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## In vivo cross-linking mass spectrometry for protein and complex structural analysis

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**TITLE:**

***In vivo* cross-linking mass spectrometry for protein and complex structural analysis**

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chemical cross-linking, mass spectrometry, protein structure, protein interaction reporter, interactome

**SUMMARY:**

We describe an integrated workflow for chemical cross-linking of proteins with mass spectrometry to study biological complexes *in vivo*. The protein interaction reporter (PIR) cross-linker presents features that enable the cross-linking of living cells with no prior protein isolation needed, providing information on protein conformations and protein-protein interactions.

**ABSTRACT**

Chemical cross-linking of proteins with mass spectrometry (XL-MS) has increasingly become a powerful technique when studying protein structures and complexes. This approach is based on the reactivity of cross-linkers to specific protein sites – usually primary amines, including side chains of lysine residues and protein N-termini which yields information on protein-protein interactions and protein conformations. Information provided by XL-MS is complementary to that from other structural methods, such as X-ray crystallography, nuclear magnetic resonance, and cryo-electron microscopy. Here, we describe a protocol for in-house synthesis and use of a peptide-based cross-linker with optimized features for interactome studies of complex biological samples. These features comprise the protein interaction reporter (PIR) technology, MS-cleavable bonds, and an affinity tag, which ultimately facilitate the identification of cross-linked

peptide pairs. The membrane permeability enables the cross-linking of living cells, tissues, and isolated organelles (e.g., nuclei and mitochondria), providing valuable structural and interaction data on proteins as they exist in their native environment. Moreover, quantitative XL-MS can be utilized for comparative interactome studies, providing information on protein conformational and interaction changes between varying biological states.

## INTRODUCTION

Biological processes are driven by multiple and complex mechanisms, with different molecules – nucleic acids, proteins, carbohydrates, lipids, etc. – playing key roles in each step. When studying proteins, several approaches can be used, but the ultimate objective is to understand how proteins with different domains and regulatory regions are structurally organized and functioning in a crowded cellular environment<sup>1,2</sup>. Besides structural information, assessing protein interactors and complexes is essential for the understanding of cellular mechanisms.

Chemical cross-linking of proteins with mass spectrometry (XL-MS), associated with other structural methods (e.g., X-ray crystallography, nuclear magnetic resonance, and cryo-electron microscopy), has become a robust approach for protein structure and interactomics studies<sup>3–5</sup>. This technique is based on the reactivity of cross-linker groups to specific side chains of proteins, usually primary amines. The distance between these reactive groups (the length of the spacer) provides constraint information useful for modeling protein structures and protein complex topologies<sup>5</sup>.

Here, we describe a workflow for in-house synthesis and *in vivo* application of a protein interaction reporter (PIR) cross-linker<sup>6</sup>, the biotin aspartate proline-N-hydroxyphthalamide (BDP-NHP)<sup>7</sup> (**Figure 1**). This cross-linker presents optimized features for interactome studies *in vivo*, such as membrane permeability, that enables the cross-linking of living cells, tissues, and isolated organelles (e.g., nuclei, vesicles, and mitochondria<sup>8</sup>), providing information on protein structure and complex assembly as close as possible to how it occurs in native and physiological conditions. Other features include a biotin tag for enrichment of cross-linked peptides – commonly found with low abundance in complex samples, and MS-cleavable bonds, which ultimately facilitate the identification of cross-linked peptides<sup>6</sup>. This is achieved by relying on a predictable mass relationship between the released reporter ion and the cross-linked peptides after the collision induced dissociation (CID)-induced cleavage of chemical bonds. Detection of this mass relationship can be done (i) “on-the-fly” during the MS analysis, with Real-time Analysis for Cross-linked peptide Technology (ReACT)<sup>9</sup>, or (ii) post-acquisition using Mango<sup>10</sup> for the *in silico* check of the mass relationship.

A quantitative XL-MS approach for interactomics studies can provide information on changes in protein conformation and complex composition when comparing different biological conditions. Our group has developed different cross-linkers and pipelines for quantitative XL-MS, including by MS1-based label-free quantitation<sup>11</sup>, targeted parallel reaction monitoring<sup>12</sup>, the stable isotope labeling of amino acids in cell culture (SILAC)-based quantitation of PIR cross-linked peptides<sup>11,12</sup>, and an isotope-labeled PIR cross-linker technology<sup>13</sup>. These quantitative XL-MS methods have been utilized to provide information on interactome changes in drug resistant

cancer cells<sup>14</sup>, study protein conformational and interaction changes induced by mitotic inhibitors<sup>15</sup> and heat shock protein 90 (Hsp90)<sup>16</sup>, and investigate the effects of phosphomimetic mutations and nucleotide binding on the interaction between Hsp90 and its cochaperone Aha1<sup>17</sup>. The *in vivo* cross-linking pipeline described here was performed with HeLa cells as a biological model (**Figure 2**), but we note that this protocol is applicable to other living systems<sup>7</sup>. To help interpret and visualize XL-MS results, we used XLinkDB<sup>18–20</sup>, a cross-linking database with algorithms to automatically generate structural models and facilitate molecular docking of cross-linked proteins. Recent updates in the platform include tools for visualization of different protein topologies and protein networks<sup>20</sup>.

The cross-linking results shown here provide insight into the HeLa cell interactome, including protein-protein interactions (inter-links) and protein conformations (intra-links), which provides information on a structural level. Moreover, monolinks – or dead-ends – are generated when one end of the cross-linker is covalently bound to a peptide and the other end is hydrolyzed<sup>21</sup>. Dead-ends can be informative on relative protein expression levels and protein structure as it is reflected in residue solvent accessibility, that ultimately translates to protein structure<sup>22</sup>. Here, we discuss ReACT and Mango mass spectrometry methods for a PIR-based cross-linking pipeline and highlight representative cross-linking results involving Hsp90B as a model. We also indicate instrument methods and *in silico* analysis for the identification of dead-ends when using the PIR technology.

## PROTOCOL

NOTE: All materials, equipment, and software used here are described in Table of Materials.

### 1. Synthesis of BDP (Figure 3)

NOTE: The BDP-NHP cross-linker was synthesized using a CEM Liberty Lite peptide synthesizer, following the manufacturer's instructions. This protocol is based on a previous publication<sup>7</sup>.

1.1. Prepare the following reagents.

1.1.1. Weigh out 0.63 g of Rink Amide resin (100–200 mesh) for 0.05 mmol.

1.1.2. Weigh out 1.73 g of aspartate (Fmoc-Asp(OtBu)-OH) and dissolve it in 21 mL of DMF.

1.1.3. Weigh out 23 g of succinic anhydride and dissolve in 23 mL of DMF.

1.1.4. Weigh out 1 g of biotinylated lysine (Fmoc-Lys(biotin)-OH) and dissolve it in 32 mL of DMF.

NOTE: Increase the solubility of biotinylated lysine in DMF by heating the solution up to 70 °C, with constant mixing.

1.1.5. Weigh out 1.42 g of proline (Fmoc-Pro-OH) and dissolve in 21 mL of DMF.

- 133
- 134 1.1.6. Weigh out 1.3 g of lysine (Fmoc-Lys(Fmoc)-OH) and dissolve it in 11 mL of DMF.
- 135
- 136 1.2. Fill the wash bottle with 400 mL of DMF.
- 137
- 138 1.3. Fill the deprotection bottle with 60 mL of the deprotection solution [20% (vol/vol)
- 139 piperidine in DMF].
- 140
- 141 1.4. Fill the activator bottle with 40 mL of activator solution (0.5 M DIC in DMF).
- 142
- 143 1.5. Fill the activator base bottle with 20 mL of 1 M Oxyma in DMF.
- 144
- 145 1.6. Run the peptide synthesizer with the following coupling steps:
- 146 Resin: 0.5-mmol resin swelling
- 147 Fmoc-Lys(biotin)-OH: 0.5-mmol triple coupling
- 148 NOTE: Divide the resin-lysine coupling in 3 separate steps due to the large volume of the lysine
- 149 solution (32 mL).
- 150 Fmoc-Lys(Fmoc)-OH: 0.5-mmol single coupling
- 151 Fmoc-Pro-OH: 0.5-mmol double coupling
- 152 Fmoc-Asp(OtBu)-OH: 0.5-mmol double coupling
- 153 Succinic anhydride: 0.5-mmol succinyl coupling
- 154
- 155 1.7. Transfer the BDP-containing resin to a 50 mL tube.
- 156

## 157 **2. Synthesis of TFA-NHP**

- 158
- 159 2.1. Weigh out 5.86 g of N-hydroxyphthalamide (NHP, 163.139 g/mol) and place in 50 mL
- 160 round bottom flask.
- 161
- 162 2.2. Add a four-fold molar excess of trifluoroacetic acid anhydride (210.03 g/mol).
- 163
- 164 2.3. Allow the reaction to proceed for 1.5 h in dry nitrogen gas atmosphere, with constant
- 165 mixing.
- 166
- 167 2.4. Evaporate excess TFA anhydride under vacuum. The product should appear as dry, white,
- 168 crystalline solid.
- 169
- 170 2.5. Transfer the content to 2 mL microcentrifuge tubes.
- 171

172 NOTE: The protocol can be paused here. Store the TFA-NHP-containing tubes at -20 °C up to a

173 year.

174

## 175 **3. BDP-NHP cross-linker esterification and purification**

176

177 3.1. Transfer the BDP-containing resin to a 50 mL tube.  
178  
179 3.2. Swell the BDP-containing resin with a minimal volume of 1 mL of DMF for 5 min.  
180  
181 3.3. Weigh out a 12-fold molar excess of TFA-NHP from 2.5 (approximately 300 mg for a 0.1  
182 mmol batch).  
183  
184 3.4. Dissolve the amount of TFA-NHP in 10 mL of dry pyridine.  
185  
186 3.5. Transfer the TFA-NHP-pyridine solution to the tube containing the swelled resin and  
187 incubate for 20 min at room temperature, with constant mixing.  
188  
189 3.6. Transfer the resulting solution from 3.5 to an empty disposable polypropylene  
190 chromatography column.  
191  
192 3.7. Using a vacuum system, wash the resin three times with 20 mL of DMF.  
193  
194 3.8. Seal the column with the outlet and incubate the resin with 20 mL of DMF for 20 min.  
195  
196 3.9. Wash the resin three times with a 20 mL of DCM.  
197  
198 3.10. Seal the column with the outlet and incubate the resin with 10 mL of DCM for 20 min.  
199  
200 3.11. Cleave the BDP-NHP cross-linker from the resin by adding 5 mL of the cleavage solution  
201 [95% trifluoroacetic acid (TFA)/ 5% DCM] for 3 h at room temperature, with constant mixing.  
202  
203 3.12. Collect the flow-through in a 15 mL tube.  
204  
205 3.13. Add 5 mL of the cleavage solution to the column and incubate for 5 min at room  
206 temperature.  
207  
208 3.14. Collect the flow-through and add the volume to the 15 mL tube from 3.12.  
209  
210 3.15. Add 150 mL of cold diethyl ether separately to four 50 mL tubes.  
211  
212 3.16. To precipitate the cross-linker, slowly add 2.5 mL of the recovered final solution from 3.12  
213 and 3.14 to each diethyl-ether-containing tube.  
214  
215 NOTE: At this point, a white precipitate should be visible.  
216  
217 3.17. Centrifuge the tubes at  $3,400 \times g$  for 30 min at 4 °C to pellet the cross-linker.  
218  
219 3.18. Suspend each resulting pellet in 5-10 mL of cold diethyl ether, combine the volumes in  
220 one 50 mL tube, and repeat the centrifugation step 3.17.

3.19. Decant the diethyl-ether to waste and completely dry the cross-linker pellet under vacuum (for approximately 20 min).

3.20. Weigh the dry pellet and suspend it in DMSO to produce a stock solution with concentration of 100-300 mM.

3.21. Calculate the yield based on the measured mass of product – usually around 95%. Convert the measured mass of dried cross-linker into moles by dividing by the average molecular mass of BDP-NHP (1,414.45 g/mol) and divide by the theoretical maximum number of moles (i.e., 0.5 mmol) on the basis of the amount of resin used.

3.22. Check the purity of the cross-linker by direct infusion ESI–MS analysis of a 1:1,000 dilution of the concentrated stock solution in a solution of 49% (vol/vol) methanol, 49% (vol/vol) water, 2% (vol/vol) acetic acid. A purity range of 80–90% is expected based on the relative intensity of the quasi-molecular ion peak for the PIR cross-linker ( $[M+H]^+ = 1,414.526\ m/z$ ) (**Figure 4**).

3.23. Measure the concentration of BDP–NHP by UV–Vis absorbance. The concentration of BDP–NHP can be measured by UV–Vis absorbance.

3.23.1. Dilute 1  $\mu$ L of the concentrated stock solution of cross-linker in 0.1 M  $\text{NH}_4\text{HCO}_3$ , pH 8.0, to achieve a concentration of 0.5 mM and quench the crosslinker, releasing free NHP with yellow color.

3.23.2. Measure the absorbance of NHP at 410 nm and compare to a calibration curve for free NHP in 0.1 M  $\text{NH}_4\text{HCO}_3$ , pH 8.0, preparing dilutions from 0.1 to 2 mM to calculate the concentration of released NHP. The concentration of BDP cross-linker in the stock solution is half the calculated concentration of NHP multiplied by the dilution factor.

3.24. The stock cross-linker solution can be stored at  $-80\ ^\circ\text{C}$  for up to 1 year.

NOTE: The protocol can be paused here.

#### **4. Cell culture and harvest**

4.1. Culture HeLa cells in 15 cm plates with 20 mL of DMEM, supplemented with 10% FBS (vol/vol) and 1% (vol/vol) penicillin–streptomycin.

4.2. Maintain the cells in a cell incubator at  $37\ ^\circ\text{C}$  with 5%  $\text{CO}_2$ .

4.3. When cells are 80-90% confluent (approximately  $2.0 \times 10^7$  cells), wash the culture twice with 5 mL of 1x PBS.

4.4. Incubate the cells with 5 mL of PBS 1  $\times$  with 20 mM EDTA, at  $37\ ^\circ\text{C}$  for 3-5 min.

265  
266 4.5. Visualize the cells in a microscope to confirm detachment of the cells from the plate.

267  
268 4.6. Transfer the cell content to a 15 mL tube, centrifuge at  $300 \times g$  for 3 min at 20 °C and  
269 discard the supernatant.

270  
271 4.7. Suspend the remaining pellet in PBS with calcium and magnesium.

272  
273 4.8. Centrifuge at  $300 \times g$  for 3 min at 20 °C and discard the supernatant.

274  
275 4.9. Suspend the cell pellet in 10 mL of 1x PBS.

276  
277 4.10. Centrifuge at  $300 \times g$  for 3 min at 20 °C and discard the supernatant.

278  
279 4.11. Repeat 4.9 and 4.10 two additional times.

280  
281 **5. *In vivo* cross-linking**

282  
283 5.1. Suspend the cell pellet from 4.11 in one-pellet volume of 170 mM  $\text{Na}_2\text{HPO}_4$   
284 (approximately 500  $\mu\text{L}$ ).

285  
286 5.2. Add 10 mM of BDP-NHP cross-linker.

287  
288 NOTE: Pipette the corresponding volume of cross-linker in the tube without touching the pipet  
289 tip to the solution – it can precipitate in the tip – and immediately vortex the sample on a gentle  
290 setting to not disrupt the integrity of the cells.

291  
292 5.3. Incubate for 30 min at room temperature, with constant mixing.

293  
294 NOTE: The solution will turn yellow as the BDP-NHP cross-linking reaction happens.

295  
296 5.4. Add one pellet volume of 0.1 M  $\text{NH}_4\text{HCO}_3$  to quench the cross-linking reaction.

297  
298 5.5. Pellet the cells by centrifugation at  $300 \times g$  for 3 min at 20 °C and discard the supernatant.

299  
300 5.6. Suspend the cell pellet in 1 mL of 0.1 M  $\text{NH}_4\text{HCO}_3$  and repeat centrifugation as in 5.5.

301  
302 5.7. Repeat 5.6 3 times or until no yellow color remains in the supernatant.

303  
304 **6. Protein extraction, reduction, alkylation, and digestion**

305  
306 6.1. Prepare the cell lysis buffer with 8 M urea in 0.1 M  $\text{NH}_4\text{HCO}_3$ .

307  
308 6.2. Suspend the cell pellet from 5.7 in 1 mL of the cell lysis buffer.



6.3. Sonicate the cells in lysis buffer using an ultrasonic processor, applying five pulses at amplitude 40 for 5 s.

6.4. Add 5 mM of TCEP-HCl to the sample to disrupt disulfide bonds. Incubate at room temperature for 30 min, with constant mixing.

6.5. Add 10 mM of IAA to alkylate reduced thiol groups. Incubate for 30 min at room temperature, with constant mixing.

NOTE: IAA is light sensitive. Protect the sample from light during the reaction.

6.6. Add 0.1 M  $\text{NH}_4\text{HCO}_3$  to dilute the sample and reduce the urea concentration to < 1 M.

6.7. Quantify the protein content using the Bradford assay – or other protein quantitation method of choice.

6.8. Add 1  $\mu\text{g}$  of sequencing-grade modified trypsin for every 200  $\mu\text{g}$  of protein (1:200 ratio) in the sample and digest for 16-18 h at 37 °C, with constant shaking at 650 rpm.

6.9. Acidify the sample with 1% TFA (vol/vol) to a pH < 3.

6.10. Centrifuge sample at  $16,000 \times g$  for 15 min at room temperature.

## **7. Sample desalting**

7.1. Prepare the reversed-phase C18 desalting column with the suitable protein capacity and wash it with one-column volume of methanol.

7.2. Add one-column volume of 0.1% (vol/vol) TFA acid in acetonitrile to condition the column.

7.3. Pass the solution through the column using the vacuum manifold.

7.4. Repeat steps 7.2 and 7.3 two additional times.

7.5. Add one-column volume of 0.1% (vol/vol) TFA acid in water to equilibrate the column.

7.6. Pass the solution through the column using the vacuum manifold.

7.7. Repeat steps 7.5 and 7.6 two additional times.

7.8. Add the supernatant from step 6.10 to the Sep-Pak column, considering the maximum volume allowed by the cartridge.

- 7.9. Pass the solution through the column using the vacuum manifold.
- 7.10. Repeat steps 7.8 and 7.9 until the entire volume from 6.10 has passed through the column.
- 7.11. Repeat steps 7.5 and 7.6 to wash the columns and eliminate remaining salts.
- 7.12. Place an open 1.5 mL microcentrifuge tube under each column outlet.
- 7.13. Add one-column volume of 80% (vol/vol) acetonitrile/ 0.1% (vol/vol) TFA acid to elute the peptides.
- 7.14. Collect the flow-through using the extraction manifold vacuum.
- 7.15. Dry out the sample by vacuum centrifugation, then reconstitute the peptides with ~10  $\mu$ L of 30% ACN, 0.1% TFA.

NOTE: The protocol can be paused here. Store samples at -80 °C.

## **8. Strong cation exchange (SCX) chromatography for sample fractionation**

- 8.1. Add 500  $\mu$ L of SCX solvent A [7 mM  $\text{KH}_2\text{PO}_4$ , pH 2.6, 30% (vol/vol) acetonitrile] to the sample from step 7.15.
- 8.2. Centrifuge the sample at 16,000  $\times g$  for 15 min at room temperature.
- 8.3. Transfer the supernatant to a 1.5 mL LC autosampler vial.
- 8.4. Inject the sample into a liquid chromatography system equipped with an SCX column (**Table of Materials**).
- 8.5. Fractionate the sample applying a 1.5 mL/min flow rate on a 97.5-min gradient with increasing concentration of SCX solvent B [7 mM  $\text{KH}_2\text{PO}_4$ , pH 2.6, 350 mM KCl, 30% (vol/vol) acetonitrile], as follows: 0% B at 0 min, 5% B at 7.5 min, 60% B at 47.5 min, 100% B at 67.5 min, 100% B at 77.5 min, 0% B at 77.51 min, and 0% B at 97.5 min.
- 8.6. Collect the 14 fractions per experiment with 500  $\mu$ L each and pool the fractions 1–5, 6–7, and 11–14.
- 8.7. Dry out each fraction (6–7, 8, 9, 10, 11–14) by vacuum centrifugation, then reconstitute the peptides with 2–3 mL of 100 mM  $\text{NH}_4\text{HCO}_3$ .

NOTE: Fractions 1–5 are usually not analyzed because most cross-linked peptides begin eluting in fraction 6. However, these fractions are useful for the identification of dead-ends.

397  
398 8.8. Adjust the pH to 8.0 using 1 M NaOH.  
399

## 400 **9. Avidin-biotin enrichment of cross-linked peptides**

401  
402 9.1. Add 200 µL of monomeric avidin resin to each resulting fraction from section 8.  
403

404 9.2. Incubate the fractions for 30 min at room temperature, with constant mixing.  
405

406 9.3. Use a disposable poly-propylene column for enrichment of BDP-cross-linked peptides  
407 from each fraction. Place the columns in the extraction manifold.  
408

409 9.4. Transfer avidin-bound peptides from each fraction to the corresponding disposable poly-  
410 propylene column.  
411

412 9.5. Add 2 mL of 0.1 M  $\text{NH}_4\text{HCO}_3$  pH 8.0 to each column.  
413

414 9.6. Remove the liquid using the extraction manifold vacuum. Discard the flow-through.  
415

416 9.7. Repeat steps 9.5 and 9.6 five additional times.  
417

418 9.8. Incubate the avidin resin with 1 mL of 70% (vol/vol) acetonitrile and 1% (vol/vol) formic  
419 acid (FA) for 5 min.  
420

421 9.9. Place a 1.5 mL microcentrifuge tube under each cartridge. Apply vacuum and collect the  
422 flow-through.  
423

424 9.10. Concentrate the fractions (6-7, 8, 9, 10, and 11-14) to a final volume of approximately 10  
425 µL in a vacuum centrifuge.  
426

427 NOTE: The experiment can be paused here. Store the samples at  $-80^\circ\text{C}$ .  
428

## 429 **10. LC-MS analysis**

430  
431 NOTE: This protocol used a high-resolution LC-MS pipeline on a Q-Exactive Plus for a Mango-  
432 oriented data analysis<sup>10</sup>, and also LC-MS on a hybrid ion trap LTQ Velos FT-ICR instrument<sup>23</sup> for  
433 the ReACT method<sup>9</sup>. Both methods apply DDA with selection of ions with charge state of +4 to  
434 +8. Briefly, Mango relies on tandem mass spectra (MS2) for the mass-relationship check and for  
435 the identification of peptides, while ReACT uses MS2 for the “on-the-fly” mass relationship check  
436 (mass of precursor = mass reporter + mass peptide 1 + mass peptide 2), and then MS3 events for  
437 the fragmentation of cross-linked peptides and further peptide search/identification. For the  
438 BDP-NHP, the mass of the reporter ion is 693.405431 Da.  
439

440 10.1. Suspend pooled fractions from section 9 in 30 µL of 0.1% (vol/vol) FA.

441  
442 10.2. Centrifuge sample fractions at  $16,000 \times g$  for 10 min at room temperature.

443  
444 10.3. Transfer the supernatant of each sample to LC autosampler vials.

445  
446 10.4. Inject 1-5  $\mu\text{L}$  of sample (approximately 1  $\mu\text{g}$ ) from each pooled fraction into the nano-LC  
447 system.

448  
449 NOTE: Analyze each fraction 2-3 times for technical replicates of the experiment.

450  
451 10.5. Load each peptide fraction onto a trap column [3 cm  $\times$  100- $\mu\text{m}$  i.d., stationary phase  
452 ReproSil-Pur C8 (5- $\mu\text{m}$  diameter and 120- $\text{\AA}$ -pore-size particles)] with a flow rate of 2  $\mu\text{L}/\text{min}$  of  
453 mobile phase: 98% (vol/vol) LC-MS solvent A [0.1% (vol/vol) FA in water] and 2% (vol/vol) LC-MS  
454 solvent B [0.1% (vol/vol) FA in acetonitrile].

455  
456 10.6. Chromatographically separate the peptides using an analytical column [60 cm  $\times$  75- $\mu\text{m}$   
457 i.d., stationary phase ReproSil-Pur C8 (5- $\mu\text{m}$  diameter and 120- $\text{\AA}$ -pore-size particles)] and apply  
458 a 240-min linear gradient: from 95% LC-MS solvent A, 5% LC-MS solvent B to 60% LC-MS solvent  
459 A, 40% LC-MS solvent B, at a flow rate of 300 nL/min.

460  
461 10.7. Apply a voltage of 2.5 kV to the spray tip for the ESI-based ionization of peptides.

462  
463 10.8. For Mango, set the high-resolution mass spectrometer (e.g., Q-Exactive Plus) to data-  
464 dependent acquisition (DDA) of the 5 most intense ions with charge state of +4 to +8, with a  
465 dynamic exclusion of 30 s and isolation window of 3 Da. Each MS1 scan (70,000 resolving power  
466 at 200  $m/z$ , automated gain control (AGC) of  $1 \times 10^6$ , scan range 400 to 2,000  $m/z$ , dynamic  
467 exclusion of 30 s) is followed by 5 MS2 scans (70,000 resolving power at 200  $m/z$ , AGC of  $5 \times 10^4$ ,  
468 normalized collision energy of 30).

469  
470 10.9. For ReACT, set the mass spectrometer, in this case a hybrid ion trap LQT Velos FT-ICR  
471 instrument, to data-dependent acquisition (DDA) of the 6 most intense ions with charge state of  
472 +4 to +8, with dynamic exclusion of 45 s and isolation window of 3 Da. Each MS1 scan (50,000  
473 resolving power at 200  $m/z$ , mass range 500 to 2,000  $m/z$ ) was followed by 1 MS2 acquisition for  
474 the “on-the-fly” mass relationship check – mass precursor = mass reporter + mass peptides –  
475 (12,500 resolving power at 200  $m/z$ , CID activation, normalized collision energy of 25), and 4 MS3  
476 acquisitions of the selected ions with a 20 ppm tolerance for mass error after the mass  
477 relationship check, and with 1+ and 2+ charge states (CID activation, normalized collision energy  
478 of 35).

479  
480 NOTE: ReACT can be performed in any instrument with a high resolution MS2 and low resolution  
481 MS3 capacity<sup>9</sup>.

10.10. For an LC-MS analysis of dead-ends, use an MS method similar to the one described in section 10.8, but with charge state of 1+ to 8+, MS1 events with 70,000 resolving power at 200  $m/z$ , and MS2 scans with 17,500 resolving power at 200  $m/z$ .

NOTE: Besides fractions 6 to 14, include pooled fractions 1 to 5 for this specific LC-MS analysis. Most cross-linked peptides begin eluting in fraction 6, with charge state of 4+ to 8+, but dead-ends will elute early during the SCX chromatography, with charge state 1+ to 8+.

## 11. Data analysis

NOTE: All required software run on a Linux operating system.

### 11.1. Mango data analysis

11.1.1. Use ReAdW to convert the instrument files, e.g., .raw files, to the .mzXML format. ReAdW is available for download at <https://sourceforge.net/projects/sashimi/files/ReAdW%20%28Xcalibur%20converter%29/>.

11.1.2. Use the Mango tool, available at <https://github.com/jpm369/mango>, to generate .ms2 files containing individual precursor masses of released peptides for each spectrum and .peaks file containing all relationships within a 20 ppm tolerance.

11.1.3. Use the following command to write the Mango parameters:

```
mango.exe -p
```

11.1.4. Use the following command to run Mango on .mzXML files:

```
mango.exe *.mzXML
```

NOTE: Hardklör<sup>24</sup> is embedded in Mango and is used for charge deconvolution and deisotoping of complex MS2 spectra.

11.1.5. Run the Comet<sup>25</sup> search engine (<http://comet-ms.sourceforge.net/>) on the .ms2 files resulted from 11.1.2.

11.1.6. Use the following command to write the comet parameters:

```
comet -p
```

11.1.7. Use the following command to run Comet on .ms2 files:

```
runCometQ *.ms2
```

11.1.8. Proceed to step 11.3.

### 11.2. ReACT data analysis

11.2.1. Use ReAdW to convert the instrument files, e.g., .raw files, to the .mzXML format.

11.2.2. Use the following command to write the comet parameters:

**comet -p**

11.2.3. Run the Comet search engine (<http://comet-ms.sourceforge.net/>) on the .mzXML files resulted from 11.2.1.

**runCometQ \*.mzXML**

11.2.4. Run react2csv to map ReACT2 results to the sequences in the database.

**react2csv \*.pep.xml**

11.2.5. Proceed to step 11.3.

11.3. XLinkProphet<sup>26</sup> for validation of results

11.3.1. Run XLinkProphet (<https://github.com/brucelab/xlinkprophet>) on the pep.xml files resulted from the Comet search to apply probability values and validate results.

11.3.2. Use the following command to run XLinkProphet parameters:

**runXLinkProphet.pl WRITEPARAMS**

11.3.3. Add the PIR cross-linker reporter mass to the command. In the case of the BDP-NHP cross-linker, the reporter mass is 693.405431, thus use the following command:

**runXLinkProphet.pl ‘\*.pep.xml’ REPORTERMASS=693.405431**

11.4. Upload the results from XLinkProphet in the .pep.xml format to XLinkDB<sup>19</sup>, available in <http://xlinkdb.gs.washington.edu/xlinkdb/>, following the platform instructions.

## REPRESENTATIVE RESULTS

In this study, we performed *in vivo* cross-linking of HeLa cells using the PIR cross-linker BDP-NHP. After SCX fractionation and biotin-avidin enrichment of cross-linked peptides, two different methods were applied for the MS analysis of the fractionated samples – Mango and ReACT, as described in section 10. We used two technical replicates from Mango and ReACT for the *in silico* analysis. PeptideProphet<sup>27</sup> and ProteinProphet<sup>28</sup> are embedded in XLinkProphet for the refinement of peptide and protein identifications, respectively, and a 1% FDR cutoff was applied for the identification of cross-linked peptides. This approach resulted in 3,002 cross-links (23% inter-links) identified, corresponding to 898 protein pairs. The complete cross-linking information is made available in **Supplementary Table 1** and online within XLinkDB ([http://xlinkdb.gs.washington.edu/xlinkdb/HeLa\\_BDP\\_JoVE\\_2020\\_Bruce.php](http://xlinkdb.gs.washington.edu/xlinkdb/HeLa_BDP_JoVE_2020_Bruce.php)).

We used different LC-MS methods and *in silico* analysis for the identification of dead-ends, as described in sections 10.10 and 11. Using a minimum probability value of 0.891 for a 1% FDR

cutoff, we identified 6,185 unique dead-ends that mapped to 1,861 proteins (**Supplementary Table 2**).

After upload of the cross-linking results on XLinkDB, an XL-MS interaction table will be generated, presenting different information on the cross-linked peptide pairs (**Figure 5**). This information includes cross-linked residues, peptide sequences, protein identifiers from UniProt<sup>29</sup>, protein structures available on the Protein Data Bank (PDB)<sup>30</sup>, visualization of cross-linking distances and residues on protein structures using NGL<sup>31</sup> or JSmol<sup>32</sup>, an interaction network for analysis and visualization of the dataset interactome (**Figure 6**), besides other options.

Moreover, XLinkDB will automatically generate structure models and docked structures for cross-linked proteins using Modeller<sup>34</sup> and PatchDock<sup>35</sup>, respectively<sup>20</sup>. The visualization of intra-links found for the heat shock protein 90 B (Hsp90B), used here as representative results, are shown in Figure 7. In the XL interaction table on XLinkDB, it is possible to filter the results for specific proteins and create an interaction network for proteins of interest, such as Hsp90 (Figure 8). The information on Hsp90A and Hsp90B inter-links (interactors) and intra-links is available in **Supplementary Table 3**.

**Figure 1. Features of the protein interaction reporter (PIR) cross-linker.** (a) The PIR technology includes a biotin tag for enrichment of cross-linked peptides, MS-cleavable bonds, and amine-reactive groups. (b) The chemical structure of the biotin aspartate proline-N-hydroxyphthalamide (BDP-NHP) cross-linker. The cross-linker is synthesized in the following sequence: biotin-lysine, lysine, proline, aspartate, succinic anhydride, followed by the reaction of amine-reactive NHP groups. Molecular formula: C<sub>64</sub>H<sub>79</sub>N<sub>13</sub>O<sub>22</sub>S; monoisotopic mass: 1413.518 Da.; protonated pseudo-molecular ion [M+H]<sup>+</sup> mass: 1,414.525 Da; reporter neutral mass: 693.399 Da. The reporter sequence is indicated within the blue lines and includes the biotin tag.

**Figure 2. *In vivo* PIR cross-linking workflow.** (a) HeLa cells were cross-linked *in vivo* with BDP-NHP. (b) Following protein extraction, the protein content was reduced, alkylated, and digested with trypsin. (c) Samples were desalted and then fractionated by strong cation exchange (SCX) chromatography. (d) Cross-linked peptides were enriched with biotin-avidin affinity chromatography. (e) Fractionated peptides were analyzed by LC-MS using the ReACT method or/and Mango. (f) Data analysis. Search of cross-linked peptides and validation of results. (g) Upload of results on XLinkDB for visualization of protein networks and structures.

**Figure 3. Synthesis of BDP-NHP cross-linker.** (a) Synthesis of N-hydroxyphthalimide trifluoroacetate ester (TFA-NHP) from NHP and TFA anhydride (steps 1-3). (b) Synthesis of the BDP-NHP crosslinker.

**Figure 4. ESI-MS profile of the BDP-NHP cross-linker.** (a) MS1 spectrum of the direct infusion of BDP-NHP. The ionized cross-linker is observed at  $m/z$  1,415.2. The ions at  $m/z$  1,181.3 and  $m/z$  1,270.1 indicate the cross-linker with two arms and one arm hydrolyzed, respectively. (b) Tandem mass spectra of the precursor ion, BDP-NHP. Reporter ion indicated at  $m/z$  695.0. The cross-linker long arm is indicated at  $m/z$  1,055.3, resulting from the cleavage of one Asp-Pro chemical bond.

**Figure 5. Representation of the XL-MS interaction table from XLinkDB.** The interaction table, made available at [http://xlinkdb.gs.washington.edu/xlinkdb/HeLa\\_BDP\\_JoVE\\_2020\\_Bruce.php](http://xlinkdb.gs.washington.edu/xlinkdb/HeLa_BDP_JoVE_2020_Bruce.php), includes cross-linked residues and peptide sequences, protein accession numbers from UniProt, PDB structures for the identified proteins, cross-linking distances based on available PDB structures, and the visualization of the intra and/or inter-links using NGL or JSmol viewer. The table shows results uniquely identified by Mango.

**Figure 6. Protein interaction network for HeLa cells cross-linked with BDP-NHP.** XLinkDB uses Cytoscape<sup>33</sup> to generate protein interaction networks for visualization and analysis of protein interactors. Distance in PDB Context (Å): in red, distances under 10, in blue, distances from 10 to 20, in orange, distances from 20 to 30, in green, 30 to 40, and in magenta, distances of 40 or greater.

**Figure 7. Visualization of cross-links found for Hsp90B.** Highlighted cross-links found for Hsp90B (HS90B\_HUMAN, PDB 5FWK) are indicated on the structure. Cross-links distances in Å are based on the PDB structures. Cross-linked lysine residues are shown in green, and lysine residues with dead-ends (K624, K435, K526, K481) are indicated in blue. The visualization of cross-links is made available in the XL-MS interaction table after upload of results on XLinkDB. The cross-linking between residues K347 and K53 with distance 43.73 Å is indicated in magenta.

**Figure 8. Interaction network for Hsp90 protein.** Cytoscape interaction network for Hsp90A and Hsp90B, including protein interactors CHRD1, ENOA, and STIP1. Distance in PDB context (Å): in red, distances under 10, in blue, distances from 10 to 20, in orange, distances from 20 to 30, in green, 30 to 40, and in magenta, distances of 40 or greater. The position of cross-linked residues is indicated in the network. The list of Hsp90 protein interactors and intra-links are available in **Supplementary Table 3.**

**Supplementary Table 1. Complete information on HeLa cells cross-linked with amide BDP-NHP.** pep A,B: cross-linked peptides; position A,B: corresponding number of the cross-linked residue in the protein sequence; accession A,B: protein accession number; Uniprot A,B: protein entry from Uniprot; modpos A,B: position of the cross-linked peptide in the protein sequence; PDB A,B: PDB structure identifier; PDB type: indicates if the PDB structure was modelled (e.g., Phyre, Modeller) or resulted from structural experiments; XL distance: distance in Å based on PDB structures; type: type of cross-linking found, if intra or inter-link. Information includes 2 technical replicates. The number of identifications, confidence (*p*-value), scan number of the identification, and ion charge are included.

**Supplementary Table 2. Information on dead-ends found for HeLa cells cross-linked with amide BDP-NHP.** Minimum probability for a 1% FDR cutoff, mono-linked peptide sequences and protein accession numbers are shown.

**Supplementary Table 3. Information on cross-links found for Hsp90A and Hsp90B.** The cross-links comprised here are related to those shown in **Figure 7.** peptide A,B: cross-linked peptides;



position: corresponding number of the cross-linked residue in the protein sequence; protein A,B: corresponding protein to which the cross-linked peptide is mapped; gene A,B: UniProt protein identifier; name: common protein name; XL distance: cross-link distance in Å; type: types of cross-linking found, if intra or inter-link.

## DISCUSSION

XL-MS can provide information on protein structure and conformation (intra-links), protein-protein interaction and complex assembly (inter-links), and protein quantitation and solvent exposure (dead-ends). One limitation of the technique when used *in vivo* for complex samples is the low-resolution structural results on protein conformation and interactome. Thus, protein structures present in the PDB are useful for the modelling of structures and for the visualization of cross-links, which is automatically done by XLinkDB – available at <http://xlinkdb.gs.washington.edu/xlinkdb/>. Distance constraints generated by mapping cross-links to PDB structures are used for the interpretation of cross-linking results. We note that BDP-NHP has a spacer arm length of 29.3 Å and a 40 Å-distance is commonly set as maximum distance between the alpha carbons of two linked residues<sup>36</sup>. Hence, intra-links with distances over 40 Å can be indicative of conformational changes not covered by the available PDB structures, whereas inter-links with distances over 40 Å potentially indicate an ensemble of differing protein complex assemblies<sup>38</sup>. Moreover, cross-linking results can provide structural information on flexible regions, e.g., intrinsically disordered regions<sup>39</sup>, that are usually not covered by other structural methods.

As representative results, we discuss the cross-links identified for Hsp90B, a constitutively expressed isoform of the homodimer chaperone Hsp90<sup>40</sup>. Hsp90 proteins have three conserved regions, the N-terminal domain, the middle domain, and the C-terminal domain<sup>41</sup>. The N-terminal domain can adopt open or closed conformations when bound to ADP or ATP, respectively<sup>41</sup>. The intra-links found for Hsp90B in this study are represented in the cryo-EM PDB structure 5FWK (**Figure 7**), with a closed conformation. Most cross-linked distances for Hsp90B are under 40 Å, thus agreeing with the PDB structure. The intra-link between residues K347 and K53 has a 43.73 Å distance, which can be an indicative of a conformational change in that region. The residue K53 is part of the ATP-bound pocket in the N-terminal region and is cross-linked to the middle domain residue K347, thus posing as evidence of a different Hsp90B conformation found in HeLa cells cross-linked *in vivo* with BDP-NHP.

The dead-end results included here are informative of solvent exposure and lysine accessibility and can be complementary to intra and inter-link information when resolving protein conformation<sup>22</sup>. **Figure 7** shows some highlighted dead-ends in the C-terminal domain of Hsp90B. We note that cross-linked peptides are frequently found as dead-ends, but not the other way around – not all dead-ends are found cross-linked, i.e., both arms of BDP-NHP cross-linked to a peptide. This is to be expected since not all lysine residues inside cells exist within a linkable distance of another lysine.

Critical steps of this protocol include specially the synthesis of the amide BDP-NHP crosslinker (steps 1-3); as described in the corresponding sections, the synthesis steps need to be carefully

performed and there are several checking points to make sure the final product is correct<sup>7</sup>. Another critical step is the addition of the crosslinker to the sample (step 5.2), once the crosslinker will precipitate in the pipette tip if in contact with the crosslinking buffer and the cells could easily lysate during the vortexing<sup>7</sup>.

Overall, this protocol provides an end-to-end pipeline for *in vivo* cross-linking with mass spectrometry of living cells and other complex biological systems. Information is obtained on the composite ensemble of protein conformations and interactions as they exist within their native cellular environment, providing unique and complementary information to that gained by other structural biology and interactome mapping techniques. The interactome results of HeLa cells presented here are publicly available on XLinkDB and can be useful for other comparative interactome studies. The continued development and application of *in vivo* cross-linking with mass spectrometry methodology to varying biological systems ultimately has the potential to provide useful molecular level insight into the roles of proteins in health and disease.

#### DATA AVAILABILITY

The datasets generated during this study are available at XLinkDB - [http://xlinkdb.gs.washington.edu/xlinkdb/HeLa\\_BDP\\_JoVE\\_2020\\_Bruce.php](http://xlinkdb.gs.washington.edu/xlinkdb/HeLa_BDP_JoVE_2020_Bruce.php). The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE <sup>42</sup> partner repository with the dataset identifier PXD023560.

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#### DISCLOSURES

The authors have nothing to disclose.

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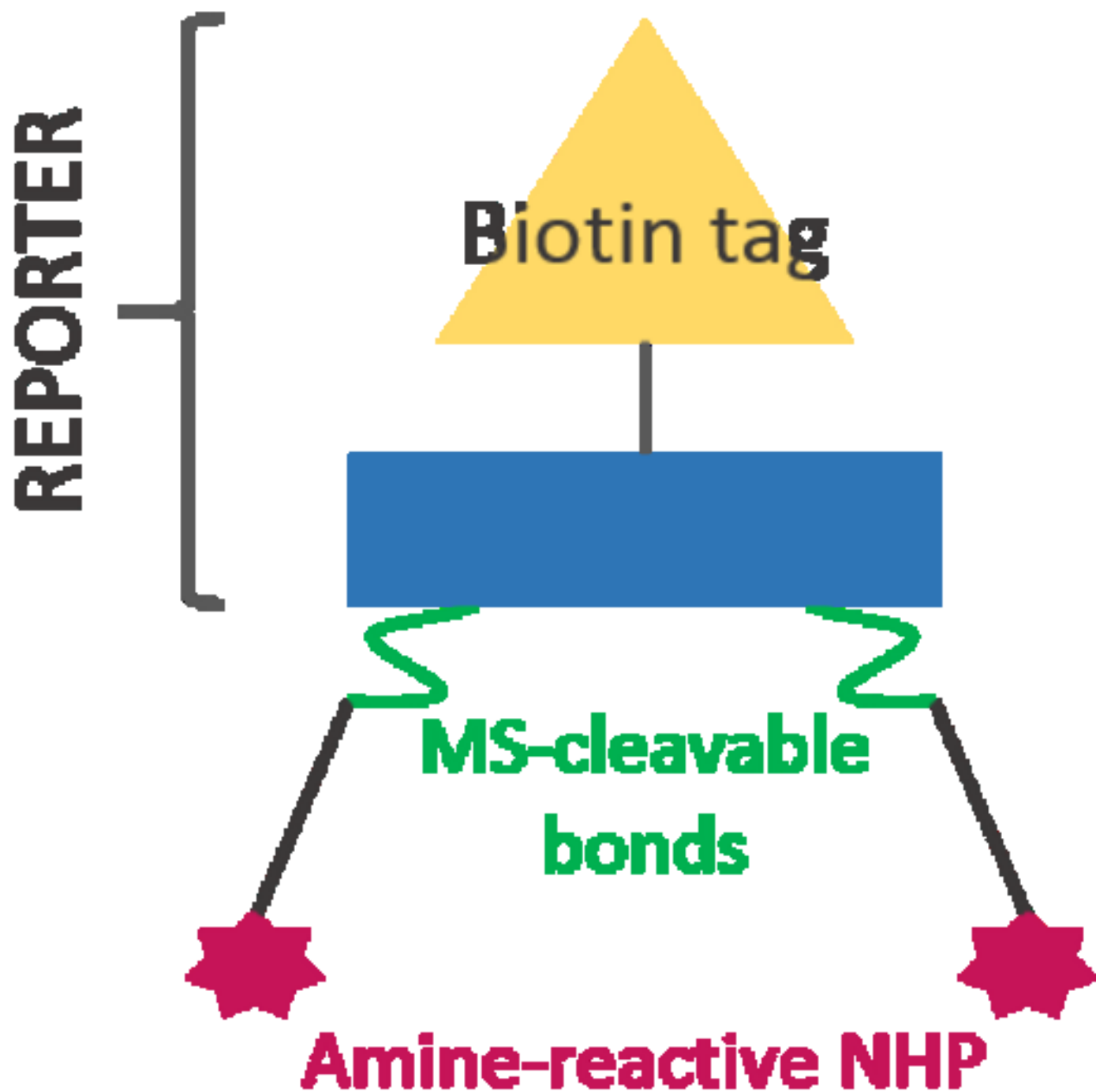
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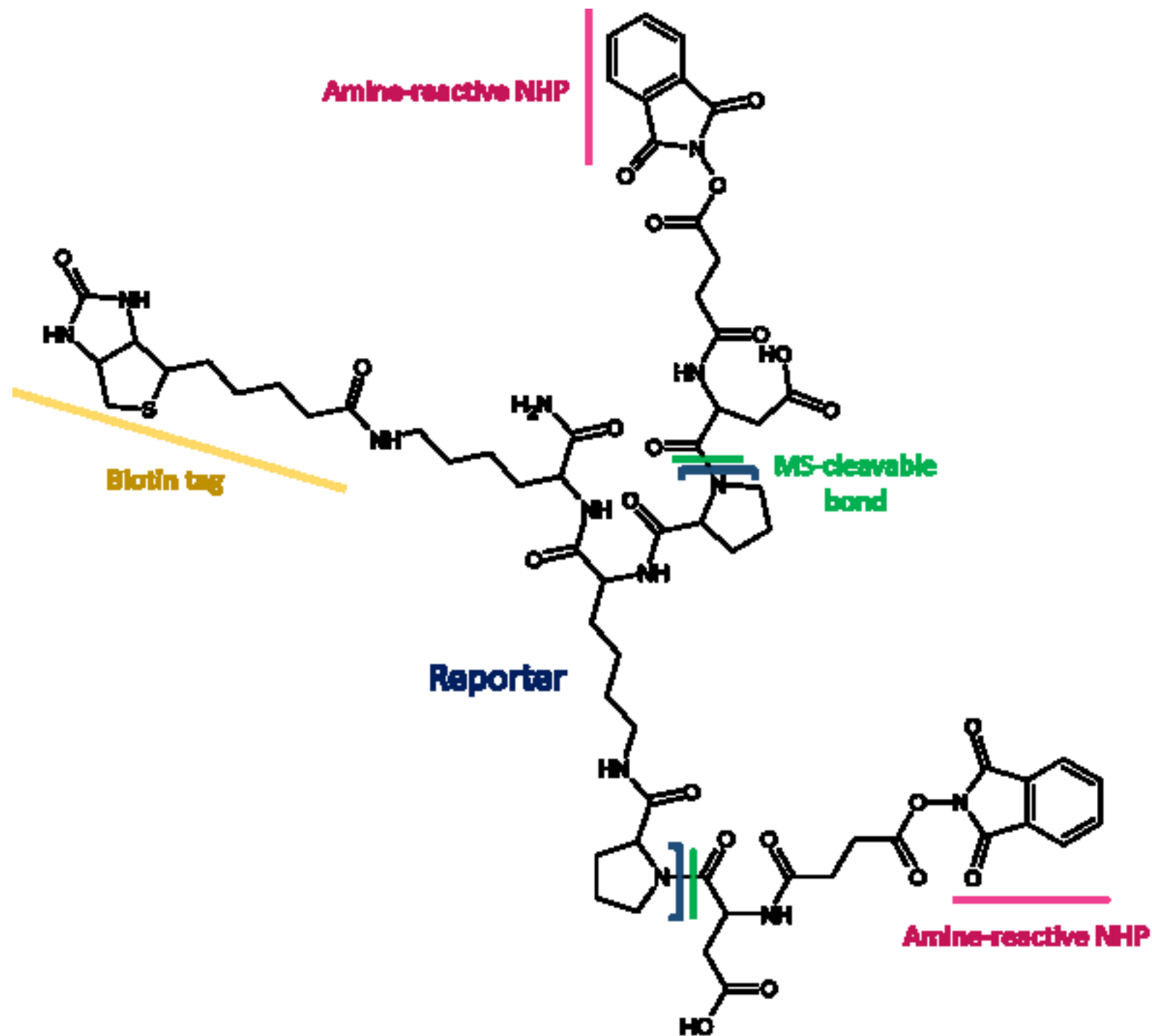
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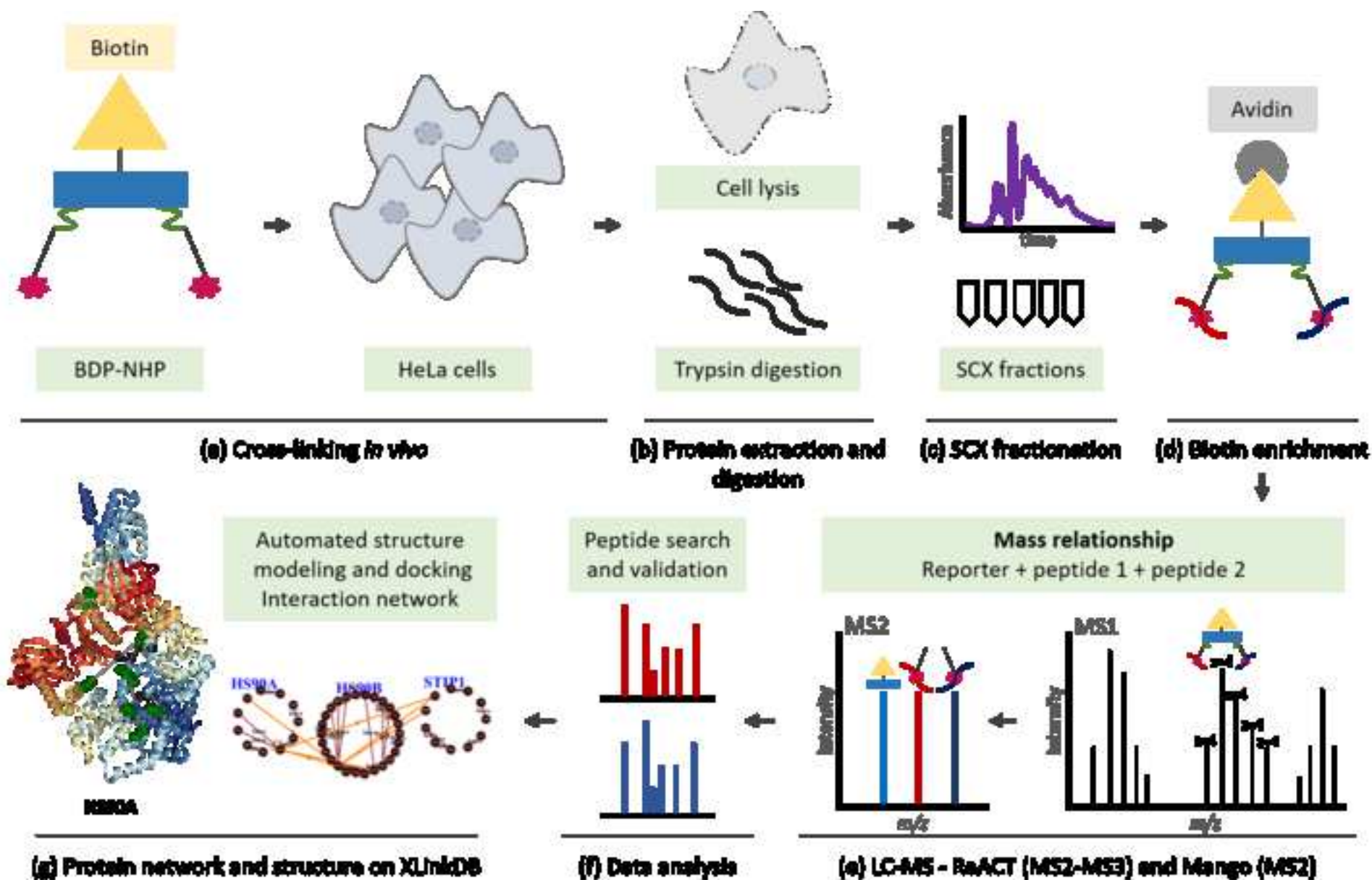
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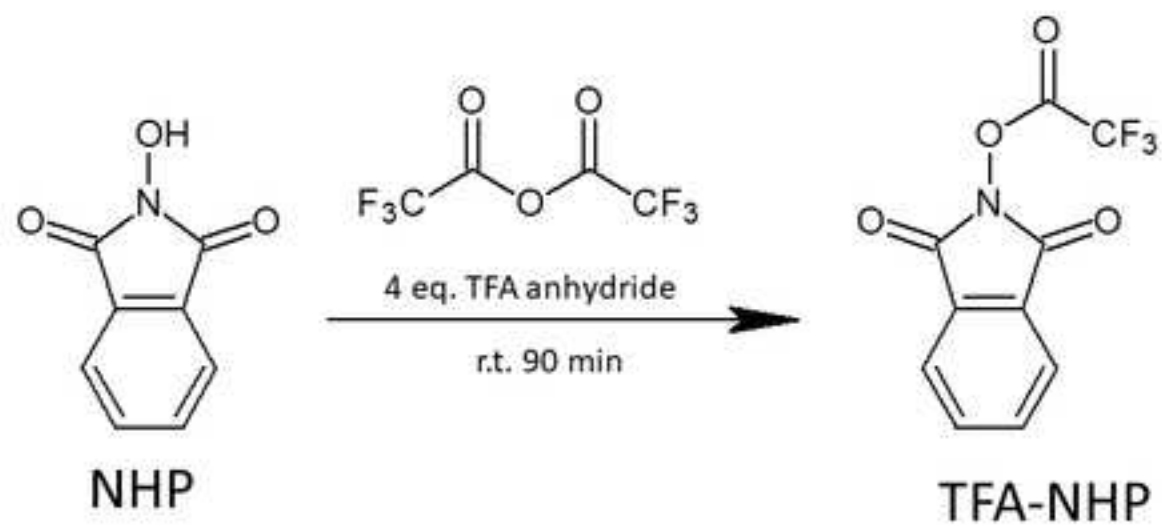
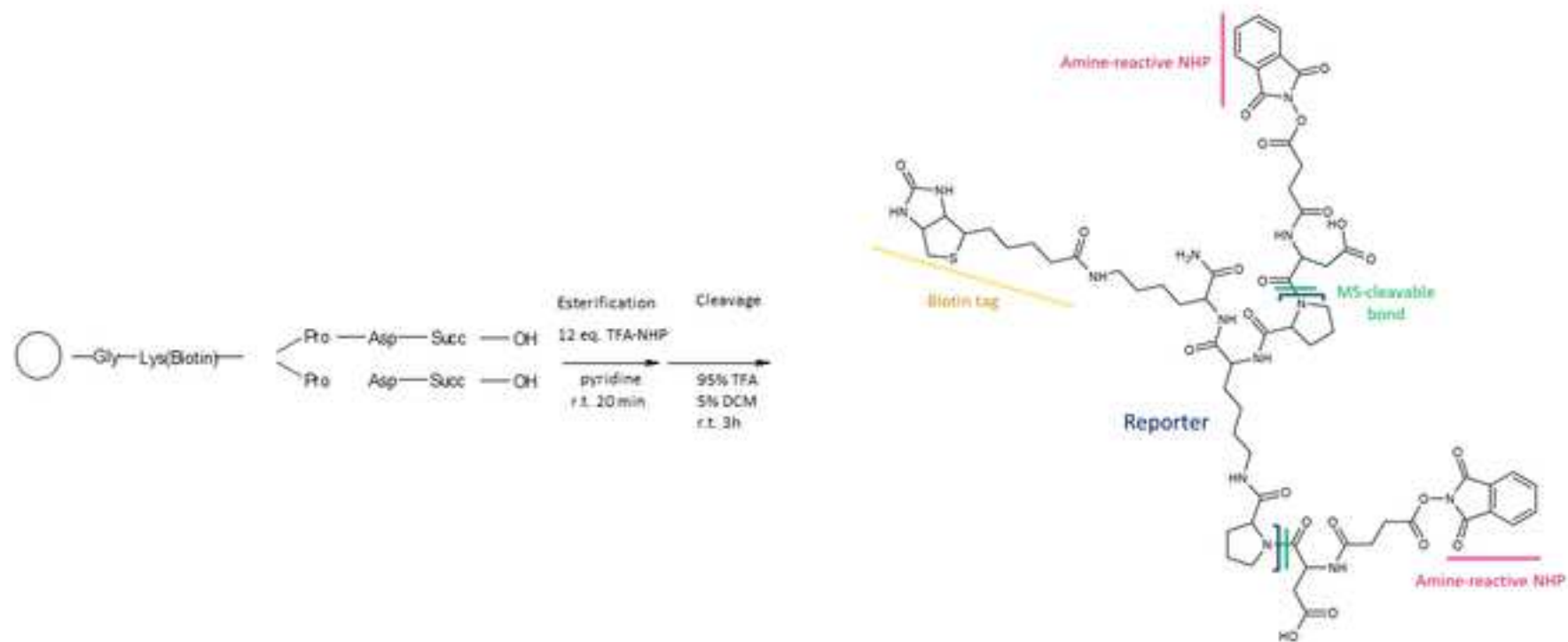


Fig 3B



WALL, BOP, APFC, 2025, Shared Networks

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Display for all countries

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Display for all projects

| Project ID | Project Name | Country | Region        | Project Type | Project ID | Project Name | Country       | Region   | Project Type |
|------------|--------------|---------|---------------|--------------|------------|--------------|---------------|----------|--------------|
| WALL-001   | WALL-001     | USA     | North America | WALL-001     | WALL-001   | USA          | North America | WALL-001 | WALL-001     |
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| WALL-0     |              |         |               |              |            |              |               |          |              |



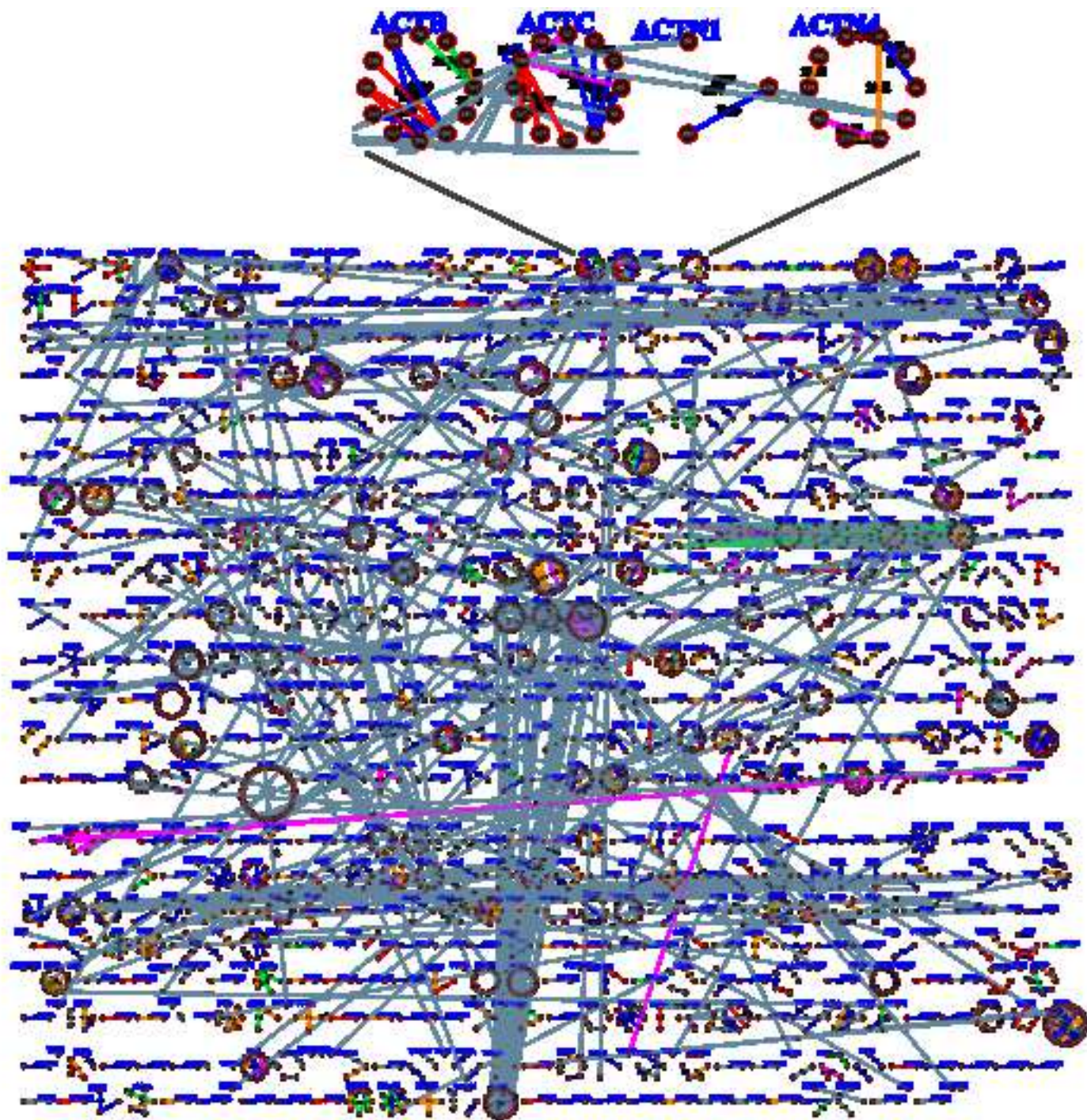




Fig 6

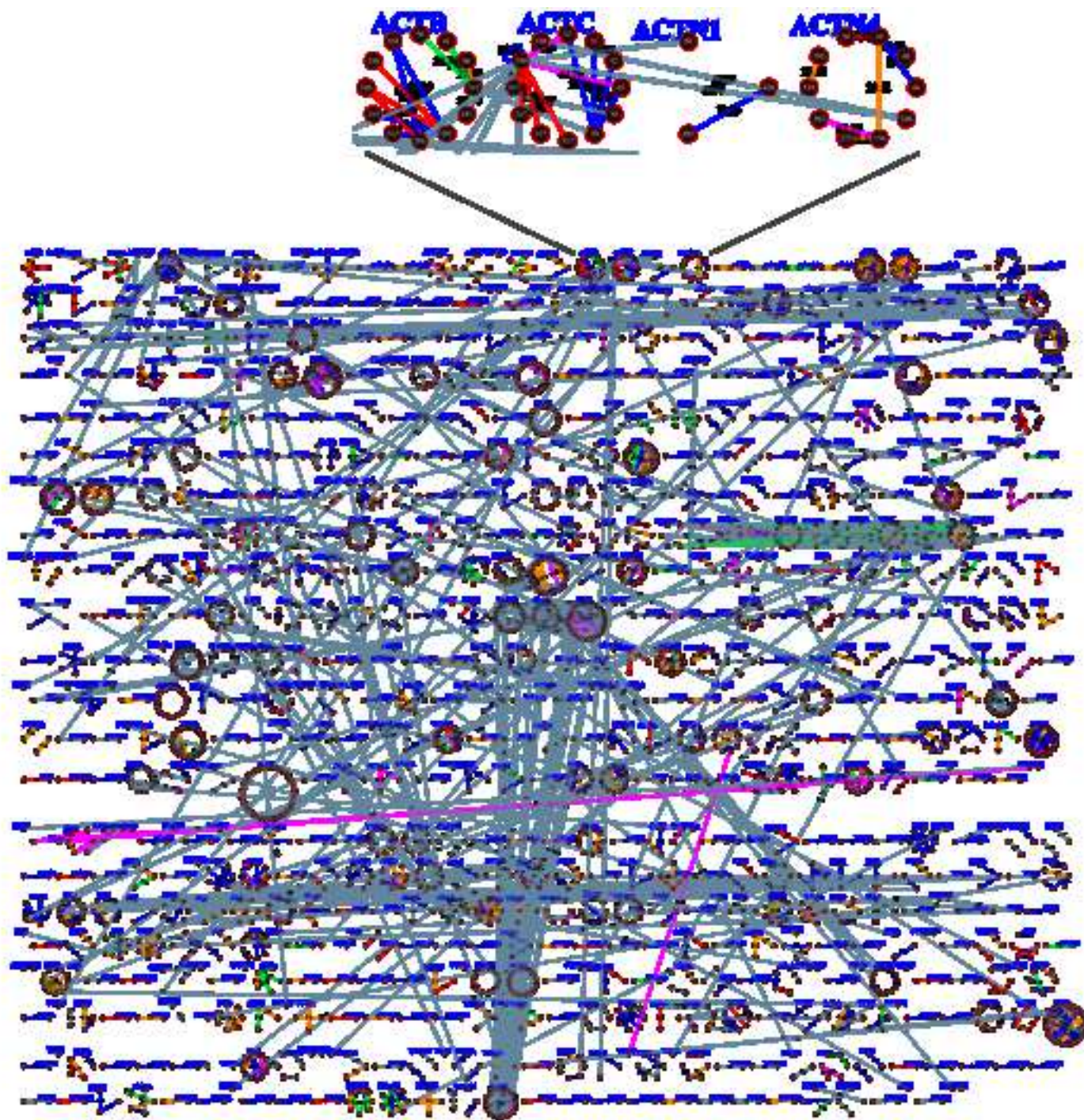
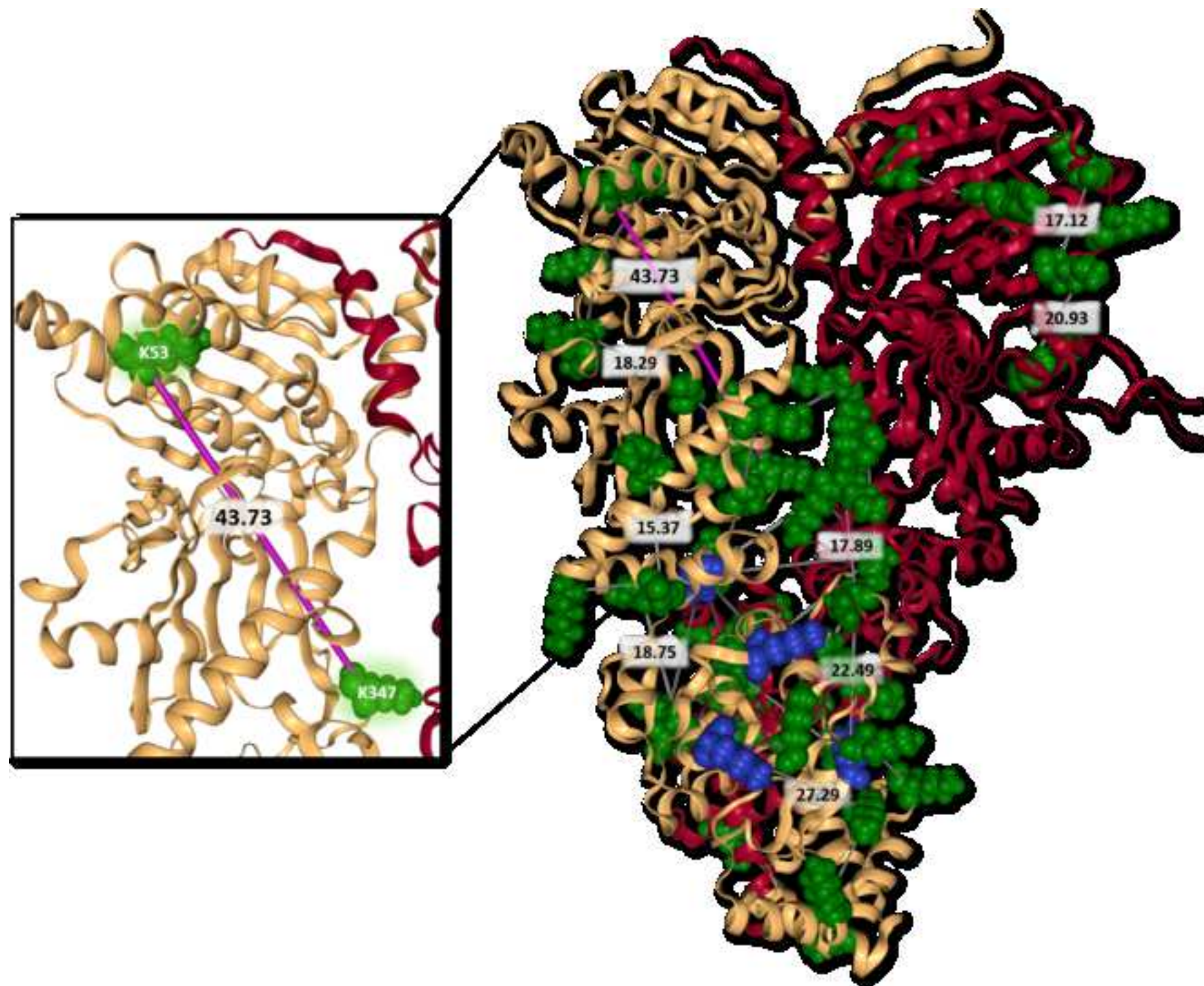
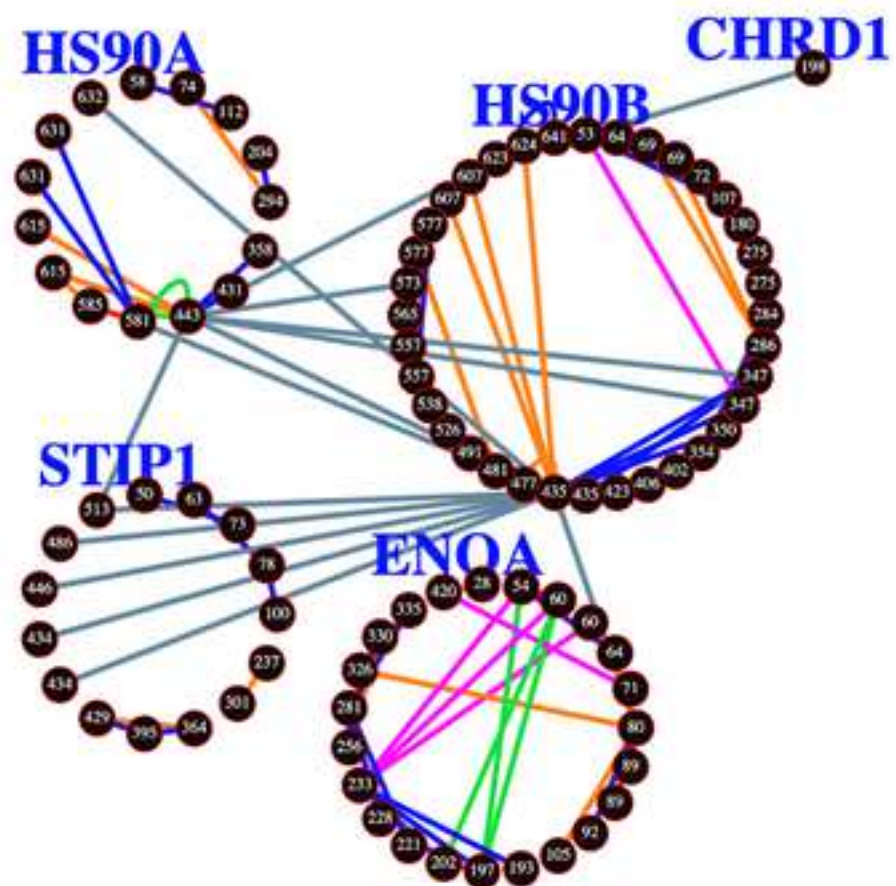




Fig 7





| Name of Material                      | Company           | Catalog Number | Comments/Description                                              |
|---------------------------------------|-------------------|----------------|-------------------------------------------------------------------|
| Acetonitrile                          | Fisher Scientific | A955           | LC–MS grade                                                       |
| Ammonium bicarbonate                  | Sigma-Aldrich     | A6141          | NH <sub>4</sub> HCO <sub>3</sub>                                  |
| Ammonium hydroxide                    | Sigma-Aldrich     | 221228         | NH <sub>4</sub> OH, ACS reagent, 28.0–30.0% NH <sub>3</sub> basis |
| Calcium chloride                      | Sigma-Aldrich     | AC42352        | CaCl <sub>2</sub>                                                 |
| Dichloromethane                       | Fisher Scientific | AC610300010    | DCM, 99,9% (wt/wt)                                                |
| Dichloromethane                       | Fisher Scientific | AC610300010    | DCM; 99.9% (wt/wt)                                                |
| Diethyl ether 99.5% (wt/wt)           | Fisher Scientific | AC364330010    |                                                                   |
| Diisopropylcarbodiimide               | Sigma-Aldrich     | D125407        | DIC                                                               |
| Dimethyl sulfoxide                    | Sigma-Aldrich     | 276855         | DMSO                                                              |
| Dimethylformamide                     | Fisher Scientific | D119           | DMF                                                               |
| DMEM                                  | Fisher Scientific | 11-965-118     | Cell culture medium                                               |
| EDTA 99% (wt/wt)                      | Fisher Scientific | AC118432500    |                                                                   |
| Ethyl cyano(hydroxyimino)acetate      | Sigma-Aldrich     | 8510860100     | Oxyma                                                             |
| Fetal bovine serum (FBS)              | Atlas Biologicals | FP-0500-A      |                                                                   |
| Fmoc-Asp(OtBu)-OH                     | Millipore Sigma   | 8520370005     |                                                                   |
| Fmoc-Gly-Wang resin                   | Bachem            | D-1745         | 100–200 mesh                                                      |
| Fmoc-L-Lys(biotin)-OH                 | P3 BioSystems     | 41084          |                                                                   |
| Fmoc-Lys(Fmoc)-OH                     | Millipore Sigma   | 8520410025     |                                                                   |
| Fmoc-Pro-OH                           | Millipore Sigma   | 8520170025     |                                                                   |
| Formic acid                           | Fisher Scientific | A117           | FA, 99.5+% (vol/vol), LC–MS grade                                 |
| HeLa cells                            | ATCC              | CCL-2          | Epithelial from human cervix                                      |
| Iodoacetamide                         | Sigma-Aldrich     | I1149          | IAA                                                               |
| Magnesium chloride                    | Sigma-Aldrich     | M8266          | MgCl <sub>2</sub>                                                 |
| Methanol                              | Fisher Scientific | A456           | LC–MS grade                                                       |
|                                       | Pierce            |                |                                                                   |
| Monomeric Avidin UltraLink Resin      | Biotechnology     | 53146          |                                                                   |
| N-hydroxyphthalimide                  | Sigma-Aldrich     | H53704         | NHP                                                               |
| Nitrogen (g) (99.998%)                | Praxair           | NI 4.8-T       |                                                                   |
| PBS                                   | Fisher Scientific | SH30256LS      |                                                                   |
| PBS with calcium and magnesium        | Fisher Scientific | SH30264FS      |                                                                   |
| Penicillin–streptomycin (10,000 U/mL) | Fisher Scientific | SV30010        |                                                                   |



|                                                                                                |                   |           |                                         |
|------------------------------------------------------------------------------------------------|-------------------|-----------|-----------------------------------------|
| Piperidine                                                                                     | Sigma-Aldrich     | 411027    | 99.5% (vol/vol)                         |
| Poly-Prep chromatography columns                                                               | Bio-Rad           | 7311550   | Disposable polypropylene columns        |
| Potassium chloride                                                                             | Sigma-Aldrich     | P9541     | KCl                                     |
| Potassium phosphate, monobasic                                                                 | Sigma-Aldrich     | P9791     |                                         |
| Pyridine                                                                                       | Millipore Sigma   | MPX20127  | DriSolv, anhydrous septum-sealed bottle |
| ReproSil-Pur, 5 micron, 120 Å                                                                  | Dr. Maisch        | r15.8e    |                                         |
| Sep-Pak Vac 3cc (500mg) C18 cartridges                                                         | Waters            | 186004619 | reversed-phase C18 desalting column     |
| Sodium chloride                                                                                | Sigma-Aldrich     | S 9888    |                                         |
| Sodium hydroxide                                                                               | Sigma-Aldrich     | 221465    |                                         |
| Sodium phosphate, dibasic                                                                      | Sigma-Aldrich     | AC20651   |                                         |
| Sodium phosphate, monobasic (NaH <sub>2</sub> PO <sub>4</sub> ; Sigma-Aldrich, cat. no. S9638) | Sigma-Aldrich     | S9638     |                                         |
| Succinic anhydride                                                                             | Sigma-Aldrich     | 239690    |                                         |
| TFA acid                                                                                       | Fisher Scientific | LS121     | LC–MS grade                             |
| Trifluoroacetic acid                                                                           | Fisher Scientific | A116      | TFA acid, Optima LC–MS grade            |
| Trifluoroacetic anhydride                                                                      | Sigma-Aldrich     | 106232    | TFA anhydride                           |
| Tris(2-carboxyethyl)phosphine hydrochloride                                                    | Fisher Scientific | 20491     | TCEP-HCl                                |
| Trypsin                                                                                        | Promega           | V5113     | sequencing grade, modified, frozen      |
| Urea                                                                                           | Sigma-Aldrich     | U5378     |                                         |
| Water                                                                                          | Fisher Scientific | W6        | LC–MS grade                             |
| Water with 0.1% (vol/vol) TFA acid                                                             | Fisher Scientific | LS119     | LC–MS grade                             |

| Name of Equipment                    | Company              | Catalog Number     | Comments/Description                    |
|--------------------------------------|----------------------|--------------------|-----------------------------------------|
| 1.5-mL LC autosampler vial           | Thermo Scientific    | MSCERT4000-39TR    |                                         |
| Analytical/preparative HPLC system   | Agilent Technologies | G1311C             |                                         |
| CEM Liberty Lite peptide synthesizer | CEM                  |                    | Automated Microwave Peptide Synthesizer |
| Conical centrifuge tubes             | Fisher Scientific    | 14-959-53A and 12- | 15 and 50 mL                            |
| Extraction manifold                  | Waters               | WAT200608          | 20 position, 16 × 75-mm tubes           |
| LC autosampler vial caps             | Fisher Scientific    | 13-622-289         |                                         |
| LC autosampler vials                 | Fisher Scientific    | 03-377-299         |                                         |

|                                          |                   |                  |                                   |
|------------------------------------------|-------------------|------------------|-----------------------------------|
| Microcentrifuge                          | Eppendorf         | 22620444         |                                   |
| Microcentrifuge tubes                    | Fisher Scientific | 02-681-320       | 1.5 mL                            |
| pH paper                                 | Fisher Scientific | 13-640-5070      |                                   |
| Poly-Prep chromatography columns         | Bio-Rad           | 7311550          |                                   |
| Q Exactive Plus                          | Thermo Scientific | IQLAAEGAAPFALGM  | High resolution mass spectrometer |
| SCX column                               | Phenomenex        | 00G-4398-N0      | Luna column                       |
| Sep-Pak Vac C18 cartridge, 3cc/500mg     | Waters            | 186004619        |                                   |
| Shaker with 15- and 1.5-mL sample blocks | Eppendorf         | 5355             | ThermoMixer R                     |
| Thermal mixer                            | Sigma-Aldrich     | T1317            | Eppendorf ThermoMixer compact     |
| Ultimate 3000                            | Thermo Scientific | ULTIM3000RSLCNAI | nano-LC system                    |
| Ultrasonic processor                     | Cole-Palmer       | EW-04714-50      |                                   |
| Vacuum centrifuge                        | SP Scientific     | EZ-2             |                                   |

#### Name of Software

ReAdW (<https://sourceforge.net/projects/sashimi/files/ReAdW%20%28Xcalibur%20converter%29/>)

Mango (<https://github.com/jpm369/mango>)

Comet 2018.01 or later (<http://comet-ms.sourceforge.net/>)

XLinkProphet (<https://github.com/brucelab/xlinkprophet>)

Perl v.5.24.0+ (<https://www.perl.org/get.html>)

All required software can be run on a standard personal computer equipped with a Linux operating system and at least 4 GB of RAM.

**Editorial and production comments:****Changes to be made by the Author(s) regarding the written manuscript:**

1. Please take this opportunity to thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues.
2. JoVE cannot publish manuscripts containing commercial language. This includes trademark symbols (™), registered symbols (®), and company names before an instrument or reagent. Please remove all commercial language from your manuscript and use generic terms instead. All commercial products should be sufficiently referenced in the Table of Materials: Poly-Prep, UltraLink, etc.

[All commercial language removed and commercial products referenced in the Table of Materials.](#)

3. Please remove the embedded figure(s) from the manuscript. All figures should be uploaded separately to your Editorial Manager account.

[All embedded figures removed](#)

4. Step 3.2: Please quantitate a minimal volume or how to do so.

[We edited the text accordingly.](#)

5. Please specify all volumes used throughout.

6. 5.1: Please quantitate a pellet volume.

[We edited the text accordingly.](#)

7. As we are a methods journal, please revise the Discussion to explicitly cover the following in detail in 3-6 paragraphs with citations:

- a) Critical steps within the protocol

[These were pointed out throughout the protocol description.](#)

- b) Any modifications and troubleshooting of the technique

- c) Any limitations of the technique

- d) The significance with respect to existing methods

- e) Any future applications of the technique

Regarding b-e, we edited the text accordingly.

**Changes to be made by the Author(s) regarding the video:**

1. Please increase the homogeneity between the video and the written manuscript. Ideally, all figures in the video would appear in the written manuscript and vice versa. The video and the written manuscript should be reflections of each other.

Homogeneity increased between video and written manuscript. Figures now appear in video and written manuscript.

2. Add a name and institution graphic for the speaker in the intro and conclusion

Added name and institution to intro.

3. Turn up the speaker's audio, it is too low

Turned up audio.

4. Please stabilize the protocol video.

Video stabilized.

5. Furthermore, please revise the narration to be more homogenous with the written manuscript. Ideally, the narration is a word for word reading of the written protocol. The headers should match up exactly as well to help anchor the user (Crosslinker QC 5:34, etc.).

Revised narration and section headers to be more homogeneous with the written manuscript.

6. At 2:01, 4:18, and 9:09 the person at the performing the protocol is looking into the camera waiting for "action" to be called, edit that out

Edited out.

7. At 3:55 and 6:51 the chapter title cards switch to different title cards where the formatting of the text has been changed. Keep the second cards, replace the first with them.

Fixed chapter title cards.

8. At 6:23 it sounds like the beginning of the voice over was cut off, bring that back in.

Added voice over back in

9. At 7:36 the audio from the video clip is audible (the pop of the centrifuge being opened), remove that.

Audio removed.

10. Please include a short conclusion section to the video.

Conclusion section added to the video.

#### **Reviewers' comments:**

##### **Reviewer #1:**

Minor Concerns:

- The authors may wish to show a schematic of the synthetic route to produce the crosslinker.
- Line 166: What is the weight of TFA-NHP that should be weighed out?

We altered the text accordingly.

- Line 194. The authors should state what the typical yield of the crosslinker is.

We altered the text accordingly.

- Line 206/Figure 3. Are the hydrolysis products due to diluting the crosslinker in water for MS analysis, or are these present in significant abundance in the stock solution?

The hydrolysis of the NHP reactive group of the BDP crosslinker occurs in the presence of aqueous solvents, either during the MS analysis or the crosslinking reaction in the  $\text{Na}_2\text{HPO}_4$  buffer.

- Line 255. Is the lysate centrifuged prior to reduction/alkylation/digestion?

It is not. The cell lysate is submitted to sonication for DNA breakage (step 6.3).

- Line 300. The fractionation details are not included in sufficient detail. What volume fractions should be collected? How many fractions should be collected over the 97.5 min gradient? This is essential to know as the authors refer to pooling of specific fraction numbers.

We altered the text accordingly to contain this information.

- Line 325. Again, details of the fractionation regime are not adequately described in this section. This is key so that someone following the protocol pools the correct fractions.

We altered the text accordingly.

- Line 335. What do the authors mean by MS3 separate events?

A third mass spectrometry event is done to fragment selected peptides to generate tandem mass spectra, used for peptide sequence identification. By separate we mean 4 individual MS3 events after each MS2 event.

- Line 362. The authors should provide numbers for these on-the-fly mass relationship checks - ie what is the mass of the reporter, and the relationship between reporter mass and the peptide masses.

We altered the text accordingly.

- Line 30 should read "side chains of lysine residues and protein N-termini which yields"

We altered the text accordingly.

- Line 88 should read "including by"

We altered the text accordingly.

- Line 98 should read "generate structural models and facilitate molecular docking..."

We altered the text accordingly.

- Line 190 should read... "suspend it in DMSO to to produce a stock solution of concentration 100-300 mM

We altered the text accordingly.

- Line 226. Delete "in a humidified ambient"

We altered the text accordingly.

- Line 311. Delete "assay for"

We altered the text accordingly.

**Reviewer #2:**

## Minor Concerns:

- I am surprised to that the length of the cross-link reported as a 'molecular ruler'. My understanding is that this hypothesis had met with little overall success in reality.

We thank the reviewer for the valid point, but the term “molecular ruler” is not present in the text. We do refer to the crosslinker as follows:

“This technique is based on the reactivity of cross-linker groups to specific side chains of proteins, usually primary amines. The distance between these reactive groups (the length of the spacer) provides constraint information useful for modeling protein structures and protein complex topologies.” (line 54)

- The concept of using dead-end links to quantify protein seems a distraction. They provide information on accessible residues; however, linear peptides are equally useful for quantifying levels of protein.

We thank the reviewer for the valid point. Indeed, dead-ends provide information on accessible residues, but considering the abundance of deadends compared to crosslinked peptides, and that it is highly probable that every crosslinked peptide has a corresponding deadend version, we chose to use this information for a “proteome” quantitation of the sample. We note that we also use other quantitative techniques, e.g., TMT and label-free, depending on the purpose of the study.

- Would it be possible to store all the data in the PRIDE database?

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the following information for login:

Project Name: In vivo cross-linking mass spectrometry for protein and complex structural analysis

Project accession: PXD023560

Reviewer account details:

Username: reviewer\_pxd023560@ebi.ac.uk

Password: OfcoLOG2



| pepA            | positionA | accessionA | uniprotA  | modposA | geneA         | pdbeA    |
|-----------------|-----------|------------|-----------|---------|---------------|----------|
| KVLELTGK        | 0         | A0A0B4J2D5 | A0A0B4J2C | 261     | LOC102724#### |          |
| KVLELTGK        | 0         | A0A0B4J2D5 | A0A0B4J2C | 261     | LOC102724#### |          |
| NNQESDCVSKK     | 9         | A6NDG6     | PGP_HUM   | 300     | PGP           | A6NDG6   |
| HSPKVVETDCPVPPK | 3         | A6NHR9     | SMHD1_HU  | 1976    | SMCHD1        | ####     |
| KQKVPGFPK       | 0         | A6NK02     | TRI75_HUN | 322     | TRIM75P       | ####     |
| KDEEVLK         | 0         | O00148     | DX39A_HU  | 155     | DDX39A        | O00148   |
| SFSLKNVK        | 4         | O00148     | DX39A_HU  | 187     | DDX39A        | O00148   |
| KGCVITISGR      | 0         | O00154     | BACH_HUN  | 286     | ACOT7         | 2QQ2     |
| HLGYKPEEYK      | 4         | O00159     | MYO1C_HU  | 704     | MYO1C         | 4BYF     |
| TEATKR          | 4         | O00159     | MYO1C_HU  | 151     | MYO1C         | 4BYF     |
| TFTWLVGKINR     | 7         | O00159     | MYO1C_HU  | 396     | MYO1C         | 4BYF     |
| TKIFIR          | 1         | O00159     | MYO1C_HU  | 714     | MYO1C         | 4BYF     |
| KWAAQTIR        | 0         | O00159     | MYO1C_HU  | 781     | MYO1C         | O00159   |
| FFQEENTEKLK     | 8         | O00232     | PSD12_HU  | 221     | PSMD12        | 5VGZ     |
| VFDVTKGR        | 5         | O00264     | PGRC1_HU  | 102     | PGRMC1        | 4X8Y     |
| GVTFNVTVDTKR    | 11        | O00299     | CLIC1_HUN | 49      | CLIC1         | 4K0N     |
| FLKSK           | 2         | O00330     | ODPX_HUN  | 488     | PDHX          | O00330   |
| DCLPELKTR       | 6         | O00429     | DNM1L_HU  | 305     | DNM1L         | 4BEJ     |
| DKLDPDMALCR     | 1         | O00469     | PLOD2_HU  | 486     | PLOD2         | ####     |
| DGITAGKAALR     | 6         | O00481     | BT3A1_HU  | 108     | BTN3A1        | ####     |
| VKFNVNR         | 1         | O00567     | NOP56_HU  | 158     | NOP56         | O00567   |
| VSISEGDDKIEYR   | 8         | P22087     | FBRL_HUM  | 131     | FBL           | 2IPX     |
| GKIGLDFCK       | 1         | O00571     | DDX3X_HU  | 335     | DDX3X         | 5E7I     |
| SGKSPILVATAVAR  | 2         | O00571     | DDX3X_HU  | 491     | DDX3X         | 5E7I     |
| ATFNPAQDKCGIR   | 8         | O00592     | PODXL_HU  | 394     | PODXL         | O00592_O |
| ATFNPAQDKCGIR   | 8         | O00592     | PODXL_HU  | 394     | PODXL         | O00592   |
| EITIHTKLPAK     | 6         | O00592     | PODXL_HU  | 418     | PODXL         | O00592   |
| LPAKDVYER       | 3         | O00592     | PODXL_HU  | 422     | PODXL         | O00592   |
| LPAKDVYER       | 3         | O00592     | PODXL_HU  | 422     | PODXL         | O00592   |
| STHIPYRDSKLTR   | 9         | O14782     | KIF3C_HUN | 321     | KIF3C         | 3B6V     |
| YFLDKLTLSR      | 4         | O14874     | BCKD_HUN  | 192     | BCKDK         | ####     |
| NPGYIKLR        | 5         | Q99623     | PHB2_HUN  | 250     | PHB2          | ####     |
| KDDVSIYYVSR     | 0         | O14975     | S27A2_HU  | 174     | SLC27A2       | ####     |
| NQQGIKAEIAR     | 5         | O15020     | SPTN2_HU  | 1953    | SPTBN2        | ####     |
| KLDFFR          | 0         | O15031     | PLXB2_HU  | 24      | PLXNB2        | O15031   |
| KLDFFR          | 0         | O15031     | PLXB2_HU  | 24      | PLXNB2        | O15031   |
| KLDFFR          | 0         | O15031     | PLXB2_HU  | 24      | PLXNB2        | O15031   |
| AFSITQGLLKDR    | 9         | O15067     | PUR4_HUN  | 900     | PFAS          | O15067   |
| NAYVWTLKGR      | 7         | O15143     | ARC1B_HU  | 82      | ARPC1B        | O15143   |
| LKLSEELSGGR     | 1         | P61158     | ARP3_HUN  | 348     | ACTR3         | P61158   |
| EKYDYVGR        | 1         | O15173     | PGRC2_HU  | 193     | PGRMC2        | O15173   |
| VTQYLPVHVAR     | 2         | O15260     | SURF4_HU  | 22      | SURF4         | ####     |
| KDFIFVSAR       | 0         | O15357     | SHIP2_HUN | 391     | INPPL1        | ####     |
| NTSKQQQQK       | 3         | O15372     | EIF3H_HUN | 269     | EIF3H         | O15372   |
| VADWTGATYQDKR   | 11        | O15371     | EIF3D_HUN | 53      | EIF3D         | ####     |
| NTSKQQQQK       | 3         | O15372     | EIF3H_HUN | 269     | EIF3H         | O15372   |

|                        |    |        |          |     |           |        |
|------------------------|----|--------|----------|-----|-----------|--------|
| GKDQQVR                | 1  | O15382 | BCAT2_HU | 111 | BCAT2     | 5MPR   |
| LCLPSFDKLELLECIR       | 7  | O15382 | BCAT2_HU | 141 | BCAT2     | 5MPR   |
| FVPLPASAKWASGLTPAQNCPR | 8  | O15533 | TPSN_HUN | 104 | TAPBP     | 3F8U   |
| SLPGPKR                | 5  | O43143 | DHX15_HU | 185 | DHX15     | 5XDR   |
| YYDILKK                | 5  | O43143 | DHX15_HU | 132 | DHX15     | 5XDR   |
| AVTKLGFK               | 3  | O43159 | RRP8_HUN | 409 | RRP8      | 2ZFU   |
| LEEVAKR                | 5  | O43169 | CYB5B_HU | 30  | CYB5B     | 3NER   |
| AYEKILFTEATR           | 3  | P48556 | PSMD8_HL | 281 | PSMD8     | 5L4K   |
| EKYLNVSR               | 1  | O43324 | MCA3_HU  | 138 | EEF1E1    | 4BL7   |
| TLIEAGLPQKVAER         | 9  | O43390 | HNRPR_HU | 41  | HNRNPR    | ####   |
| DFIEKR                 | 4  | O43678 | NDUA2_HL | 39  | NDUFA2    | 1S3A   |
| KANPDLPIILIR           | 0  | O43678 | NDUA2_HL | 46  | NDUFA2    | 1S3A   |
| EALEKTEK               | 4  | O43707 | ACTN4_HU | 518 | ACTN4     | O43707 |
| KTAPYK                 | 0  | O43707 | ACTN4_HU | 176 | ACTN4     | O43707 |
| KTAPYK                 | 0  | O43707 | ACTN4_HU | 176 | ACTN4     | O43707 |
| KTAPYK                 | 0  | O43707 | ACTN4_HU | 176 | ACTN4     | 2R00   |
| KTFTAWCNSHLR           | 0  | O43707 | ACTN4_HU | 54  | ACTN4     | 2R00   |
| KTFTAWCNSHLR           | 0  | O43707 | ACTN4_HU | 54  | ACTN4     | 2R00   |
| KTFTAWCNSHLR           | 0  | O43707 | ACTN4_HU | 54  | ACTN4     | 2R00   |
| IKIAPPER               | 1  | P68032 | ACTC_HUN | 330 | ACTC1     | P68032 |
| VHKINNVNK              | 2  | O43707 | ACTN4_HU | 108 | ACTN4     | 2R00   |
| AICIDPAYSKAYGR         | 9  | O43765 | SGTA_HUN | 160 | SGTA      | 2VYI   |
| IFDSEEILAGYKR          | 11 | O43776 | SYNC_HUN | 490 | NARS      | O43776 |
| TEASKLVMSYVAACVGK      | 4  | O43795 | MYO1B_HL | 119 | MYO1B     | O43795 |
| LQKLVAK                | 2  | O43818 | U3IP2_HU | 125 | RRP9      | ####   |
| LAKLYLEQLR             | 2  | O43818 | U3IP2_HU | 84  | RRP9      | ####   |
| IITKAK                 | 3  | P51553 | IDH3G_HU | 194 | IDH3G     | 5GRI   |
| FAQKR                  | 3  | O43852 | CALU_HUN | 102 | CALU      | O43852 |
| LGKIVSK                | 2  | O43852 | CALU_HUN | 75  | CALU      | O43852 |
| LYQLSKAGK              | 5  | O43865 | SAHH2_HU | 267 | AHCYL1    | 3MTG   |
| LYQLSKAGK              | 5  | O43865 | SAHH2_HU | 267 | AHCYL1    | 3MTG   |
| DFNQFIKANEK            | 6  | O60264 | SMCA5_HL | 855 | SMARCA5   | ####   |
| ESVEQQADSFKATR         | 10 | O60313 | OPA1_HUN | 568 | OPA1      | O60313 |
| KLCEK                  | 0  | O60353 | FZD6_HUN | 97  | FZD6      | ####   |
| FEQKGFR                | 3  | O60361 | NDK8_HUN | 16  | NME2P1    | O60361 |
| NVMSKVQEMNYIQK         | 4  | O60488 | ACSL4_HU | 388 | ACSL4     | O60488 |
| NVMSKVQEMNYIQK         | 4  | O60488 | ACSL4_HU | 388 | ACSL4     | O60488 |
| IYDRKFLECK             | 5  | O60516 | 4EBP3_HU | 43  | EIF4EBP3  | ####   |
| KEACWTISNITAGNR        | 0  | O60684 | IMA7_HUN | 354 | KPNA6     | 4UAD   |
| VVKAASGALR             | 2  | O60716 | CTND1_HU | 728 | CTNND1    | 3L6X   |
| AVTKYTSK               | 3  | O60814 | H2B1K_HU | 121 | HIST1H2BK | 2CV5   |
| AVTKYTSK               | 3  | O60814 | H2B1K_HU | 121 | HIST1H2BK | 2CV5   |
| KAVTK                  | 0  | O60814 | H2B1K_HU | 17  | HIST1H2BK | ####   |
| LLPGELAKHAVSEGTK       | 8  | O60814 | H2B1K_HU | 109 | HIST1H2BK | 2CV5   |
| SAPAPKK                | 5  | O60814 | H2B1K_HU | 12  | HIST1H2BK | ####   |
| GKQGGK                 | 1  | P04908 | H2A1B_HU | 6   | HIST1H2AB | P04908 |
| KGGGK                  | 0  | P25490 | TYY1_HUN | 174 | YY1       | ####   |

|                        |    |        |           |      |                |
|------------------------|----|--------|-----------|------|----------------|
| AVTKYTSAK              | 3  | O60814 | H2B1K_HU  | 121  | HIST1H2BK 2CV5 |
| TKQTAR                 | 1  | Q16695 | H31T_HUN  | 5    | HIST3H3 Q16695 |
| GLKLSGGEK              | 2  | O75027 | ABCB7_HU  | 608  | ABCB7 O75027   |
| GGKIFIER               | 2  | O75054 | IGSF3_HUN | 92   | IGSF3 #####    |
| KYSSTER                | 0  | O75165 | DJC13_HUI | 305  | DNAJC13 #####  |
| NCLALADDKK             | 8  | O75367 | H2AY_HUN  | 304  | H2AFY 1ZR5     |
| ETTDFKVDTK             | 5  | O75369 | FLNB_HUN  | 476  | FLNB #####     |
| GAGIGGLGITVEGPSESKINCR | 17 | O75369 | FLNB_HUN  | 1372 | FLNB #####     |
| IKVFGPGIEGK            | 1  | O75369 | FLNB_HUN  | 1232 | FLNB #####     |
| VKIAGPGLGSGVR          | 1  | O75369 | FLNB_HUN  | 1425 | FLNB #####     |
| VKIAGPGLGSGVR          | 1  | O75369 | FLNB_HUN  | 1425 | FLNB #####     |
| GFSIPECQKLLPK          | 8  | O75390 | CISY_HUM  | 103  | CS O75390      |
| KDTPR                  | 0  | P26641 | EF1G_HUN  | 228  | EEF1G #####    |
| DLQQYQSQAKQLFR         | 9  | O75396 | SC22B_HUI | 38   | SEC22B O75396  |
| KLNEQSPTR              | 0  | O75396 | SC22B_HUI | 43   | SEC22B O75396  |
| KQAFNAYK               | 0  | O75400 | PR40A_HU  | 438  | PRPF40A #####  |
| YFKQQEILWR             | 2  | O75436 | VP26A_HU  | 288  | VPS26A 2FAU    |
| KYTEQITNEK             | 0  | Q16718 | NDUA5_HL  | 46   | NDUFA5 Q16718  |
| AKWDAWNALGSLPK         | 1  | O75521 | ECI2_HUM  | 92   | ECI2 #####     |
| LLLKLK                 | 3  | O75533 | SF3B1_HUI | 503  | SF3B1 5IFE     |
| TGKPIAVK               | 2  | O75534 | CSDE1_HUI | 81   | CSDE1 #####    |
| KLPEEVVK               | 0  | O75643 | U520_HUN  | 1134 | SNRNP200 5URJ  |
| KVLLTGETSTDLC          | 0  | O75643 | U520_HUN  | 1404 | SNRNP200 5URJ  |
| LLGKGNIIISTPEK         | 3  | O75643 | U520_HUN  | 1421 | SNRNP200 5URJ  |
| SLVQEMVGSFGKR          | 11 | O75643 | U520_HUN  | 557  | SNRNP200 5URJ  |
| LQAIAEKR               | 6  | O75781 | PALM_HUN  | 21   | PALM #####     |
| VKILYK                 | 1  | O75935 | DCTN3_HU  | 55   | DCTN3 #####    |
| AGLVDDFEKK             | 8  | O75947 | ATP5H_HU  | 72   | ATP5H O75947   |
| IVEYEKEMEK             | 5  | O75947 | ATP5H_HU  | 117  | ATP5H O75947   |
| IVEYEKEM[147.04]EK     | 5  | O75947 | ATP5H_HU  | 117  | ATP5H O75947   |
| SCAEWVSLSKAR           | 9  | O75947 | ATP5H_HU  | 109  | ATP5H O75947   |
| ANVAKAGLVDDFEK         | 4  | O75947 | ATP5H_HU  | 63   | ATP5H O75947   |
| SCAEWVSLSKAR           | 9  | O75947 | ATP5H_HU  | 109  | ATP5H O75947   |
| SQQALVQKR              | 7  | P24539 | AT5F1_HUI | 162  | ATP5F1 P24539  |
| LTGVSISQVNHKPLR        | 11 | O75955 | FLOT1_HUI | 422  | FLOT1 O75955_O |
| TKQQIEEQR              | 1  | O75955 | FLOT1_HUI | 246  | FLOT1 #####    |
| AEAYQKYGDAAK           | 5  | Q14254 | FLOT2_HUI | 350  | FLOT2 #####    |
| EKELEAR                | 1  | O75955 | FLOT1_HUI | 277  | FLOT1 #####    |
| IQQIAEGEKVK            | 8  | Q14254 | FLOT2_HUI | 305  | FLOT2 #####    |
| AIQSLKK                | 5  | O75964 | ATP5L_HUI | 54   | ATP5L #####    |
| AWKETNMAR              | 2  | O76024 | WFS1_HUN  | 679  | WFS1 #####     |
| ALSKHLPSSDSMSLK        | 3  | O76094 | SRP72_HUI | 504  | SRP72 #####    |
| DQNVFDSKKK             | 8  | O76094 | SRP72_HUI | 284  | SRP72 O76094   |
| GKYYAVNYPLR            | 1  | Q13547 | HDAC1_HU  | 220  | HDAC1 4BKX     |
| VGCKYQAEIPDR           | 3  | O94776 | MTA2_HUI  | 152  | MTA2 O94776    |
| KTPEGR                 | 0  | O94826 | TOM70_HL  | 84   | TOMM70 #####   |
| YFKAGK                 | 2  | O94826 | TOM70_HL  | 126  | TOMM70 O94826  |

|                         |    |        |           |     |        |        |
|-------------------------|----|--------|-----------|-----|--------|--------|
| LLAKAR                  | 3  | O94906 | PRP6_HUN  | 667 | PRPF6  | 509Z   |
| AKLLAR                  | 1  | Q14689 | DIP2A_HUI | 44  | DIP2A  | Q14689 |
| FITALKSTGLR             | 5  | O94925 | GLSK_HUM  | 164 | GLS    | 3UO9   |
| LSKAFVELTK              | 2  | O95394 | AGM1_HUI  | 189 | PGM3   | O95394 |
| GAGSKTLQQNAESR          | 4  | O95816 | BAG2_HUN  | 200 | BAG2   | ####   |
| LLEHSGKAGSK             | 5  | O95816 | BAG2_HUN  | 195 | BAG2   | ####   |
| NIENSDKAIK              | 6  | O95816 | BAG2_HUN  | 186 | BAG2   | O95816 |
| AGAEVKSR                | 5  | O95831 | AIFM1_HU  | 278 | AIFM1  | 5KVI   |
| AGAEVKSR                | 5  | O95831 | AIFM1_HU  | 278 | AIFM1  | 5KVI   |
| IIKDGEQHEDLNEVAK        | 2  | O95831 | AIFM1_HU  | 593 | AIFM1  | 5KVI   |
| KAALSASEGEEVPQDK        | 0  | O95831 | AIFM1_HU  | 112 | AIFM1  | ####   |
| KIGDFR                  | 0  | O95831 | AIFM1_HU  | 286 | AIFM1  | 5KVI   |
| LLLKLK                  | 3  | O95831 | AIFM1_HU  | 382 | AIFM1  | 5KVI   |
| SLEKISR                 | 3  | O95831 | AIFM1_HU  | 295 | AIFM1  | 5KVI   |
| IVSGKDYNVTANSK          | 4  | P00338 | LDHA_HUN  | 81  | LDHA   | 5W8J   |
| IVSGKDYNVTANSK          | 4  | P00338 | LDHA_HUN  | 81  | LDHA   | 5W8J   |
| KSADTLWGIQK             | 0  | P00338 | LDHA_HUN  | 318 | LDHA   | 5W8J   |
| KSADTLWGIQK             | 0  | P00338 | LDHA_HUN  | 318 | LDHA   | 5W8J   |
| KSADTLWGIQK             | 0  | P00338 | LDHA_HUN  | 318 | LDHA   | 5W8J   |
| LSGFPKNR                | 5  | P00338 | LDHA_HUN  | 155 | LDHA   | 5W8J   |
| IVSGKDYNVTANSK          | 4  | P00338 | LDHA_HUN  | 81  | LDHA   | 5W8J   |
| IVSGKDYNVTANSK          | 4  | P00338 | LDHA_HUN  | 81  | LDHA   | 5W8J   |
| INPKNYTDNELEK           | 3  | P00367 | DHE3_HUN  | 191 | GLUD1  | 1L1F   |
| INPKNYTDNELEK           | 3  | P00367 | DHE3_HUN  | 191 | GLUD1  | 1L1F   |
| TAMKYNLGLDLR            | 3  | P00367 | DHE3_HUN  | 527 | GLUD1  | 1L1F   |
| KSNPIIR                 | 0  | P00387 | NB5R3_HU  | 164 | CYB5R3 | 1UMK   |
| NKHSAR                  | 1  | P00387 | NB5R3_HU  | 228 | CYB5R3 | 1UMK   |
| VLQKLGAHAVGM[147.04]STV | 3  | P00491 | PNPH_HUN  | 211 | PNP    | ####   |
| DTNSKK                  | 4  | P00505 | AATM_HUI  | 58  | GOT2   | 5AX8   |
| DVFLPKPTWGNHTPIFR       | 5  | P00505 | AATM_HUI  | 159 | GOT2   | 5AX8   |
| EFSIYMTKDGR             | 7  | P00505 | AATM_HUI  | 404 | GOT2   | 5AX8   |
| KAEAQIAAK               | 0  | P00505 | AATM_HUI  | 82  | GOT2   | 5AX8   |
| KQWLQEVK                | 0  | P00505 | AATM_HUI  | 338 | GOT2   | 5AX8   |
| KQWLQEVK                | 0  | P00505 | AATM_HUI  | 338 | GOT2   | 5AX8   |
| TQLVSNLKK               | 7  | P00505 | AATM_HUI  | 363 | GOT2   | 5AX8   |
| LTKIICAQQCSGR           | 2  | P00533 | EGFR_HUN  | 212 | EGFR   | 3QWQ   |
| VKIPVAIK                | 1  | P00533 | EGFR_HUN  | 739 | EGFR   | ####   |
| AEPKIEAFR               | 4  | P00558 | PGK1_HUN  | 146 | PGK1   | 2WZD   |
| AEPKIEAFR               | 4  | P00558 | PGK1_HUN  | 146 | PGK1   | 2WZD   |
| AGGFLMKK                | 6  | P00558 | PGK1_HUN  | 191 | PGK1   | 2WZD   |
| AGGFLMKK                | 6  | P00558 | PGK1_HUN  | 191 | PGK1   | 2WZD   |
| AGGFLMKK                | 6  | P00558 | PGK1_HUN  | 191 | PGK1   | 2WZD   |
| AGGFLMKK                | 6  | P00558 | PGK1_HUN  | 191 | PGK1   | 2WZD   |
| AGGFLMKK                | 6  | P00558 | PGK1_HUN  | 191 | PGK1   | 2WZD   |
| AGGFLM[147.04]KK        | 6  | P00558 | PGK1_HUN  | 191 | PGK1   | 2WZD   |
| AGGFLM[147.04]KK        | 6  | P00558 | PGK1_HUN  | 191 | PGK1   | 2WZD   |
| ALESPERPFLAILGGAKVADK   | 16 | P00558 | PGK1_HUN  | 216 | PGK1   | 2WZD   |

|                      |    |        |          |     |       |           |
|----------------------|----|--------|----------|-----|-------|-----------|
| ASLSKLGDVYVNDAFGTAHR | 4  | P00558 | PGK1_HUM | 156 | PGK1  | 2WZD      |
| DASGNKVK             | 5  | P00558 | PGK1_HUM | 139 | PGK1  | P00558    |
| IKA AVPSIK           | 1  | P00558 | PGK1_HUM | 41  | PGK1  | 2WZD      |
| IKA AVPSIK           | 1  | P00558 | PGK1_HUM | 41  | PGK1  | 2WZD      |
| IKA AVPSIK           | 1  | P00558 | PGK1_HUM | 41  | PGK1  | 2WZD      |
| IKA AVPSIK           | 1  | P00558 | PGK1_HUM | 41  | PGK1  | 2WZD      |
| IVKDLMSK             | 2  | P00558 | PGK1_HUM | 267 | PGK1  | 2WZD      |
| KELNYFAK             | 0  | P00558 | PGK1_HUM | 192 | PGK1  | 2WZD      |
| VDFNVPMKNNQITNNQR    | 7  | P00558 | PGK1_HUM | 30  | PGK1  | 2WZD      |
| VKA EPAK             | 1  | P00558 | PGK1_HUM | 141 | PGK1  | P00558    |
| KGVPVK               | 0  | P00966 | ASSY_HUM | 229 | ASS1  | P00966_PC |
| LQSKVTAK             | 3  | P00966 | ASSY_HUM | 408 | ASS1  | ####      |
| KWEAAR               | 0  | P01889 | 1B07_HUM | 170 | HLA-B | 4U1H      |
| EAALSTALSEKR         | 10 | P02545 | LMNA_HUI | 155 | LMNA  | ####      |
| KEGDLIAAQAR          | 0  | P02545 | LMNA_HUI | 123 | LMNA  | ####      |
| KLESTESR             | 0  | P02545 | LMNA_HUI | 420 | LMNA  | P02545    |
| KLESTESR             | 0  | P02545 | LMNA_HUI | 420 | LMNA  | P02545    |
| KLESTESR             | 0  | P02545 | LMNA_HUI | 420 | LMNA  | P02545    |
| KLLEGEER             | 0  | P02545 | LMNA_HUI | 378 | LMNA  | ####      |
| KLLEGEER             | 0  | P02545 | LMNA_HUI | 378 | LMNA  | ####      |
| KTLD SVAK            | 0  | P02545 | LMNA_HUI | 90  | LMNA  | ####      |
| KTLD SVAK            | 0  | P02545 | LMNA_HUI | 90  | LMNA  | ####      |
| KTLD SVAK            | 0  | P02545 | LMNA_HUI | 90  | LMNA  | ####      |
| LEAALGEAKK           | 8  | P02545 | LMNA_HUI | 180 | LMNA  | ####      |
| LEAALGEAKK           | 8  | P02545 | LMNA_HUI | 180 | LMNA  | ####      |
| LQEKEDLQELNDR        | 3  | P02545 | LMNA_HUI | 32  | LMNA  | ####      |
| LQLELSKVR            | 6  | P02545 | LMNA_HUI | 108 | LMNA  | ####      |
| LQTMKEELDFQK         | 4  | P02545 | LMNA_HUI | 201 | LMNA  | ####      |
| LVEIDNGKQR           | 7  | P02545 | LMNA_HUI | 233 | LMNA  | ####      |
| TLDSVAKER            | 6  | P02545 | LMNA_HUI | 97  | LMNA  | ####      |
| TYSAKLDNAR           | 4  | P02545 | LMNA_HUI | 270 | LMNA  | ####      |
| TYSAKLDNAR           | 4  | P02545 | LMNA_HUI | 270 | LMNA  | ####      |
| AKLQIELGK            | 1  | P20700 | LMNB1_HL | 102 | LMNB1 | ####      |
| LKLSPSPSSR           | 1  | P20700 | LMNB1_HL | 389 | LMNB1 | ####      |
| LQEKEELR             | 3  | P20700 | LMNB1_HL | 33  | LMNB1 | ####      |
| AATVTGKLVHANFGTK     | 6  | P02786 | TFR1_HUM | 231 | TFRC  | 3S9L      |
| ADIKEMGLSLQWLYSAR    | 3  | P02786 | TFR1_HUM | 633 | TFRC  | 3S9L      |
| AGKITFAEK            | 2  | P02786 | TFR1_HUM | 261 | TFRC  | 3S9L      |
| AGKITFAEK            | 2  | P02786 | TFR1_HUM | 261 | TFRC  | 3S9L      |
| AGKITFAEK            | 2  | P02786 | TFR1_HUM | 261 | TFRC  | 3S9L      |
| AGKITFAEK            | 2  | P02786 | TFR1_HUM | 261 | TFRC  | 3S9L      |
| AGKITFAEK            | 2  | P02786 | TFR1_HUM | 261 | TFRC  | 3S9L      |
| AGKITFAEK            | 2  | P02786 | TFR1_HUM | 261 | TFRC  | 3S9L      |
| AGKITFAEK            | 2  | P02786 | TFR1_HUM | 261 | TFRC  | 3S9L      |
| DQH FVKIQVK          | 5  | P02786 | TFR1_HUM | 189 | TFRC  | 3S9L      |
| DQH FVKIQVK          | 5  | P02786 | TFR1_HUM | 189 | TFRC  | 3S9L      |
| DSAQNSVIIVDKNGR      | 11 | P02786 | TFR1_HUM | 205 | TFRC  | 3S9L      |

|                      |    |        |          |     |       |      |
|----------------------|----|--------|----------|-----|-------|------|
| EAGSQKDENLALYVENQFR  | 5  | P02786 | TFR1_HUM | 161 | TFRC  | 3S9L |
| EFKLSK               | 2  | P02786 | TFR1_HUM | 177 | TFRC  | 3S9L |
| EFKLSK               | 2  | P02786 | TFR1_HUM | 177 | TFRC  | 3S9L |
| EFKLSK               | 2  | P02786 | TFR1_HUM | 177 | TFRC  | 3S9L |
| EFKLSK               | 2  | P02786 | TFR1_HUM | 177 | TFRC  | 3S9L |
| EFKLSK               | 2  | P02786 | TFR1_HUM | 177 | TFRC  | 3S9L |
| EFKLSK               | 2  | P02786 | TFR1_HUM | 177 | TFRC  | 3S9L |
| EFKLSK               | 2  | P02786 | TFR1_HUM | 177 | TFRC  | 3S9L |
| EFKLSK               | 2  | P02786 | TFR1_HUM | 177 | TFRC  | 3S9L |
| FVMKK                | 3  | P02786 | TFR1_HUM | 672 | TFRC  | 3S9L |
| IPELNKVAR            | 5  | P02786 | TFR1_HUM | 585 | TFRC  | 3S9L |
| IPELNKVAR            | 5  | P02786 | TFR1_HUM | 585 | TFRC  | 3S9L |
| IPELNKVAR            | 5  | P02786 | TFR1_HUM | 585 | TFRC  | 3S9L |
| IPELNKVAR            | 5  | P02786 | TFR1_HUM | 585 | TFRC  | 3S9L |
| IPELNKVAR            | 5  | P02786 | TFR1_HUM | 585 | TFRC  | 3S9L |
| IQVKDSAQNSVIIVDK     | 3  | P02786 | TFR1_HUM | 193 | TFRC  | 3S9L |
| IQVKDSAQNSVIIVDK     | 3  | P02786 | TFR1_HUM | 193 | TFRC  | 3S9L |
| KLNDR                | 0  | P02786 | TFR1_HUM | 673 | TFRC  | 3S9L |
| KLNDR                | 0  | P02786 | TFR1_HUM | 673 | TFRC  | 3S9L |
| KLNDR                | 0  | P02786 | TFR1_HUM | 673 | TFRC  | 3S9L |
| KLNDR                | 0  | P02786 | TFR1_HUM | 673 | TFRC  | 3S9L |
| KLSEK                | 0  | P02786 | TFR1_HUM | 130 | TFRC  | 3S9L |
| KLSEK                | 0  | P02786 | TFR1_HUM | 130 | TFRC  | 3S9L |
| KLSEK                | 0  | P02786 | TFR1_HUM | 130 | TFRC  | 3S9L |
| LAQMFSDMVLKDGFPQR    | 10 | P02786 | TFR1_HUM | 439 | TFRC  | 3S9L |
| LDSTDFGTIKLLNENSYPVR | 10 | P02786 | TFR1_HUM | 145 | TFRC  | 3S9L |
| LFGNMEGDCPSDWKTDSTCR | 13 | P02786 | TFR1_HUM | 358 | TFRC  | 3S9L |
| LTDFGNAEKTDR         | 9  | P02786 | TFR1_HUM | 665 | TFRC  | 3S9L |
| LTDFGNAEKTDR         | 9  | P02786 | TFR1_HUM | 665 | TFRC  | 3S9L |
| LTDFGNAEKTDR         | 9  | P02786 | TFR1_HUM | 665 | TFRC  | 3S9L |
| LVHANFGTKK           | 8  | P02786 | TFR1_HUM | 240 | TFRC  | 3S9L |
| LVHANFGTKK           | 8  | P02786 | TFR1_HUM | 240 | TFRC  | 3S9L |
| LYWDDLKR             | 6  | P02786 | TFR1_HUM | 128 | TFRC  | 3S9L |
| LYWDDLKR             | 6  | P02786 | TFR1_HUM | 128 | TFRC  | 3S9L |
| LYWDDLKR             | 6  | P02786 | TFR1_HUM | 128 | TFRC  | 3S9L |
| LYWDDLKR             | 6  | P02786 | TFR1_HUM | 128 | TFRC  | 3S9L |
| MVTSESKNVK           | 6  | P02786 | TFR1_HUM | 371 | TFRC  | 3S9L |
| M[147.04]VTSESKNVK   | 6  | P02786 | TFR1_HUM | 371 | TFRC  | 3S9L |
| NVKLTVSNVLK          | 2  | P02786 | TFR1_HUM | 374 | TFRC  | 3S9L |
| NVKLTVSNVLK          | 2  | P02786 | TFR1_HUM | 374 | TFRC  | 3S9L |
| NVKLTVSNVLK          | 2  | P02786 | TFR1_HUM | 374 | TFRC  | 3S9L |
| NVKLTVSNVLK          | 2  | P02786 | TFR1_HUM | 374 | TFRC  | 3S9L |
| RLYWDDLKR            | 7  | P02786 | TFR1_HUM | 128 | TFRC  | 3S9L |
| VEYHFLSPYVSPKESPR    | 12 | P02786 | TFR1_HUM | 693 | TFRC  | 3S9L |
| VEYHFLSPYVSPKESPR    | 12 | P02786 | TFR1_HUM | 693 | TFRC  | 3S9L |
| IPELNKVAR            | 5  | P02786 | TFR1_HUM | 585 | TFRC  | 3S9L |
| KIDDR                | 0  | Q02880 | TOP2B_HU | 678 | TOP2B | 3QX3 |

|                      |           |          |              |        |
|----------------------|-----------|----------|--------------|--------|
| KIDDR                | 0 Q02880  | TOP2B_HU | 678 TOP2B    | 3QX3   |
| DAQIFIQKK            | 7 P04040  | CATA_HUN | 476 CAT      | P04040 |
| DPASDQMQRHWKEQR      | 10 P04040 | CATA_HUN | 16 CAT       | P04040 |
| ALQASALKAWGGK        | 7 P04075  | ALDOA_HU | 312 ALDOA    | P04075 |
| AWGGKK               | 4 P04075  | ALDOA_HU | 317 ALDOA    | P04075 |
| GILAADESTGSIKR       | 13 P04075 | ALDOA_HU | 42 ALDOA     | P04075 |
| KDGADFAK             | 0 P04075  | ALDOA_HU | 140 ALDOA    | P04075 |
| GILAADESTGSIKR       | 13 P04075 | ALDOA_HU | 42 ALDOA     | P04075 |
| DLAKDITSDTSGDFR      | 3 P04083  | ANXA1_HU | 166 ANXA1    | 1AIN   |
| KALTGHLEEVVLALLK     | 0 P04083  | ANXA1_HU | 98 ANXA1     | 1AIN   |
| NALLSLAKGDR          | 7 P04083  | ANXA1_HU | 185 ANXA1    | 1AIN   |
| NALLSLAKGDR          | 7 P04083  | ANXA1_HU | 185 ANXA1    | 1AIN   |
| GELLEAIKR            | 7 P04179  | SODM_HU  | 122 SOD2     | 5T30   |
| AGAHLQGGAKR          | 9 P04406  | G3P_HUM  | 117 GAPDH    | 1U8F   |
| AVGKVIPELNGK         | 3 P04406  | G3P_HUM  | 219 GAPDH    | 1U8F   |
| DPSKIK               | 3 P04406  | G3P_HUM  | 84 GAPDH     | 1U8F   |
| DPSKIK               | 3 P04406  | G3P_HUM  | 84 GAPDH     | 1U8F   |
| DPSKIK               | 3 P04406  | G3P_HUM  | 84 GAPDH     | 1U8F   |
| DPSKIK               | 3 P04406  | G3P_HUM  | 84 GAPDH     | 1U8F   |
| GALQNIIPASTGAAKAVGK  | 14 P04406 | G3P_HUM  | 215 GAPDH    | 1U8F   |
| LEKPAK               | 2 P04406  | G3P_HUM  | 251 GAPDH    | 1U8F   |
| TVDGPGSKLWR          | 7 P04406  | G3P_HUM  | 194 GAPDH    | 1U8F   |
| TVDGPGSKLWR          | 7 P04406  | G3P_HUM  | 194 GAPDH    | 1U8F   |
| TVDGPGSKLWR          | 7 P04406  | G3P_HUM  | 194 GAPDH    | 1U8F   |
| TVDGPGSKLWR          | 7 P04406  | G3P_HUM  | 194 GAPDH    | 1U8F   |
| TVDGPGSKLWR          | 7 P04406  | G3P_HUM  | 194 GAPDH    | 1U8F   |
| TVDGPGSKLWR          | 7 P04406  | G3P_HUM  | 194 GAPDH    | 1U8F   |
| VVDLMAHMASKE         | 10 P04406 | G3P_HUM  | 334 GAPDH    | 1U8F   |
| VVKQASEGPLK          | 2 P04406  | G3P_HUM  | 263 GAPDH    | 1U8F   |
| VVKQASEGPLK          | 2 P04406  | G3P_HUM  | 263 GAPDH    | 1U8F   |
| YDDIKK               | 4 P04406  | G3P_HUM  | 259 GAPDH    | 1U8F   |
| YDDIKK               | 4 P04406  | G3P_HUM  | 259 GAPDH    | 1U8F   |
| YDDIKK               | 4 P04406  | G3P_HUM  | 259 GAPDH    | 1U8F   |
| YDDIKK               | 4 P04406  | G3P_HUM  | 259 GAPDH    | 1U8F   |
| VVDLMAHM[147.04]ASKE | 10 P04406 | G3P_HUM  | 334 GAPDH    | 1U8F   |
| ELVLKSAVEAER         | 4 P04843  | RPN1_HUN | 564 RPN1     | P04843 |
| LISGKR               | 4 P04843  | RPN1_HUN | 592 RPN1     | P04843 |
| LISGKR               | 4 P04843  | RPN1_HUN | 592 RPN1     | P04843 |
| LKTEGSDLCDR          | 1 P04843  | RPN1_HUN | 538 RPN1     | P04843 |
| LKTEGSDLCDR          | 1 P04843  | RPN1_HUN | 538 RPN1     | P04843 |
| LVAGKLK              | 4 P04843  | RPN1_HUN | 576 RPN1     | P04843 |
| LVAGKLK              | 4 P04843  | RPN1_HUN | 576 RPN1     | P04843 |
| NVESYTKLGNPTR        | 6 P04843  | RPN1_HUN | 187 RPN1     | ####   |
| VSEMQKLDAQVK         | 5 P04843  | RPN1_HUN | 553 RPN1     | P04843 |
| GKQGGK               | 1 P04908  | H2A1B_HU | 6 HIST1H2AB  | ####   |
| NDEELNKLGR           | 6 P04908  | H2A1B_HU | 96 HIST1H2AB | 5B0Z   |
| KGNYSER              | 0 P04908  | H2A1B_HU | 37 HIST1H2AB | 5B0Z   |



|                         |           |          |                      |
|-------------------------|-----------|----------|----------------------|
| KGNYSER                 | 0 P04908  | H2A1B_HU | 37 HIST1H2AB5B0Z     |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| GKQGGK                  | 1 P04908  | H2A1B_HU | 6 HIST1H2AB P04908   |
| GKQGGK                  | 1 P04908  | H2A1B_HU | 6 HIST1H2AB P04908   |
| YQKSTELLIR              | 2 P68431  | H31_HUM/ | 57 HIST1H3A 5AV9     |
| DNKKTR                  | 2 P04908  | H2A1B_HU | 75 HIST1H2AB5B0Z     |
| KTESHHK                 | 0 P04908  | H2A1B_HU | 120 HIST1H2AB P04908 |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| QGGKAR                  | 3 P04908  | H2A1B_HU | 10 HIST1H2AB P04908  |
| VTIMPKDIQLAR            | 5 Q16695  | H31T_HUN | 123 HIST3H3 3A6N     |
| KGNYSER                 | 0 P04908  | H2A1B_HU | 37 HIST1H2AB5B0Z     |
| KGNYSER                 | 0 P04908  | H2A1B_HU | 37 HIST1H2AB5B0Z     |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| GKQGGK                  | 1 P04908  | H2A1B_HU | 6 HIST1H2AB P04908   |
| NDEELNKLLGK             | 6 Q96KK5  | H2A1H_HU | 96 HIST1H2AH Q96KK5  |
| NDEELNKLLGR             | 6 P04908  | H2A1B_HU | 96 HIST1H2AB5B0Z     |
| SLAGQSGQGKPR            | 9 P04920  | B3A2_HUN | 893 SLC4A2 #####     |
| AVFQANQENLPILKR         | 13 P05023 | AT1A1_HU | 444 ATP1A1 P05023    |
| IVEIPFNSTNKYQLSIHK      | 10 P05023 | AT1A1_HU | 487 ATP1A1 P05023    |
| VIMVTGDHPITAKAIK        | 12 P05023 | AT1A1_HU | 625 ATP1A1 P05023    |
| IVEIPFNSTNKYQLSIHK      | 10 P05023 | AT1A1_HU | 487 ATP1A1 P05023    |
| YKDSAQR                 | 1 P05026  | AT1B1_HU | 113 ATP1B1 P05026    |
| YNPNVLPVQCTGKR          | 12 P05026 | AT1B1_HU | 216 ATP1B1 P05026    |
| YNPNVLPVQCTGKR          | 12 P05026 | AT1B1_HU | 216 ATP1B1 P05026    |
| YNPNVLPVQCTGKR          | 12 P05026 | AT1B1_HU | 216 ATP1B1 P05026    |
| AAYFGIYDTAKGMLPDPK      | 10 P05141 | ADT2_HUN | 199 SLC25A5 P05141   |
| AFFKGAWSNVLR            | 3 P05141  | ADT2_HUN | 272 SLC25A5 P05141   |
| DEGGKAFFK               | 4 P05141  | ADT2_HUN | 268 SLC25A5 P05141   |
| GLGDCLVKIYK             | 7 P05141  | ADT2_HUN | 163 SLC25A5 P05141   |
| IYKSDGIK                | 2 P05141  | ADT2_HUN | 166 SLC25A5 P05141   |
| IYKSDGIK                | 2 P05141  | ADT2_HUN | 166 SLC25A5 P05141   |
| IYKSDGIK                | 2 P05141  | ADT2_HUN | 166 SLC25A5 P05141   |
| KGTDIM[147.04]YGTGLDCWR | 0 P05141  | ADT2_HUN | 245 SLC25A5 P05141   |
| LAADVKGAGAER            | 6 P05141  | ADT2_HUN | 147 SLC25A5 P05141   |
| LAADVKGAGAER            | 6 P05141  | ADT2_HUN | 147 SLC25A5 P05141   |
| LAADVKGAGAER            | 6 P05141  | ADT2_HUN | 147 SLC25A5 P05141   |
| LAADVKGAGAER            | 6 P05141  | ADT2_HUN | 147 SLC25A5 P05141   |
| LAADVKGAGAER            | 6 P05141  | ADT2_HUN | 147 SLC25A5 P05141   |
| LAADVKGAGAER            | 6 P05141  | ADT2_HUN | 147 SLC25A5 P05141   |
| LAADVKGAGAER            | 6 P05141  | ADT2_HUN | 147 SLC25A5 P05141   |
| QIFLGGVDKR              | 8 P05141  | ADT2_HUN | 105 SLC25A5 P05141   |

|                      |           |           |             |           |
|----------------------|-----------|-----------|-------------|-----------|
| QIFLGGVDKR           | 8 P05141  | ADT2_HUM  | 105 SLC25A5 | P05141    |
| YFPTQALNFAFKDK       | 11 P05141 | ADT2_HUM  | 92 SLC25A5  | P05141    |
| YFPTQALNFAFKDKYK     | 13 P05141 | ADT2_HUM  | 94 SLC25A5  | P05141    |
| YKQIFLGGVDK          | 1 P05141  | ADT2_HUM  | 96 SLC25A5  | P05141    |
| YKQIFLGGVDK          | 1 P05141  | ADT2_HUM  | 96 SLC25A5  | P05141    |
| YKQIFLGGVDKR         | 1 P05141  | ADT2_HUM  | 96 SLC25A5  | P05141    |
| LAADVKGAGAER         | 6 P05141  | ADT2_HUM  | 147 SLC25A5 | P05141    |
| GSSIFGLAPGKAR        | 10 P05187 | PPB1_HUM  | 403 ALPP    | 1EW2      |
| GSSIFGLAPGKAR        | 10 P05187 | PPB1_HUM  | 403 ALPP    | 1EW2      |
| KYMFR                | 0 P05187  | PPB1_HUM  | 227 ALPP    | 1EW2      |
| LTPQAVKIR            | 6 P05198  | IF2A_HUM. | 190 EIF2S1  | P05198    |
| LTPQAVKIR            | 6 P05198  | IF2A_HUM. | 190 EIF2S1  | P05198    |
| LTPQAVKIR            | 6 P05198  | IF2A_HUM. | 190 EIF2S1  | P05198    |
| KELLLPGNNR           | 0 P05362  | ICAM1_HU  | 67 ICAM1    | 1MQ8      |
| KVTNVNLSR            | 0 P05362  | ICAM1_HU  | 469 ICAM1   | ####      |
| KVTNVNLSR            | 0 P05362  | ICAM1_HU  | 469 ICAM1   | ####      |
| KILDSVGIEADDDRLNK    | 0 P05387  | RLA2_HUM  | 25 RPLP2    | 4BEH      |
| DMLLANKVPAAAR        | 6 P05388  | RLA0_HUM  | 106 RPLP0   | P05388    |
| GKAVVLMGK            | 1 P05388  | RLA0_HUM  | 50 RPLP0    | P05388    |
| GNVGFVFTKEDLTEIR     | 8 P05388  | RLA0_HUM  | 92 RPLP0    | P05388    |
| NVLSLTNKGEVFNELVGK   | 7 P05556  | ITB1_HUM. | 228 ITGB1   | 4WK0      |
| SKGTAEK              | 1 P05556  | ITB1_HUM. | 100 ITGB1   | P05556    |
| SKGTAEK              | 1 P05556  | ITB1_HUM. | 100 ITGB1   | P05556    |
| DYAKDDPLEFK          | 3 P06756  | ITAV_HUM  | 112 ITGAV   | 3IJE      |
| VVFNLNTYKTK          | 8 P17301  | ITA2_HUM  | 230 ITGA2   | 1V7P      |
| EHLEKK               | 4 P05783  | K1C18_HU  | 118 KRT18   | P05783    |
| EHLEKK               | 4 P05783  | K1C18_HU  | 118 KRT18   | P05783    |
| EHLEKK               | 4 P05783  | K1C18_HU  | 118 KRT18   | P05783    |
| KGPQVR               | 0 P05783  | K1C18_HU  | 119 KRT18   | ####      |
| KGPQVR               | 0 P05783  | K1C18_HU  | 119 KRT18   | ####      |
| KGPQVR               | 0 P05783  | K1C18_HU  | 119 KRT18   | ####      |
| KNHEEEVK             | 0 P05783  | K1C18_HU  | 215 KRT18   | ####      |
| KNHEEEVK             | 0 P05783  | K1C18_HU  | 215 KRT18   | ####      |
| KNHEEEVK             | 0 P05783  | K1C18_HU  | 215 KRT18   | ####      |
| KNHEEEVK             | 0 P05783  | K1C18_HU  | 215 KRT18   | ####      |
| KVIDDTNITR           | 0 P05783  | K1C18_HU  | 187 KRT18   | ####      |
| KVIDDTNITR           | 0 P05783  | K1C18_HU  | 187 KRT18   | ####      |
| KVIDDTNITR           | 0 P05783  | K1C18_HU  | 187 KRT18   | ####      |
| KVIDDTNITR           | 0 P05783  | K1C18_HU  | 187 KRT18   | ####      |
| LESKIR               | 3 P05783  | K1C18_HU  | 111 KRT18   | P05783    |
| LESKIR               | 3 P05783  | K1C18_HU  | 111 KRT18   | P05783_PC |
| LESKIR               | 3 P05783  | K1C18_HU  | 111 KRT18   | P05783    |
| NLKASLENSLR          | 2 P05783  | K1C18_HU  | 317 KRT18   | ####      |
| NLKASLENSLR          | 2 P05783  | K1C18_HU  | 317 KRT18   | ####      |
| NLKASLENSLR          | 2 P05783  | K1C18_HU  | 317 KRT18   | ####      |
| SQDLAKIM[147.04]ADIR | 5 P05783  | K1C18_HU  | 247 KRT18   | ####      |
| VKLEAEIATYR          | 1 P05783  | K1C18_HU  | 372 KRT18   | ####      |

|                       |          |           |           |        |
|-----------------------|----------|-----------|-----------|--------|
| VVSETNDTKVLR          | 8 P05783 | K1C18_HUI | 426 KRT18 | ####   |
| AVVVVK                | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVVK                | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| EHLEKK                | 4 P05783 | K1C18_HUI | 118 KRT18 | P05783 |
| GELAIKDANAK           | 5 P05787 | K2C8_HUM  | 347 KRT8  | P05787 |
| KDVDEAYMKN            | 0 P05787 | K2C8_HUM  | 198 KRT8  | P05787 |
| KGPQVR                | 0 P05783 | K1C18_HUI | 119 KRT18 | ####   |
| KGPQVR                | 0 P05783 | K1C18_HUI | 119 KRT18 | ####   |
| KGPQVR                | 0 P05783 | K1C18_HUI | 119 KRT18 | ####   |
| KGPQVR                | 0 P05783 | K1C18_HUI | 119 KRT18 | ####   |
| KGPQVR                | 0 P05783 | K1C18_HUI | 119 KRT18 | ####   |
| KLLEGEESR             | 0 P05787 | K2C8_HUM  | 393 KRT8  | P05787 |
| KLLEGEESR             | 0 P05787 | K2C8_HUM  | 393 KRT8  | P05787 |
| KLLEGEESR             | 0 P05787 | K2C8_HUM  | 393 KRT8  | P05787 |
| KLLEGEESR             | 0 P05787 | K2C8_HUM  | 393 KRT8  | P05787 |
| KLLEGEESR             | 0 P05787 | K2C8_HUM  | 393 KRT8  | P05787 |
| KLLEGEESR             | 0 P05787 | K2C8_HUM  | 393 KRT8  | P05787 |
| KNHEEEVK              | 0 P05783 | K1C18_HUI | 215 KRT18 | ####   |
| KNREELDK              | 0 P05783 | K1C18_HUI | 262 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR            | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| LESKIR                | 3 P05783 | K1C18_HUI | 111 KRT18 | P05783 |
| LESKIR                | 3 P05783 | K1C18_HUI | 111 KRT18 | P05783 |
| MLETKWSLLQQQK         | 4 P05787 | K2C8_HUM  | 122 KRT8  | P05787 |
| MLETKWSLLQQQK         | 4 P05787 | K2C8_HUM  | 122 KRT8  | P05787 |
| M[147.04]LETKWSLLQQQK | 4 P05787 | K2C8_HUM  | 122 KRT8  | P05787 |
| NLKASLENSLR           | 2 P05783 | K1C18_HUI | 317 KRT18 | ####   |
| NLKASLENSLR           | 2 P05783 | K1C18_HUI | 317 KRT18 | ####   |
| NLKASLENSLR           | 2 P05783 | K1C18_HUI | 317 KRT18 | ####   |
| NLKASLENSLR           | 2 P05783 | K1C18_HUI | 317 KRT18 | ####   |
| RLESKIR               | 4 P05783 | K1C18_HUI | 111 KRT18 | P05783 |
| RLESKIR               | 4 P05783 | K1C18_HUI | 111 KRT18 | P05783 |
| SQDLAKIMADIR          | 5 P05783 | K1C18_HUI | 247 KRT18 | ####   |
| SQDLAKIMADIR          | 5 P05783 | K1C18_HUI | 247 KRT18 | ####   |
| SYKVSTSGPR            | 2 P05787 | K2C8_HUM  | 11 KRT8   | ####   |
| SYKVSTSGPR            | 2 P05787 | K2C8_HUM  | 11 KRT8   | ####   |
| SYKVSTSGPR            | 2 P05787 | K2C8_HUM  | 11 KRT8   | ####   |
| TKTEISEMNR            | 1 P05787 | K2C8_HUM  | 304 KRT8  | P05787 |
| TLNNKFASFIDK          | 4 P05787 | K2C8_HUM  | 101 KRT8  | P05787 |
| TQEKEQIK              | 3 P05787 | K2C8_HUM  | 92 KRT8   | P05787 |

|                 |          |           |           |        |
|-----------------|----------|-----------|-----------|--------|
| TQEKEQIK        | 3 P05787 | K2C8_HUM  | 92 KRT8   | P05787 |
| VKLEAEIATYR     | 1 P05783 | K1C18_HUI | 372 KRT18 | ####   |
| VTQKSYK         | 3 P05787 | K2C8_HUM  | 8 KRT8    | ####   |
| VTQKSYK         | 3 P05787 | K2C8_HUM  | 8 KRT8    | ####   |
| VVSETNDTKVLR    | 8 P05783 | K1C18_HUI | 426 KRT18 | ####   |
| VVSETNDTKVLR    | 8 P05783 | K1C18_HUI | 426 KRT18 | ####   |
| VVSETNDTKVLR    | 8 P05783 | K1C18_HUI | 426 KRT18 | ####   |
| YEDEINKR        | 6 P05787 | K2C8_HUM  | 185 KRT8  | P05787 |
| FANYIDKVR       | 6 P08670 | VIME_HUM  | 120 VIM   | P08670 |
| KVIDDTNITR      | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR      | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR      | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| NLKASLENSLR     | 2 P05783 | K1C18_HUI | 317 KRT18 | ####   |
| SKFADLSEAANR    | 1 P08670 | VIME_HUM  | 294 VIM   | ####   |
| GELALKDAR       | 5 P08729 | K2C7_HUM  | 348 KRT7  | P08729 |
| IVDGKVVSETNDTK  | 4 P05783 | K1C18_HUI | 417 KRT18 | ####   |
| KGPQVR          | 0 P05783 | K1C18_HUI | 119 KRT18 | ####   |
| KGPQVR          | 0 P05783 | K1C18_HUI | 119 KRT18 | ####   |
| KVIDDTNITR      | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR      | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| KVIDDTNITR      | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| LLETQWTLQEQK    | 4 P08729 | K2C7_HUM  | 122 KRT7  | ####   |
| NLKASLENSLR     | 2 P05783 | K1C18_HUI | 317 KRT18 | ####   |
| NLKASLENSLR     | 2 P05783 | K1C18_HUI | 317 KRT18 | ####   |
| SAKSSR          | 2 P08729 | K2C7_HUM  | 133 KRT7  | ####   |
| KVIDDTNITR      | 0 P05783 | K1C18_HUI | 187 KRT18 | ####   |
| AKQDMAR         | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AKQDMAR         | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AKQDMAR         | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AKQDMAR         | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AKQDM[147.04]AR | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AKQDM[147.04]AR | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AKQDM[147.04]AR | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AKQDM[147.04]AR | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AKQDM[147.04]AR | 1 P05787 | K2C8_HUM  | 364 KRT8  | P05787 |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| AVVVKK          | 4 P05787 | K2C8_HUM  | 464 KRT8  | ####   |
| DGKLVSSESDVLPK  | 2 P05787 | K2C8_HUM  | 472 KRT8  | ####   |
| DGKLVSSESDVLPK  | 2 P05787 | K2C8_HUM  | 472 KRT8  | ####   |
| EQIKTLNNK       | 3 P05787 | K2C8_HUM  | 96 KRT8   | P05787 |

|                    |          |          |          |           |
|--------------------|----------|----------|----------|-----------|
| FASFIDKVR          | 6 P05787 | K2C8_HUM | 108 KRT8 | P05787    |
| FASFIDKVR          | 6 P05787 | K2C8_HUM | 108 KRT8 | P05787    |
| FASFIDKVR          | 6 P05787 | K2C8_HUM | 108 KRT8 | P05787    |
| FASFIDKVR          | 6 P05787 | K2C8_HUM | 108 KRT8 | P05787    |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8 | P05787_PC |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8 | P05787    |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8 | P05787    |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8 | P05787    |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8 | P05787    |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8 | P05787    |
| KLETR              | 0 P05787 | K2C8_HUM | 465 KRT8 | ####      |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787_PC |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| KLLEGEESR          | 0 P05787 | K2C8_HUM | 393 KRT8 | P05787    |
| LQAEIEGLKGQR       | 8 P05787 | K2C8_HUM | 325 KRT8 | P05787    |
| LQAEIEGLKGQR       | 8 P05787 | K2C8_HUM | 325 KRT8 | P05787    |
| LQAEIEGLKGQR       | 8 P05787 | K2C8_HUM | 325 KRT8 | P05787_PC |
| LQAEIEGLKGQR       | 8 P05787 | K2C8_HUM | 325 KRT8 | P05787    |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8  | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8  | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8  | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8  | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8  | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8  | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8  | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8  | ####      |
| TKTEISEMNR         | 1 P05787 | K2C8_HUM | 304 KRT8 | P05787    |
| TKTEISEMNR         | 1 P05787 | K2C8_HUM | 304 KRT8 | P05787    |
| TKTEISEMNR         | 1 P05787 | K2C8_HUM | 304 KRT8 | P05787    |
| TKTEISEMNR         | 1 P05787 | K2C8_HUM | 304 KRT8 | P05787    |
| TKTEISEMNR         | 1 P05787 | K2C8_HUM | 304 KRT8 | P05787    |
| TKTEISEM[147.04]NR | 1 P05787 | K2C8_HUM | 304 KRT8 | P05787    |
| TKTEISEM[147.04]NR | 1 P05787 | K2C8_HUM | 304 KRT8 | P05787    |

|                    |          |          |           |           |
|--------------------|----------|----------|-----------|-----------|
| TKTEISEM[147.04]NR | 1 P05787 | K2C8_HUM | 304 KRT8  | P05787    |
| TKTEISEM[147.04]NR | 1 P05787 | K2C8_HUM | 304 KRT8  | P05787    |
| TLNNKFASFIDK       | 4 P05787 | K2C8_HUM | 101 KRT8  | P05787    |
| TQEKEQIK           | 3 P05787 | K2C8_HUM | 92 KRT8   | P05787    |
| TQEKEQIK           | 3 P05787 | K2C8_HUM | 92 KRT8   | P05787    |
| TQEKEQIK           | 3 P05787 | K2C8_HUM | 92 KRT8   | P05787    |
| TQEKEQIK           | 3 P05787 | K2C8_HUM | 92 KRT8   | P05787    |
| TQEKEQIK           | 3 P05787 | K2C8_HUM | 92 KRT8   | P05787    |
| VTQKSYK            | 3 P05787 | K2C8_HUM | 8 KRT8    | ####      |
| VTQKSYK            | 3 P05787 | K2C8_HUM | 8 KRT8    | ####      |
| VTQKSYK            | 3 P05787 | K2C8_HUM | 8 KRT8    | ####      |
| VTQKSYK            | 3 P05787 | K2C8_HUM | 8 KRT8    | ####      |
| VTQKSYK            | 3 P05787 | K2C8_HUM | 8 KRT8    | ####      |
| VTQKSYK            | 3 P05787 | K2C8_HUM | 8 KRT8    | ####      |
| WSLLQQQKTAR        | 7 P05787 | K2C8_HUM | 130 KRT8  | P05787    |
| WSLLQQQKTAR        | 7 P05787 | K2C8_HUM | 130 KRT8  | P05787    |
| WSLLQQQKTAR        | 7 P05787 | K2C8_HUM | 130 KRT8  | P05787_PC |
| EKLQEMLQR          | 1 P08670 | VIME_HUM | 188 VIM   | 3UF1      |
| FANYIDKVR          | 6 P08670 | VIME_HUM | 120 VIM   | P08670    |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8  | P05787    |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8  | P05787    |
| KVESLQEEIAFLK      | 0 P08670 | VIME_HUM | 223 VIM   | 3UF1      |
| LQAEIEGLKGQR       | 8 P05787 | K2C8_HUM | 325 KRT8  | P05787    |
| QAKQESTEYR         | 2 P08670 | VIME_HUM | 313 VIM   | ####      |
| SKFADLSEAANR       | 1 P08670 | VIME_HUM | 294 VIM   | ####      |
| SKFADLSEAANR       | 1 P08670 | VIME_HUM | 294 VIM   | ####      |
| SKFADLSEAANR       | 1 P08670 | VIME_HUM | 294 VIM   | ####      |
| SKFADLSEAANR       | 1 P08670 | VIME_HUM | 294 VIM   | ####      |
| SKFADLSEAANR       | 1 P08670 | VIME_HUM | 294 VIM   | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8   | ####      |
| TLLIKTVETR         | 4 P08670 | VIME_HUM | 445 VIM   | ####      |
| TLLIKTVETR         | 4 P08670 | VIME_HUM | 445 VIM   | ####      |
| TLNNKFASFIDK       | 4 P05787 | K2C8_HUM | 101 KRT8  | P05787    |
| TLNNKFASFIDK       | 4 P05787 | K2C8_HUM | 101 KRT8  | P05787    |
| AKLEAAIAEAER       | 1 P08729 | K2C7_HUM | 331 KRT7  | P08729    |
| AKQDMAR            | 1 P05787 | K2C8_HUM | 364 KRT8  | P05787    |
| AKQDM[147.04]AR    | 1 P05787 | K2C8_HUM | 364 KRT8  | P05787    |
| DGKLVSSESDVLPK     | 2 P05787 | K2C8_HUM | 472 KRT8  | ####      |
| GELAIKDANAK        | 5 P05787 | K2C8_HUM | 347 KRT8  | P05787    |
| GELALKDAR          | 5 P08729 | K2C7_HUM | 348 KRT7  | P08729    |
| GELALKDAR          | 5 P08729 | K2C7_HUM | 348 KRT7  | P08729    |
| LQAEIEGLKGQR       | 8 P05787 | K2C8_HUM | 325 KRT8  | P05787    |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8   | ####      |
| SYKVSTSGPR         | 2 P05787 | K2C8_HUM | 11 KRT8   | ####      |
| TQEKEQIK           | 3 P05787 | K2C8_HUM | 92 KRT8   | P05787    |
| KLTGSTDQHDHR       | 0 Q6ZNG1 | ZN600_HU | 65 ZNF600 | ####      |
| KLLEGESR           | 0 P05787 | K2C8_HUM | 393 KRT8  | P05787    |

|                            |    |        |           |     |        |        |
|----------------------------|----|--------|-----------|-----|--------|--------|
| TSFDKILLR                  | 4  | P06213 | INSR_HUM  | 511 | INSR   | 4ZXB   |
| GPIKTK                     | 3  | P06576 | ATPB_HUM  | 159 | ATP5B  | P06576 |
| LVPLKETIK                  | 4  | P06576 | ATPB_HUM  | 485 | ATP5B  | P06576 |
| ITTTKK                     | 4  | P06576 | ATPB_HUM  | 350 | ATP5B  | P06576 |
| VYKEVK                     | 2  | P24539 | AT5F1_HUI | 191 | ATP5F1 | P24539 |
| ADKLAEEHSS                 | 2  | P06576 | ATPB_HUM  | 522 | ATP5B  | P06576 |
| AMKQVAGTMK                 | 2  | P25705 | ATPA_HUM  | 427 | ATP5A1 | P25705 |
| AMKQVAGTM[147.04]K         | 2  | P25705 | ATPA_HUM  | 427 | ATP5A1 | P25705 |
| AM[147.04]KQVAGTMK         | 2  | P25705 | ATPA_HUM  | 427 | ATP5A1 | P25705 |
| AM[147.04]KQVAGTM[147.04]K | 2  | P25705 | ATPA_HUM  | 427 | ATP5A1 | P25705 |
| ITTTKK                     | 4  | P06576 | ATPB_HUM  | 350 | ATP5B  | P06576 |
| ITTTKK                     | 4  | P06576 | ATPB_HUM  | 350 | ATP5B  | P06576 |
| GQKVLDSGAPIK               | 2  | P06576 | ATPB_HUM  | 124 | ATP5B  | P06576 |
| GQKVLDSGAPIK               | 2  | P06576 | ATPB_HUM  | 124 | ATP5B  | P06576 |
| IGEKYVDMSVK                | 3  | P48047 | ATPO_HUM  | 192 | ATP5O  | P48047 |
| EGDKHTLSK                  | 3  | P06703 | S10A6_HUI | 26  | S100A6 | 1K8U   |
| AVNEKSCNCLLK               | 4  | P06733 | ENOA_HUM  | 335 | ENO1   | 2PSN   |
| AVNEKSCNCLLK               | 4  | P06733 | ENOA_HUM  | 335 | ENO1   | 2PSN   |
| DNDKTR                     | 3  | P06733 | ENOA_HUM  | 54  | ENO1   | 2PSN   |
| DNDKTR                     | 3  | P06733 | ENOA_HUM  | 54  | ENO1   | 2PSN   |
| DNDKTR                     | 3  | P06733 | ENOA_HUM  | 54  | ENO1   | 2PSN   |
| EGLELLKTAIGK               | 6  | P06733 | ENOA_HUM  | 228 | ENO1   | 2PSN   |
| IAKAVNEK                   | 2  | P06733 | ENOA_HUM  | 330 | ENO1   | 2PSN   |
| IAKAVNEK                   | 2  | P06733 | ENOA_HUM  | 330 | ENO1   | 2PSN   |
| IAKAVNEK                   | 2  | P06733 | ENOA_HUM  | 330 | ENO1   | 2PSN   |
| IEEELGSKAK                 | 7  | P06733 | ENOA_HUM  | 420 | ENO1   | 2PSN   |
| IEEELGSKAK                 | 7  | P06733 | ENOA_HUM  | 420 | ENO1   | 2PSN   |
| NVIEK                      | 3  | P06733 | ENOA_HUM  | 197 | ENO1   | 2PSN   |
| NVIEK                      | 3  | P06733 | ENOA_HUM  | 197 | ENO1   | 2PSN   |
| NVIEK                      | 3  | P06733 | ENOA_HUM  | 197 | ENO1   | 2PSN   |
| NVIEK                      | 3  | P06733 | ENOA_HUM  | 197 | ENO1   | 2PSN   |
| SGKYDLDFK                  | 2  | P06733 | ENOA_HUM  | 256 | ENO1   | 2PSN   |
| TAIGKAGYTDK                | 4  | P06733 | ENOA_HUM  | 233 | ENO1   | 2PSN   |
| TAIGKAGYTDK                | 4  | P06733 | ENOA_HUM  | 233 | ENO1   | 2PSN   |
| TIAPALVSKK                 | 8  | P06733 | ENOA_HUM  | 80  | ENO1   | 2PSN   |
| TIAPALVSKK                 | 8  | P06733 | ENOA_HUM  | 80  | ENO1   | 2PSN   |
| TIAPALVSKK                 | 8  | P06733 | ENOA_HUM  | 80  | ENO1   | 2PSN   |
| TIAPALVSKK                 | 8  | P06733 | ENOA_HUM  | 80  | ENO1   | 2PSN   |
| TIAPALVSKK                 | 8  | P06733 | ENOA_HUM  | 80  | ENO1   | 2PSN   |
| TIAPALVSKK                 | 8  | P06733 | ENOA_HUM  | 80  | ENO1   | 2PSN   |
| YISPDQLADLYKSFIK           | 11 | P06733 | ENOA_HUM  | 281 | ENO1   | 2PSN   |
| YMGKGVSK                   | 3  | P06733 | ENOA_HUM  | 60  | ENO1   | 2PSN   |
| YM[147.04]GKGVSK           | 3  | P06733 | ENOA_HUM  | 60  | ENO1   | 2PSN   |
| YM[147.04]GKGVSK           | 3  | P06733 | ENOA_HUM  | 60  | ENO1   | 2PSN   |
| TIAPALVSKK                 | 8  | P06733 | ENOA_HUM  | 80  | ENO1   | 2PSN   |
| IKIAPPER                   | 1  | P68032 | ACTC_HUM  | 330 | ACTC1  | P68032 |
| ELQAAGKSPEDLER             | 6  | P06744 | G6PI_HUM  | 454 | GPI    | 1JIQ   |

|                        |           |          |           |        |
|------------------------|-----------|----------|-----------|--------|
| HFVALSTNTTKVK          | 10 P06744 | G6PI_HUM | 252 GPI   | 1JIQ   |
| YITKSGTR               | 3 P06744  | G6PI_HUM | 366 GPI   | 1JIQ   |
| YITKSGTR               | 3 P06744  | G6PI_HUM | 366 GPI   | 1JIQ   |
| AKMQASIEK              | 1 P06748  | NPM_HUM  | 250 NPM1  | ####   |
| AKMQASIEK              | 1 P06748  | NPM_HUM  | 250 NPM1  | ####   |
| AKMQASIEK              | 1 P06748  | NPM_HUM  | 250 NPM1  | ####   |
| AKM[147.04]QASIEK      | 1 P06748  | NPM_HUM  | 250 NPM1  | ####   |
| AKM[147.04]QASIEK      | 1 P06748  | NPM_HUM  | 250 NPM1  | ####   |
| DSKPSSTPR              | 2 P06748  | NPM_HUM  | 215 NPM1  | ####   |
| DTPAKNAQK              | 4 P06748  | NPM_HUM  | 202 NPM1  | ####   |
| FINYVKNCFR             | 5 P06748  | NPM_HUM  | 273 NPM1  | ####   |
| GGSLPKVEAK             | 5 P06748  | NPM_HUM  | 263 NPM1  | ####   |
| GQESFKK                | 5 P06748  | NPM_HUM  | 229 NPM1  | ####   |
| KQEKTPK                | 0 P06748  | NPM_HUM  | 230 NPM1  | ####   |
| KQEKTPK                | 3 P06748  | NPM_HUM  | 233 NPM1  | ####   |
| KQEKTPK                | 3 P06748  | NPM_HUM  | 233 NPM1  | ####   |
| LLSISGKR               | 6 P06748  | NPM_HUM  | 141 NPM1  | ####   |
| LLSISGKR               | 6 P06748  | NPM_HUM  | 141 NPM1  | ####   |
| SKGQESFK               | 1 P06748  | NPM_HUM  | 223 NPM1  | ####   |
| SKGQESFK               | 1 P06748  | NPM_HUM  | 223 NPM1  | ####   |
| SKGQESFK               | 1 P06748  | NPM_HUM  | 223 NPM1  | ####   |
| SKGQESFK               | 1 P06748  | NPM_HUM  | 223 NPM1  | ####   |
| SKGQESFK               | 1 P06748  | NPM_HUM  | 223 NPM1  | ####   |
| SKGQESFK               | 1 P06748  | NPM_HUM  | 223 NPM1  | ####   |
| SKGQESFKK              | 7 P06748  | NPM_HUM  | 229 NPM1  | ####   |
| TPKGPSSVEDIK           | 2 P06748  | NPM_HUM  | 239 NPM1  | ####   |
| TPKGPSSVEDIK           | 2 P06748  | NPM_HUM  | 239 NPM1  | ####   |
| TPKGPSSVEDIK           | 2 P06748  | NPM_HUM  | 239 NPM1  | ####   |
| TVSLGAGAKDELHIVEAEAMNY | 8 P06748  | NPM_HUM  | 54 NPM1   | 5EHD   |
| VEAKFINYVK             | 3 P06748  | NPM_HUM  | 267 NPM1  | ####   |
| VEAKFINYVK             | 3 P06748  | NPM_HUM  | 267 NPM1  | ####   |
| VEAKFINYVK             | 3 P06748  | NPM_HUM  | 267 NPM1  | ####   |
| GMKVIENR               | 2 P06753  | TPM3_HUM | 129 TPM3  | P06753 |
| GMKVIENR               | 2 P06753  | TPM3_HUM | 129 TPM3  | P06753 |
| KYEEVAR                | 0 P06753  | TPM3_HUM | 162 TPM3  | P06753 |
| SVAKLEK                | 3 P06753  | TPM3_HUM | 249 TPM3  | P06753 |
| KYEEVAR                | 0 P06753  | TPM3_HUM | 162 TPM3  | P06753 |
| GM[147.04]KVIENR       | 2 P06753  | TPM3_HUM | 129 TPM3  | P06753 |
| SKQDKILACAPLYHWR       | 4 P06756  | ITAV_HUM | 134 ITGAV | 3IJE   |
| TCSLPGTALKVSCFNVR      | 9 P06756  | ITAV_HUM | 499 ITGAV | 3IJE   |
| YDPNVYSIKYNNQLATR      | 8 P06756  | ITAV_HUM | 233 ITGAV | 3IJE   |
| EAEGKPLCSGR            | 4 P18084  | ITB5_HUM | 519 ITGB5 | P18084 |
| KGFNSVATAR             | 0 P07099  | HYEP_HUM | 197 EPHX1 | P07099 |
| IVADKDYSVTANSK         | 4 P07195  | LDHB_HUM | 82 LDHB   | 1I0Z   |
| IVADKDYSVTANSK         | 4 P07195  | LDHB_HUM | 82 LDHB   | 1I0Z   |
| KSADTLWDIQQ            | 0 P07195  | LDHB_HUM | 319 LDHB  | 1I0Z   |
| KSADTLWDIQQ            | 0 P07195  | LDHB_HUM | 319 LDHB  | 1I0Z   |



|                         |           |           |              |        |
|-------------------------|-----------|-----------|--------------|--------|
| LKDDEVAQLK              | 1 P07195  | LDHB_HUM  | 310 LDHB     | 110Z   |
| GYPTIKFFR               | 5 P07237  | PDIA1_HUI | 103 P4HB     | 4EKZ   |
| GYPTIKFFR               | 5 P07237  | PDIA1_HUI | 103 P4HB     | 4EKZ   |
| GYPTIKFFR               | 5 P07237  | PDIA1_HUI | 103 P4HB     | 4EKZ   |
| KEECPAVR                | 0 P07237  | PDIA1_HUI | 309 P4HB     | 4EKZ   |
| LKAEGSEIR               | 1 P07237  | PDIA1_HUI | 71 P4HB      | 4EKZ   |
| NGDTASPKEYTAGR          | 7 P07237  | PDIA1_HUI | 114 P4HB     | 4EKZ   |
| NGDTASPKEYTAGR          | 7 P07237  | PDIA1_HUI | 114 P4HB     | 4EKZ   |
| DKVLIR                  | 1 P07355  | ANXA2_HU  | 286 ANXA2    | 5LPU   |
| DLYDAGVKR               | 7 P07355  | ANXA2_HU  | 204 ANXA2    | 5LPU   |
| DLYDAGVKR               | 7 P07355  | ANXA2_HU  | 204 ANXA2    | 5LPU   |
| KELASALK                | 0 P07355  | ANXA2_HU  | 81 ANXA2     | 5LPU   |
| KGTDVPK                 | 0 P07355  | ANXA2_HU  | 206 ANXA2    | 5LPU   |
| KGTDVPK                 | 0 P07355  | ANXA2_HU  | 206 ANXA2    | 5LPU   |
| KGTDVPK                 | 0 P07355  | ANXA2_HU  | 206 ANXA2    | 5LPU   |
| KGTDVPK                 | 0 P07355  | ANXA2_HU  | 206 ANXA2    | 5LPU   |
| KLMVALAK                | 0 P07355  | ANXA2_HU  | 169 ANXA2    | 5LPU   |
| KLMVALAK                | 0 P07355  | ANXA2_HU  | 169 ANXA2    | 5LPU   |
| KLM[147.04]VALAK        | 0 P07355  | ANXA2_HU  | 169 ANXA2    | 5LPU   |
| LYDSMKGK                | 5 P07355  | ANXA2_HU  | 279 ANXA2    | 5LPU   |
| SEVDMLKIR               | 6 P07355  | ANXA2_HU  | 302 ANXA2    | 5LPU   |
| SEVDMLKIR               | 6 P07355  | ANXA2_HU  | 302 ANXA2    | 5LPU   |
| SEVDMLKIR               | 6 P07355  | ANXA2_HU  | 302 ANXA2    | 5LPU   |
| SEVDM[147.04]LKIR       | 6 P07355  | ANXA2_HU  | 302 ANXA2    | 5LPU   |
| SVPHLQKVFDK             | 6 P07355  | ANXA2_HU  | 227 ANXA2    | 5LPU   |
| SVPHLQKVFDK             | 6 P07355  | ANXA2_HU  | 227 ANXA2    | 5LPU   |
| VYKEMYK                 | 2 P07355  | ANXA2_HU  | 148 ANXA2    | 5LPU   |
| VYKEM[147.04]YK         | 2 P07355  | ANXA2_HU  | 148 ANXA2    | 5LPU   |
| DTFKR                   | 3 Q9HCH5  | SYTL2_HUM | 725 SYTL2    | ####   |
| KLAVNMVPFPR             | 0 P07437  | TBB5_HUM  | 252 TUBB     | 5N5N   |
| KLAVNMVPFPR             | 0 P07437  | TBB5_HUM  | 252 TUBB     | 5N5N   |
| STGGAPTFNVTVTCTDK       | 13 P07737 | PROF1_HU  | 105 PFN1     | 4X1L   |
| TDKTLVLLMGK             | 2 P07737  | PROF1_HU  | 108 PFN1     | 4X1L   |
| TFVNITPAEVGVLVGKDR      | 15 P07737 | PROF1_HU  | 54 PFN1      | 4X1L   |
| TKSTGGAPTFNVTCTDK       | 1 P07737  | PROF1_HU  | 91 PFN1      | 4X1L   |
| SSFYVNGTLGGQKCSVIR      | 13 P07737 | PROF1_HU  | 70 PFN1      | 4X1L   |
| AYVDDTPAEQMKAER         | 11 P07814 | SYEP_HUM  | 300 EPRS     | P07814 |
| AYVDDTPAEQM[147.04]KAER | 11 P07814 | SYEP_HUM  | 300 EPRS     | P07814 |
| EVAKHPK                 | 3 P07814  | SYEP_HUM  | 532 EPRS     | ####   |
| IWAFNKK                 | 5 P07814  | SYEP_HUM  | 497 EPRS     | P07814 |
| KLKTEK                  | 0 P07814  | SYEP_HUM  | 917 EPRS     | ####   |
| KVIDPVAPR               | 0 P07814  | SYEP_HUM  | 498 EPRS     | P07814 |
| DILEKK                  | 4 P07900  | HS90A_HU  | 581 HSP90AA1 | 3Q6M   |
| DILEKK                  | 4 P07900  | HS90A_HU  | 581 HSP90AA1 | 3Q6M   |
| DILEKK                  | 4 P07900  | HS90A_HU  | 581 HSP90AA1 | 3Q6M   |
| ELISNSSDALDKIR          | 11 P07900 | HS90A_HU  | 58 HSP90AA1  | P07900 |
| FYEQFSKNIK              | 6 P07900  | HS90A_HU  | 443 HSP90AA1 | 3Q6M   |

|                     |    |        |          |     |          |           |
|---------------------|----|--------|----------|-----|----------|-----------|
| FYEQFSKNIK          | 6  | P07900 | HS90A_HU | 443 | HSP90AA1 | 3Q6M      |
| IKELVK              | 1  | P07900 | HS90A_HU | 204 | HSP90AA1 | P07900    |
| IMKAQALR            | 2  | P07900 | HS90A_HU | 615 | HSP90AA1 | 3Q6M      |
| IM[147.04]KAQALR    | 2  | P07900 | HS90A_HU | 615 | HSP90AA1 | 3Q6M      |
| IM[147.04]KAQALR    | 2  | P07900 | HS90A_HU | 615 | HSP90AA1 | 3Q6M      |
| KNNIK               | 0  | P07900 | HS90A_HU | 358 | HSP90AA1 | P07900    |
| TKPIWTR             | 1  | P07900 | HS90A_HU | 294 | HSP90AA1 | P07900    |
| APFDLFENKK          | 8  | P08238 | HS90B_HU | 347 | HSP90AB1 | P08238    |
| DILEKK              | 4  | P07900 | HS90A_HU | 581 | HSP90AA1 | 3Q6M      |
| EILDKK              | 4  | P08238 | HS90B_HU | 573 | HSP90AB1 | P08238    |
| FYEAFSKNLK          | 6  | P08238 | HS90B_HU | 435 | HSP90AB1 | 3PRY      |
| FYEAFSKNLK          | 6  | P08238 | HS90B_HU | 435 | HSP90AB1 | 3PRY      |
| FYEQFSKNIK          | 6  | P07900 | HS90A_HU | 443 | HSP90AA1 | 3Q6M      |
| FYEQFSKNIK          | 6  | P07900 | HS90A_HU | 443 | HSP90AA1 | 3Q6M      |
| FYEQFSKNIK          | 6  | P07900 | HS90A_HU | 443 | HSP90AA1 | 3Q6M      |
| AVVPSKR             | 5  | P07910 | HNRPC_HU | 157 | HNRNPC   | ####      |
| AVVPSKR             | 5  | P07910 | HNRPC_HU | 157 | HNRNPC   | ####      |
| AVVPSKR             | 5  | P07910 | HNRPC_HU | 157 | HNRNPC   | ####      |
| GSSKSGK             | 3  | P07910 | HNRPC_HU | 184 | HNRNPC   | ####      |
| GSSKSGK             | 3  | P07910 | HNRPC_HU | 184 | HNRNPC   | ####      |
| KELTQIK             | 0  | P07910 | HNRPC_HU | 198 | HNRNPC   | P07910_PC |
| KELTQIK             | 0  | P07910 | HNRPC_HU | 198 | HNRNPC   | ####      |
| KELTQIK             | 0  | P07910 | HNRPC_HU | 198 | HNRNPC   | ####      |
| KELTQIK             | 0  | P07910 | HNRPC_HU | 198 | HNRNPC   | ####      |
| KSDVEAIFSK          | 0  | P07910 | HNRPC_HU | 30  | HNRNPC   | 2MZ1      |
| KSDVEAIFSK          | 0  | P07910 | HNRPC_HU | 30  | HNRNPC   | 2MZ1      |
| YGKIVGCSVHK         | 2  | P07910 | HNRPC_HU | 42  | HNRNPC   | ####      |
| YGKIVGCSVHK         | 2  | P07910 | HNRPC_HU | 42  | HNRNPC   | 2MZ1      |
| IKAAMPR             | 1  | P07954 | FUMH_HUI | 263 | FH       | 3.00E+04  |
| IKAAMPR             | 1  | P07954 | FUMH_HUI | 263 | FH       | 3.00E+04  |
| IKAAMPR             | 1  | P07954 | FUMH_HUI | 263 | FH       | 3.00E+04  |
| IKAAM[147.04]PR     | 1  | P07954 | FUMH_HUI | 263 | FH       | 3.00E+04  |
| IKAAM[147.04]PR     | 1  | P07954 | FUMH_HUI | 263 | FH       | 3.00E+04  |
| MPTPVIKAFGILK       | 6  | P07954 | FUMH_HUI | 94  | FH       | 3.00E+04  |
| MPTPVIKAFGILK       | 6  | P07954 | FUMH_HUI | 94  | FH       | 3.00E+04  |
| STMNFKIGGVTER       | 5  | P07954 | FUMH_HUI | 80  | FH       | 3.00E+04  |
| STMNFKIGGVTER       | 5  | P07954 | FUMH_HUI | 80  | FH       | 3.00E+04  |
| ASCESDVLHFTSTTTSKNR | 16 | P08069 | IGF1R_HU | 502 | IGF1R    | ####      |
| QSKGDINTR           | 2  | P08069 | IGF1R_HU | 474 | IGF1R    | 1IGR      |
| QSKGDINTR           | 2  | P08069 | IGF1R_HU | 474 | IGF1R    | 1IGR      |
| VCEEEKK             | 5  | P08069 | IGF1R_HU | 336 | IGF1R    | 1IGR      |
| DLIADLKYELTGK       | 6  | P08133 | ANXA6_HU | 75  | ANXA6    | P08133_PC |
| IPGEKDSVICLK        | 4  | P08174 | DAF_HUM  | 76  | CD55     | 1OK3      |
| KSCPNPGEIR          | 0  | P08174 | DAF_HUM  | 161 | CD55     | 1OK3      |
| TRLAADVGKSGTER      | 8  | P12236 | ADT3_HUN | 147 | SLC25A6  | P12236    |
| EDFDSLLQSAKK        | 10 | P08195 | 4F2_HUM  | 298 | SLC3A2   | 2DH2      |
| EDFDSLLQSAKK        | 10 | P08195 | 4F2_HUM  | 298 | SLC3A2   | 2DH2      |

|                       |           |          |              |           |
|-----------------------|-----------|----------|--------------|-----------|
| GENSWFSTQVDTVATKVK    | 15 P08195 | 4F2_HUMA | 329 SLC3A2   | 2DH2      |
| GENSWFSTQVDTVATKVK    | 15 P08195 | 4F2_HUMA | 329 SLC3A2   | 2DH2      |
| GENSWFSTQVDTVATKVK    | 15 P08195 | 4F2_HUMA | 329 SLC3A2   | 2DH2      |
| GLVLGPIHKNQK          | 8 P08195  | 4F2_HUMA | 266 SLC3A2   | 2DH2      |
| GLVLGPIHKNQK          | 8 P08195  | 4F2_HUMA | 266 SLC3A2   | 2DH2      |
| GLVLGPIHKNQK          | 8 P08195  | 4F2_HUMA | 266 SLC3A2   | 2DH2      |
| IGDLQAFQGHGAGNLAGLKGR | 18 P08195 | 4F2_HUMA | 245 SLC3A2   | P08195_PC |
| LDYLSSLKVK            | 7 P08195  | 4F2_HUMA | 255 SLC3A2   | 2DH2      |
| LDYLSSLKVK            | 7 P08195  | 4F2_HUMA | 255 SLC3A2   | 2DH2      |
| LDYLSSLKVK            | 7 P08195  | 4F2_HUMA | 255 SLC3A2   | 2DH2      |
| VKGLVLGPIHK           | 1 P08195  | 4F2_HUMA | 257 SLC3A2   | 2DH2      |
| VKGLVLGPIHK           | 1 P08195  | 4F2_HUMA | 257 SLC3A2   | 2DH2      |
| AGLQVYNKCWK           | 7 P13987  | CD59_HUN | 63 CD59      | 2J8B      |
| AGLQVYNKCWK           | 7 P13987  | CD59_HUN | 63 CD59      | 2J8B      |
| LKLEPHEGLLLR          | 1 P08195  | 4F2_HUMA | 615 SLC3A2   | 2DH2      |
| KDVLETFTVK            | 0 P21926  | CD9_HUM  | 170 CD9      | P21926    |
| GGVVLKEDALPGQK        | 5 P35613  | BASI_HUM | 179 BSG      | 4U0Q      |
| IIGLKPEGVPR           | 4 P54709  | AT1B3_HU | 182 ATP1B3   | P54709    |
| IIGLKPEGVPR           | 4 P54709  | AT1B3_HU | 182 ATP1B3   | P54709    |
| LKLEPHEGLLLR          | 1 P08195  | 4F2_HUMA | 615 SLC3A2   | 2DH2      |
| NAKFYPVTR             | 2 P54851  | EMP2_HUN | 129 EMP2     | P54851    |
| KSFEQISANITK          | 0 P08237  | PFKAM_HL | 476 PFKM     | 4OMT      |
| APFDLFENKK            | 8 P08238  | HS90B_HU | 347 HSP90AB1 | P08238    |
| APFDLFENKK            | 8 P08238  | HS90B_HU | 347 HSP90AB1 | P08238    |
| EILDKK                | 4 P08238  | HS90B_HU | 573 HSP90AB1 | P08238    |
| ELISNASDALDKIR        | 11 P08238 | HS90B_HU | 53 HSP90AB1  | P08238    |
| ETQKSIYYITGESK        | 3 P08238  | HS90B_HU | 481 HSP90AB1 | 3PRY      |
| FYEAFSKNLK            | 6 P08238  | HS90B_HU | 435 HSP90AB1 | 3PRY      |
| FYEAFSKNLK            | 6 P08238  | HS90B_HU | 435 HSP90AB1 | 3PRY      |
| FYEAFSKNLK            | 6 P08238  | HS90B_HU | 435 HSP90AB1 | 3PRY      |
| FYEAFSKNLK            | 6 P08238  | HS90B_HU | 435 HSP90AB1 | P08238    |
| FYEAFSKNLK            | 6 P08238  | HS90B_HU | 435 HSP90AB1 | P08238    |
| FYEAFSKNLK            | 6 P08238  | HS90B_HU | 435 HSP90AB1 | 3PRY      |
| GTKVILHLK             | 2 P08238  | HS90B_HU | 180 HSP90AB1 | P08238    |
| GTKVILHLK             | 2 P08238  | HS90B_HU | 180 HSP90AB1 | P08238    |
| GTKVILHLK             | 2 P08238  | HS90B_HU | 180 HSP90AB1 | P08238    |
| IMKAQALR              | 2 P08238  | HS90B_HU | 607 HSP90AB1 | P08238    |
| IMKAQALR              | 2 P08238  | HS90B_HU | 607 HSP90AB1 | P08238    |
| IMKAQALR              | 2 P08238  | HS90B_HU | 607 HSP90AB1 | P08238    |
| IM[147.04]KAQALR      | 2 P08238  | HS90B_HU | 607 HSP90AB1 | P08238    |
| IM[147.04]KAQALR      | 2 P08238  | HS90B_HU | 607 HSP90AB1 | P08238    |
| IM[147.04]KAQALR      | 2 P08238  | HS90B_HU | 607 HSP90AB1 | P08238    |
| KM[147.04]EESKAK      | 5 P08238  | HS90B_HU | 557 HSP90AB1 | P08238    |
| KNIVK                 | 0 P08238  | HS90B_HU | 406 HSP90AB1 | 3PRY      |
| KNNIK                 | 0 P08238  | HS90B_HU | 350 HSP90AB1 | 3PRY      |
| KVEKVTISNR            | 3 P08238  | HS90B_HU | 577 HSP90AB1 | P08238    |
| LDSGKELK              | 4 P08238  | HS90B_HU | 69 HSP90AB1  | P08238    |

|                    |    |        |           |     |          |           |
|--------------------|----|--------|-----------|-----|----------|-----------|
| LDSGKELK           | 4  | P08238 | HS90B_HU  | 69  | HSP90AB1 | P08238    |
| MEESKAK            | 4  | P08238 | HS90B_HU  | 557 | HSP90AB1 | P08238    |
| MEESKAK            | 4  | P08238 | HS90B_HU  | 557 | HSP90AB1 | P08238    |
| M[147.04]KETQK     | 1  | P08238 | HS90B_HU  | 477 | HSP90AB1 | 3PRY      |
| NNIKLYVR           | 3  | P08238 | HS90B_HU  | 354 | HSP90AB1 | P08238    |
| NNIKLYVR           | 3  | P08238 | HS90B_HU  | 354 | HSP90AB1 | 3PRY      |
| QKAEADKNDK         | 1  | P08238 | HS90B_HU  | 641 | HSP90AB1 | P08238_PC |
| RAPFDLFENKK        | 9  | P08238 | HS90B_HU  | 347 | HSP90AB1 | P08238    |
| TKPIWTR            | 1  | P08238 | HS90B_HU  | 286 | HSP90AB1 | P08238    |
| TKPIWTR            | 1  | P08238 | HS90B_HU  | 286 | HSP90AB1 | P08238    |
| VEKVTISNR          | 2  | P08238 | HS90B_HU  | 577 | HSP90AB1 | P08238    |
| YESLTDPSKLD SGK    | 8  | P08238 | HS90B_HU  | 64  | HSP90AB1 | P08238    |
| FYEAFSKNLK         | 6  | P08238 | HS90B_HU  | 435 | HSP90AB1 | 3PRY      |
| FYEAFSKNLK         | 6  | P08238 | HS90B_HU  | 435 | HSP90AB1 | 3PRY      |
| HDSPEDVKR          | 7  | P31948 | STIP1_HUN | 486 | STIP1    | P31948    |
| KAAALEAMK          | 0  | P31948 | STIP1_HUN | 434 | STIP1    | P31948    |
| KAAALEAM[147.04]K  | 0  | P31948 | STIP1_HUN | 434 | STIP1    | P31948    |
| ELISNASDALDKIR     | 11 | P08238 | HS90B_HU  | 53  | HSP90AB1 | P08238    |
| TDSDIISKMR         | 7  | P08579 | RU2B_HUN  | 93  | SNRPB2   | 1A9N      |
| EKLQEEMLQR         | 1  | P08670 | VIME_HUN  | 188 | VIM      | P08670    |
| EKLQEEMLQR         | 1  | P08670 | VIME_HUN  | 188 | VIM      | P08670    |
| EKLQEEMLQR         | 1  | P08670 | VIME_HUN  | 188 | VIM      | P08670    |
| EKLQEEMLQR         | 1  | P08670 | VIME_HUN  | 188 | VIM      | P08670    |
| EKLQEEMLQR         | 1  | P08670 | VIME_HUN  | 188 | VIM      | P08670    |
| EKLQEEMLQR         | 1  | P08670 | VIME_HUN  | 188 | VIM      | P08670    |
| EKLQEEM[147.04]LQR | 1  | P08670 | VIME_HUN  | 188 | VIM      | P08670    |
| ETNLDSLPLVDTHSKR   | 14 | P08670 | VIME_HUN  | 439 | VIM      | ####      |
| ETNLDSLPLVDTHSKR   | 14 | P08670 | VIME_HUN  | 439 | VIM      | ####      |
| ETNLDSLPLVDTHSKR   | 14 | P08670 | VIME_HUN  | 439 | VIM      | ####      |
| FANYIDKVR          | 6  | P08670 | VIME_HUN  | 120 | VIM      | ####      |
| FANYIDKVR          | 6  | P08670 | VIME_HUN  | 120 | VIM      | P08670    |
| FANYIDKVR          | 6  | P08670 | VIME_HUN  | 120 | VIM      | P08670    |
| FANYIDKVR          | 6  | P08670 | VIME_HUN  | 120 | VIM      | P08670    |
| FANYIDKVR          | 6  | P08670 | VIME_HUN  | 120 | VIM      | P08670    |
| FANYIDKVR          | 6  | P08670 | VIME_HUN  | 120 | VIM      | P08670    |
| FANYIDKVR          | 6  | P08670 | VIME_HUN  | 120 | VIM      | P08670    |
| GQGKSR             | 3  | P08670 | VIME_HUN  | 143 | VIM      | P08670    |
| GQGKSR             | 3  | P08670 | VIME_HUN  | 143 | VIM      | P08670    |
| GQGKSR             | 3  | P08670 | VIME_HUN  | 143 | VIM      | ####      |
| ILLAELEQLKGQ GK    | 9  | P08670 | VIME_HUN  | 139 | VIM      | P08670    |
| ILLAELEQLKGQ GK    | 9  | P08670 | VIME_HUN  | 139 | VIM      | P08670    |
| ILLAELEQLKGQ GK    | 9  | P08670 | VIME_HUN  | 139 | VIM      | 3UF1      |
| KLLEGEESR          | 0  | P08670 | VIME_HUN  | 402 | VIM      | ####      |
| KLLEGEESR          | 0  | P08670 | VIME_HUN  | 402 | VIM      | ####      |
| KLLEGEESR          | 0  | P08670 | VIME_HUN  | 402 | VIM      | ####      |
| KLLEGEESR          | 0  | P08670 | VIME_HUN  | 402 | VIM      | ####      |
| KLLEGEESR          | 0  | P08670 | VIME_HUN  | 402 | VIM      | ####      |

|                     |          |           |            |        |
|---------------------|----------|-----------|------------|--------|
| KLLEGEESR           | 0 P08670 | VIME_HUN  | 402 VIM    | ####   |
| KLLEGEESR           | 0 P08670 | VIME_HUN  | 402 VIM    | ####   |
| KLLEGEESR           | 0 P08670 | VIME_HUN  | 402 VIM    | ####   |
| KLLEGEESR           | 0 P08670 | VIME_HUN  | 402 VIM    | ####   |
| KVESLQEEIAFLK       | 0 P08670 | VIME_HUN  | 223 VIM    | 3UF1   |
| KVESLQEEIAFLK       | 0 P08670 | VIME_HUN  | 223 VIM    | ####   |
| KVESLQEEIAFLK       | 0 P08670 | VIME_HUN  | 223 VIM    | ####   |
| LQDEIQNMKEEMAR      | 8 P08670 | VIME_HUN  | 373 VIM    | ####   |
| LQDEIQNMKEEMAR      | 8 P08670 | VIME_HUN  | 373 VIM    | ####   |
| NLQEAEEWYKSK        | 9 P08670 | VIME_HUN  | 292 VIM    | ####   |
| QAKQESTEYR          | 2 P08670 | VIME_HUN  | 313 VIM    | ####   |
| QAKQESTEYR          | 2 P08670 | VIME_HUN  | 313 VIM    | ####   |
| QAKQESTEYR          | 2 P08670 | VIME_HUN  | 313 VIM    | ####   |
| QAKQESTEYRR         | 2 P08670 | VIME_HUN  | 313 VIM    | ####   |
| QQYESVAAKNLQEAEEWYK | 8 P08670 | VIME_HUN  | 282 VIM    | ####   |
| QVDQLTNDKAR         | 8 P08670 | VIME_HUN  | 168 VIM    | 3UF1   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TLLIKTVETR          | 4 P08670 | VIME_HUN  | 445 VIM    | ####   |
| TNEKVELQELNDR       | 3 P08670 | VIME_HUN  | 104 VIM    | P08670 |
| TNEKVELQELNDR       | 3 P08670 | VIME_HUN  | 104 VIM    | P08670 |
| TNEKVELQELNDR       | 3 P08670 | VIME_HUN  | 104 VIM    | P08670 |
| TNEKVELQELNDR       | 3 P08670 | VIME_HUN  | 104 VIM    | P08670 |
| GELALKDAR           | 5 P08729 | K2C7_HUN  | 348 KRT7   | P08729 |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| SKFADLSEAA NR       | 1 P08670 | VIME_HUN  | 294 VIM    | ####   |
| EQLQKNK             | 4 Q5T655 | CFA58_HUI | 837 CFAP58 | ####   |
| VIIKEYYTR           | 4 P08708 | RS17_HUM  | 19 RPS17   | 5FLX   |

|                    |    |        |          |      |         |           |
|--------------------|----|--------|----------|------|---------|-----------|
| VIIEKYYTR          | 4  | P08708 | RS17_HUM | 19   | RPS17   | 5FLX      |
| VIIEKYYTR          | 4  | P08708 | RS17_HUM | 19   | RPS17   | 5FLX      |
| AKLEAAIAEAEER      | 1  | P08729 | K2C7_HUM | 331  | KRT7    | P08729    |
| AKQEELEAALQR       | 1  | P08729 | K2C7_HUM | 353  | KRT7    | P08729    |
| FASFIDKVR          | 6  | P08729 | K2C7_HUM | 108  | KRT7    | ####      |
| GELALKDAR          | 5  | P08729 | K2C7_HUM | 348  | KRT7    | P08729    |
| GELALKDAR          | 5  | P08729 | K2C7_HUM | 348  | KRT7    | P08729    |
| KDVDAAYMSK         | 0  | P08729 | K2C7_HUM | 199  | KRT7    | ####      |
| KDVDAAYM[147.04]SK | 0  | P08729 | K2C7_HUM | 199  | KRT7    | ####      |
| KLLEGEESR          | 0  | P08729 | K2C7_HUM | 394  | KRT7    | P08729    |
| KLLEGEESR          | 0  | P08729 | K2C7_HUM | 394  | KRT7    | P08729    |
| KLLEGEESR          | 0  | P08729 | K2C7_HUM | 394  | KRT7    | P08729    |
| KLLEGEESR          | 0  | P08729 | K2C7_HUM | 394  | KRT7    | P08729    |
| KLLEGEESR          | 0  | P08729 | K2C7_HUM | 394  | KRT7    | P08729    |
| LQAEIDNIKNQR       | 8  | P08729 | K2C7_HUM | 326  | KRT7    | P08729    |
| LQAEIDNIKNQR       | 8  | P08729 | K2C7_HUM | 326  | KRT7    | P08729_PC |
| DLIDKTK            | 4  | Q00872 | MYPC1_HL | 792  | MYBPC1  | ####      |
| GEVAPDAKSFVLNLGK   | 7  | P09382 | LEG1_HUM | 29   | LGALS1  | 4Q27      |
| VRGEVAPDAKSFVLNLGK | 9  | P09382 | LEG1_HUM | 29   | LGALS1  | 4Q27      |
| FKDPNAPK           | 1  | P09429 | HMGB1_HI | 90   | HMGB1   | 2YRQ      |
| IKGEHPGLSIGDVAK    | 1  | P09429 | HMGB1_HI | 114  | HMGB1   | 2YRQ      |
| KCSER              | 0  | P09429 | HMGB1_HI | 44   | HMGB1   | 2YRQ      |
| TMSAKEK            | 4  | P09429 | HMGB1_HI | 55   | HMGB1   | 2YRQ      |
| KQEAEWK            | 0  | P09496 | CLCA_HUM | 130  | CLTA    | P09496    |
| LCDFNPKSSK         | 6  | P09496 | CLCA_HUM | 223  | CLTA    | ####      |
| AVNYFSKVK          | 6  | Q00610 | CLH1_HUM | 1441 | CLTC    | Q00610    |
| LCDFNPKSSK         | 6  | P09496 | CLCA_HUM | 223  | CLTA    | ####      |
| QDEQLQKTK          | 6  | P09496 | CLCA_HUM | 156  | CLTA    | P09496    |
| SVLISLKQAPLVH      | 6  | P09496 | CLCA_HUM | 242  | CLTA    | ####      |
| SVLISLKQAPLVH      | 6  | P09496 | CLCA_HUM | 242  | CLTA    | ####      |
| SVLISLKQAPLVH      | 6  | P09496 | CLCA_HUM | 242  | CLTA    | ####      |
| LCDFNPKSSK         | 6  | P09496 | CLCA_HUM | 223  | CLTA    | ####      |
| VAQLCDFNPKSSK      | 9  | P09497 | CLCB_HUM | 204  | CLTB    | ####      |
| VAQLCDFNPKSSK      | 9  | P09497 | CLCB_HUM | 204  | CLTB    | ####      |
| ILGQKSTDR          | 4  | P09622 | DLDH_HUM | 445  | DLD     | 5J5Z      |
| ILQKQGFK           | 3  | P09622 | DLDH_HUM | 267  | DLD     | 5J5Z      |
| ILQKQGFK           | 3  | P09622 | DLDH_HUM | 267  | DLD     | 5J5Z      |
| LNTKVTGATK         | 3  | P09622 | DLDH_HUM | 277  | DLD     | 5J5Z      |
| DPNTRK             | 4  | P09651 | ROA1_HUM | 52   | HNRNPA1 | ####      |
| DPNTRK             | 4  | P09651 | ROA1_HUM | 52   | HNRNPA1 | 1L3K      |
| DPNTRK             | 4  | P09651 | ROA1_HUM | 52   | HNRNPA1 | P09651    |
| KLFVGGLK           | 0  | P09651 | ROA1_HUM | 106  | HNRNPA1 | P09651    |
| SESPKEPEQLR        | 4  | P09651 | ROA1_HUM | 8    | HNRNPA1 | 1L3K      |
| SSGPYGGGGQYFAKPR   | 13 | P09651 | ROA1_HUM | 350  | HNRNPA1 | ####      |
| SSGPYGGGGQYFAKPR   | 13 | P09651 | ROA1_HUM | 350  | HNRNPA1 | ####      |
| VVEPKR             | 4  | P09651 | ROA1_HUM | 87   | HNRNPA1 | 1L3K      |
| VVEPKR             | 4  | P09651 | ROA1_HUM | 87   | HNRNPA1 | P09651    |

|                       |    |        |           |      |                 |
|-----------------------|----|--------|-----------|------|-----------------|
| EESGKPGAHVTVK         | 4  | P22626 | ROA2_HUN  | 104  | HNRNPA2B5WWG    |
| EKEQFR                | 1  | P22626 | ROA2_HUN  | 17   | HNRNPA2B5WWG    |
| INEILSNALKR           | 9  | P52272 | HNRPM_HI  | 381  | HNRNPM #####    |
| SSGPYGGGGQYFAKPR      | 13 | P09651 | ROA1_HUN  | 350  | HNRNPA1 #####   |
| YIGIVKQAGLER          | 5  | P52597 | HNRPF_HU  | 224  | HNRNPF P52597   |
| SSGPYGGGGQYFAKPR      | 13 | P09651 | ROA1_HUN  | 350  | HNRNPA1 #####   |
| KNNM[147.04]AAK       | 0  | Q16534 | HLF_HUM/  | 234  | HLF Q16534      |
| LKGLLQSGQIPGR         | 1  | P09661 | RU2A_HUN  | 221  | SNRPA1 #####    |
| IEKGQVR               | 2  | P09874 | PARP1_HU  | 134  | PARP1 #####     |
| LYEKTGNAWHSK          | 4  | P09874 | PARP1_HU  | 621  | PARP1 4DQY      |
| LYEKTGNAWHSK          | 4  | P09874 | PARP1_HU  | 621  | PARP1 4DQY      |
| YAAKFYR               | 3  | P09914 | IFIT1_HUM | 259  | IFIT1 5UDI      |
| TKAVSR                | 1  | P0C0S5 | H2AZ_HUN  | 16   | H2AFZ P0C0S5    |
| AMTKDNNLLGR           | 3  | P0DMV8 | HS71A_HU  | 451  | HSPA1A P0DMV8   |
| AMTKDNNLLGR           | 3  | P0DMV8 | HS71A_HU  | 451  | HSPA1A P0DMV8   |
| AM[147.04]TKDNNLLGR   | 3  | P0DMV8 | HS71A_HU  | 451  | HSPA1A P0DMV8   |
| AM[147.04]TKDNNLLGR   | 3  | P0DMV8 | HS71A_HU  | 451  | HSPA1A P0DMV8   |
| DAKLDK                | 2  | P0DMV8 | HS71A_HU  | 325  | HSPA1A 5BN8     |
| LSKEEIER              | 2  | P0DMV8 | HS71A_HU  | 512  | HSPA1A P0DMV8   |
| LSKEEIER              | 2  | P0DMV8 | HS71A_HU  | 512  | HSPA1A P0DMV8   |
| STLEPVEKALR           | 7  | P0DMV8 | HS71A_HU  | 319  | HSPA1A 5BN8     |
| VFDKDGNGYISAAELR      | 3  | P0DP23 | CALM1_HL  | 95   | CALM1 4DJC      |
| TPKIQVYSR             | 2  | P61769 | B2MG_HUI  | 26   | B2M 5J1A        |
| VNHVTLSPQKIVK         | 9  | P61769 | B2MG_HUI  | 111  | B2M 5J1A        |
| AKKPAGAAK             | 1  | P10412 | H14_HUM/  | 129  | HIST1H1E P10412 |
| KAKAAKPK              | 0  | P10412 | H14_HUM/  | 175  | HIST1H1E P10412 |
| KSAGAAK               | 0  | P10412 | H14_HUM/  | 26   | HIST1H1E P10412 |
| KEINK                 | 0  | P10515 | ODP2_HUN  | 462  | DLAT P10515     |
| AGLGEEFEKEIR          | 8  | P10586 | PTPRF_HUI | 906  | PTPRF #####     |
| AWTSKSGPLSPSIQSR      | 4  | P10586 | PTPRF_HUI | 994  | PTPRF #####     |
| AWTSKSGPLSPSIQSR      | 4  | P10586 | PTPRF_HUI | 994  | PTPRF #####     |
| AWTSKSGPLSPSIQSR      | 4  | P10586 | PTPRF_HUI | 994  | PTPRF #####     |
| LAANKR                | 3  | P10586 | PTPRF_HUI | 895  | PTPRF #####     |
| LEEKSR                | 3  | P10586 | PTPRF_HUI | 1455 | PTPRF 1LAR      |
| TMPVEQVFAKNFR         | 9  | P10586 | PTPRF_HUI | 1016 | PTPRF #####     |
| TM[147.04]PVEQVFAKNFR | 9  | P10586 | PTPRF_HUI | 1016 | PTPRF #####     |
| LLPGELAKHAVSEGTK      | 8  | Q93079 | H2B1H_HU  | 109  | HIST1H2BHQ93079 |
| VGEFSGANKEK           | 8  | P10599 | THIO_HUM  | 94   | TXN 4OO4        |
| EDLKEEEEGK            | 3  | P82970 | HMG5_H    | 257  | HMG5 P82970     |
| KGLDPYNVLAPK          | 0  | P10606 | COX5B_HU  | 57   | COX5B P10606    |
| AQIEKR                | 4  | P10809 | CH60_HUN  | 369  | HSPD1 4PJ1      |
| DGVTVAKSIDLK          | 6  | P10809 | CH60_HUN  | 82   | HSPD1 4PJ1      |
| DGVTVAKSIDLK          | 6  | P10809 | CH60_HUN  | 82   | HSPD1 4PJ1      |
| DKYKNIGAK             | 3  | P10809 | CH60_HUN  | 91   | HSPD1 4PJ1      |
| DKYKNIGAK             | 3  | P10809 | CH60_HUN  | 91   | HSPD1 4PJ1      |
| DVKFGADAR             | 2  | P10809 | CH60_HUN  | 31   | HSPD1 4PJ1      |
| DVKFGADAR             | 2  | P10809 | CH60_HUN  | 31   | HSPD1 4PJ1      |





|                       |    |        |          |     |        |        |
|-----------------------|----|--------|----------|-----|--------|--------|
| YKNIGAK               | 1  | P10809 | CH60_HUN | 91  | HSPD1  | 4PJ1   |
| GKGKD                 | 1  | P21741 | MK_HUMA  | 140 | MDK    | ####   |
| LKVGLQVVAVK           | 1  | P10809 | CH60_HUN | 292 | HSPD1  | 4PJ1   |
| SQGKVLQATVVAVGSGSK    | 3  | P61604 | CH10_HUN | 40  | HSPE1  | P61604 |
| EVEKAK                | 3  | P11021 | BIP_HUMA | 294 | HSPA5  | 6ASY   |
| FAEEDKK               | 5  | P11021 | BIP_HUMA | 553 | HSPA5  | 6ASY   |
| IPKIQQLVK             | 2  | P11021 | BIP_HUMA | 370 | HSPA5  | 6ASY   |
| NKITITNDQNR           | 1  | P11021 | BIP_HUMA | 523 | HSPA5  | 6ASY   |
| NKITITNDQNR           | 1  | P11021 | BIP_HUMA | 523 | HSPA5  | 6ASY   |
| NQIGDKEK              | 5  | P11021 | BIP_HUMA | 579 | HSPA5  | 6ASY   |
| NTVVPTKK              | 6  | P11021 | BIP_HUMA | 446 | HSPA5  | 6ASY   |
| QATKDAGTIAGLNVMR      | 3  | P11021 | BIP_HUMA | 185 | HSPA5  | 6ASY   |
| STM[147.04]KPVQK      | 3  | P11021 | BIP_HUMA | 340 | HSPA5  | 6ASY   |
| TGKDVR                | 2  | P11021 | BIP_HUMA | 276 | HSPA5  | 6ASY   |
| VTAEDKGTGNK           | 5  | P11021 | BIP_HUMA | 516 | HSPA5  | 6ASY   |
| DAKLDK                | 2  | P11142 | HSP7C_HU | 325 | HSPA8  | 4H5R   |
| DISENKR               | 5  | P11142 | HSP7C_HU | 257 | HSPA8  | 4H5R   |
| DISENKR               | 5  | P11142 | HSP7C_HU | 257 | HSPA8  | 4H5R   |
| DISENKR               | 5  | P11142 | HSP7C_HU | 257 | HSPA8  | 4H5R   |
| DISENKR               | 5  | P11142 | HSP7C_HU | 257 | HSPA8  | 4H5R   |
| GTLDPVEKALR           | 7  | P11142 | HSP7C_HU | 319 | HSPA8  | 4H5R   |
| IPKIQK                | 2  | P11142 | HSP7C_HU | 345 | HSPA8  | 4H5R   |
| KVGAER                | 0  | P11142 | HSP7C_HU | 188 | HSPA8  | P11142 |
| LSKEDIER              | 2  | P11142 | HSP7C_HU | 512 | HSPA8  | P11142 |
| LSKEDIER              | 2  | P11142 | HSP7C_HU | 512 | HSPA8  | P11142 |
| QATKDAGTIAGLNVLR      | 3  | P11142 | HSP7C_HU | 159 | HSPA8  | 4H5R   |
| LSKEEVER              | 2  | P17066 | HSP76_HU | 514 | HSPA6  | ####   |
| SIGAAAKSQVISNAK       | 6  | P34932 | HSP74_HU | 53  | HSPA4  | P34932 |
| SDLEDKR               | 5  | P11233 | RALA_HUN | 134 | RALA   | 2BOV   |
| VVESTKDGLGR           | 5  | P11277 | SPTB1_HU | 981 | SPTB   | ####   |
| EHIDKYKN              | 6  | P11310 | ACADM_HI | 420 | ACADM  | 2A1T   |
| FYGDEEKDKGLQTSQDAR    | 6  | P27797 | CALR_HUN | 62  | CALR   | 3POW   |
| GIPVVEHKVEK           | 7  | P11388 | TOP2A_HU | 131 | TOP2A  | P11388 |
| GKILNVR               | 1  | P11388 | TOP2A_HU | 489 | TOP2A  | 4FM9   |
| NVKLPDAYER            | 2  | P11413 | G6PD_HUN | 432 | G6PD   | 1QKI   |
| AAQAPSSFQLLYDLKLPVEDK | 14 | P11586 | C1TC_HUN | 819 | MTHFD1 | P11586 |
| GFSNLKK               | 5  | P11586 | C1TC_HUN | 739 | MTHFD1 | P11586 |
| ANKEVPCYVFDEELR       | 2  | P11717 | MPRI_HUN | 170 | IGF2R  | P11717 |
| VLQEGKAR              | 5  | P11717 | MPRI_HUN | 527 | IGF2R  | P11717 |
| AKEFTNVYIK            | 1  | P11940 | PABP1_HU | 188 | PABPC1 | P11940 |
| IVATKPLYVALAQR        | 4  | P11940 | PABP1_HU | 361 | PABPC1 | P11940 |
| KFEQMK                | 0  | P11940 | PABP1_HU | 279 | PABPC1 | P11940 |
| KVFBVGR               | 0  | P11940 | PABP1_HU | 167 | PABPC1 | 4F02   |
| KVFBVGR               | 0  | P11940 | PABP1_HU | 167 | PABPC1 | 4F02   |
| KVFBVGR               | 0  | P11940 | PABP1_HU | 167 | PABPC1 | 4F02   |
| KVFBVGR               | 0  | P11940 | PABP1_HU | 167 | PABPC1 | 4F02   |
| KVFBVGR               | 0  | P11940 | PABP1_HU | 167 | PABPC1 | P11940 |

|                     |           |          |             |           |
|---------------------|-----------|----------|-------------|-----------|
| KVFBVGR             | 0 P11940  | PABP1_HU | 167 PABPC1  | 4F02      |
| KVFBVGR             | 0 P11940  | PABP1_HU | 167 PABPC1  | 4F02      |
| KVFBVGR             | 0 P11940  | PABP1_HU | 167 PABPC1  | 4F02      |
| SKGFGFVCFSSPEEATK   | 1 P11940  | PABP1_HU | 333 PABPC1  | P11940    |
| SKGFGFVCFSSPEEATK   | 1 P11940  | PABP1_HU | 333 PABPC1  | P11940    |
| ILKCAGNEDIITLR      | 2 P12004  | PCNA_HUN | 80 PCNA     | ####      |
| KVLEALK             | 0 P12004  | PCNA_HUN | 14 PCNA     | 1U7B      |
| LVQGSILKK           | 7 P12004  | PCNA_HUN | 13 PCNA     | 1U7B      |
| GLKQQK              | 2 P12081  | SYHC_HUN | 22 HARS     | ####      |
| AAYFGVYDTAKGMLPDPK  | 10 P12236 | ADT3_HUN | 199 SLC25A6 | P12236    |
| LAADVGKSGTER        | 6 P12236  | ADT3_HUN | 147 SLC25A6 | P12236    |
| LAADVGKSGTER        | 6 P12236  | ADT3_HUN | 147 SLC25A6 | P12236    |
| LAADVGKSGTER        | 6 P12236  | ADT3_HUN | 147 SLC25A6 | P12236    |
| LAADVGKSGTER        | 6 P12236  | ADT3_HUN | 147 SLC25A6 | P12236    |
| LAADVGKSGTER        | 6 P12236  | ADT3_HUN | 147 SLC25A6 | P12236    |
| LAADVGKSGTER        | 6 P12236  | ADT3_HUN | 147 SLC25A6 | P12236_P1 |
| LAADVGKSGTER        | 6 P12236  | ADT3_HUN | 147 SLC25A6 | P12236    |
| YFPTQALNFAFKDK      | 11 P12236 | ADT3_HUN | 92 SLC25A6  | P12236    |
| YKQIFLGGVDK         | 1 P12236  | ADT3_HUN | 96 SLC25A6  | P12236    |
| TRLAADVGKSGTER      | 8 P12236  | ADT3_HUN | 147 SLC25A6 | P12236    |
| KLTSDLGR            | 0 Q9P2E9  | RRBP1_HU | 1358 RRBPI  | Q9P2E9    |
| DVFEAKAR            | 5 P12268  | IMDH2_HU | 134 IMPDH2  | ####      |
| DVFEAKAR            | 5 P12268  | IMDH2_HU | 134 IMPDH2  | ####      |
| KYEQGFITDPVVLSPK    | 0 P12268  | IMDH2_HU | 109 IMPDH2  | 1NF7      |
| QKDYETATLSEIK       | 1 P12814  | ACTN1_HU | 420 ACTN1   | P12814    |
| VHKISNVNK           | 2 P12814  | ACTN1_HU | 89 ACTN1    | P12814_P1 |
| IKIIPPER            | 1 P68032  | ACTC_HUN | 330 ACTC1   | P68032    |
| AYGLKSGLK           | 4 P12956  | XRCC6_HU | 591 XRCC6   | ####      |
| ALKPPPIK            | 2 P12956  | XRCC6_HU | 282 XRCC6   | ####      |
| KLCVFK              | 0 P13010  | XRCC5_HU | 233 XRCC5   | P13010    |
| IAAYKSILQER         | 4 P13010  | XRCC5_HU | 265 XRCC5   | 1JEY      |
| YAYDKR              | 4 P13010  | XRCC5_HU | 399 XRCC5   | 1JEY      |
| HLSASQKALK          | 6 P13073  | COX41_HU | 60 COX4I1   | P13073    |
| EDLYLKPIQR          | 5 P13639  | EF2_HUMA | 445 EE2     | P13639    |
| EETAKLIEK           | 4 P13639  | EF2_HUMA | 314 EE2     | P13639    |
| FSKSATSPEGK         | 2 P13639  | EF2_HUMA | 275 EE2     | P13639    |
| GLKEGIPALDNFLDKL    | 2 P13639  | EF2_HUMA | 845 EE2     | P13639    |
| IM[147.04]GPNYTPGKK | 9 P13639  | EF2_HUMA | 438 EE2     | P13639    |
| KDEQER              | 0 P13639  | EF2_HUMA | 61 EE2      | P13639    |
| KDEQER              | 0 P13639  | EF2_HUMA | 61 EE2      | P13639    |
| KEETAKLIEK          | 5 P13639  | EF2_HUMA | 314 EE2     | P13639    |
| KLWGDR              | 0 P13639  | EF2_HUMA | 259 EE2     | P13639    |
| KLWGDR              | 0 P13639  | EF2_HUMA | 259 EE2     | P13639    |
| KLWGDR              | 0 P13639  | EF2_HUMA | 259 EE2     | P13639    |
| KLWGDR              | 0 P13639  | EF2_HUMA | 259 EE2     | P13639    |
| KLWGDR              | 0 P13639  | EF2_HUMA | 259 EE2     | P13639    |
| KSDPVVSUR           | 0 P13639  | EF2_HUMA | 572 EE2     | P13639    |

|                         |           |          |             |        |
|-------------------------|-----------|----------|-------------|--------|
| KVEDMMK                 | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDMMK                 | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDMMK                 | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDMMK                 | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDMM[147.04]K         | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDMM[147.04]K         | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDMM[147.04]K         | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDMM[147.04]K         | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDM[147.04]MK         | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDM[147.04]M[147.04]K | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| KVEDM[147.04]M[147.04]K | 0 P13639  | EF2_HUMA | 252 EEF2    | ####   |
| LIEKLDIK                | 3 P13639  | EF2_HUMA | 318 EEF2    | P13639 |
| LIEKLDIK                | 3 P13639  | EF2_HUMA | 318 EEF2    | P13639 |
| LIEKLDIK                | 3 P13639  | EF2_HUMA | 318 EEF2    | P13639 |
| SATSPGKK                | 7 P13639  | EF2_HUMA | 283 EEF2    | P13639 |
| SATSPGKK                | 7 P13639  | EF2_HUMA | 283 EEF2    | P13639 |
| SATSPGKK                | 7 P13639  | EF2_HUMA | 283 EEF2    | P13639 |
| VAVEAKNPADLPK           | 5 P13639  | EF2_HUMA | 512 EEF2    | P13639 |
| VFSGLVSTGLKVR           | 10 P13639 | EF2_HUMA | 426 EEF2    | P13639 |
| VFSGLVSTGLKVR           | 10 P13639 | EF2_HUMA | 426 EEF2    | P13639 |
| DKDPPIPAK               | 1 P13667  | PDIA4_HU | 111 PDIA4   | 3IDV   |
| FQSKYEPR                | 3 P13667  | PDIA4_HU | 366 PDIA4   | P13667 |
| KFAMEPEEFDSOTLR         | 0 P13667  | PDIA4_HU | 485 PDIA4   | P13667 |
| SKVLEPAK                | 1 P13667  | PDIA4_HU | 437 PDIA4   | P13667 |
| AESMLQQADKLGR           | 9 P13797  | PLST_HUM | 346 PLS3    | 1AOA   |
| IKIIPPER                | 1 P68032  | ACTC_HUN | 330 ACTC1   | P68032 |
| VAQDLCKVAGIAK           | 6 P13804  | ETFA_HUM | 69 ETFA     | 2A1U   |
| KGAGK                   | 0 P13805  | TNNT1_HU | 266 TNNT1   | ####   |
| TNNFNVELKGAVER          | 9 P13807  | GYS1_HUN | 381 GYS1    | P13807 |
| KILIEDWK                | 0 P14314  | GLU2B_HU | 142 PRKCSH  | ####   |
| KILIEDWK                | 0 P14314  | GLU2B_HU | 142 PRKCSH  | ####   |
| KLIELQAGK               | 0 P14314  | GLU2B_HU | 158 PRKCSH  | ####   |
| LVSQPKK                 | 4 P14314  | GLU2B_HU | 436 PRKCSH  | P14314 |
| GADFLVTEVENGGSLSKK      | 17 P14618 | KPYM_HU  | 206 PKM     | 3GR4   |
| KVLGEK                  | 0 P14618  | KPYM_HU  | 256 PKM     | 3GR4   |
| KVLGEK                  | 0 P14618  | KPYM_HU  | 256 PKM     | 3GR4   |
| KVLGEK                  | 0 P14618  | KPYM_HU  | 256 PKM     | 3GR4   |
| LNFSHGTHEYHAETIKNVR     | 15 P14618 | KPYM_HU  | 89 PKM      | 3GR4   |
| NICKVVEVGSK             | 3 P14618  | KPYM_HU  | 166 PKM     | 3GR4   |
| SVETLKEMIK              | 5 P14618  | KPYM_HU  | 62 PKM      | 3GR4   |
| SVETLKEMIK              | 5 P14618  | KPYM_HU  | 62 PKM      | 3GR4   |
| AQAYQTGKDISTNYYASQK     | 7 P14625  | ENPL_HUM | 671 HSP90B1 | P14625 |
| EELVKNLGTIAK            | 4 P14625  | ENPL_HUM | 161 HSP90B1 | 4NH9   |
| EGVKFDESEK              | 3 P14625  | ENPL_HUM | 597 HSP90B1 | P14625 |
| FDESEKTK                | 5 P14625  | ENPL_HUM | 603 HSP90B1 | ####   |
| FQNVAKGK                | 5 P14625  | ENPL_HUM | 593 HSP90B1 | P14625 |
| GLFDEYGSKK              | 8 P14625  | ENPL_HUM | 404 HSP90B1 | P14625 |

|                     |           |           |             |        |
|---------------------|-----------|-----------|-------------|--------|
| GLFDEYGSKK          | 8 P14625  | ENPL_HUM  | 404 HSP90B1 | P14625 |
| GLFDEYGSKK          | 8 P14625  | ENPL_HUM  | 404 HSP90B1 | P14625 |
| GLFDEYGSKK          | 8 P14625  | ENPL_HUM  | 404 HSP90B1 | P14625 |
| ILKVIR              | 2 P14625  | ENPL_HUM  | 458 HSP90B1 | P14625 |
| ILKVIR              | 2 P14625  | ENPL_HUM  | 458 HSP90B1 | P14625 |
| ILKVIR              | 2 P14625  | ENPL_HUM  | 458 HSP90B1 | P14625 |
| IMKAQAYQTGK         | 2 P14625  | ENPL_HUM  | 663 HSP90B1 | P14625 |
| IMKAQAYQTGK         | 2 P14625  | ENPL_HUM  | 663 HSP90B1 | P14625 |
| IM[147.04]KAQAYQTGK | 2 P14625  | ENPL_HUM  | 663 HSP90B1 | P14625 |
| KEAESSPFVER         | 0 P14625  | ENPL_HUM  | 547 HSP90B1 | P14625 |
| KEAESSPFVER         | 0 P14625  | ENPL_HUM  | 547 HSP90B1 | P14625 |
| KSDYIK              | 0 P14625  | ENPL_HUM  | 405 HSP90B1 | P14625 |
| KSDYIK              | 0 P14625  | ENPL_HUM  | 405 HSP90B1 | P14625 |
| KSDYIK              | 0 P14625  | ENPL_HUM  | 405 HSP90B1 | P14625 |
| KTFEINPR            | 0 P14625  | ENPL_HUM  | 683 HSP90B1 | P14625 |
| KTFEINPR            | 0 P14625  | ENPL_HUM  | 683 HSP90B1 | P14625 |
| KTFEINPR            | 0 P14625  | ENPL_HUM  | 683 HSP90B1 | P14625 |
| KTFEINPR            | 0 P14625  | ENPL_HUM  | 683 HSP90B1 | P14625 |
| KTFEINPR            | 0 P14625  | ENPL_HUM  | 683 HSP90B1 | P14625 |
| LAKLLR              | 2 P14625  | ENPL_HUM  | 508 HSP90B1 | P14625 |
| LIINSLYKNK          | 7 P14625  | ENPL_HUM  | 95 HSP90B1  | 4NH9   |
| GWVNTLVGGQKEGAR     | 10 P14735 | IDE_HUMA  | 364 IDE     | 2WK3   |
| IVPIKDIR            | 4 P14735  | IDE_HUMA  | 308 IDE     | 2WK3   |
| KLSAECAC            | 0 P14735  | IDE_HUMA  | 899 IDE     | 2WK3   |
| KLSAECAC            | 0 P14735  | IDE_HUMA  | 899 IDE     | 2WK3   |
| FSTPEQAANKR         | 8 P14866  | HNRPL_HU  | 493 HNRNPL  | 3TO8   |
| RPSSVKVFSGK         | 5 P14866  | HNRPL_HU  | 533 HNRNPL  | 3TO8   |
| VFSGKSER            | 4 P14866  | HNRPL_HU  | 538 HNRNPL  | P14866 |
| LTSSLTTKGASSFK      | 7 P22695  | QCR2_HUM  | 92 UQCRC2   | 5XTE   |
| IKAIAAK             | 1 P15121  | ALDR_HUM  | 235 AKR1B1  | 1US0   |
| NLVVIPKSVTPER       | 6 P15121  | ALDR_HUM  | 263 AKR1B1  | 1US0   |
| KVGFNPK             | 0 P15170  | ERF3A_HUI | 247 GSPT1   | P15170 |
| LVPFLKK             | 5 P15170  | ERF3A_HUI | 246 GSPT1   | P15170 |
| VGFNPKK             | 5 P15170  | ERF3A_HUI | 253 GSPT1   | P15170 |
| VVKCR               | 2 P15529  | MCP_HUM   | 227 CD46    | 5FO8   |
| YKLLGGLAVR          | 1 P23396  | RS3_HUM/  | 108 RPS3    | P23396 |
| ALYKAISVPR          | 3 P15924  | DESP_HUM  | 154 DSP     | ####   |
| FQKQALEASNR         | 2 P15924  | DESP_HUM  | 1789 DSP    | ####   |
| IDKQIDFR            | 2 P15924  | DESP_HUM  | 872 DSP     | ####   |
| ISYKDAINR           | 3 P15924  | DESP_HUM  | 2786 DSP    | ####   |
| ISYKDAINR           | 3 P15924  | DESP_HUM  | 2786 DSP    | ####   |
| KEEAIR              | 0 P15924  | DESP_HUM  | 1874 DSP    | ####   |
| KLEDSTR             | 0 P15924  | DESP_HUM  | 1916 DSP    | ####   |
| KQQLEVELR           | 0 P15924  | DESP_HUM  | 1444 DSP    | ####   |
| LPVEEAYKR           | 7 P15924  | DESP_HUM  | 2317 DSP    | 5DZZ   |
| SLSEEIKR            | 6 P15924  | DESP_HUM  | 1410 DSP    | ####   |
| TVKDQDITR           | 2 P15924  | DESP_HUM  | 1552 DSP    | ####   |

|                     |           |          |              |        |
|---------------------|-----------|----------|--------------|--------|
| YVQKGEYR            | 3 P16070  | CD44_HUN | 158 CD44     | 1UUH   |
| TDMAGPKATK          | 6 P16152  | CBR1_HUN | 239 CBR1     | 1WMA   |
| TDM[147.04]AGPKATK  | 6 P16152  | CBR1_HUN | 239 CBR1     | 1WMA   |
| AAGAGAAKR           | 7 P16401  | H15_HUM/ | 35 HIST1H1B  | P16401 |
| AVAASKER            | 5 P16401  | H15_HUM/ | 55 HIST1H1B  | P16401 |
| IKLGLK              | 1 P16401  | H15_HUM/ | 84 HIST1H1B  | P16401 |
| KAASGEAKPK          | 0 P16401  | H15_HUM/ | 113 HIST1H1B | P16401 |
| LGLKSLVSK           | 3 P16401  | H15_HUM/ | 88 HIST1H1B  | P16401 |
| AVAASKER            | 5 P16403  | H12_HUM/ | 52 HIST1H1C  | P16403 |
| AVAASKER            | 5 P16403  | H12_HUM/ | 52 HIST1H1C  | P16403 |
| IKLGLK              | 1 P16403  | H12_HUM/ | 81 HIST1H1C  | P16403 |
| IKLGLK              | 1 P16403  | H12_HUM/ | 81 HIST1H1C  | P16403 |
| KASGPPVSELITK       | 0 P16403  | H12_HUM/ | 34 HIST1H1C  | ####   |
| LGLKSLVSK           | 3 P16403  | H12_HUM/ | 85 HIST1H1C  | P16403 |
| LGLKSLVSK           | 3 P16403  | H12_HUM/ | 85 HIST1H1C  | P16403 |
| SGVSLAALKK          | 8 P16403  | H12_HUM/ | 63 HIST1H1C  | P16403 |
| SLVSKGTLVQTK        | 4 P16403  | H12_HUM/ | 90 HIST1H1C  | P16403 |
| LVALKK              | 4 Q92772  | CDKL2_HU | 33 CDKL2     | 4AAA   |
| KLNQGTER            | 0 P16435  | NCPR_HUN | 291 POR      | 3QE2   |
| IEVASSVKLCR         | 7 P16615  | AT2A2_HU | 611 ATP2A2   | P16615 |
| IEVASSVKLCR         | 7 P16615  | AT2A2_HU | 611 ATP2A2   | P16615 |
| KSVQR               | 0 P16615  | AT2A2_HU | 135 ATP2A2   | P16615 |
| NYLEPGKECVQPATK     | 6 P16615  | AT2A2_HU | 995 ATP2A2   | ####   |
| GLFKENNER           | 3 P17301  | ITA2_HUM | 718 ITGA2    | P17301 |
| MGDVYKCPVDLSTATCEK  | 5 P17301  | ITA2_HUM | 82 ITGA2     | P17301 |
| NALDTKNLIK          | 5 P17301  | ITA2_HUM | 323 ITGA2    | 1V7P   |
| ITLQDLKR            | 6 Q9Y5P8  | P2R3B_HU | 459 PPP2R3B  | 4I5L   |
| AALVYSDDKLER        | 8 P17342  | ANPRC_HU | 208 NPR3     | 1YK0   |
| LIDFLECGKTNL        | 8 P17844  | DDX5_HUN | 236 DDX5     | 4A4D   |
| AVAFSPVTELKK        | 10 P17858 | PFKAL_HU | 726 PFKL     | P17858 |
| NVIFQPVAELKK        | 10 Q01813 | PFKAP_HU | 736 PFKP     | 4XYJ   |
| ACAAQTKATFLK        | 6 P17980  | PRS6A_HU | 245 PSMC3    | 5M32   |
| DNKQAGVFEPTIVK      | 2 P17987  | TCPA_HUN | 499 TCP1     | P17987 |
| LACKEAVR            | 3 P17987  | TCPA_HUN | 126 TCP1     | P17987 |
| ANEVSKLYAVHQEGNK    | 6 P50990  | TCPQ_HUN | 466 CCT8     | P50990 |
| DCLINAAKTSMSSK      | 7 P17987  | TCPA_HUN | 153 TCP1     | P17987 |
| LACKEAVR            | 3 P17987  | TCPA_HUN | 126 TCP1     | P17987 |
| TSLGPKGMDK          | 5 P50991  | TCPD_HUN | 55 CCT4      | P50991 |
| LACKEAVR            | 3 P17987  | TCPA_HUN | 126 TCP1     | P17987 |
| LACKEAVR            | 3 P17987  | TCPA_HUN | 126 TCP1     | P17987 |
| KVVVVR              | 0 P40429  | RL13A_HU | 32 RPL13A    | P40429 |
| VIWGVKTR            | 4 P18077  | RL35A_HU | 73 RPL35A    | ####   |
| DAPEGGFDAVLQAAVCKEK | 16 P18084 | ITB5_HUM | 260 ITGB5    | P18084 |
| EKIGWR              | 1 P18084  | ITB5_HUM | 262 ITGB5    | P18084 |
| KLTSNFR             | 0 P18084  | ITB5_HUM | 170 ITGB5    | P18084 |
| GYGKINK             | 3 P18124  | RL7_HUM  | 161 RPL7     | P18124 |
| KVLQLLR             | 0 P18124  | RL7_HUM  | 107 RPL7     | P18124 |

|                       |           |           |           |           |
|-----------------------|-----------|-----------|-----------|-----------|
| KVLQLLR               | 0 P18124  | RL7_HUMA  | 107 RPL7  | P18124    |
| EYKVVGR               | 2 Q02543  | RL18A_HUI | 11 RPL18A | Q02543    |
| ILLVAKR               | 5 P18206  | VINC_HUM  | 768 VCL   | 1TR2      |
| KSAEFLHMLKNAESNAELK   | 10 P18621 | RL17_HUM  | 96 RPL17  | ####      |
| VHFKNTR               | 3 P18621  | RL17_HUM  | 27 RPL17  | P18621    |
| ALPFWNEEIVPQIKEGK     | 13 P18669 | PGAM1_HI  | 176 PGAM1 | 4GPZ      |
| FSGWYDADLSPAGHEEAKR   | 17 P18669 | PGAM1_HI  | 39 PGAM1  | 4GPZ      |
| HGEAQVKIWR            | 6 P18669  | PGAM1_HI  | 113 PGAM1 | 4GPZ      |
| KAMEAVAAQ GK          | 0 P18669  | PGAM1_HI  | 241 PGAM1 | 4GPZ      |
| AFSSFKNR              | 5 P19256  | LFA3_HUM  | 78 CD58   | 1CCZ      |
| AAATPAKK              | 6 P19338  | NUCL_HUN  | 95 NCL    | ####      |
| AAVTPGKK              | 6 P19338  | NUCL_HUN  | 87 NCL    | ####      |
| ALELTGLKVF GNEIK      | 7 P19338  | NUCL_HUN  | 370 NCL   | 2KRR      |
| ALELTGLKVF GNEIK      | 7 P19338  | NUCL_HUN  | 370 NCL   | 2KRR      |
| EALNSCNKR             | 7 P19338  | NUCL_HUN  | 545 NCL   | P19338    |
| EALNSCNKR             | 7 P19338  | NUCL_HUN  | 545 NCL   | P19338    |
| ETGSSKGFGFVDFNSEEDAK  | 5 P19338  | NUCL_HUN  | 610 NCL   | P19338    |
| KA AVTPGK             | 0 P19338  | NUCL_HUN  | 80 NCL    | ####      |
| KTVTPAK               | 0 P19338  | NUCL_HUN  | 96 NCL    | ####      |
| LVSKDGK               | 3 P19338  | NUCL_HUN  | 424 NCL   | 2KRR      |
| LVSKDGK               | 3 P19338  | NUCL_HUN  | 424 NCL   | 2KRR      |
| LVSKDGK               | 3 P19338  | NUCL_HUN  | 424 NCL   | 2KRR      |
| SAPELKTGISDVFAK       | 5 P19338  | NUCL_HUN  | 324 NCL   | 2KRR      |
| SKGIAYIEFK            | 1 P19338  | NUCL_HUN  | 429 NCL   | P19338    |
| SKGIAYIEFK            | 1 P19338  | NUCL_HUN  | 429 NCL   | 2KRR      |
| SKGIAYIEFK            | 1 P19338  | NUCL_HUN  | 429 NCL   | 2KRR      |
| SQPSKTLFVK            | 4 P19338  | NUCL_HUN  | 572 NCL   | P19338    |
| SQPSKTLFVK            | 4 P19338  | NUCL_HUN  | 572 NCL   | P19338    |
| TLLAKNL PYK           | 4 P19338  | NUCL_HUN  | 398 NCL   | P19338    |
| TLLAKNL PYK           | 4 P19338  | NUCL_HUN  | 398 NCL   | P19338    |
| TLLAKNL PYK           | 4 P19338  | NUCL_HUN  | 398 NCL   | 2KRR      |
| TLLAKNL PYK           | 4 P19338  | NUCL_HUN  | 398 NCL   | 2KRR      |
| TLLAKNL PYK           | 4 P19338  | NUCL_HUN  | 398 NCL   | 2KRR      |
| TLLAKNL PYK           | 4 P19338  | NUCL_HUN  | 398 NCL   | P19338    |
| TLLAKNL PYK           | 4 P19338  | NUCL_HUN  | 398 NCL   | P19338_P1 |
| VFGNEIKLEKPK          | 6 P19338  | NUCL_HUN  | 377 NCL   | 2KRR      |
| VTLDWAKPK             | 6 P19338  | NUCL_HUN  | 646 NCL   | P19338    |
| VTLDWAKPK             | 6 P19338  | NUCL_HUN  | 646 NCL   | P19338    |
| NYPEGHKA AAVLPVLDLAQR | 6 P19404  | NDUV2_HI  | 75 NDUFV2 | 5XTB      |
| IKA AFK               | 1 P20073  | ANXA7_HU  | 224 ANXA7 | P20073    |
| TATADDKK              | 6 P20290  | BTF3_HUM  | 86 BTF3   | ####      |
| ICIVTKEGIR            | 5 P20618  | PSB1_HUM  | 228 PSMB1 | 5LE5      |
| ICIVTKEGIR            | 5 P20618  | PSB1_HUM  | 228 PSMB1 | 5LE5      |
| LVKDV FISAAER         | 2 P20618  | PSB1_HUM  | 204 PSMB1 | 5LE5      |
| ATAGAYIASQTVKK        | 12 P28074 | PSB5_HUM  | 91 PSMB5  | ####      |
| ATAGAYIASQTVKK        | 12 P28074 | PSB5_HUM  | 91 PSMB5  | ####      |
| ATAGAYIASQTVKK        | 12 P28074 | PSB5_HUM  | 91 PSMB5  | ####      |

|                   |    |        |          |      |       |           |
|-------------------|----|--------|----------|------|-------|-----------|
| LVKDVFISAAER      | 2  | P20618 | PSB1_HUM | 204  | PSMB1 | 5LE5      |
| ELALVKR           | 5  | P20645 | MPRD_HUI | 50   | M6PR  | P20645    |
| GKESEK            | 1  | P20645 | MPRD_HUI | 40   | M6PR  | P20645    |
| ELTGLKALYETELADAR | 5  | P20700 | LMNB1_HL | 79   | LMNB1 | P20700_P2 |
| ESDLNGAQIKLR      | 9  | P20700 | LMNB1_HL | 134  | LMNB1 | ####      |
| KIGDTSVSYK        | 0  | P20700 | LMNB1_HL | 474  | LMNB1 | 3JT0      |
| LKLSPSPSSR        | 1  | P20700 | LMNB1_HL | 389  | LMNB1 | ####      |
| LKLSPSPSSR        | 1  | P20700 | LMNB1_HL | 389  | LMNB1 | ####      |
| LQEKEELR          | 3  | P20700 | LMNB1_HL | 33   | LMNB1 | ####      |
| DKGEYTLVVK        | 1  | P21333 | FLNA_HUM | 2623 | FLNA  | ####      |
| GKLDVQFSGLTK      | 1  | P21333 | FLNA_HUM | 906  | FLNA  | ####      |
| IKVSGLGEK         | 1  | P21333 | FLNA_HUM | 975  | FLNA  | ####      |
| VKAEGPGLSR        | 1  | P21333 | FLNA_HUM | 876  | FLNA  | ####      |
| VVAKGLGLSK        | 3  | P21333 | FLNA_HUM | 2563 | FLNA  | ####      |
| MKVIYPAVEGR       | 1  | P21589 | 5NTD_HUM | 536  | NT5E  | 4H1S      |
| DVFTKGYGFLIK      | 4  | P21796 | VDAC1_HU | 20   | VDAC1 | 5XDO      |
| IKTGYK            | 1  | P21796 | VDAC1_HU | 115  | VDAC1 | 5XDO      |
| IKTGYK            | 1  | P21796 | VDAC1_HU | 115  | VDAC1 | 5XDO      |
| IKTGYK            | 1  | P21796 | VDAC1_HU | 115  | VDAC1 | 5XDO      |
| IKTGYK            | 1  | P21796 | VDAC1_HU | 115  | VDAC1 | 5XDO      |
| LTFDSSFSPNTGKK    | 12 | P21796 | VDAC1_HU | 109  | VDAC1 | 5XDO      |
| LTFDSSFSPNTGKK    | 12 | P21796 | VDAC1_HU | 109  | VDAC1 | 5XDO      |
| LTFDSSFSPNTGKK    | 12 | P21796 | VDAC1_HU | 109  | VDAC1 | 5XDO      |
| NAKIK             | 2  | P21796 | VDAC1_HU | 113  | VDAC1 | 5XDO      |
| VTGSLETKYR        | 7  | P21796 | VDAC1_HU | 61   | VDAC1 | 5XDO      |
| KDVLETFTVK        | 0  | P21926 | CD9_HUM/ | 170  | CD9   | P21926    |
| TKDEPQR           | 1  | P21926 | CD9_HUM/ | 135  | CD9   | P21926    |
| TKDEPQR           | 1  | P21926 | CD9_HUM/ | 135  | CD9   | P21926    |
| TKDEPQR           | 1  | P21926 | CD9_HUM/ | 135  | CD9   | P21926    |
| TKDEPQR           | 1  | P21926 | CD9_HUM/ | 135  | CD9   | P21926    |
| EVQEFYKDTYNK      | 6  | P21926 | CD9_HUM/ | 126  | CD9   | P21926    |
| AIYKGPGSEAGP      | 3  | P21964 | COMT_HUI | 263  | COMT  | 4PYI      |
| GKEDALVTK         | 1  | P22087 | FBRL_HUM | 102  | FBL   | ####      |
| NLVPGESVYGEKR     | 11 | P22087 | FBRL_HUM | 121  | FBL   | 2IPX      |
| VSISEGDDKIEYR     | 8  | P22087 | FBRL_HUM | 131  | FBL   | ####      |
| DQKLPHLER         | 2  | P22102 | PUR2_HUM | 598  | GART  | P22102    |
| FAKEFMDR          | 2  | P22102 | PUR2_HUM | 111  | GART  | 2QK4      |
| DKQSYR            | 1  | P22234 | PUR6_HUM | 228  | PAICS | ####      |
| IATGSFLKR         | 7  | P22234 | PUR6_HUM | 110  | PAICS | P22234_P2 |
| IATGSFLKR         | 7  | P22234 | PUR6_HUM | 110  | PAICS | 2H31      |
| KACGNFGIPCELR     | 0  | P22234 | PUR6_HUM | 286  | PAICS | 2H31      |
| KACGNFGIPCELR     | 0  | P22234 | PUR6_HUM | 286  | PAICS | 2H31      |
| KACGNFGIPCELR     | 0  | P22234 | PUR6_HUM | 286  | PAICS | 2H31      |
| KACGNFGIPCELR     | 0  | P22234 | PUR6_HUM | 286  | PAICS | 2H31      |
| KNFEWVAER         | 0  | P22234 | PUR6_HUM | 247  | PAICS | P22234    |
| KNFEWVAER         | 0  | P22234 | PUR6_HUM | 247  | PAICS | 2H31      |
| KLSFK             | 0  | P22314 | UBA1_HUM | 300  | UBA1  | 4P22      |

|                          |           |          |                  |           |
|--------------------------|-----------|----------|------------------|-----------|
| GLVGEIHKR                | 7 P22392  | NDKB_HUM | 26 NME2          | 1NSK      |
| NIIHGSDSVKSAEK           | 9 P22392  | NDKB_HUM | 124 NME2         | 1NSK      |
| NIIHGSDSVKSAEK           | 9 P22392  | NDKB_HUM | 124 NME2         | 1NSK      |
| TFIAIKPDGVQR             | 5 P22392  | NDKB_HUM | 12 NME2          | 1NSK      |
| VMLGETNPADSKPGTIR        | 11 P22392 | NDKB_HUM | 100 NME2         | 1NSK      |
| VM[147.04]LGETNPADSKPGTI | 11 P22392 | NDKB_HUM | 100 NME2         | 1NSK      |
| VKTVWLVGR                | 1 P22570  | ADRO_HUM | 221 FDXR         | P22570    |
| DPASKR                   | 4 P22626  | ROA2_HUM | 59 HNRNPA2B5WWG  |           |
| DPASKR                   | 4 P22626  | ROA2_HUM | 59 HNRNPA2B5WWG  |           |
| DPASKR                   | 4 P22626  | ROA2_HUM | 59 HNRNPA2B5WWG  |           |
| DPASKR                   | 4 P22626  | ROA2_HUM | 59 HNRNPA2B5WWG  |           |
| DPASKR                   | 4 P22626  | ROA2_HUM | 59 HNRNPA2B5WWG  |           |
| EESGKPGAHVTVK            | 4 P22626  | ROA2_HUM | 104 HNRNPA2B5WWG |           |
| EKEQFR                   | 1 P22626  | ROA2_HUM | 17 HNRNPA2B5WWG  |           |
| EKEQFR                   | 1 P22626  | ROA2_HUM | 17 HNRNPA2B5WWG  |           |
| EKEQFR                   | 1 P22626  | ROA2_HUM | 17 HNRNPA2B5WWG  |           |
| EKEQFR                   | 1 P22626  | ROA2_HUM | 17 HNRNPA2B5WWG  |           |
| EKEQFR                   | 1 P22626  | ROA2_HUM | 17 HNRNPA2B5WWG  |           |
| KALSR                    | 0 P22626  | ROA2_HUM | 186 HNRNPA2B5WWG |           |
| KLFIGGLSFETTEESLR        | 0 P22626  | ROA2_HUM | 22 HNRNPA2B5WWG  | P22626_P2 |
| KLFVGGLK                 | 0 P22626  | ROA2_HUM | 113 HNRNPA2B5WWG |           |
| VVEPKR                   | 4 P22626  | ROA2_HUM | 94 HNRNPA2B5WWG  |           |
| VVEPKR                   | 4 P22626  | ROA2_HUM | 94 HNRNPA2B5WWG  |           |
| VVEPKR                   | 4 P22626  | ROA2_HUM | 94 HNRNPA2B5WWG  |           |
| VVEPKR                   | 4 P22626  | ROA2_HUM | 94 HNRNPA2B5WWG  | P22626_P2 |
| GGLGLSGAKANYR            | 8 P22695  | QCR2_HUM | 250 UQCRC2       | 5XTE      |
| IGLFIKAGSR               | 5 P22695  | QCR2_HUM | 66 UQCRC2        | 5XTE      |
| KFVSGQK                  | 0 P22695  | QCR2_HUM | 430 UQCRC2       | 5XTE      |
| GIVEFASKPAAR             | 7 P23246  | SFPQ_HUM | 421 SFPQ         | 4WIJ      |
| GIVEFASKPAAR             | 7 P23246  | SFPQ_HUM | 421 SFPQ         | 4WIJ      |
| GKGFGFIK                 | 1 P23246  | SFPQ_HUM | 332 SFPQ         | 4WIJ      |
| GKGFGFIK                 | 1 P23246  | SFPQ_HUM | 332 SFPQ         | 4WIJ      |
| GKGFGFIK                 | 1 P23246  | SFPQ_HUM | 332 SFPQ         | 4WIJ      |
| KAFER                    | 0 P23246  | SFPQ_HUM | 426 SFPQ         | 4WIJ      |
| KAFER                    | 0 P23246  | SFPQ_HUM | 426 SFPQ         | 4WIJ      |
| KAFER                    | 0 P23246  | SFPQ_HUM | 426 SFPQ         | P23246    |
| LAQKNPMYQK               | 3 P23246  | SFPQ_HUM | 466 SFPQ         | 4WIJ      |
| LAQKNPM[147.04]YQK       | 3 P23246  | SFPQ_HUM | 466 SFPQ         | 4WIJ      |
| LFAKYGEPGEVFINK          | 3 P23246  | SFPQ_HUM | 319 SFPQ         | 4WIJ      |
| GIVEFASKPAAR             | 7 P23246  | SFPQ_HUM | 421 SFPQ         | 4WIJ      |
| KEMQLR                   | 0 P23246  | SFPQ_HUM | 561 SFPQ         | 4WIJ      |
| YGKAGEVFIHK              | 2 Q15233  | NONO_HUM | 99 NONO          | 3SDE      |
| FPDENFKLK                | 6 P23284  | PPIB_HUM | 129 PPIB         | 3ICH      |
| GDGTGGKSIYGER            | 6 P23284  | PPIB_HUM | 116 PPIB         | 3ICH      |
| GDGTGGKSIYGER            | 6 P23284  | PPIB_HUM | 116 PPIB         | ####      |
| GDGTGGKSIYGER            | 6 P23284  | PPIB_HUM | 116 PPIB         | 3ICH      |
| GDGTGGKSIYGER            | 6 P23284  | PPIB_HUM | 116 PPIB         | 3ICH      |



|                  |           |           |            |           |
|------------------|-----------|-----------|------------|-----------|
| GDGTGGKSIYGER    | 6 P23284  | PPIB_HUM  | 116 PPIB   | 3ICH      |
| IEVEKPFAIAK      | 4 P23284  | PPIB_HUM  | 209 PPIB   | 3ICH      |
| IEVEKPFAIAKE     | 10 P23284 | PPIB_HUM  | 215 PPIB   | 3ICH      |
| KVESTK           | 0 P23284  | PPIB_HUM  | 181 PPIB   | 3ICH      |
| NSKFHR           | 2 P23284  | PPIB_HUM  | 92 PPIB    | 3ICH      |
| VIFGLFGKTVPK     | 7 P23284  | PPIB_HUM  | 67 PPIB    | 3ICH      |
| VIFGLFGKTVPK     | 7 P23284  | PPIB_HUM  | 67 PPIB    | 3ICH      |
| VIFGLFGKTVPK     | 7 P23284  | PPIB_HUM  | 67 PPIB    | 3ICH      |
| LKPLEVELR        | 1 P49755  | TMEDA_HL  | 145 TMED10 | ####      |
| AYIKLNQLEK       | 3 Q8IVL5  | P3H2_HUN  | 160 P3H2   | ####      |
| IDKELINR         | 2 P23381  | SYWC_HUN  | 114 WARS   | 5UJJ      |
| MLVSLKMSYK       | 5 P23381  | SYWC_HUN  | 47 WARS    | 5UJJ      |
| NVVKIQK          | 3 P23381  | SYWC_HUN  | 253 WARS   | 5UJJ      |
| ELTAVVQKR        | 7 P23396  | RS3_HUM   | 75 RPS3    | 1WH9      |
| ELTAVVQKR        | 7 P23396  | RS3_HUM   | 75 RPS3    | 1WH9      |
| ELTAVVQKR        | 7 P23396  | RS3_HUM   | 75 RPS3    | P23396    |
| TQNVLGEKGR       | 7 P23396  | RS3_HUM   | 62 RPS3    | 1WH9      |
| TQNVLGEKGR       | 7 P23396  | RS3_HUM   | 62 RPS3    | P23396    |
| YKLLGGLAVR       | 1 P23396  | RS3_HUM   | 108 RPS3   | P23396    |
| KKGPNANS         | 0 P62861  | RS30_HUM  | 52 FAU     | 5FLX      |
| YKLLGGLAVR       | 1 P23396  | RS3_HUM   | 108 RPS3   | P23396    |
| LPSGSKK          | 5 P62917  | RL8_HUM   | 155 RPL8   | P62917    |
| VKLPSGSKK        | 7 P62917  | RL8_HUM   | 155 RPL8   | P62917    |
| KLTGIK           | 0 P23528  | COF1_HUN  | 127 CFL1   | 5L6W      |
| KLTGIK           | 0 P23528  | COF1_HUN  | 127 CFL1   | 5L6W      |
| KSSTPEEVK        | 0 P23528  | COF1_HUN  | 22 CFL1    | 5L6W      |
| VNVDKVLER        | 4 P23763  | VAMP1_HL  | 54 VAMP1   | P23763    |
| AKKPALVAK        | 1 P24534  | EF1B_HUM  | 132 EEF1B2 | P24534    |
| KPALVAK          | 0 P24534  | EF1B_HUM  | 133 EEF1B2 | P24534    |
| TIEKFEK          | 3 P68104  | EF1A1_HUI | 41 EEF1A1  | P68104    |
| VYKEVK           | 2 P24539  | AT5F1_HUI | 191 ATP5F1 | P24539    |
| VYKEVK           | 2 P24539  | AT5F1_HUI | 191 ATP5F1 | P24539    |
| AGIPKEEVK        | 4 P24752  | THIL_HUM  | 83 ACAT1   | 2IB8      |
| GSTPYGGVKLEDLIVK | 8 P24752  | THIL_HUM  | 174 ACAT1  | 2IB8      |
| LKTVFQK          | 1 P24752  | THIL_HUM  | 268 ACAT1  | 2IB8      |
| LKTVFQK          | 1 P24752  | THIL_HUM  | 268 ACAT1  | 2IB8      |
| VDFSKVPK         | 4 P24752  | THIL_HUM  | 263 ACAT1  | 2IB8      |
| TVLIACNVKQMSK    | 8 P25205  | MCM3_HU   | 266 MCM3   | P25205    |
| KGGGK            | 0 P25490  | TYY1_HUM  | 174 YY1    | ####      |
| AMKQVAGTMK       | 2 P25705  | ATPA_HUN  | 427 ATP5A1 | P25705    |
| FNDGSDEKKK       | 8 P25705  | ATPA_HUN  | 240 ATP5A1 | P25705    |
| GPIGSKTR         | 5 P25705  | ATPA_HUN  | 167 ATP5A1 | P25705_P2 |
| GPIGSKTR         | 5 P25705  | ATPA_HUN  | 167 ATP5A1 | P25705    |
| GYLDKLEPSK       | 4 P25705  | ATPA_HUN  | 498 ATP5A1 | P25705    |
| TLIDKAR          | 4 P28066  | PSA5_HUN  | 91 PSMA5   | ####      |
| LNLYELKEGR       | 6 P49720  | PSB3_HUN  | 77 PSMB3   | 5LE5      |
| YKYGYEIPVDMLCK   | 1 P60900  | PSA6_HUN  | 104 PSMA6  | 5LE5      |

|                        |          |           |           |           |
|------------------------|----------|-----------|-----------|-----------|
| YKYGYEIPVDM[147.04]LCK | 1 P60900 | PSA6_HUM  | 104 PSMA6 | 5LE5      |
| EKEELM[147.04]ER       | 1 P26038 | MOES_HUI  | 344 MSN   | P26038    |
| KAPDFVIFYAPR           | 0 P26038 | MOES_HUI  | 263 MSN   | 1E5W      |
| KPDTIEVQQMK            | 0 P26038 | MOES_HUI  | 296 MSN   | 1E5W      |
| QLFDQVVKTIGLR          | 7 P26038 | MOES_HUI  | 35 MSN    | 1E5W      |
| KPSAPK                 | 0 P26373 | RL13_HUM  | 130 RPL13 | P26373    |
| KPSAPK                 | 0 P26373 | RL13_HUM  | 130 RPL13 | P26373    |
| LKEYR                  | 1 P26373 | RL13_HUM  | 118 RPL13 | P26373    |
| LKEYR                  | 1 P26373 | RL13_HUM  | 118 RPL13 | P26373    |
| SKLILFPR               | 1 P26373 | RL13_HUM  | 123 RPL13 | P26373    |
| SKLILFPR               | 1 P26373 | RL13_HUM  | 123 RPL13 | P26373    |
| SKLILFPR               | 1 P26373 | RL13_HUM  | 123 RPL13 | P26373    |
| YHTKVR                 | 3 P26373 | RL13_HUM  | 69 RPL13  | P26373    |
| YHLSKR                 | 4 Q86UK5 | LBN_HUM/  | 590 EVC2  | ####      |
| SNEFKNLR               | 4 P26440 | IVD_HUMA  | 75 IVD    | 1IVH      |
| ELPSFLGKR              | 7 P26447 | S10A4_HUI | 48 S100A4 | 3C1V      |
| ELPSFLGKR              | 7 P26447 | S10A4_HUI | 48 S100A4 | 3C1V      |
| LNKSELK                | 2 P26447 | S10A4_HUI | 31 S100A4 | 3C1V      |
| SELKELLTR              | 3 P26447 | S10A4_HUI | 35 S100A4 | 3C1V      |
| ELKTDSSPNQAR           | 2 P26599 | PTBP1_HUI | 137 PTBP1 | P26599    |
| IDFSKLTSLNVK           | 4 P26599 | PTBP1_HUI | 259 PTBP1 | 3ZZY      |
| ILFNKK                 | 4 P26599 | PTBP1_HUI | 373 PTBP1 | ####      |
| LTSLNVKYNNNDK          | 6 P26599 | PTBP1_HUI | 266 PTBP1 | 3ZZY      |
| VKILFNK                | 1 P26599 | PTBP1_HUI | 368 PTBP1 | ####      |
| VKILFNKK               | 1 P26599 | PTBP1_HUI | 368 PTBP1 | ####      |
| YNNDKSR                | 4 P26599 | PTBP1_HUI | 271 PTBP1 | 3ZZY      |
| YNNDKSR                | 4 P26599 | PTBP1_HUI | 271 PTBP1 | 3ZZY      |
| GGVVLKEDALPGQK         | 5 P35613 | BASI_HUM  | 179 BSG   | 4U0Q      |
| FQEEAKNR               | 5 P26639 | SYTC_HUM  | 319 TARS  | P26639    |
| IHKNSSTYWEGK           | 2 P26639 | SYTC_HUM  | 279 TARS  | P26639    |
| KDTPR                  | 0 P26641 | EF1G_HUM  | 228 EE1G  | ####      |
| KDTPR                  | 0 P26641 | EF1G_HUM  | 228 EE1G  | ####      |
| KFAETQPK               | 0 P26641 | EF1G_HUM  | 220 EE1G  | ####      |
| KFPAGK                 | 0 P26641 | EF1G_HUM  | 52 EE1G   | 5JPO      |
| LQIGVKK                | 5 P26885 | FKBP2_HUI | 36 FKBP2  | ####      |
| FKFPGR                 | 1 P27635 | RL10_HUM  | 158 RPL10 | 2PA2      |
| GAFGKPQGTVAR           | 4 P27635 | RL10_HUM  | 121 RPL10 | P27635    |
| GAFGKPQGTVAR           | 4 P27635 | RL10_HUM  | 121 RPL10 | P27635    |
| GAFGKPQGTVAR           | 4 P27635 | RL10_HUM  | 121 RPL10 | P27635    |
| GPLDKWR                | 4 P27635 | RL10_HUM  | 208 RPL10 | P27635_P2 |
| GPLDKWR                | 4 P27635 | RL10_HUM  | 208 RPL10 | P27635    |
| GVPDAKIR               | 5 P27635 | RL10_HUM  | 30 RPL10  | P27635    |
| LIPDGCGVKYIPNR         | 8 P27635 | RL10_HUM  | 198 RPL10 | P27635    |
| DKQDEEQR               | 1 P27797 | CALR_HUM  | 360 CALR  | 3POW      |
| GKNVLINK               | 1 P27797 | CALR_HUM  | 153 CALR  | P27797    |
| GKNVLINK               | 1 P27797 | CALR_HUM  | 153 CALR  | 3POW      |
| HKSDFGK                | 1 P27797 | CALR_HUM  | 43 CALR   | 3POW      |

|                         |           |          |               |        |
|-------------------------|-----------|----------|---------------|--------|
| HKNPK                   | 1 P27824  | CALX_HUM | 207 CANX      | P27824 |
| KDDTDDEIAK              | 0 P27824  | CALX_HUM | 90 CANX       | ####   |
| LLSKTPELNLDQFHDK        | 3 P27824  | CALX_HUM | 170 CANX      | P27824 |
| KCLEELQK                | 0 P49721  | PSB2_HUM | 162 PSMB2     | ####   |
| IPQAIAQLSKEAGVEK        | 9 Q16795  | NDUA9_HU | 157 NDUFA9    | Q16795 |
| KAYGQALAK               | 0 P29401  | TKT_HUM  | 319 TKT       | 4KXW   |
| KAYGQALAK               | 0 P29401  | TKT_HUM  | 319 TKT       | 4KXW   |
| KAYGQALAK               | 0 P29401  | TKT_HUM  | 319 TKT       | 4KXW   |
| KAYGQALAK               | 0 P29401  | TKT_HUM  | 319 TKT       | 4KXW   |
| KAYGQALAK               | 0 P29401  | TKT_HUM  | 319 TKT       | 4KXW   |
| KAYGQALAK               | 0 P29401  | TKT_HUM  | 319 TKT       | 4KXW   |
| KEHPDR                  | 0 P29401  | TKT_HUM  | 353 TKT       | 4KXW   |
| KLILDSAR                | 0 P29401  | TKT_HUM  | 543 TKT       | 4KXW   |
| SGKPAELLK               | 2 P29401  | TKT_HUM  | 597 TKT       | 4KXW   |
| VGDKIATR                | 3 P29401  | TKT_HUM  | 314 TKT       | 4KXW   |
| VGDKIATR                | 3 P29401  | TKT_HUM  | 314 TKT       | 4KXW   |
| VVLKSK                  | 3 P29401  | TKT_HUM  | 497 TKT       | 4KXW   |
| YKSQDPR                 | 1 P29401  | TKT_HUM  | 59 TKT        | 4KXW   |
| LVNLEKSSPGHR            | 5 P29692  | EF1D_HUM | 117 EEF1D     | ####   |
| FDTQYPYGEKQDEFKR        | 9 P30040  | ERP29_HU | 69 ERP29      | 2QC7   |
| KGAEKEEL                | 0 P30040  | ERP29_HU | 254 ERP29     | 2QC7   |
| AAKLAPEFAK              | 2 P30041  | PRDX6_HU | 56 PRDX6      | 5B6M   |
| LAPEFAKR                | 6 P30041  | PRDX6_HU | 63 PRDX6      | 5B6M   |
| LAPEFAKR                | 6 P30041  | PRDX6_HU | 63 PRDX6      | 5B6M   |
| AHKAEGK                 | 2 P30044  | PRDX5_HU | 142 PRDX5     | ####   |
| ALKEPPR                 | 2 P30050  | RL12_HUM | 86 RPL12      | 5A8L   |
| IGPLGLSPKK              | 8 P30050  | RL12_HUM | 40 RPL12      | 5A8L   |
| EGMTAFVEKR              | 8 P30084  | ECHM_HU  | 282 ECHS1     | P30084 |
| KANFK                   | 0 P30084  | ECHM_HU  | 284 ECHS1     | P30084 |
| VLTPQVQKNRPTSISWDGLDSGI | 7 P30086  | PEBP1_HU | 47 PEBP1      | 1BEH   |
| DGKALER                 | 2 P30101  | PDIA3_HU | 347 PDIA3     | 3F8U   |
| KFLDAGHK                | 0 P30101  | PDIA3_HU | 289 PDIA3     | 3F8U   |
| KYEGGR                  | 0 P30101  | PDIA3_HU | 466 PDIA3     | 3F8U   |
| KYEGGR                  | 0 P30101  | PDIA3_HU | 466 PDIA3     | 3F8U   |
| TAKGEK                  | 2 P30101  | PDIA3_HU | 332 PDIA3     | 3F8U   |
| TAKGEK                  | 2 P30101  | PDIA3_HU | 332 PDIA3     | 3F8U   |
| TEEEFKK                 | 5 P30101  | PDIA3_HU | 146 PDIA3     | 3F8U   |
| ALCTGEKGFGYK            | 6 P30405  | PPIF_HUM | 86 PPIF       | 4O8H   |
| ALSTGEKGFGYK            | 6 P62937  | PPIA_HUM | 44 PPIA       | 4N1M   |
| LSPQAVNSIAKR            | 10 P30626 | SORCN_HU | 146 SRI       | 1JUO   |
| VGSVLQEGCGKISK          | 10 P31040 | SDHA_HUM | 538 SDHA      | P31040 |
| AVTKYTSSK               | 3 P62807  | H2B1C_HU | 121 HIST1H2BC | 5GT0   |
| AAVDYQKVVR              | 6 P31153  | METK2_HU | 81 MAT2A      | 5A1I   |
| KPIYQR                  | 0 P31153  | METK2_HU | 368 MAT2A     | 5A1I   |
| KPIYQR                  | 0 P31153  | METK2_HU | 368 MAT2A     | 5A1I   |
| LNAKLAE LR              | 3 P31153  | METK2_HU | 163 MAT2A     | 5A1I   |
| SLVKGGLCR               | 3 P31153  | METK2_HU | 307 MAT2A     | 5A1I   |

|                          |           |           |             |        |
|--------------------------|-----------|-----------|-------------|--------|
| AMLSTGFKIPQK             | 7 P31327  | CPSM_HUN  | 1356 CPS1   | 5DOT   |
| EIGFSDKQISK              | 6 P31327  | CPSM_HUN  | 915 CPS1    | 5DOT   |
| EIGFSDKQISK              | 6 P31327  | CPSM_HUN  | 915 CPS1    | 5DOT   |
| EPLFGISTGNLITGLAAGAKTYK  | 19 P31327 | CPSM_HUN  | 307 CPS1    | 5DOT   |
| GTMLGKIEFEGQPVDVDPNK     | 5 P31327  | CPSM_HUN  | 182 CPS1    | 5DOT   |
| GVLKEYGVK                | 3 P31327  | CPSM_HUN  | 527 CPS1    | 5DOT   |
| IAKAFAISGPFNVQFLVK       | 2 P31327  | CPSM_HUN  | 1232 CPS1   | 5DOT   |
| IAKAFAISGPFNVQFLVK       | 2 P31327  | CPSM_HUN  | 1232 CPS1   | 5DOT   |
| IALGIPLPEIKNVVSGK        | 10 P31327 | CPSM_HUN  | 751 CPS1    | 5DOT   |
| IGSSMKSVGEVMAIGR         | 5 P31327  | CPSM_HUN  | 793 CPS1    | 5DOT   |
| IGSSMKSVGEVMAIGR         | 5 P31327  | CPSM_HUN  | 793 CPS1    | 5DOT   |
| IPQKGILIGIQQSFRR         | 3 P31327  | CPSM_HUN  | 1360 CPS1   | 5DOT   |
| KELSEPSSTR               | 0 P31327  | CPSM_HUN  | 841 CPS1    | 5DOT   |
| KELSEPSSTR               | 0 P31327  | CPSM_HUN  | 841 CPS1    | P31327 |
| KELSEPSSTR               | 0 P31327  | CPSM_HUN  | 841 CPS1    | 5DOT   |
| KELSEPSSTR               | 0 P31327  | CPSM_HUN  | 841 CPS1    | 5DOT   |
| KELSEPSSTR               | 0 P31327  | CPSM_HUN  | 841 CPS1    | 5DOT   |
| KELSEPSSTR               | 0 P31327  | CPSM_HUN  | 841 CPS1    | 5DOT   |
| KFLEEATR                 | 0 P31327  | CPSM_HUN  | 1150 CPS1   | 5DOT   |
| KFLEEATR                 | 0 P31327  | CPSM_HUN  | 1150 CPS1   | 5DOT   |
| KFLEEATR                 | 0 P31327  | CPSM_HUN  | 1150 CPS1   | 5DOT   |
| KFLEEATR                 | 0 P31327  | CPSM_HUN  | 1150 CPS1   | 5DOT   |
| LFAEAVQKSR               | 7 P31327  | CPSM_HUN  | 1479 CPS1   | 5DOT   |
| LPMNKEWPSNLDLR           | 4 P31327  | CPSM_HUN  | 831 CPS1    | 5DOT   |
| NVVSGKTSACFEPSLDYMVTK    | 5 P31327  | CPSM_HUN  | 757 CPS1    | 5DOT   |
| NVVSGKTSACFEPSLDYM[147.] | 5 P31327  | CPSM_HUN  | 757 CPS1    | 5DOT   |
| QISKCLGLTEAQTR           | 3 P31327  | CPSM_HUN  | 919 CPS1    | 5DOT   |
| QISKCLGLTEAQTR           | 3 P31327  | CPSM_HUN  | 919 CPS1    | 5DOT   |
| VSQEHPPVLTKFVEGAR        | 10 P31327 | CPSM_HUN  | 1168 CPS1   | 5DOT   |
| VSQEHPPVLTKFVEGAR        | 10 P31327 | CPSM_HUN  | 1168 CPS1   | 5DOT   |
| KQQMGK                   | 0 P31946  | 1433B_HU  | 77 YWHAB    | 5N10   |
| KQQM[147.04]GK           | 0 P31946  | 1433B_HU  | 77 YWHAB    | 5N10   |
| VISSIEQKTER              | 7 P31946  | 1433B_HU  | 70 YWHAB    | 5N10   |
| DAKLYSNR                 | 2 P31948  | STIP1_HUN | 395 STIP1   | P31948 |
| DAKLYSNR                 | 2 P31948  | STIP1_HUN | 395 STIP1   | P31948 |
| DCEECIQLEPTFIKGYTR       | 13 P31948 | STIP1_HUN | 429 STIP1   | P31948 |
| KAAALEFLNR               | 0 P31948  | STIP1_HUN | 78 STIP1    | P31948 |
| KAAALEFLNR               | 0 P31948  | STIP1_HUN | 78 STIP1    | P31948 |
| QIAKAYAR                 | 3 P31948  | STIP1_HUN | 301 STIP1   | 1ELR   |
| SAAYAKK                  | 5 P31948  | STIP1_HUN | 50 STIP1    | P31948 |
| DDIYEHIKEK               | 7 P37058  | DHB3_HUN  | 117 HSD17B3 | P37058 |
| LMAEGAPKWPK              | 7 P32004  | L1CAM_HL  | 137 L1CAM   | ####   |
| LM[147.04]AEGAPKWPK      | 7 P32004  | L1CAM_HL  | 137 L1CAM   | P32004 |
| LM[147.04]AEGAPKWPK      | 7 P32004  | L1CAM_HL  | 137 L1CAM   | ####   |
| STIEKK                   | 4 P32004  | L1CAM_HL  | 530 L1CAM   | P32004 |
| STIEKK                   | 4 P32004  | L1CAM_HL  | 530 L1CAM   | P32004 |
| TLQLLKVGEEDDGEYR         | 5 P32004  | L1CAM_HL  | 301 L1CAM   | P32004 |

|                         |           |          |           |           |
|-------------------------|-----------|----------|-----------|-----------|
| TLQLLKVGEEDDGEYR        | 5 P32004  | L1CAM_HL | 301 L1CAM | P32004    |
| IGKPAPDFK               | 2 P32119  | PRDX2_HU | 10 PRDX2  | 5IJT      |
| IGKPAPDFK               | 2 P32119  | PRDX2_HU | 10 PRDX2  | 5IJT      |
| IGKPAPDFK               | 2 P32119  | PRDX2_HU | 10 PRDX2  | 5IJT      |
| KEGGLGPLNIPLADVTR       | 0 P32119  | PRDX2_HU | 92 PRDX2  | 5IJT      |
| LSDYK GK                | 4 P32119  | PRDX2_HU | 34 PRDX2  | 5IJT      |
| LSDYK GK                | 4 P32119  | PRDX2_HU | 34 PRDX2  | 5IJT      |
| IGKPAPDFK               | 2 P32119  | PRDX2_HU | 10 PRDX2  | 5IJT      |
| IGKPAPDFK               | 2 P32119  | PRDX2_HU | 10 PRDX2  | 5IJT      |
| KQGGLGPMNIPLVSDPK       | 0 Q06830  | PRDX1_HU | 93 PRDX1  | 4XCS      |
| IFKGCNIENACYPLGICAER    | 2 P32320  | CDD_HUM  | 51 CDA    | 1MQ0      |
| KELATVR                 | 0 P32969  | RL9_HUM  | 65 RPL9   | P32969    |
| KELATVR                 | 0 P32969  | RL9_HUM  | 65 RPL9   | 2CQL      |
| KELATVR                 | 0 P32969  | RL9_HUM  | 65 RPL9   | 2CQL      |
| NFLGEKYIR               | 5 P32969  | RL9_HUM  | 121 RPL9  | P32969    |
| TVIVKGPR                | 4 P32969  | RL9_HUM  | 28 RPL9   | 2CQL      |
| KELATVR                 | 0 P32969  | RL9_HUM  | 65 RPL9   | 2CQL      |
| KNDLR                   | 0 Q9H2U1  | DHX36_HU | 192 DHX36 | Q9H2U1    |
| KLFVQDLATR              | 0 P33176  | KINH_HUM | 801 KIF5B | ####      |
| KLFVQDLATR              | 0 P33176  | KINH_HUM | 801 KIF5B | ####      |
| SKNM[147.04]AR          | 1 P33176  | KINH_HUM | 909 KIF5B | ####      |
| AVVKTDIQIALPSGCGYR      | 3 P33316  | DUT_HUM  | 155 DUT   | 3ARA      |
| GSGGFGSTGKN             | 9 P33316  | DUT_HUM  | 251 DUT   | ####      |
| ALADDDFLTVTGKTVR        | 12 P33991 | MCM4_HU  | 858 MCM4  | ####      |
| KPDIYER                 | 0 P33991  | MCM4_HU  | 455 MCM4  | P33991    |
| LFSEKR                  | 4 P33991  | MCM4_HU  | 444 MCM4  | P33991    |
| TPALKYQQLFEDIR          | 4 P33991  | MCM4_HU  | 819 MCM4  | P33991_P3 |
| DSLLGDKGQTAR            | 6 P33993  | MCM7_HU  | 648 MCM7  | P33993    |
| EAWASKDATYTSAR          | 5 P33993  | MCM7_HU  | 596 MCM7  | P33993    |
| AVDPKTGR                | 4 P34897  | GLYM_HU  | 302 SHMT2 | P34897    |
| EYSLQVLKNAR             | 7 P34897  | GLYM_HU  | 356 SHMT2 | P34897    |
| LNPKTGLIDYNQLALTAR      | 3 P34897  | GLYM_HU  | 200 SHMT2 | P34897_P3 |
| LQDFKSFLK               | 4 P34897  | GLYM_HU  | 469 SHMT2 | P34897    |
| SFLLKDSETSQR            | 4 P34897  | GLYM_HU  | 474 SHMT2 | P34897    |
| TAKLQDFK                | 2 P34897  | GLYM_HU  | 464 SHMT2 | P34897    |
| TAKLQDFK                | 2 P34897  | GLYM_HU  | 464 SHMT2 | P34897    |
| VVDFIDEGVNIGLEVSK       | 15 P34897 | GLYM_HU  | 459 SHMT2 | P34897    |
| YSEGYPGKR               | 7 P34897  | GLYM_HU  | 103 SHMT2 | P34897    |
| YSEGYPGKR               | 7 P34897  | GLYM_HU  | 103 SHMT2 | P34897    |
| YSEGYPGKR               | 7 P34897  | GLYM_HU  | 103 SHMT2 | P34897    |
| VTPQSDGSSSKVK           | 10 P34932 | HSP74_HU | 477 HSPA4 | P34932    |
| KVAQVPLGPECSR           | 0 P35052  | GPC1_HU  | 236 GPC1  | 4AD7      |
| QIYGAKGFSLSVDPQAEISGEHL | 5 P35052  | GPC1_HU  | 42 GPC1   | 4AD7      |
| FVVEKAEQQK              | 4 P35232  | PHB_HUM  | 202 PHB   | P35232_P3 |
| FVVEKAEQQK              | 4 P35232  | PHB_HUM  | 202 PHB   | P35232    |
| VLPSITTEILKSVVAR        | 10 P35232 | PHB_HUM  | 128 PHB   | P35232    |
| AKQEQR                  | 1 Q99623  | PHB2_HU  | 218 PHB2  | Q99623    |

|                       |          |          |           |        |
|-----------------------|----------|----------|-----------|--------|
| AKQEQR                | 1 Q99623 | PHB2_HUM | 218 PHB2  | Q99623 |
| AQFLVEKAK             | 6 Q99623 | PHB2_HUM | 216 PHB2  | ####   |
| AQFLVEKAK             | 6 Q99623 | PHB2_HUM | 216 PHB2  | ####   |
| FVVEKAEQQK            | 4 P35232 | PHB_HUM/ | 202 PHB   | P35232 |
| FVVEKAEQQK            | 4 P35232 | PHB_HUM/ | 202 PHB   | P35232 |
| KISSPTGSK             | 0 Q99623 | PHB2_HUM | 89 PHB2   | Q99623 |
| SVVAKFNASQLITQR       | 4 Q99623 | PHB2_HUM | 147 PHB2  | Q99623 |
| YTKLTDAQILTR          | 2 P35250 | RFC2_HUM | 192 RFC2  | P35250 |
| YTKLTDAQILTR          | 2 P35250 | RFC2_HUM | 192 RFC2  | P35250 |
| KYTWNDVGQLVEK         | 0 P35573 | GDE_HUM/ | 191 AGL   | ####   |
| EEELVKVR              | 5 P35579 | MYH9_HUI | 856 MYH9  | P35579 |
| EKETKALSLAR           | 4 P35579 | MYH9_HUI | 1477 MYH9 | ####   |
| INKALDK               | 2 P35579 | MYH9_HUI | 435 MYH9  | P35579 |
| KDQGELER              | 0 P35579 | MYH9_HUI | 202 MYH9  | P35579 |
| LEVNLQAMKAQFER        | 8 P35579 | MYH9_HUI | 1566 MYH9 | ####   |
| LNKQFR                | 2 P35579 | MYH9_HUI | 1500 MYH9 | ####   |
| LNKQFR                | 2 P35579 | MYH9_HUI | 1500 MYH9 | ####   |
| QKLQLEK               | 1 P35579 | MYH9_HUI | 961 MYH9  | ####   |
| QSACNLEKK             | 7 P35579 | MYH9_HUI | 1441 MYH9 | ####   |
| TDLLEPYNKYR           | 9 P35579 | MYH9_HUI | 299 MYH9  | P35579 |
| TDLLEPYNKYR           | 9 P35579 | MYH9_HUI | 299 MYH9  | P35579 |
| TDLLEPYNKYR           | 9 P35579 | MYH9_HUI | 299 MYH9  | P35579 |
| VKANLEK               | 1 P35579 | MYH9_HUI | 1212 MYH9 | ####   |
| VLLQGKGDSEHK          | 5 P35579 | MYH9_HUI | 1240 MYH9 | ####   |
| YKASITALEAK           | 1 P35579 | MYH9_HUI | 1806 MYH9 | ####   |
| INKALDR               | 2 P35580 | MYH10_HL | 442 MYH10 | 4PD3   |
| GGVVLKEDALPGQK        | 5 P35613 | BASI_HUM | 179 BSG   | 4U0Q   |
| GGVVLKEDALPGQK        | 5 P35613 | BASI_HUM | 179 BSG   | 4U0Q   |
| GGVVLKEDALPGQK        | 5 P35613 | BASI_HUM | 179 BSG   | 4U0Q   |
| VKAVK                 | 1 P35613 | BASI_HUM | 224 BSG   | 4U0Q   |
| VKAVK                 | 1 P35613 | BASI_HUM | 224 BSG   | 4U0Q   |
| VKAVK                 | 1 P35613 | BASI_HUM | 224 BSG   | 4U0Q   |
| VKAVK                 | 1 P35613 | BASI_HUM | 224 BSG   | 4U0Q   |
| WLKGGVVLK             | 2 P35613 | BASI_HUM | 173 BSG   | 4U0Q   |
| KTGQPMINLYTDR         | 0 P35637 | FUS_HUM/ | 316 FUS   | ####   |
| KTGQPM[147.04]INLYTDR | 0 P35637 | FUS_HUM/ | 316 FUS   | ####   |
| QIGIIKTNK             | 5 P35637 | FUS_HUM/ | 312 FUS   | ####   |
| QIGIIKTNK             | 5 P35637 | FUS_HUM/ | 312 FUS   | ####   |
| ELKPAR                | 2 P36542 | ATPG_HUM | 64 ATP5C1 | P36542 |
| AWNDIKK               | 5 P36578 | RL4_HUM/ | 181 RPL4  | P36578 |
| AWNDIKK               | 5 P36578 | RL4_HUM/ | 181 RPL4  | P36578 |
| KAASLK                | 0 P36578 | RL4_HUM/ | 269 RPL4  | P36578 |
| KAASLK                | 0 P36578 | RL4_HUM/ | 269 RPL4  | P36578 |
| KPVVGK                | 0 P36578 | RL4_HUM/ | 375 RPL4  | P36578 |
| VNTTQKR               | 5 P36578 | RL4_HUM/ | 120 RPL4  | P36578 |
| VNTTQKR               | 5 P36578 | RL4_HUM/ | 120 RPL4  | P36578 |
| VNTTQKR               | 5 P36578 | RL4_HUM/ | 120 RPL4  | P36578 |

|                  |           |           |            |           |
|------------------|-----------|-----------|------------|-----------|
| VNTTQKR          | 5 P36578  | RL4_HUMA  | 120 RPL4   | P36578    |
| ILKSPEIQR        | 2 P36578  | RL4_HUMA  | 294 RPL4   | P36578    |
| ILKSPEIQR        | 2 P36578  | RL4_HUMA  | 294 RPL4   | P36578    |
| KAASLK           | 0 P36578  | RL4_HUMA  | 269 RPL4   | P36578    |
| KAASLK           | 0 P36578  | RL4_HUMA  | 269 RPL4   | P36578    |
| LLVKLYR          | 3 Q07020  | RL18_HUM  | 30 RPL18   | Q07020    |
| AGVTCIVLPAENKK   | 12 P36776 | LONM_HUI  | 917 LONP1  | P36776    |
| AGVTCIVLPAENKK   | 12 P36776 | LONM_HUI  | 917 LONP1  | P36776    |
| ALSLLKK          | 5 P36776  | LONM_HUI  | 367 LONP1  | ####      |
| ALSLLKK          | 5 P36776  | LONM_HUI  | 367 LONP1  | ####      |
| EFELSKLQQR       | 5 P36776  | LONM_HUI  | 374 LONP1  | ####      |
| KEFELSK          | 0 P36776  | LONM_HUI  | 368 LONP1  | ####      |
| LKELVVPK         | 1 P36776  | LONM_HUI  | 426 LONP1  | P36776    |
| LYKALSLLK        | 2 P36776  | LONM_HUI  | 361 LONP1  | ####      |
| TIAAKR           | 4 P36776  | LONM_HUI  | 903 LONP1  | P36776    |
| SFVGKQFSANDK     | 4 P36871  | PGM1_HUI  | 457 PGM1   | 5JN5      |
| SKNILVK          | 1 P36897  | TGFR1_HU  | 337 TGFR1  | 1B6C      |
| KTQCR            | 0 P36941  | TNR3_HUN  | 121 LTBR   | ####      |
| KISTVVSSK        | 0 P37108  | SRP14_HUI | 66 SRP14   | P37108    |
| TKPIPK           | 1 P37108  | SRP14_HUI | 38 SRP14   | P37108    |
| FAADAVKLER       | 6 P37837  | TALDO_HU  | 321 TALDO1 | 1F05      |
| KLGGSQEDQIK      | 0 P37837  | TALDO_HU  | 71 TALDO1  | 1F05      |
| VIDYAVKIR        | 6 P38117  | ETFB_HUM  | 19 ETFB    | 1EFV      |
| VLAKLAEK         | 3 P38117  | ETFB_HUM  | 110 ETFB   | 1EFV      |
| SGGPPPKR         | 6 P38159  | RBMX_HUI  | 163 RBMX   | ####      |
| VEQATKPSFESGR    | 5 P38159  | RBMX_HUI  | 86 RBMX    | 2MB0      |
| DKGTGR           | 1 P38646  | GRP75_HU  | 537 HSPA9  | P38646_p3 |
| DKGTGR           | 1 P38646  | GRP75_HU  | 537 HSPA9  | P38646    |
| DKGTGR           | 1 P38646  | GRP75_HU  | 537 HSPA9  | P38646    |
| HIVKEFK          | 3 P38646  | GRP75_HU  | 288 HSPA9  | 4KBO      |
| HLNMKLTR         | 4 P38646  | GRP75_HU  | 345 HSPA9  | 4KBO      |
| KDSETGENIR       | 0 P38646  | GRP75_HU  | 625 HSPA9  | P38646    |
| KDSETGENIR       | 0 P38646  | GRP75_HU  | 625 HSPA9  | P38646    |
| LKEEISK          | 1 P38646  | GRP75_HU  | 612 HSPA9  | P38646    |
| LVGMPAKR         | 6 P38646  | GRP75_HU  | 106 HSPA9  | 4KBO      |
| MPKVQQTVDLFGR    | 2 P38646  | GRP75_HU  | 394 HSPA9  | 4KBO      |
| MPKVQQTVDLFGR    | 2 P38646  | GRP75_HU  | 394 HSPA9  | 4KBO      |
| MPKVQQTVDLFGR    | 2 P38646  | GRP75_HU  | 394 HSPA9  | 4KBO      |
| QATKDAGQISGLNVLR | 3 P38646  | GRP75_HU  | 206 HSPA9  | 4KBO      |
| QATKDAGQISGLNVLR | 3 P38646  | GRP75_HU  | 206 HSPA9  | 4KBO      |
| ESIMKEFR         | 4 P38919  | IF4A3_HUN | 321 EIF4A3 | 4C9B      |
| KGVAINFVK        | 0 P38919  | IF4A3_HUN | 374 EIF4A3 | 4C9B      |
| ESIMKEFR         | 4 P38919  | IF4A3_HUN | 321 EIF4A3 | 4C9B      |
| GSKSVAR          | 2 P39019  | RS19_HUM  | 97 RPS19   | 5FLX      |
| IAGQVAAANKK      | 9 P39019  | RS19_HUM  | 143 RPS19  | P39019    |
| GLIKLVSK         | 3 P62851  | RS25_HUM  | 98 RPS25   | P62851    |
| ALEKIDLK         | 3 P39023  | RL3_HUMA  | 362 RPL3   | P39023    |

|                 |          |           |            |           |
|-----------------|----------|-----------|------------|-----------|
| YKIGQGYLIK      | 2 P39023 | RL3_HUMA  | 286 RPL3   | P39023    |
| YKIGQGYLIK      | 2 P39023 | RL3_HUMA  | 286 RPL3   | P39023    |
| KYCQVIR         | 0 P39023 | RL3_HUMA  | 155 RPL3   | P39023    |
| SLLVQTKR        | 6 P39023 | RL3_HUMA  | 356 RPL3   | P39023    |
| KGDLLK          | 0 Q8WXHO | SYNE2_HUI | 4586 SYNE2 | ####      |
| TSTGAPAAIKK     | 9 P40121 | CAPG_HUN  | 137 CAPG   | 1J72      |
| QAPPSKGPTVR     | 5 P40189 | IL6RB_HUN | 521 IL6ST  | 3L5H      |
| QAPPSKGPTVR     | 5 P40189 | IL6RB_HUN | 521 IL6ST  | 3L5H      |
| SKLESLCR        | 1 P40222 | TXLNA_HU  | 240 TXLNA  | ####      |
| KFIEDR          | 0 P40227 | TCPZ_HUM  | 265 CCT6A  | P40227    |
| SVTLLIKGPNK     | 6 P40227 | TCPZ_HUM  | 377 CCT6A  | P40227    |
| TEVNSGFFYKSAEER | 9 P40227 | TCPZ_HUM  | 251 CCT6A  | P40227    |
| HKSETDTSLIR     | 1 P40227 | TCPZ_HUM  | 199 CCT6A  | P40227    |
| SVTLLIKGPNK     | 6 P40227 | TCPZ_HUM  | 377 CCT6A  | P40227    |
| KFAYLGR         | 0 P40429 | RL13A_HUI | 134 RPL13A | P40429    |
| KFAYLGR         | 0 P40429 | RL13A_HUI | 134 RPL13A | P40429    |
| KVVVVR          | 0 P40429 | RL13A_HUI | 32 RPL13A  | P40429    |
| KVVVVR          | 0 P40429 | RL13A_HUI | 32 RPL13A  | P40429    |
| MVVPAALKVVR     | 7 P40429 | RL13A_HUI | 125 RPL13A | P40429    |
| GAAVIKAR        | 5 P40925 | MDHC_HU   | 236 MDH1   | P40925    |
| GAAVIKAR        | 5 P40925 | MDHC_HU   | 236 MDH1   | P40925    |
| ANTFVAELKGLDPAR | 8 P40926 | MDHM_HL   | 185 MDH2   | 2DFD      |
| ANTFVAELKGLDPAR | 8 P40926 | MDHM_HL   | 185 MDH2   | 2DFD      |
| ANTFVAELKGLDPAR | 8 P40926 | MDHM_HL   | 185 MDH2   | 2DFD      |
| ASIKKGEDFVK     | 3 P40926 | MDHM_HL   | 328 MDH2   | 2DFD      |
| IQEAGTEVVKAK    | 9 P40926 | MDHM_HL   | 239 MDH2   | 2DFD      |
| IQEAGTEVVKAK    | 9 P40926 | MDHM_HL   | 239 MDH2   | 2DFD      |
| IQEAGTEVVKAK    | 9 P40926 | MDHM_HL   | 239 MDH2   | 2DFD      |
| KGEDFVK         | 0 P40926 | MDHM_HL   | 329 MDH2   | 2DFD      |
| KGEDFVK         | 0 P40926 | MDHM_HL   | 329 MDH2   | 2DFD      |
| KGEDFVK         | 0 P40926 | MDHM_HL   | 329 MDH2   | 2DFD      |
| KPGMTR          | 0 P40926 | MDHM_HL   | 105 MDH2   | 2DFD      |
| KPGM[147.04]TR  | 0 P40926 | MDHM_HL   | 105 MDH2   | 2DFD      |
| KPGM[147.04]TR  | 0 P40926 | MDHM_HL   | 105 MDH2   | 2DFD      |
| FGELVMTKESK     | 7 P40939 | ECHA_HUN  | 334 HADHA  | P40939    |
| FGELVMTKESK     | 7 P40939 | ECHA_HUN  | 334 HADHA  | P40939    |
| FVDLYGAQKIVDR   | 8 P40939 | ECHA_HUN  | 728 HADHA  | P40939    |
| GLYPAPLKIIDVVK  | 7 P40939 | ECHA_HUN  | 303 HADHA  | P40939_P4 |
| GKLVQVNSR       | 1 P41221 | WNT5A_HI  | 283 WNT5A  | P41221    |
| DADKSIIR        | 3 P41252 | SYIC_HUM, | 375 IARS   | P41252    |
| FPGAYLK GK      | 6 P41252 | SYIC_HUM, | 285 IARS   | P41252    |
| TIPIKYPLK       | 4 P41252 | SYIC_HUM, | 844 IARS   | P41252    |
| TLKEQGR         | 2 P41252 | SYIC_HUM, | 382 IARS   | P41252    |
| TLKEQGR         | 2 P41252 | SYIC_HUM, | 382 IARS   | P41252    |
| RVPVLGKEYTEK    | 6 Q9P2J5 | SYLC_HUM  | 1133 LARS  | ####      |
| DDQLKVHGF       | 4 P41567 | EIF1_HUM, | 109 EIF1   | 4KZY      |
| KATASR          | 0 P42126 | ECI1_HUM, | 260 ECI1   | 1SG4      |



|                         |           |           |             |        |
|-------------------------|-----------|-----------|-------------|--------|
| KATASR                  | 0 P42126  | ECI1_HUM  | 260 ECI1    | 1SG4   |
| AEVGEKTEER              | 5 P42167  | LAP2B_HUI | 334 TMPO    | ####   |
| KVIEEQLEPAVEK           | 0 P42704  | LPPRC_HUI | 1224 LRPPRC | P42704 |
| VGIPKETPALTINR          | 4 P42765  | THIM_HUN  | 81 ACAA2    | 4C2K   |
| KEEIIK                  | 0 P42766  | RL35_HUM  | 14 RPL35    | P42766 |
| KSIAR                   | 0 P42766  | RL35_HUM  | 52 RPL35    | P42766 |
| VAKVTGGAASK             | 2 P42766  | RL35_HUM  | 35 RPL35    | P42766 |
| KTCLPR                  | 0 P42892  | ECE1_HUM  | 426 ECE1    | ####   |
| EGKIVR                  | 2 P43003  | EAA1_HUN  | 160 SLC1A3  | P43003 |
| EGKIVR                  | 2 P43003  | EAA1_HUN  | 160 SLC1A3  | P43003 |
| EGKIVR                  | 2 P43003  | EAA1_HUN  | 160 SLC1A3  | P43003 |
| TNYEKR                  | 4 P43003  | EAA1_HUN  | 196 SLC1A3  | ####   |
| AQLVKEDKDAQFYCELNYR     | 7 P43121  | MUC18_HL  | 217 MCAM    | P43121 |
| EDKDAQFYCELNYR          | 2 P43121  | MUC18_HL  | 217 MCAM    | P43121 |
| EDKDAQFYCELNYR          | 2 P43121  | MUC18_HL  | 217 MCAM    | P43121 |
| EVTVPVFYPTTEKVVLEVEPVGM | 11 P43121 | MUC18_HL  | 251 MCAM    | P43121 |
| EVTVPVFYPTTEKVVLEVEPVGM | 11 P43121 | MUC18_HL  | 251 MCAM    | P43121 |
| FLNKLAEER               | 3 P43243  | MATR3_HL  | 836 MATR3   | ####   |
| TGFYCKLCSLFYTNEEVAK     | 5 P43243  | MATR3_HL  | 804 MATR3   | ####   |
| DIFNKGFGFGLVK           | 4 P45880  | VDAC2_HU  | 31 VDAC2    | P45880 |
| DIFNKGFGFGLVK           | 4 P45880  | VDAC2_HU  | 31 VDAC2    | P45880 |
| DIFNKGFGFGLVK           | 4 P45880  | VDAC2_HU  | 31 VDAC2    | P45880 |
| LDVKT                   | 3 P45880  | VDAC2_HU  | 43 VDAC2    | P45880 |
| LTFTDTFSPNTGKK          | 12 P45880 | VDAC2_HU  | 120 VDAC2   | P45880 |
| LTFTDTFSPNTGKK          | 12 P45880 | VDAC2_HU  | 120 VDAC2   | P45880 |
| SCSGVEFSTSGSSNTDTGKVTGT | 18 P45880 | VDAC2_HU  | 64 VDAC2    | P45880 |
| SSYKR                   | 3 P45880  | VDAC2_HU  | 130 VDAC2   | P45880 |
| SKGAVAIADAIR            | 1 P46060  | RAGP1_HU  | 279 RANGAP1 | P46060 |
| SKGAVAIADAIR            | 1 P46060  | RAGP1_HU  | 279 RANGAP1 | P46060 |
| ILGPGLNKAGK             | 7 P62906  | RL10A_HUI | 130 RPL10A  | P62906 |
| KQFSQYIK                | 0 P46777  | RL5_HUM   | 221 RPL5    | P46777 |
| TTTGNKVFGALK            | 5 P46777  | RL5_HUM   | 158 RPL5    | P46777 |
| TTTGNKVFGALK            | 5 P46777  | RL5_HUM   | 158 RPL5    | P46777 |
| TTTGNKVFGALK            | 5 P46777  | RL5_HUM   | 158 RPL5    | P46777 |
| YNTPKYR                 | 4 P46777  | RL5_HUM   | 48 RPL5     | P46777 |
| YQVKFR                  | 3 P46777  | RL5_HUM   | 19 RPL5     | P46777 |
| DSFLKR                  | 4 P46778  | RL21_HUM  | 107 RPL21   | P46778 |
| GVVVVIKR                | 6 P46779  | RL28_HUM  | 65 RPL28    | ####   |
| GVVVVIKR                | 6 P46779  | RL28_HUM  | 65 RPL28    | ####   |
| GVVVVIKR                | 6 P46779  | RL28_HUM  | 65 RPL28    | ####   |
| KPATSYVR                | 0 P46779  | RL28_HUM  | 72 RPL28    | ####   |
| NCSSFLIKR               | 7 P46779  | RL28_HUM  | 19 RPL28    | ####   |
| TTINKNAR                | 4 P46779  | RL28_HUM  | 84 RPL28    | ####   |
| FTLAKIR                 | 4 P46781  | RS9_HUM   | 52 RPS9     | 5FLX   |
| KQVVNIPSFIVR            | 0 P46781  | RS9_HUM   | 139 RPS9    | 5FLX   |
| KTYVTPR                 | 0 P46781  | RS9_HUM   | 11 RPS9     | 5FLX   |
| KTYVTPR                 | 0 P46781  | RS9_HUM   | 11 RPS9     | 5FLX   |

|                       |    |        |           |      |         |           |
|-----------------------|----|--------|-----------|------|---------|-----------|
| KTYVTPR               | 0  | P46781 | RS9_HUM/  | 11   | RPS9    | 5FLX      |
| MKLDYILGLK            | 1  | P46781 | RS9_HUM/  | 93   | RPS9    | 5FLX      |
| VKFTLAK               | 1  | P46781 | RS9_HUM/  | 47   | RPS9    | 5FLX      |
| KQVVNIPSFIVR          | 0  | P46781 | RS9_HUM/  | 139  | RPS9    | P46781    |
| YAAKR                 | 3  | P46782 | RS5_HUM/  | 59   | RPS5    | 5FLX      |
| YAAKR                 | 3  | P46782 | RS5_HUM/  | 59   | RPS5    | 5FLX      |
| ATYDKLCK              | 4  | P62851 | RS25_HUM  | 57   | RPS25   | P62851    |
| EVPNYKLITPAVVSR       | 5  | P62851 | RS25_HUM  | 66   | RPS25   | P62851    |
| EKIQTGLK              | 1  | P46940 | IQGA1_HU  | 1458 | IQGAP1  | ####      |
| ITLQDVVSHSKK          | 10 | P46940 | IQGA1_HU  | 935  | IQGAP1  | ####      |
| MHQARKR               | 5  | P46940 | IQGA1_HU  | 823  | IQGAP1  | ####      |
| TILLNTRK              | 6  | P46940 | IQGA1_HU  | 1389 | IQGAP1  | ####      |
| MNFLKK                | 4  | P46940 | IQGA1_HU  | 773  | IQGAP1  | ####      |
| IKIIPPER              | 1  | P68032 | ACTC_HUN  | 330  | ACTC1   | P68032    |
| DILQAVKEAAVQR         | 6  | Q96TA1 | NIBL1_HUN | 554  | FAM129B | ####      |
| KVPLDER               | 0  | Q96TA1 | NIBL1_HUN | 62   | FAM129B | ####      |
| DKVVGK                | 1  | P47756 | CAPZB_HU  | 53   | CAPZB   | P47756    |
| KLEVEANNAFDQYR        | 0  | P47756 | CAPZB_HU  | 95   | CAPZB   | P47756    |
| KLEVEANNAFDQYR        | 0  | P47756 | CAPZB_HU  | 95   | CAPZB   | P47756    |
| ILSYKIGK              | 4  | P52907 | CAZA1_HU  | 278  | CAPZA1  | P52907    |
| ILSYKIGK              | 4  | P52907 | CAZA1_HU  | 278  | CAPZA1  | P52907    |
| ILSYKIGK              | 4  | P52907 | CAZA1_HU  | 278  | CAPZA1  | P52907    |
| LEAMCFDGVKR           | 9  | P47813 | IF1AX_HUN | 56   | EIF1AX  | 4KZY      |
| KILQLVATGAVR          | 0  | P47897 | SYQ_HUM/  | 498  | QARS    | P47897    |
| KILQLVATGAVR          | 0  | P47897 | SYQ_HUM/  | 498  | QARS    | 4YE6      |
| KILQLVATGAVR          | 0  | P47897 | SYQ_HUM/  | 498  | QARS    | 4YE6      |
| TVTLKEDPGKV           | 4  | P47897 | SYQ_HUM/  | 769  | QARS    | 4YE6      |
| VKYTPHHR              | 1  | P47897 | SYQ_HUM/  | 421  | QARS    | 4YE6      |
| LSDIPEGKNMAFK         | 7  | P47985 | UCRI_HUM  | 163  | UQCRFS1 | 5XTE      |
| LSDIPEGKNM[147.04]AFK | 7  | P47985 | UCRI_HUM  | 163  | UQCRFS1 | 5XTE      |
| SFLSQGQVLKLEAK        | 9  | P48047 | ATPO_HUN  | 172  | ATP50   | ####      |
| VAQILKEPK             | 5  | P48047 | ATPO_HUN  | 70   | ATP50   | P48047    |
| ISDDKYGR              | 4  | P48444 | COPD_HUN  | 309  | ARCN1   | P48444    |
| KVEDAK                | 0  | P48643 | TCPE_HUM  | 242  | CCT5    | 5UYX      |
| FFDKVQDLGR            | 3  | P48960 | CD97_HUN  | 281  | CD97    | ####      |
| APKSACGVCPGR          | 2  | P49207 | RL34_HUM  | 43   | RPL34   | P49207    |
| IVVKVLK               | 3  | P49207 | RL34_HUM  | 105  | RPL34   | P49207    |
| IVYLYTKK              | 6  | P49207 | RL34_HUM  | 36   | RPL34   | P49207    |
| IVVKVLK               | 3  | P49207 | RL34_HUM  | 105  | RPL34   | P49207    |
| NKPYPVR               | 1  | P49257 | LMAN1_HL  | 197  | LMAN1   | P49257_P4 |
| YVSSLTEEISKR          | 10 | P49257 | LMAN1_HL  | 372  | LMAN1   | P49257_P4 |
| KRKPEEESPR            | 0  | P49321 | NASP_HUN  | 719  | NASP    | ####      |
| EGVFAKEVR             | 5  | P49327 | FAS_HUM/  | 673  | FASN    | P49327    |
| TGYQAKQVR             | 5  | P49327 | FAS_HUM/  | 1927 | FASN    | 4PIV      |
| VFTTVGSAEKR           | 9  | P49327 | FAS_HUM/  | 1704 | FASN    | P49327    |
| VFTTVGSAEKR           | 9  | P49327 | FAS_HUM/  | 1704 | FASN    | P49327    |
| VFTTVGSAEKR           | 9  | P49327 | FAS_HUM/  | 1704 | FASN    | P49327    |

|                    |           |          |              |        |
|--------------------|-----------|----------|--------------|--------|
| VFTTVGSAEKR        | 9 P49327  | FAS_HUM  | 1704 FASN    | P49327 |
| YMAQKGKHIGK        | 5 P49327  | FAS_HUM  | 1847 FASN    | P49327 |
| YMAQKGKHIGK        | 5 P49327  | FAS_HUM  | 1847 FASN    | P49327 |
| YM[147.04]AQGKHIGK | 5 P49327  | FAS_HUM  | 1847 FASN    | P49327 |
| ILAEGGGAKFK        | 8 P49411  | EFTU_HUN | 88 TUFM      | ####   |
| KAESLK             | 0 P49588  | SYAC_HUN | 766 AARS     | P49588 |
| KAESLK             | 0 P49588  | SYAC_HUN | 766 AARS     | P49588 |
| KAESLK             | 0 P49588  | SYAC_HUN | 766 AARS     | P49588 |
| SVLGEADQKGSVLAPDR  | 8 P49588  | SYAC_HUN | 625 AARS     | P49588 |
| LNLVELKEGR         | 6 P49720  | PSB3_HUN | 77 PSMB3     | 5LE5   |
| IIEYKR             | 4 Q5H9M0  | MUML1_H  | 686 MUM1L1   | ####   |
| KYIIYAK            | 0 P49736  | MCM2_HU  | 722 MCM2     | P49736 |
| EKITAFVVER         | 1 P49748  | ACADV_HU | 278 ACADVL   | 3B96   |
| GKELSGLGSAK        | 1 P49748  | ACADV_HU | 482 ACADVL   | 3B96   |
| KPAKAESKFAVGMFK    | 0 P49748  | ACADV_HU | 64 ACADVL    | ####   |
| SISKALVER          | 3 P49748  | ACADV_HU | 639 ACADVL   | 3B96   |
| TPVTDPATGAVKEK     | 11 P49748 | ACADV_HU | 276 ACADVL   | 3B96   |
| LMTPKPVSIATNR      | 4 P49790  | NU153_HU | 371 NUP153   | ####   |
| AKLYR              | 1 P49792  | RBP2_HUN | 2338 RANBP2  | ####   |
| AVPGNVAKLR         | 7 P49792  | RBP2_HUN | 550 RANBP2   | ####   |
| GIGDIKILQNYDNK     | 5 P49792  | RBP2_HUN | 2358 RANBP2  | ####   |
| LKGSLSR            | 1 P49821  | NDUV1_HU | 54 NDUFV1    | 5XTB   |
| SGNIVAGIANESKK     | 12 P49915 | GUAA_HU  | 182 GMPS     | 2VXO   |
| VADGFKVVAR         | 5 P49915  | GUAA_HU  | 165 GMPS     | 2VXO   |
| FKIPGSPPEMGR       | 1 P50395  | GDIB_HUN | 57 GDI2      | P50395 |
| EQLKIWMGK          | 3 P50454  | SERPH_HU | 291 SERPINH1 | P50454 |
| KAVASLPK           | 0 P50454  | SERPH_HU | 300 SERPINH1 | P50454 |
| NVYKDLR            | 3 P50570  | DYN2_HUN | 598 DNM2     | 2YS1   |
| TGQKVALK           | 3 P50750  | CDK9_HUN | 44 CDK9      | 4EC9   |
| AAPAPKAQK          | 5 P50914  | RL14_HUN | 193 RPL14    | ####   |
| APAPKASGK          | 4 P50914  | RL14_HUN | 209 RPL14    | ####   |
| APAQKAPAPK         | 4 P50914  | RL14_HUN | 204 RPL14    | ####   |
| ATGQKAAPAPK        | 4 P50914  | RL14_HUN | 187 RPL14    | ####   |
| GQKAPAQK           | 2 P50914  | RL14_HUN | 199 RPL14    | ####   |
| ITAASKK            | 5 P50914  | RL14_HUN | 171 RPL14    | ####   |
| KAPAQK             | 0 P50914  | RL14_HUN | 172 RPL14    | ####   |
| KITAASK            | 0 P50914  | RL14_HUN | 165 RPL14    | ####   |
| KITAASKK           | 6 P50914  | RL14_HUN | 171 RPL14    | ####   |
| LCKTVGATALPR       | 2 P50990  | TCPQ_HUN | 326 CCT8     | P50990 |
| LNSKWDLR           | 3 P50990  | TCPQ_HUN | 318 CCT8     | P50990 |
| LNSKWDLR           | 3 P50990  | TCPQ_HUN | 318 CCT8     | P50990 |
| LNSKWDLR           | 3 P50990  | TCPQ_HUN | 318 CCT8     | P50990 |
| VPEEDLKR           | 6 Q99832  | TCPH_HUN | 320 CCT7     | Q99832 |
| AYILNLVKQIK        | 7 P50991  | TCPD_HUN | 288 CCT4     | P50991 |
| AYILNLVKQIK        | 7 P50991  | TCPD_HUN | 288 CCT4     | P50991 |
| DKPAQIR            | 1 P50991  | TCPD_HUN | 29 CCT4      | P50991 |
| DKPAQIR            | 1 P50991  | TCPD_HUN | 29 CCT4      | P50991 |

|                     |          |           |              |           |
|---------------------|----------|-----------|--------------|-----------|
| GSNKLVEEAER         | 3 P50991 | TCPD_HUN  | 395 CCT4     | P50991    |
| KTGCNVLLIQK         | 0 P50991 | TCPD_HUN  | 292 CCT4     | P50991    |
| KTGCNVLLIQK         | 0 P50991 | TCPD_HUN  | 292 CCT4     | P50991    |
| DKPAQIR             | 1 P50991 | TCPD_HUN  | 29 CCT4      | P50991    |
| GKGAYQDR            | 1 P50991 | TCPD_HUN  | 21 CCT4      | ####      |
| KTGCNVLLIQK         | 0 P50991 | TCPD_HUN  | 292 CCT4     | P50991    |
| VAEIEHAEKEK         | 8 P78371 | TCPB_HUN  | 272 CCT2     | P78371    |
| AYKAEFK             | 2 P50995 | ANX11_HU  | 315 ANXA11   | ####      |
| FLNQIKVQEK          | 5 P51398 | RT29_HUM  | 203 DAP3     | P51398    |
| YLLYGEKGTGK         | 6 P51398 | RT29_HUM  | 130 DAP3     | P51398    |
| KEKAQDR             | 0 P51532 | SMCA4_HL  | 1602 SMARCA4 | ####      |
| SGSGKVYQGPAK        | 4 P51659 | DHB4_HUN  | 674 HSD17B4  | ####      |
| VVK TALDAFGR        | 2 P51659 | DHB4_HUN  | 84 HSD17B4   | 1ZBQ      |
| VVEPKR              | 4 P51991 | ROA3_HUN  | 108 HNRNPA3  | P51991    |
| GCGVVKFESPEVAER     | 5 P52272 | HNRPM_HI  | 698 HNRNPM   | P52272    |
| INEILSNALKR         | 9 P52272 | HNRPM_HI  | 381 HNRNPM   | ####      |
| KACQIFVR            | 0 P52272 | HNRPM_HI  | 651 HNRNPM   | P52272    |
| NLPDFTWKMLK         | 8 P52272 | HNRPM_HI  | 667 HNRNPM   | P52272    |
| KQSFVLK             | 0 P52565 | GDIR1_HUI | 99 ARHGDI    | 1HH4      |
| YIGIVKQAGLER        | 5 P52597 | HNRPF_HU  | 224 HNRNPF   | P52597    |
| GWVSKR              | 4 P52701 | MSH6_HUI  | 145 MSH6     | ####      |
| YIKGYR              | 2 P53041 | PPP5_HUM  | 97 PPP5C     | 1WAO      |
| AQKLLGVGDEK         | 2 P53396 | ACLY_HUM  | 151 ACLY     | 5TE1      |
| GIKEGR              | 2 P53396 | ACLY_HUM  | 732 ACLY     | 5TE1      |
| LTLLNPKGR           | 6 P53396 | ACLY_HUM  | 272 ACLY     | 5TE1      |
| FEEAVEKFR           | 6 P53621 | COPA_HUN  | 1028 COPA    | P53621    |
| VKGNNVYCLDR         | 1 P53621 | COPA_HUN  | 574 COPA     | P53621    |
| ALSSSKQSSSR         | 5 P53999 | TCP4_HUM  | 53 SUB1      | ####      |
| ALSSSKQSSSR         | 5 P53999 | TCP4_HUM  | 53 SUB1      | ####      |
| DDNMFQIGKMR         | 8 P53999 | TCP4_HUM  | 68 SUB1      | 1PCF      |
| DDNMFQIGKM[147.04]R | 8 P53999 | TCP4_HUM  | 68 SUB1      | 1PCF      |
| DDNM[147.04]FQIGKMR | 8 P53999 | TCP4_HUM  | 68 SUB1      | 1PCF      |
| KGISLNPEQWSQLK      | 0 P53999 | TCP4_HUM  | 101 SUB1     | 1PCF      |
| KGISLNPEQWSQLK      | 0 P53999 | TCP4_HUM  | 101 SUB1     | 1PCF      |
| QKTGETSR            | 1 P53999 | TCP4_HUM  | 41 SUB1      | ####      |
| KAGAEVVK            | 0 P54577 | SYYC_HUM  | 147 YARS     | P54577_P5 |
| KAGAEVVK            | 0 P54577 | SYYC_HUM  | 147 YARS     | 1N3L      |
| VLKDVK              | 2 P54578 | UBP14_HU  | 345 USP14    | 2AYN      |
| DKFLGR              | 1 P54709 | AT1B3_HU  | 266 ATP1B3   | P54709    |
| DKFLGR              | 1 P54709 | AT1B3_HU  | 266 ATP1B3   | P54709    |
| EVTVECKIDGSANLK     | 6 P54709 | AT1B3_HU  | 251 ATP1B3   | P54709    |
| IDGSANLKSQDDRDK     | 7 P54709 | AT1B3_HU  | 259 ATP1B3   | P54709    |
| IDGSANLKSQDDRDK     | 7 P54709 | AT1B3_HU  | 259 ATP1B3   | P54709    |
| IIGLKPEGVPR         | 4 P54709 | AT1B3_HU  | 182 ATP1B3   | P54709    |
| IIGLKPEGVPR         | 4 P54709 | AT1B3_HU  | 182 ATP1B3   | P54709    |
| SQDDRDKFLGR         | 6 P54709 | AT1B3_HU  | 266 ATP1B3   | P54709    |
| VMFKITAR            | 3 P54709 | AT1B3_HU  | 274 ATP1B3   | P54709    |

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|------------------------|----|--------|-----------|------|----------|--------|
| VMFKITAR               | 3  | P54709 | AT1B3_HU  | 274  | ATP1B3   | P54709 |
| VM[147.04]FKITAR       | 3  | P54709 | AT1B3_HU  | 274  | ATP1B3   | P54709 |
| YFPYYGKK               | 6  | P54709 | AT1B3_HU  | 220  | ATP1B3   | P54709 |
| NAKFYPVTR              | 2  | P54851 | EMP2_HUN  | 129  | EMP2     | ####   |
| NAKFYPVTR              | 2  | P54851 | EMP2_HUN  | 129  | EMP2     | P54851 |
| FASYLTFSPEVKSRLR       | 12 | P54886 | P5CS_HUM  | 662  | ALDH18A1 | ####   |
| LAAPLLKR               | 6  | P54886 | P5CS_HUM  | 424  | ALDH18A1 | 2H5G   |
| VEQVKIHAGPK            | 4  | P54886 | P5CS_HUM  | 643  | ALDH18A1 | 2H5G   |
| GDTVLLKGK              | 6  | P55072 | TERA_HUN  | 60   | VCP      | 5C1B   |
| KAFEEAEK               | 0  | P55072 | TERA_HUN  | 288  | VCP      | 5C1B   |
| KSPVAKDVDLEFLAK        | 5  | P55072 | TERA_HUN  | 668  | VCP      | 5C1B   |
| KYEMFAQTLQQSR          | 0  | P55072 | TERA_HUN  | 754  | VCP      | 5C1B   |
| KYEM[147.04]FAQTLQQSR  | 0  | P55072 | TERA_HUN  | 754  | VCP      | 5C1B   |
| KYEM[147.04]FAQTLQQSR  | 0  | P55072 | TERA_HUN  | 754  | VCP      | 5C1B   |
| VAILKANLR              | 4  | P55072 | TERA_HUN  | 658  | VCP      | 5C1B   |
| AQPAVNGKLGVPNGR        | 7  | P55199 | ELL_HUMA  | 355  | ELL      | ####   |
| NLQVKCAQIEAK           | 4  | P55209 | NP1L1_HU  | 87   | NAP1L1   | P55209 |
| NLQVKCAQIEAK           | 4  | P55209 | NP1L1_HU  | 87   | NAP1L1   | P55209 |
| KIGELVR                | 0  | P55265 | DSRAD_HU  | 715  | ADAR     | ####   |
| VSIYDSKR               | 6  | P55265 | DSRAD_HU  | 1115 | ADAR     | ####   |
| AWKADR                 | 2  | P55809 | SCOT1_HU  | 214  | OXCT1    | 3DLX   |
| KEGDGEAK               | 0  | P55809 | SCOT1_HU  | 286  | OXCT1    | P55809 |
| SAKPGDDVR              | 2  | P55809 | SCOT1_HU  | 296  | OXCT1    | P55809 |
| ASKELVER               | 2  | P55884 | EIF3B_HUN | 744  | EIF3B    | P55884 |
| WSPKGYLATFHQR          | 3  | P55884 | EIF3B_HUN | 345  | EIF3B    | P55884 |
| IKGSEADR               | 1  | P56192 | SYMC_HUN  | 729  | MARS     | 5GL7   |
| IPSGGDGKTLK            | 7  | P56199 | ITA1_HUM  | 628  | ITGA1    | ####   |
| KEAFTEAR               | 0  | P56199 | ITA1_HUM  | 259  | ITGA1    | ####   |
| GQLLPVSKALQQGLVGLELK   | 7  | P58107 | EPIPL_HUN | 97   | EPPK1    | ####   |
| KGLIPWEQAAR            | 0  | P58107 | EPIPL_HUN | 1028 | EPPK1    | ####   |
| QALSTATATVSVGKFR       | 13 | P58107 | EPIPL_HUN | 502  | EPPK1    | ####   |
| QLIEKAEALR             | 4  | P58107 | EPIPL_HUN | 2000 | EPPK1    | ####   |
| ELKQLYLER              | 2  | P61160 | ARP2_HUN  | 322  | ACTR2    | P61160 |
| EAGITEKVVFEQTK         | 6  | P60174 | TPIS_HUM  | 179  | TPI1     | 4POC   |
| ELASQPDVDGFLVGASLKPEFV | 18 | P60174 | TPIS_HUM  | 275  | TPI1     | 4POC   |
| GWLKSNVSDAVAQSTR       | 3  | P60174 | TPIS_HUM  | 231  | TPI1     | 4POC   |
| TKSLSFR                | 1  | P60228 | EIF3E_HUN | 409  | EIF3E    | P60228 |
| TKSLSFR                | 1  | P60228 | EIF3E_HUN | 409  | EIF3E    | P60228 |
| QVLKDLVK               | 3  | P60228 | EIF3E_HUN | 275  | EIF3E    | P60228 |
| TKSLSFR                | 1  | P60228 | EIF3E_HUN | 409  | EIF3E    | P60228 |
| YLTAVITNKDVR           | 9  | P60228 | EIF3E_HUN | 265  | EIF3E    | P60228 |
| KNASCGTR               | 0  | P60468 | SC61B_HU  | 35   | SEC61B   | ####   |
| ALGQNPTNAEVLKVLGNPK    | 12 | P60660 | MYL6_HUN  | 50   | MYL6     | P60660 |
| NKDQGTIEDYVEGLR        | 1  | P60660 | MYL6_HUN  | 81   | MYL6     | P60660 |
| DLTDYLMKILTER          | 7  | P60709 | ACTB_HUN  | 191  | ACTB     | 6ANU   |
| DSYVGDEAQSKR           | 10 | P60709 | ACTB_HUN  | 61   | ACTB     | 6ANU   |
| EITALAPSTMKIK          | 10 | P60709 | ACTB_HUN  | 326  | ACTB     | 6ANU   |

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|------------------------|----|--------|-----------|-----|---------|-----------|
| EITALAPSTMKIK          | 10 | P60709 | ACTB_HUN  | 326 | ACTB    | 6ANU      |
| EITALAPSTM[147.04]KIK  | 10 | P60709 | ACTB_HUN  | 326 | ACTB    | 6ANU      |
| EITALAPSTM[147.04]KIK  | 10 | P60709 | ACTB_HUN  | 326 | ACTB    | 6ANU      |
| IKIIPPER               | 1  | P60709 | ACTB_HUN  | 328 | ACTB    | 6ANU      |
| IKIIPPER               | 1  | P60709 | ACTB_HUN  | 328 | ACTB    | 6ANU      |
| MQKEITALAPSTMK         | 2  | P60709 | ACTB_HUN  | 315 | ACTB    | 6ANU      |
| MQKEITALAPSTM[147.04]K | 2  | P60709 | ACTB_HUN  | 315 | ACTB    | 6ANU      |
| VAPEEHPVLLTEAPLNPKANR  | 17 | P60709 | ACTB_HUN  | 113 | ACTB    | 6ANU      |
| VAPEEHPVLLTEAPLNPKANR  | 17 | P60709 | ACTB_HUN  | 113 | ACTB    | 6ANU      |
| VAPEEHPVLLTEAPLNPKANR  | 17 | P60709 | ACTB_HUN  | 113 | ACTB    | 6ANU      |
| VAPEEHPVLLTEAPLNPKANR  | 17 | P60709 | ACTB_HUN  | 113 | ACTB    | 6ANU      |
| VAPEEHPVLLTEAPLNPKANR  | 17 | P60709 | ACTB_HUN  | 113 | ACTB    | 6ANU      |
| DSYVGDEAQSKR           | 10 | P60709 | ACTB_HUN  | 61  | ACTB    | 6ANU      |
| GFKDQIYDIFQK           | 2  | P60842 | IF4A1_HUN | 193 | EIF4A1  | 3EIQ      |
| KEELTLEGIR             | 0  | P60842 | IF4A1_HUN | 238 | EIF4A1  | 3EIQ      |
| KEELTLEGIR             | 0  | P60842 | IF4A1_HUN | 238 | EIF4A1  | 3EIQ      |
| YLSPKYIK               | 4  | P60842 | IF4A1_HUN | 174 | EIF4A1  | 3EIQ      |
| GFKDQIYDIFQK           | 2  | P60842 | IF4A1_HUN | 193 | EIF4A1  | 3EIQ      |
| GYLTKEDLR              | 4  | P60903 | S10AA_HU  | 28  | S100A10 | 1A4P      |
| KCSTPEEIK              | 0  | P60981 | DEST_HUN  | 22  | DSTN    | P60981    |
| KLEGNPQGSNQGVK         | 0  | P61006 | RAB8A_HU  | 176 | RAB8A   | 5SZI      |
| IKLQLWDTAGQER          | 1  | P61106 | RAB14_HU  | 61  | RAB14   | P61106    |
| QEYQEKGVK              | 5  | P61160 | ARP2_HUN  | 381 | ACTR2   | P61160    |
| STTKVGNIEIK            | 3  | P61160 | ARP2_HUN  | 46  | ACTR2   | ####      |
| KEGYDFHSSSEFEIVK       | 0  | P61163 | ACTZ_HUN  | 200 | ACTR1A  | P61163    |
| LLSEVKK                | 5  | P61163 | ACTZ_HUN  | 319 | ACTR1A  | P61163    |
| LGKLYLER               | 2  | P61201 | CSN2_HUN  | 157 | COPS2   | 4D10      |
| KDETK                  | 0  | P61221 | ABCE1_HU  | 191 | ABCE1   | P61221    |
| KDETK                  | 0  | P61221 | ABCE1_HU  | 191 | ABCE1   | P61221    |
| KDETK                  | 0  | P61221 | ABCE1_HU  | 191 | ABCE1   | P61221    |
| LFCVGFTKK              | 7  | P61247 | RS3A_HUN  | 144 | RPS3A   | 5FLX      |
| NIGKTLVTR              | 3  | P61247 | RS3A_HUN  | 46  | RPS3A   | 5FLX      |
| AKLVSK                 | 1  | P61289 | PSME3_HU  | 188 | PSME3   | P61289_P6 |
| LKVDSFR                | 1  | P61289 | PSME3_HU  | 14  | PSME3   | P61289    |
| LLIEKCNTVK             | 4  | P61289 | PSME3_HU  | 132 | PSME3   | P61289    |
| KVTAAMGK               | 0  | P61353 | RL27_HUM  | 52  | RPL27   | P61353    |
| YSVDIPLDKTVVNK         | 8  | P61353 | RL27_HUM  | 93  | RPL27   | P61353    |
| GGIMLPEKSQ GK          | 7  | P61604 | CH10_HUN  | 36  | HSPE1   | 4PJ1      |
| GKGGEIQPVSVK           | 1  | P61604 | CH10_HUN  | 56  | HSPE1   | 4PJ1      |
| GKGGEIQPVSVK           | 1  | P61604 | CH10_HUN  | 56  | HSPE1   | 4PJ1      |
| KFLPLFDR               | 0  | P61604 | CH10_HUN  | 8   | HSPE1   | 4PJ1      |
| KFLPLFDR               | 0  | P61604 | CH10_HUN  | 8   | HSPE1   | 4PJ1      |
| KFLPLFDR               | 0  | P61604 | CH10_HUN  | 8   | HSPE1   | 4PJ1      |
| KFLPLFDR               | 0  | P61604 | CH10_HUN  | 8   | HSPE1   | 4PJ1      |
| KFLPLFDR               | 0  | P61604 | CH10_HUN  | 8   | HSPE1   | 4PJ1      |
| KFLPLFDR               | 0  | P61604 | CH10_HUN  | 8   | HSPE1   | 4PJ1      |
| SAAETVTKGGIMLPEK       | 7  | P61604 | CH10_HUN  | 28  | HSPE1   | 4PJ1      |

|                          |    |        |           |     |        |        |
|--------------------------|----|--------|-----------|-----|--------|--------|
| SAAETVTKGGIM[147.04]LPEK | 7  | P61604 | CH10_HUM  | 28  | HSPE1  | 4PJ1   |
| VGDKVLLPEYGGTK           | 3  | P61604 | CH10_HUM  | 70  | HSPE1  | 4PJ1   |
| VGDKVLLPEYGGTK           | 3  | P61604 | CH10_HUM  | 70  | HSPE1  | 4PJ1   |
| VGDKVLLPEYGGTK           | 3  | P61604 | CH10_HUM  | 70  | HSPE1  | 4PJ1   |
| VGDKVLLPEYGGTK           | 3  | P61604 | CH10_HUM  | 70  | HSPE1  | 4PJ1   |
| VVLDDKDYFLFR             | 5  | P61604 | CH10_HUM  | 86  | HSPE1  | 4PJ1   |
| VVLDDKDYFLFR             | 5  | P61604 | CH10_HUM  | 86  | HSPE1  | 4PJ1   |
| TPKIQVYSR                | 2  | P61769 | B2MG_HUI  | 26  | B2M    | 5J1A   |
| KPTLDFK                  | 0  | Q96RW7 | HMCN1_HI  | 326 | HMCN1  | ####   |
| DLAGSIIGKGGQR            | 8  | P61978 | HNRPK_HU  | 405 | HNRNPK | 1ZZK   |
| IILDLISESPIKGR           | 11 | P61978 | HNRPK_HU  | 219 | HNRNPK | P61978 |
| IILDLISESPIKGR           | 11 | P61978 | HNRPK_HU  | 219 | HNRNPK | P61978 |
| NIKALR                   | 2  | P61978 | HNRPK_HU  | 66  | HNRNPK | P61978 |
| VVLIGGKPDR               | 6  | P61978 | HNRPK_HU  | 198 | HNRNPK | P61978 |
| KIEMVR                   | 0  | P61981 | 1433G_HU  | 78  | YWHAG  | 3UZD   |
| NLLSVAYKNVVGAR           | 7  | P61981 | 1433G_HU  | 50  | YWHAG  | 3UZD   |
| ILPKPTR                  | 3  | P62081 | RS7_HUM   | 103 | RPS7   | 5FLX   |
| KLTGK                    | 0  | P62081 | RS7_HUM   | 179 | RPS7   | 5FLX   |
| VKLDGSR                  | 1  | P62081 | RS7_HUM   | 147 | RPS7   | 5FLX   |
| IYGFYDECKR               | 8  | P62136 | PP1A_HUM  | 141 | PPP1CA | 4G9J   |
| LNKCGVISPR               | 2  | P62244 | RS15A_HU  | 71  | RPS15A | 5FLX   |
| LNKCGVISPR               | 2  | P62244 | RS15A_HU  | 71  | RPS15A | 5FLX   |
| LNKCGVISPR               | 2  | P62244 | RS15A_HU  | 71  | RPS15A | 5FLX   |
| SINNAEKR                 | 6  | P62244 | RS15A_HU  | 19  | RPS15A | 5FLX   |
| LNKCGVISPR               | 2  | P62244 | RS15A_HU  | 71  | RPS15A | 5FLX   |
| TATAVAHCKR               | 8  | P62249 | RS16_HUM  | 26  | RPS16  | 5FLX   |
| YVDEASKK                 | 6  | P62249 | RS16_HUM  | 105 | RPS16  | 5FLX   |
| YVDEASKK                 | 6  | P62249 | RS16_HUM  | 105 | RPS16  | 5FLX   |
| GLIKLVSK                 | 3  | P62851 | RS25_HUM  | 98  | RPS25  | P62851 |
| VFYKMK                   | 4  | P62258 | 1433E_HUI | 123 | YWHAE  | 3UBW   |
| VVSSIEQKTEGAEK           | 7  | P63104 | 1433Z_HUI | 68  | YWHAZ  | 1QJB   |
| FKVVK                    | 1  | P62266 | RS23_HUM  | 121 | RPS23  | P62266 |
| FKVVK                    | 1  | P62266 | RS23_HUM  | 121 | RPS23  | P62266 |
| KGHAVGDIPGVR             | 0  | P62266 | RS23_HUM  | 108 | RPS23  | ####   |
| KADIDLT                  | 0  | P62269 | RS18_HUM  | 47  | RPS18  | 5FLX   |
| EQIYKLAK                 | 4  | P62277 | RS13_HUM  | 39  | RPS13  | 5FLX   |
| EQIYKLAK                 | 4  | P62277 | RS13_HUM  | 39  | RPS13  | 5FLX   |
| FVTGNKILR                | 5  | P62277 | RS13_HUM  | 70  | RPS13  | 5FLX   |
| FVTGNKILR                | 5  | P62277 | RS13_HUM  | 70  | RPS13  | 5FLX   |
| FVTGNKILR                | 5  | P62277 | RS13_HUM  | 70  | RPS13  | 5FLX   |
| FVTGNKILR                | 5  | P62277 | RS13_HUM  | 70  | RPS13  | 5FLX   |
| KAVAVR                   | 0  | P62277 | RS13_HUM  | 94  | RPS13  | 5FLX   |
| KAVAVR                   | 0  | P62277 | RS13_HUM  | 94  | RPS13  | 5FLX   |
| KHLER                    | 0  | P62277 | RS13_HUM  | 100 | RPS13  | 5FLX   |
| SVPTWLKLTSDDVK           | 6  | P62277 | RS13_HUM  | 27  | RPS13  | 5FLX   |
| VLLGETGKEK               | 7  | P62280 | RS11_HUM  | 30  | RPS11  | 5FLX   |
| YYKNIGLGFK               | 2  | P62280 | RS11_HUM  | 38  | RPS11  | 5FLX   |

|                       |    |        |           |     |          |        |
|-----------------------|----|--------|-----------|-----|----------|--------|
| AILYKR                | 4  | P62424 | RL7A_HUM  | 72  | RPL7A    | P62424 |
| AILYKR                | 4  | P62424 | RL7A_HUM  | 72  | RPL7A    | P62424 |
| AILYKR                | 4  | P62424 | RL7A_HUM  | 72  | RPL7A    | P62424 |
| GDVPTKRPPVLR          | 5  | P62424 | RL7A_HUM  | 131 | RPL7A    | P62424 |
| HWGGNVLGPKSVAR        | 9  | P62424 | RL7A_HUM  | 245 | RPL7A    | P62424 |
| IAKLEK                | 2  | P62424 | RL7A_HUM  | 252 | RPL7A    | P62424 |
| AKELATK               | 1  | P62424 | RL7A_HUM  | 259 | RPL7A    | P62424 |
| AMELLKVSK             | 5  | Q9Y3U8 | RL36_HUM  | 62  | RPL36    | Q9Y3U8 |
| AMELLKVSK             | 5  | Q9Y3U8 | RL36_HUM  | 62  | RPL36    | Q9Y3U8 |
| AMELLKVSK             | 5  | Q9Y3U8 | RL36_HUM  | 62  | RPL36    | Q9Y3U8 |
| AM[147.04]ELLKVSK     | 5  | Q9Y3U8 | RL36_HUM  | 62  | RPL36    | Q9Y3U8 |
| AM[147.04]ELLKVSK     | 5  | Q9Y3U8 | RL36_HUM  | 62  | RPL36    | Q9Y3U8 |
| LTKHTK                | 2  | Q9Y3U8 | RL36_HUM  | 35  | RPL36    | Q9Y3U8 |
| IVSQKQMSDR            | 4  | P62491 | RB11A_HU  | 179 | RAB11A   | 5C46   |
| IVSQKQIADR            | 4  | Q15907 | RB11B_HU  | 179 | RAB11B   | 2F9M   |
| FIKIDGK               | 2  | P62701 | RS4X_HUM  | 71  | RPS4X    | 5A2Q   |
| IDGKVR                | 3  | P62701 | RS4X_HUM  | 75  | RPS4X    | 5A2Q   |
| ITPEEAKYK             | 6  | P62701 | RS4X_HUM  | 120 | RPS4X    | 5A2Q   |
| KIFVGTK               | 0  | P62701 | RS4X_HUM  | 128 | RPS4X    | 5A2Q   |
| LIYDTKGR              | 5  | P62701 | RS4X_HUM  | 106 | RPS4X    | 5A2Q   |
| VAPEEHPTLLTEAPLNPKANR | 17 | P62736 | ACTA_HUM  | 115 | ACTA2    | P62736 |
| KAYVR                 | 0  | P62750 | RL23A_HUI | 135 | RPL23A   | P62750 |
| KAYVR                 | 0  | P62750 | RL23A_HUI | 135 | RPL23A   | P62750 |
| DAVYTEHAKR            | 9  | P62805 | H4_HUMAI  | 78  | HIST1H4A | 5B0Z   |
| DAVYTEHAKR            | 9  | P62805 | H4_HUMAI  | 78  | HIST1H4A | 5B0Z   |
| DAVYTEHAKR            | 9  | P62805 | H4_HUMAI  | 78  | HIST1H4A | 5B0Z   |
| DAVYTEHAKR            | 9  | P62805 | H4_HUMAI  | 78  | HIST1H4A | 5B0Z   |
| DAVYTEHAKR            | 9  | P62805 | H4_HUMAI  | 78  | HIST1H4A | 5B0Z   |
| DAVYTEHAKR            | 9  | P62805 | H4_HUMAI  | 78  | HIST1H4A | 5B0Z   |
| DAVYTEHAKR            | 9  | P62805 | H4_HUMAI  | 78  | HIST1H4A | 5B0Z   |
| DNIQGITKPAIR          | 7  | P62805 | H4_HUMAI  | 32  | HIST1H4A | 5B0Z   |
| GGAKR                 | 3  | P62805 | H4_HUMAI  | 17  | HIST1H4A | P62805 |
| GKGGK                 | 1  | P62805 | H4_HUMAI  | 6   | HIST1H4A | P62805 |
| GVLKVFLENVIR          | 3  | P62805 | H4_HUMAI  | 60  | HIST1H4A | 5B0Z   |
| TVTAMDVVYALKR         | 11 | P62805 | H4_HUMAI  | 92  | HIST1H4A | 5B0Z   |
| TVTAMDVVYALKR         | 11 | P62805 | H4_HUMAI  | 92  | HIST1H4A | 5B0Z   |
| TVTAM[147.04]DVVYALKR | 11 | P62805 | H4_HUMAI  | 92  | HIST1H4A | 5B0Z   |
| TVTAM[147.04]DVVYALKR | 11 | P62805 | H4_HUMAI  | 92  | HIST1H4A | 5B0Z   |
| RGGVKR                | 4  | P62805 | H4_HUMAI  | 45  | HIST1H4A | 5B0Z   |
| RGGVKR                | 4  | P62805 | H4_HUMAI  | 45  | HIST1H4A | 5B0Z   |
| RGGVKR                | 4  | P62805 | H4_HUMAI  | 45  | HIST1H4A | 5B0Z   |
| DAVYTEHAKR            | 9  | P62805 | H4_HUMAI  | 78  | HIST1H4A | 5B0Z   |
| DNIQGITKPAIR          | 7  | P62805 | H4_HUMAI  | 32  | HIST1H4A | 5B0Z   |
| DNIQGITKPAIR          | 7  | P62805 | H4_HUMAI  | 32  | HIST1H4A | 5B0Z   |
| EIAQDFKTDLR           | 6  | Q16695 | H31T_HUN  | 80  | HIST3H3  | 3A6N   |
| EIAQDFKTDLR           | 6  | Q16695 | H31T_HUN  | 80  | HIST3H3  | 3A6N   |
| EIAQDFKTDLR           | 6  | Q16695 | H31T_HUN  | 80  | HIST3H3  | 3A6N   |



|                      |          |           |               |        |
|----------------------|----------|-----------|---------------|--------|
| EIAQDFKTDLR          | 6 Q16695 | H31T_HUN  | 80 HIST3H3    | 3A6N   |
| GLGKGGAK             | 3 P62805 | H4_HUMAI  | 13 HIST1H4A   | P62805 |
| KLPFQR               | 0 Q16695 | H31T_HUN  | 65 HIST3H3    | 3A6N   |
| RGGVKR               | 4 P62805 | H4_HUMAI  | 45 HIST1H4A   | 5B0Z   |
| TKQTAR               | 1 Q16695 | H31T_HUN  | 5 HIST3H3     | Q16695 |
| TKQTAR               | 1 Q16695 | H31T_HUN  | 5 HIST3H3     | Q16695 |
| VTIMPKDIQLAR         | 5 Q16695 | H31T_HUN  | 123 HIST3H3   | 3A6N   |
| VTIM[147.04]PKDIQLAR | 5 Q16695 | H31T_HUN  | 123 HIST3H3   | 3A6N   |
| YQKSTELLIR           | 2 Q16695 | H31T_HUN  | 57 HIST3H3    | 3A6N   |
| YQKSTELLIR           | 2 Q16695 | H31T_HUN  | 57 HIST3H3    | 3A6N   |
| KESYSIYVYK           | 0 Q8N257 | H2B3B_HU  | 35 HIST3H2BB  | Q8N257 |
| KESYSIYVYK           | 0 Q8N257 | H2B3B_HU  | 35 HIST3H2BB  | Q8N257 |
| AVTKYTSSK            | 3 Q93079 | H2B1H_HU  | 121 HIST1H2BH | Q93079 |
| DAVTYTEHAKR          | 9 P62805 | H4_HUMAI  | 78 HIST1H4A   | 5B0Z   |
| GGKGLGK              | 2 P62805 | H4_HUMAI  | 9 HIST1H4A    | P62805 |
| GLGKGGAK             | 3 P62805 | H4_HUMAI  | 13 HIST1H4A   | P62805 |
| HAVSEGTKAVTK         | 7 Q93079 | H2B1H_HU  | 117 HIST1H2BH | Q93079 |
| KESYSVYVYK           | 0 Q93079 | H2B1H_HU  | 35 HIST1H2BH  | Q93079 |
| KESYSVYVYK           | 0 Q93079 | H2B1H_HU  | 35 HIST1H2BH  | Q93079 |
| KESYSVYVYK           | 0 Q93079 | H2B1H_HU  | 35 HIST1H2BH  | Q93079 |
| KTVTAMDVVYALK        | 0 P62805 | H4_HUMAI  | 80 HIST1H4A   | 5B0Z   |
| LAHYNKR              | 5 Q93079 | H2B1H_HU  | 86 HIST1H2BH  | Q93079 |
| LAHYNKR              | 5 Q93079 | H2B1H_HU  | 86 HIST1H2BH  | Q93079 |
| LAHYNKR              | 5 Q93079 | H2B1H_HU  | 86 HIST1H2BH  | Q93079 |
| LAHYNKR              | 5 Q93079 | H2B1H_HU  | 86 HIST1H2BH  | Q93079 |
| RKTVTAMDVVYALK       | 1 P62805 | H4_HUMAI  | 80 HIST1H4A   | 5B0Z   |
| KGNYAER              | 0 Q96KK5 | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5 |
| KGNYAER              | 0 Q96KK5 | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5 |
| KGNYAER              | 0 Q96KK5 | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5 |
| NDEELNKLLGK          | 6 Q96KK5 | H2A1H_HU  | 96 HIST1H2AH  | Q96KK5 |
| NDEELNKLLGK          | 6 Q96KK5 | H2A1H_HU  | 96 HIST1H2AH  | Q96KK5 |
| NDEELNKLLGK          | 6 Q96KK5 | H2A1H_HU  | 96 HIST1H2AH  | Q96KK5 |
| NDEELNKLLGK          | 6 Q96KK5 | H2A1H_HU  | 96 HIST1H2AH  | Q96KK5 |
| KGGAGGK              | 0 Q53EL6 | PDCD4_HU  | 115 PDCD4     | ####   |
| AKSIVFHR             | 1 P62826 | RAN_HUM.  | 134 RAN       | 5CIQ   |
| AKSIVFHR             | 1 P62826 | RAN_HUM.  | 134 RAN       | 5CIQ   |
| GPIKFNVWDTAGQEK      | 3 P62826 | RAN_HUM.  | 60 RAN        | 5CIQ   |
| KNLQYYDISAK          | 0 P62826 | RAN_HUM.  | 142 RAN       | 5CIQ   |
| VDIKDR               | 3 P62826 | RAN_HUM.  | 127 RAN       | 5CIQ   |
| VTYKNVPNWHR          | 3 P62826 | RAN_HUM.  | 99 RAN        | 5CIQ   |
| VTYKNVPNWHR          | 3 P62826 | RAN_HUM.  | 99 RAN        | 5CIQ   |
| VTYKNVPNWHR          | 3 P62826 | RAN_HUM.  | 99 RAN        | 5CIQ   |
| KFMTNR               | 0 P62847 | RS24_HUM  | 11 RPS24      | 5FLX   |
| KFVLR                | 0 P62854 | RS26_HUM  | 38 RPS26      | P62854 |
| VTKVLGR              | 2 P62857 | RS28_HUM  | 16 RPS28      | 5FLX   |
| KFVLR                | 0 Q6T423 | S22AP_HUI | 173 SLC22A25  | Q6T423 |
| KGPNANS              | 0 P62861 | RS30_HUM  | 53 FAU        | 5FLX   |

|                   |    |        |           |     |          |        |
|-------------------|----|--------|-----------|-----|----------|--------|
| TFVSGACDASIKLWDVR | 11 | P62879 | GBB2_HUM  | 209 | GNB2     | P62879 |
| KSLESINSR         | 0  | P62888 | RL30_HUM  | 9   | RPL30    | 3VI6   |
| LQLVMKSGK         | 5  | P62888 | RL30_HUM  | 23  | RPL30    | 3VI6   |
| SGKYVLGYK         | 2  | P62888 | RL30_HUM  | 26  | RPL30    | 3VI6   |
| ALKEIR            | 2  | P62899 | RL31_HUM  | 47  | RPL31    | P62899 |
| IHGVGFKK          | 6  | P62899 | RL31_HUM  | 39  | RPL31    | P62899 |
| AVDIPHMDIEALKK    | 12 | P62906 | RL10A_HUI | 91  | RPL10A   | P62906 |
| ILGPGLNKAGK       | 7  | P62906 | RL10A_HUI | 130 | RPL10A   | P62906 |
| ILGPGLNKAGK       | 7  | P62906 | RL10A_HUI | 130 | RPL10A   | P62906 |
| STIKFQMK          | 3  | P62906 | RL10A_HUI | 156 | RPL10A   | P62906 |
| VDEVKSTIK         | 4  | P62906 | RL10A_HUI | 152 | RPL10A   | P62906 |
| KGGLGGK           | 0  | Q15050 | RRS1_HUM  | 335 | RRS1     | ####   |
| KAIVER            | 0  | P62910 | RL32_HUM  | 109 | RPL32    | P62910 |
| KAIVER            | 0  | P62910 | RL32_HUM  | 109 | RPL32    | P62910 |
| KLCLNICVGESGDR    | 0  | P62913 | RL11_HUM  | 19  | RPL11    | 4XXB   |
| KGAAR             | 0  | P62917 | RL8_HUM   | 24  | RPL8     | P62917 |
| KGAGSVFR          | 0  | P62917 | RL8_HUM   | 10  | RPL8     | P62917 |
| VKLPSGSK          | 1  | P62917 | RL8_HUM   | 149 | RPL8     | P62917 |
| ALSTGEKGFYK       | 6  | P62937 | PPIA_HUM  | 44  | PPIA     | 4N1M   |
| ALSTGEKGFYK       | 6  | P62937 | PPIA_HUM  | 44  | PPIA     | 4N1M   |
| ALSTGEKGFYK       | 6  | P62937 | PPIA_HUM  | 44  | PPIA     | 4N1M   |
| GFGYKGSCFHR       | 4  | P62937 | PPIA_HUM  | 49  | PPIA     | 4N1M   |
| HVVFGKVK          | 5  | P62937 | PPIA_HUM  | 131 | PPIA     | 4N1M   |
| KITIADCGQLE       | 0  | P62937 | PPIA_HUM  | 155 | PPIA     | 4N1M   |
| KITIADCGQLE       | 0  | P62937 | PPIA_HUM  | 155 | PPIA     | 4N1M   |
| VPKTAENFR         | 2  | P62937 | PPIA_HUM  | 31  | PPIA     | P62937 |
| VSFELFADKVPK      | 8  | P62937 | PPIA_HUM  | 28  | PPIA     | 4N1M   |
| VSFELFADKVPK      | 8  | P62937 | PPIA_HUM  | 28  | PPIA     | 4N1M   |
| AKIQDK            | 1  | P62987 | RL40_HUM  | 29  | UBA52    | 5HPL   |
| IQDKEGIPPDQQR     | 3  | P62987 | RL40_HUM  | 33  | UBA52    | 5HPL   |
| IQDKEGIPPDQQR     | 3  | P62987 | RL40_HUM  | 33  | UBA52    | 5HPL   |
| LIFAGKQLEDGR      | 5  | P62987 | RL40_HUM  | 48  | UBA52    | 5HPL   |
| LIFAGKQLEDGR      | 5  | P62987 | RL40_HUM  | 48  | UBA52    | 5HPL   |
| MQIFVKTLTGK       | 5  | P62987 | RL40_HUM  | 6   | UBA52    | 5HPL   |
| TKQTAR            | 1  | P68431 | H31_HUM   | 5   | HIST1H3A | P68431 |
| EIAQDFKTDLR       | 6  | Q16695 | H31T_HUM  | 80  | HIST3H3  | 3A6N   |
| YQKSTELLIR        | 2  | Q16695 | H31T_HUM  | 57  | HIST3H3  | 3A6N   |
| LIFAGKQLEDGR      | 5  | P62987 | RL40_HUM  | 48  | UBA52    | 5HPL   |
| KQQMAR            | 0  | P63104 | 1433Z_HUI | 75  | YWHAZ    | 1QJB   |
| KQQM[147.04]AR    | 0  | P63104 | 1433Z_HUI | 75  | YWHAZ    | 1QJB   |
| KQQM[147.04]AR    | 0  | P63104 | 1433Z_HUI | 75  | YWHAZ    | 1QJB   |
| NLLSVAYKNVVGAR    | 7  | P63104 | 1433Z_HUI | 49  | YWHAZ    | 1QJB   |
| NLLSVAYKNVVGAR    | 7  | P63104 | 1433Z_HUI | 49  | YWHAZ    | 1QJB   |
| VFYLKMK           | 4  | P63104 | 1433Z_HUI | 120 | YWHAZ    | 1QJB   |
| EGEYIKLK          | 5  | P63165 | SUMO1_HI  | 23  | SUMO1    | 1WYW   |
| DKTIK             | 1  | P63244 | RACK1_HU  | 127 | RACK1    | 4AOW   |
| VEYEKR            | 4  | P63279 | UBC9_HUN  | 146 | UBE2I    | 2GRR   |

|                          |           |           |               |           |
|--------------------------|-----------|-----------|---------------|-----------|
| VLGTVKWFNVR              | 5 P67809  | YBOX1_HU  | 64 YBX1       | P67809    |
| KYEEVAR                  | 0 P67936  | TPM4_HUN  | 125 TPM4      | P67936    |
| TVAKLEK                  | 3 P67936  | TPM4_HUN  | 212 TPM4      | P67936    |
| DSYVGDEAQSQR             | 10 P68032 | ACTC_HUN  | 63 ACTC1      | P68032    |
| HQGVMVGMGQKDSYVGDEAC     | 10 P68032 | ACTC_HUN  | 52 ACTC1      | P68032    |
| HQGVMVGM[147.04]GQKDSY   | 10 P68032 | ACTC_HUN  | 52 ACTC1      | P68032    |
| HQGVM[147.04]VGMGQKDSY   | 10 P68032 | ACTC_HUN  | 52 ACTC1      | P68032    |
| HQGVM[147.04]VGM[147.04] | 10 P68032 | ACTC_HUN  | 52 ACTC1      | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032_P6 |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| IKIIAPPER                | 1 P68032  | ACTC_HUN  | 330 ACTC1     | P68032    |
| KYGEK                    | 0 P68036  | UB2L3_HU  | 146 UBE2L3    | 4Q5E      |
| AAGAGKVTK                | 5 P68104  | EF1A1_HUI | 450 EEF1A1    | ####      |
| EVSTYIKK                 | 6 P68104  | EF1A1_HUI | 179 EEF1A1    | P68104    |
| EVSTYIKK                 | 6 P68104  | EF1A1_HUI | 179 EEF1A1    | P68104    |
| EVSTYIKK                 | 6 P68104  | EF1A1_HUI | 179 EEF1A1    | P68104    |
| KAAGAGK                  | 0 P68104  | EF1A1_HUI | 444 EEF1A1    | P68104    |
| LPLQDVYKIGGIGTVPVGR      | 7 P68104  | EF1A1_HUI | 255 EEF1A1    | P68104    |
| LPLQDVYKIGGIGTVPVGR      | 7 P68104  | EF1A1_HUI | 255 EEF1A1    | P68104_P6 |
| LPLQDVYKIGGIGTVPVGR      | 7 P68104  | EF1A1_HUI | 255 EEF1A1    | P68104    |
| QTVAVGVIAVDK             | 8 P68104  | EF1A1_HUI | 439 EEF1A1    | P68104    |
| SAQKAQK                  | 3 P68104  | EF1A1_HUI | 457 EEF1A1    | ####      |
| SAQKAQK                  | 3 P68104  | EF1A1_HUI | 457 EEF1A1    | ####      |
| TIEKFEK                  | 3 P68104  | EF1A1_HUI | 41 EEF1A1     | P68104    |
| VTKSAQK                  | 2 P68104  | EF1A1_HUI | 453 EEF1A1    | ####      |
| AVTKYTSSK                | 3 Q93079  | H2B1H_HU  | 121 HIST1H2BH | Q93079    |
| FDLMYAKR                 | 6 P68366  | TBA4A_HU  | 401 TUBA4A    | P68366    |
| KQLATKAAR                | 0 P68431  | H31_HUM/  | 19 HIST1H3A   | P68431    |
| KQLATKAAR                | 5 P68431  | H31_HUM/  | 24 HIST1H3A   | P68431    |
| KSAPATGGVK               | 0 P68431  | H31_HUM/  | 28 HIST1H3A   | P68431    |
| KSTGGK                   | 0 P68431  | H31_HUM/  | 10 HIST1H3A   | P68431    |
| KSTGGK                   | 0 P68431  | H31_HUM/  | 10 HIST1H3A   | P68431    |
| TKQTAR                   | 1 P68431  | H31_HUM/  | 5 HIST1H3A    | P68431    |
| TKQTAR                   | 1 P68431  | H31_HUM/  | 5 HIST1H3A    | P68431    |
| TKQTAR                   | 1 P68431  | H31_HUM/  | 5 HIST1H3A    | P68431    |
| AVTKYTSSK                | 3 Q93079  | H2B1H_HU  | 121 HIST1H2BH | Q93079    |
| KMVDQLFCK                | 0 P78347  | GTF2I_HUN | 468 GTF2I     | ####      |
| KQVEELFER                | 0 P78347  | GTF2I_HUN | 363 GTF2I     | ####      |
| LEKIQVGNR                | 2 P78347  | GTF2I_HUN | 526 GTF2I     | ####      |

|                      |           |           |             |           |
|----------------------|-----------|-----------|-------------|-----------|
| KIGVNPQPK            | 0 P78371  | TCPB_HUM  | 223 CCT2    | P78371    |
| SLHDALCVLAQTVKDSR    | 13 P78371 | TCPB_HUM  | 402 CCT2    | P78371_P7 |
| KEFTK                | 0 P78417  | GSTO1_HU  | 148 GSTO1   | 4YQU      |
| KEFTK                | 0 P78417  | GSTO1_HU  | 148 GSTO1   | 4YQU      |
| SLGKGSAPPGPVPEGSIR   | 3 P78417  | GSTO1_HU  | 11 GSTO1    | 4YQU      |
| ALKLNSNEAR           | 2 P78527  | PRKDC_HU  | 3455 PRKDC  | P78527    |
| ATQMPEGGQGAPPMYQLYKR | 18 P78527 | PRKDC_HU  | 963 PRKDC   | 5LUQ      |
| DQEKLSLMYAR          | 3 P78527  | PRKDC_HU  | 2738 PRKDC  | P78527    |
| GKPLPEYHVR           | 1 P78527  | PRKDC_HU  | 3710 PRKDC  | P78527    |
| KAALSALESFLK         | 0 P78527  | PRKDC_HU  | 310 PRKDC   | 5LUQ      |
| KGVAEQK              | 0 P78527  | PRKDC_HU  | 2746 PRKDC  | P78527    |
| KGVAEQK              | 0 P78527  | PRKDC_HU  | 2746 PRKDC  | P78527    |
| KSLNSIEFR            | 0 P78527  | PRKDC_HU  | 71 PRKDC    | 5LUQ      |
| KSLNSIEFR            | 0 P78527  | PRKDC_HU  | 71 PRKDC    | 5LUQ      |
| MGQKIAPYSVEIK        | 3 P78527  | PRKDC_HU  | 99 PRKDC    | P78527    |
| NTCTSVYTKDR          | 8 P78527  | PRKDC_HU  | 117 PRKDC   | 5LUQ      |
| AYYSPVGKK            | 7 P78536  | ADA17_HU  | 375 ADAM17  | ####      |
| AVKFQR               | 2 P83731  | RL24_HUM  | 77 RPL24    | 5A2Q      |
| NQKPEVR              | 2 P83731  | RL24_HUM  | 97 RPL24    | 5A2Q      |
| NQKPEVR              | 2 P83731  | RL24_HUM  | 97 RPL24    | 5A2Q      |
| KGTANAR              | 0 P84098  | RL19_HUM  | 82 RPL19    | P84098    |
| KGTANAR              | 0 P84098  | RL19_HUM  | 82 RPL19    | P84098    |
| KNTLAR               | 0 P84098  | RL19_HUM  | 65 RPL19    | P84098    |
| KNTLAR               | 0 P84098  | RL19_HUM  | 65 RPL19    | P84098    |
| ADLIAYLKK            | 7 P99999  | CYC_HUM   | 100 CYCS    | 5TY3      |
| AEWQVYKEISR          | 6 Q00059  | TFAM_HUM  | 111 TFAM    | 3TQ6      |
| ELPDSKK              | 5 Q00059  | TFAM_HUM  | 95 TFAM     | 3TQ6      |
| KIYQDAYR             | 0 Q00059  | TFAM_HUM  | 97 TFAM     | 3TQ6      |
| KPVSSYLK             | 0 Q00059  | TFAM_HUM  | 52 TFAM     | 3TQ6      |
| MYKEEGLK             | 2 Q00325  | MPCP_HUM  | 209 SLC25A3 | Q00325    |
| AKAGLLER             | 1 Q00341  | VIGLN_HUM | 1031 HDLBP  | 2CTK      |
| KGAVITQIR            | 0 Q00341  | VIGLN_HUM | 1071 HDLBP  | ####      |
| YHPKIIGR             | 3 Q00341  | VIGLN_HUM | 1066 HDLBP  | ####      |
| FIIGKK               | 4 Q00341  | VIGLN_HUM | 382 HDLBP   | ####      |
| AVNYFSKVK            | 6 Q00610  | CLH1_HUM  | 1441 CLTC   | Q00610    |
| IAAYLFKGNR           | 6 Q00610  | CLH1_HUM  | 1516 CLTC   | Q00610    |
| KANSTR               | 0 Q00610  | CLH1_HUM  | 1246 CLTC   | Q00610    |
| KANSTR               | 0 Q00610  | CLH1_HUM  | 1246 CLTC   | Q00610    |
| KDSLYK               | 0 Q00610  | CLH1_HUM  | 1530 CLTC   | Q00610    |
| KFNALFAQGNYSEAAK     | 0 Q00610  | CLH1_HUM  | 367 CLTC    | Q00610    |
| KVGYPDWIFLLR         | 0 Q00610  | CLH1_HUM  | 507 CLTC    | Q00610    |
| QKWLLLTGISAQQNR      | 1 Q00610  | CLH1_HUM  | 163 CLTC    | 4G55      |
| VDKLDASESLR          | 2 Q00610  | CLH1_HUM  | 1612 CLTC   | Q00610    |
| VKNFLK               | 1 Q00610  | CLH1_HUM  | 760 CLTC    | Q00610    |
| VVGKYCEK             | 3 Q00610  | CLH1_HUM  | 907 CLTC    | Q00610    |
| WKQSVELCK            | 1 Q00610  | CLH1_HUM  | 1522 CLTC   | Q00610    |
| YIQAAACKTGQIK        | 6 Q00610  | CLH1_HUM  | 737 CLTC    | Q00610    |

|                         |           |           |             |          |
|-------------------------|-----------|-----------|-------------|----------|
| YLQMARKK                | 6 Q00610  | CLH1_HUM  | 1162 CLTC   | ####     |
| APQCLGKFIEIAAR          | 6 Q00839  | HNRPU_HL  | 565 HNRNPU  | ####     |
| APQCLGKFIEIAAR          | 6 Q00839  | HNRPU_HL  | 565 HNRNPU  | ####     |
| APQCLGKFIEIAAR          | 6 Q00839  | HNRPU_HL  | 565 HNRNPU  | ####     |
| APQCLGKFIEIAAR          | 6 Q00839  | HNRPU_HL  | 565 HNRNPU  | ####     |
| APQCLGKFIEIAAR          | 6 Q00839  | HNRPU_HL  | 565 HNRNPU  | ####     |
| DEDYKQR                 | 4 Q00839  | HNRPU_HL  | 614 HNRNPU  | ####     |
| KAVVVC PK               | 0 Q00839  | HNRPU_HL  | 602 HNRNPU  | ####     |
| KAVVVC PK               | 0 Q00839  | HNRPU_HL  | 602 HNRNPU  | ####     |
| KAVVVC PK               | 0 Q00839  | HNRPU_HL  | 602 HNRNPU  | ####     |
| KAVVVC PK               | 0 Q00839  | HNRPU_HL  | 602 HNRNPU  | ####     |
| KMCLFAGFQR              | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KMCLFAGFQR              | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KMCLFAGFQR              | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KMCLFAGFQR              | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KMCLFAGFQR              | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KMCLFAGFQR              | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KMCLFAGFQR              | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KM[147.04]CLFAGFQR      | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KM[147.04]CLFAGFQR      | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| KM[147.04]CLFAGFQR      | 0 Q00839  | HNRPU_HL  | 592 HNRNPU  | ####     |
| QMADTGKLN TLLQR         | 6 Q00839  | HNRPU_HL  | 551 HNRNPU  | ####     |
| QMADTGKLN TLLQR         | 6 Q00839  | HNRPU_HL  | 551 HNRNPU  | ####     |
| QM[147.04]ADTGKLN TLLQR | 6 Q00839  | HNRPU_HL  | 551 HNRNPU  | ####     |
| VC FEMKVTEK             | 5 Q00839  | HNRPU_HL  | 339 HNRNPU  | Q00839   |
| EASLGEASKLQQFLR         | 8 Q01082  | SPTB2_HUI | 1063 SPTBN1 | ####     |
| EASLGEASKLQQFLR         | 8 Q01082  | SPTB2_HUI | 1063 SPTBN1 | ####     |
| ELEAENYHDIKR            | 10 Q01082 | SPTB2_HUI | 497 SPTBN1  | Q01082   |
| FYHDAKEIFGR             | 5 Q01082  | SPTB2_HUI | 1815 SPTBN1 | 3EDV     |
| HYASEEIKEK              | 7 Q01082  | SPTB2_HUI | 1989 SPTBN1 | 3EDV     |
| LEKAEHER                | 2 Q01082  | SPTB2_HUI | 401 SPTBN1  | Q01082   |
| TTLKNR                  | 3 Q01082  | SPTB2_HUI | 1052 SPTBN1 | ####     |
| DLAALGDKVNSLGETAER      | 7 Q13813  | SPTN1_HUI | 1288 SPTAN1 | ####     |
| EKLTVLSEER              | 1 Q13813  | SPTN1_HUI | 441 SPTAN1  | ####     |
| LVSQDNFGFDLP AVEAATKK   | 18 Q01082 | SPTB2_HUI | 462 SPTBN1  | Q01082   |
| LLQEKYQR                | 4 Q8WWI1  | LMO7_HUI  | 1248 LMO7   | ####     |
| EFHLNESGDPSSKSTEIK      | 12 Q01105 | SET_HUMA  | 167 SET     | 2.00E+50 |
| SGKDLTK                 | 2 Q01105  | SET_HUMA  | 177 SET     | ####     |
| STEIKWK                 | 4 Q01105  | SET_HUMA  | 172 SET     | 2.00E+50 |
| STEIKWK                 | 4 Q01105  | SET_HUMA  | 172 SET     | 2.00E+50 |
| VEVTEFEDIKSGYR          | 9 Q01105  | SET_HUMA  | 132 SET     | 2.00E+50 |
| VEVTEFEDIKSGYR          | 9 Q01105  | SET_HUMA  | 132 SET     | 2.00E+50 |
| YNKLR                   | 2 Q01105  | SET_HUMA  | 75 SET      | 2.00E+50 |
| ALAAPAAEEKEEAR          | 9 Q01650  | LAT1_HUM  | 19 SLC7A5   | ####     |
| IKEAR                   | 1 Q01813  | PFKAP_HUI | 702 PFKP    | 4XYJ     |
| LKAACNLLQR              | 1 Q01813  | PFKAP_HUI | 109 PFKP    | 4XYJ     |
| NFGTKISAR               | 4 Q01813  | PFKAP_HUI | 688 PFKP    | 4XYJ     |
| NFGTKISAR               | 4 Q01813  | PFKAP_HUI | 688 PFKP    | 4XYJ     |

|                   |           |           |             |          |
|-------------------|-----------|-----------|-------------|----------|
| NFGTKISAR         | 4 Q01813  | PFKAP_HUI | 688 PFKP    | 4XYJ     |
| NVIFQPVAELKK      | 10 Q01813 | PFKAP_HUI | 736 PFKP    | 4XYJ     |
| NVIFQPVAELKK      | 10 Q01813 | PFKAP_HUI | 736 PFKP    | 4XYJ     |
| SFAGNLNTYKR       | 9 Q01813  | PFKAP_HUI | 395 PFKP    | 4XYJ     |
| KLADISLGK         | 0 Q02413  | DSG1_HUM  | 757 DSG1    | ####     |
| EYKVVGR           | 2 Q02543  | RL18A_HUI | 11 RPL18A   | Q02543   |
| VKNFGIWLR         | 1 Q02543  | RL18A_HUI | 76 RPL18A   | Q02543   |
| GTVYFKEGK         | 5 Q02790  | FKBP4_HUI | 282 FKBP4   | 1QZ2     |
| GTVYFKEGK         | 5 Q02790  | FKBP4_HUI | 282 FKBP4   | 1QZ2     |
| LEQSTIVKER        | 7 Q02790  | FKBP4_HUI | 274 FKBP4   | 1QZ2     |
| IDISNVKIPK        | 6 Q02878  | RL6_HUM   | 207 RPL6    | Q02878   |
| GKILNVR           | 1 Q02880  | TOP2B_HU  | 510 TOP2B   | 3QX3     |
| TPATKR            | 4 Q04637  | IF4G1_HUM | 1183 EIF4G1 | ####     |
| CQSSCGQVKCR       | 8 Q04721  | NOTC2_HU  | 1350 NOTCH2 | ####     |
| KPDDGKMK          | 5 Q04760  | LGUL_HUM  | 157 GLO1    | 3W0T     |
| KPDDGKM[147.04]K  | 5 Q04760  | LGUL_HUM  | 157 GLO1    | 3W0T     |
| KSLDFYTR          | 0 Q04760  | LGUL_HUM  | 44 GLO1     | 3W0T     |
| VQPEAQAKVDVFR     | 7 Q06323  | PSME1_HU  | 13 PSME1    | 1AVO     |
| DISLSDYKGK        | 7 Q06830  | PRDX1_HU  | 35 PRDX1    | 4XCS     |
| DISLSDYKGK        | 7 Q06830  | PRDX1_HU  | 35 PRDX1    | 4XCS     |
| DISLSDYKGK        | 7 Q06830  | PRDX1_HU  | 35 PRDX1    | 4XCS     |
| KQGGLGPMNIPLVSDPK | 0 Q06830  | PRDX1_HU  | 93 PRDX1    | 4XCS     |
| ENKTAVVVGTITDDVR  | 2 Q07020  | RL18_HUM  | 78 RPL18    | Q07020   |
| HNKDR             | 2 Q07020  | RL18_HUM  | 9 RPL18     | Q07020   |
| LLVKLYR           | 3 Q07020  | RL18_HUM  | 30 RPL18    | Q07020   |
| TNSTFNQVVLKR      | 10 Q07020 | RL18_HUM  | 49 RPL18    | Q07020   |
| VQEVPKLK          | 5 Q07020  | RL18_HUM  | 97 RPL18    | Q07020   |
| KVAGEK            | 0 Q07021  | C1QBP_HU  | 123 C1QBP   | 1P32     |
| KVAGEK            | 0 Q07021  | C1QBP_HU  | 123 C1QBP   | 1P32     |
| KVAGEK            | 0 Q07021  | C1QBP_HU  | 123 C1QBP   | 1P32     |
| ALKEAVK           | 2 Q07065  | CKAP4_HU  | 290 CKAP4   | Q07065   |
| AVKQGESEVSR       | 2 Q07065  | CKAP4_HU  | 191 CKAP4   | Q07065   |
| DLSDGIHVVKDAR     | 9 Q07065  | CKAP4_HU  | 223 CKAP4   | Q07065   |
| ELVSLKQEQQAFK     | 5 Q07065  | CKAP4_HU  | 332 CKAP4   | Q07065_Q |
| IHEKV             | 3 Q07065  | CKAP4_HU  | 601 CKAP4   | ####     |
| ISEVLQKLQNEILK    | 6 Q07065  | CKAP4_HU  | 206 CKAP4   | Q07065_Q |
| SQKEINDMK         | 2 Q07065  | CKAP4_HU  | 264 CKAP4   | Q07065   |
| SQKEINDM[147.04]K | 2 Q07065  | CKAP4_HU  | 264 CKAP4   | Q07065   |
| GTPGEGKPR         | 5 Q07092  | COGA1_HL  | 864 COL16A1 | ####     |
| LGPDDPNVAKTK      | 9 Q07866  | KLC1_HUM  | 382 KLC1    | 3NF1     |
| ILAKLPIEPR        | 3 Q08211  | DHX9_HUM  | 857 DHX9    | Q08211   |
| KLEAGIR           | 0 Q08211  | DHX9_HUM  | 497 DHX9    | Q08211   |
| LDSELKELR         | 5 Q08378  | GOGA3_HL  | 881 GOLGA3  | ####     |
| TFVPKNER          | 4 Q08J23  | NSUN2_HL  | 692 NSUN2   | ####     |
| TFVPKNER          | 4 Q08J23  | NSUN2_HL  | 692 NSUN2   | ####     |
| GPDWHLKMPK        | 6 Q09666  | AHNK_HUM  | 748 AHNK    | ####     |
| LQGSQVSLASKK      | 10 Q09666 | AHNK_HUM  | 5858 AHNK   | ####     |

|                  |           |          |             |        |
|------------------|-----------|----------|-------------|--------|
| KTAAVCVAK        | 0 Q10567  | AP1B1_HU | 139 AP1B1   | 4P6Z   |
| FCPTENVAKINR     | 8 Q10713  | MPPA_HU  | 232 PMPCA   | Q10713 |
| FCPTENVAKINR     | 8 Q10713  | MPPA_HU  | 232 PMPCA   | Q10713 |
| GQSHWVKR         | 6 Q96EE3  | SEH1_HU  | 105 SEH1L   | Q96EE3 |
| KGWLFASCAK       | 0 Q12788  | TBL3_HU  | 387 TBL3    | Q12788 |
| AKGLFLPEDENLR    | 1 Q12797  | ASPH_HU  | 609 ASPH    | 5JQY   |
| QVGSYKK          | 5 Q12905  | ILF2_HU  | 109 ILF2    | Q12905 |
| QKCLAALASLR      | 1 Q12906  | ILF3_HU  | 202 ILF3    | Q12906 |
| VKPAPDETSFSEALLK | 1 Q12905  | ILF2_HU  | 45 ILF2     | Q12905 |
| ALKGVLR          | 2 Q96KR1  | ZFR_HU   | 786 ZFR     | Q96KR1 |
| HALIKK           | 4 Q12931  | TRAP1_HU | 652 TRAP1   | Q12931 |
| KDAEK            | 0 Q12931  | TRAP1_HU | 432 TRAP1   | 5Y3N   |
| KVLIQTK          | 0 Q12931  | TRAP1_HU | 369 TRAP1   | 5Y3N   |
| LNELLVKALER      | 6 Q12931  | TRAP1_HU | 699 TRAP1   | Q12931 |
| MQQLAKTQEER      | 5 Q12931  | TRAP1_HU | 629 TRAP1   | ####   |
| ELKTVTFSK        | 2 Q13011  | ECH1_HU  | 321 ECH1    | ####   |
| NAMNKVFWR        | 4 Q13011  | ECH1_HU  | 83 ECH1     | 2VRE   |
| NAMNKVFWR        | 4 Q13011  | ECH1_HU  | 83 ECH1     | 2VRE   |
| SVQATTENKELK     | 8 Q13011  | ECH1_HU  | 318 ECH1    | ####   |
| AVAEGKR          | 5 Q13057  | COASY_HU | 464 COASY   | Q13057 |
| GSVLEPEGTVEIKFR  | 12 Q13085 | ACACA_HU | 2127 ACACA  | 4ASI   |
| KVFGVGR          | 0 Q13148  | TADBP_HU | 192 TADBP   | Q13148 |
| KLFVGGGLK        | 0 Q13151  | ROA0_HU  | 99 HNRNPA0  | Q13151 |
| KLFVGGGLK        | 0 Q13151  | ROA0_HU  | 99 HNRNPA0  | Q13151 |
| EKDVER           | 1 Q13243  | SRSF5_HU | 18 SRSF5    | Q13243 |
| LNVEEKK          | 5 Q13283  | G3BP1_HU | 413 G3BP1   | ####   |
| KVFGVGR          | 0 Q13310  | PABP4_HU | 167 PABPC4  | Q13310 |
| KGAAPAPPR        | 0 Q13428  | TCOF_HU  | 449 TCOF1   | ####   |
| KGAAPAPPR        | 0 Q13428  | TCOF_HU  | 449 TCOF1   | ####   |
| KGWESR           | 0 Q13428  | TCOF_HU  | 1340 TCOF1  | ####   |
| KGWESR           | 0 Q13428  | TCOF_HU  | 1340 TCOF1  | ####   |
| EKFLITR          | 1 Q13443  | ADAM9_HU | 290 ADAM9   | Q13443 |
| MSFVKGWGPDYPR    | 4 Q13485  | SMAD4_HU | 507 SMAD4   | 1DD1   |
| IKQQQPNPVEQR     | 1 Q13496  | MTM1_HU  | 546 MTM1    | ####   |
| AYLLGKEDAAAR     | 5 Q13501  | SQSTM_HU | 13 SQSTM1   | ####   |
| AADKLAPAQYIR     | 3 Q13573  | SNW1_HU  | 170 SNW1    | 5MQF   |
| TLQSLACGKAR      | 8 Q13619  | CUL4A_HU | 635 CUL4A   | 2HYE   |
| LDVPQNLNMFQKWK   | 10 Q13740 | CD166_HU | 55 ALCAM    | 5A2F   |
| SVQYDDVPEYKDR    | 10 Q13740 | CD166_HU | 87 ALCAM    | 5A2F   |
| ADLEKAWVQR       | 4 Q13813  | SPTN1_HU | 1432 SPTAN1 | 3FB2   |
| ITKEAGSVSLR      | 2 Q13813  | SPTN1_HU | 1057 SPTAN1 | ####   |
| KLLVGSSEDYGR     | 0 Q13813  | SPTN1_HU | 1784 SPTAN1 | ####   |
| KLLVGSSEDYGR     | 0 Q13813  | SPTN1_HU | 1784 SPTAN1 | ####   |
| LAQFVEHWKELK     | 8 Q13813  | SPTN1_HU | 1853 SPTAN1 | ####   |
| LKDINK           | 1 Q13813  | SPTN1_HU | 1148 SPTAN1 | ####   |
| LKGLALQR         | 1 Q13813  | SPTN1_HU | 241 SPTAN1  | ####   |
| LLQAQKLVQYLR     | 5 Q13813  | SPTN1_HU | 150 SPTAN1  | ####   |

|                   |    |        |           |      |         |          |
|-------------------|----|--------|-----------|------|---------|----------|
| QGFVPAAYVKK       | 9  | Q13813 | SPTN1_HU  | 1022 | SPTAN1  | ####     |
| QKLEDSYR          | 1  | Q13813 | SPTN1_HU  | 39   | SPTAN1  | ####     |
| SKLGESQTLQQFSR    | 1  | Q13813 | SPTN1_HU  | 1546 | SPTAN1  | ####     |
| FSKYMPNVK         | 2  | Q13838 | DX39B_HU  | 138  | DDX39B  | 1XTK     |
| KDEEVLK           | 0  | Q13838 | DX39B_HU  | 156  | DDX39B  | 1XTK     |
| YQQFKDFQR         | 4  | Q13838 | DX39B_HU  | 334  | DDX39B  | 1XTK     |
| YQQFKDFQR         | 4  | Q13838 | DX39B_HU  | 334  | DDX39B  | 1XTK     |
| DLKDYFSK          | 2  | Q14103 | HNRPD_HL  | 114  | HNRNPD  | 5IMO     |
| KIFVGGLSPDTPEEK   | 0  | Q14103 | HNRPD_HL  | 183  | HNRNPD  | Q14103   |
| MFIGGLSWDTTKK     | 11 | Q14103 | HNRPD_HL  | 110  | HNRNPD  | 5IMO     |
| TKEPVKK           | 1  | Q14103 | HNRPD_HL  | 178  | HNRNPD  | Q14103   |
| VIDPKR            | 4  | Q14103 | HNRPD_HL  | 170  | HNRNPD  | 5IMO     |
| DNWISVDSVTSEIKLAK | 13 | Q14126 | DSG2_HUN  | 448  | DSG2    | 5ERD     |
| EGEDLSKK          | 6  | Q14126 | DSG2_HUN  | 66   | DSG2    | 5ERD     |
| ITYKYTGK          | 3  | Q14126 | DSG2_HUN  | 88   | DSG2    | 5ERD     |
| LAKLPDFESR        | 2  | Q14126 | DSG2_HUN  | 451  | DSG2    | 5ERD     |
| YVKLEDR           | 2  | Q14126 | DSG2_HUN  | 430  | DSG2    | 5ERD     |
| AEKDR             | 2  | Q14152 | EIF3A_HUN | 1360 | EIF3A   | ####     |
| KAEEER            | 0  | Q14152 | EIF3A_HUN | 606  | EIF3A   | ####     |
| LEEIPLIKSAYEEQR   | 7  | Q14152 | EIF3A_HUN | 711  | EIF3A   | ####     |
| AKELLGQGLLLR      | 1  | Q99613 | EIF3C_HUN | 643  | EIF3C   | Q99613   |
| KLCDNLR           | 0  | Q14152 | EIF3A_HUN | 196  | EIF3A   | Q14152   |
| LTKGQVGGTFAR      | 2  | Q14181 | DPOA2_HL  | 564  | POLA2   | 4Y97     |
| DLSSQLLKVLGTR     | 7  | Q14204 | DYHC1_HU  | 394  | DYNC1H1 | Q14204   |
| FKVQYPQSQACK      | 1  | Q14204 | DYHC1_HU  | 624  | DYNC1H1 | Q14204   |
| KIIDSVR           | 0  | Q14204 | DYHC1_HU  | 2286 | DYNC1H1 | 5NUG     |
| LLEKQR            | 3  | Q14204 | DYHC1_HU  | 1199 | DYNC1H1 | Q14204   |
| LLEKQR            | 3  | Q14204 | DYHC1_HU  | 1199 | DYNC1H1 | Q14204   |
| STALLKSLSAER      | 5  | Q14204 | DYHC1_HU  | 3480 | DYNC1H1 | 5NUG     |
| VLLKALER          | 3  | Q14204 | DYHC1_HU  | 2239 | DYNC1H1 | 5NUG     |
| KLEEQR            | 0  | Q14247 | SRC8_HUN  | 390  | CTTN    | ####     |
| ALKTFVK           | 2  | Q14566 | MCM6_HU   | 95   | MCM6    | Q14566   |
| DGSGVTKSSWR       | 6  | Q14566 | MCM6_HU   | 611  | MCM6    | Q14566   |
| DGSGVTKSSWR       | 6  | Q14566 | MCM6_HU   | 611  | MCM6    | Q14566   |
| KEIPLAK           | 0  | Q14566 | MCM6_HU   | 102  | MCM6    | Q14566   |
| LLNKSIR           | 3  | Q14566 | MCM6_HU   | 654  | MCM6    | Q14566   |
| EFEEKVK           | 5  | Q14683 | SMC1A_HL  | 796  | SMC1A   | ####     |
| IKLEGIITR         | 1  | Q9UQE7 | SMC3_HUN  | 820  | SMC3    | ####     |
| KLMMTLK           | 0  | Q14690 | RRP5_HUN  | 516  | PDCD11  | ####     |
| MKFFFK            | 1  | Q14690 | RRP5_HUN  | 1832 | PDCD11  | Q14690   |
| KFADGEVVR         | 0  | Q14739 | LBR_HUM   | 5    | LBR     | ####     |
| IEGEGSVLQAKLK     | 10 | Q14764 | MVP_HUN   | 745  | MVP     | Q14764_Q |
| EIESLKVSISQLTR    | 5  | Q14789 | GOGB1_HL  | 2608 | GOLGB1  | Q14789   |
| KELLQR            | 0  | Q14789 | GOGB1_HL  | 1003 | GOLGB1  | ####     |
| KEYLEKIQGAQK      | 0  | Q14789 | GOGB1_HL  | 1988 | GOLGB1  | ####     |
| YQEKISALER        | 3  | Q14789 | GOGB1_HL  | 2034 | GOLGB1  | ####     |
| KELLQR            | 0  | Q14789 | GOGB1_HL  | 1003 | GOLGB1  | ####     |



|                       |    |        |           |      |         |        |
|-----------------------|----|--------|-----------|------|---------|--------|
| ELVKEPAR              | 3  | Q14980 | NUMA1_HI  | 939  | NUMA1   | ####   |
| QVDPVQKK              | 6  | Q9Y6V0 | PCLO_HUN  | 797  | PCLO    | ####   |
| WKSFNLVK              | 1  | Q14997 | PSME4_HU  | 916  | PSME4   | ####   |
| KVVAAR                | 0  | Q15004 | PAF15_HUI | 15   | PCLAF   | ####   |
| KTYDK                 | 0  | Q15008 | PSMD6_HL  | 126  | PSMD6   | 5M32   |
| VQKLSR                | 2  | Q15008 | PSMD6_HL  | 382  | PSMD6   | 5M32   |
| KAPTSSQR              | 0  | Q15029 | U5S1_HUN  | 359  | EFTUD2  | 509Z   |
| STPVTVVLPTDKGK        | 11 | Q15029 | U5S1_HUN  | 194  | EFTUD2  | 509Z   |
| AVGWWKR               | 5  | Q15041 | AR6P1_HU  | 124  | ARL6IP1 | Q15041 |
| FLMKSYDQVHSGK         | 3  | Q15067 | ACOX1_HU  | 437  | ACOX1   | Q15067 |
| FLMKSYDQVHSGK         | 3  | Q15067 | ACOX1_HU  | 437  | ACOX1   | Q15067 |
| FLMKSYDQVHSGK         | 3  | Q15067 | ACOX1_HU  | 437  | ACOX1   | Q15067 |
| FLM[147.04]KSYDQVHSGK | 3  | Q15067 | ACOX1_HU  | 437  | ACOX1   | Q15067 |
| LQTKVLELQR            | 3  | Q15075 | EEA1_HUM  | 1312 | EEA1    | 1JOC   |
| KAATALK               | 0  | Q15084 | PDIA6_HUI | 67   | PDIA6   | Q15084 |
| LTPEWKK               | 5  | Q15084 | PDIA6_HUI | 66   | PDIA6   | Q15084 |
| QLVKDR                | 3  | Q15084 | PDIA6_HUI | 136  | PDIA6   | ####   |
| AKVEEAR               | 1  | Q15149 | PLEC_HUM  | 2154 | PLEC    | ####   |
| ALAEKMLK              | 4  | Q15149 | PLEC_HUM  | 2447 | PLEC    | ####   |
| AQAEVEGLGKGVAR        | 9  | Q15149 | PLEC_HUM  | 1175 | PLEC    | 5J1I   |
| AQAQAAAELR            | 8  | Q15149 | PLEC_HUM  | 2274 | PLEC    | ####   |
| AQFEQLKDGK            | 6  | Q15149 | PLEC_HUM  | 3469 | PLEC    | ####   |
| DKLLSAER              | 1  | Q15149 | PLEC_HUM  | 4140 | PLEC    | ####   |
| DPYTGQSVSLFQALKK      | 14 | Q15149 | PLEC_HUM  | 3258 | PLEC    | ####   |
| EAAAATQKR             | 7  | Q15149 | PLEC_HUM  | 1886 | PLEC    | ####   |
| EAKELQQR              | 2  | Q15149 | PLEC_HUM  | 1528 | PLEC    | ####   |
| EAKELQQR              | 2  | Q15149 | PLEC_HUM  | 1528 | PLEC    | ####   |
| FAKQYINAIK            | 2  | Q15149 | PLEC_HUM  | 1410 | PLEC    | ####   |
| GAEKAENVETTQVYTEETRR  | 3  | Q15149 | PLEC_HUM  | 3685 | PLEC    | ####   |
| GHLSGLAKR             | 7  | Q15149 | PLEC_HUM  | 923  | PLEC    | ####   |
| GKAEQAVR              | 1  | Q15149 | PLEC_HUM  | 1815 | PLEC    | ####   |
| GLVDKIMVDR            | 4  | Q15149 | PLEC_HUM  | 4480 | PLEC    | ####   |
| ISYKDALDR             | 3  | Q15149 | PLEC_HUM  | 4584 | PLEC    | ####   |
| ITVEKIK               | 4  | Q15149 | PLEC_HUM  | 3091 | PLEC    | ####   |
| KAALEEVR              | 0  | Q15149 | PLEC_HUM  | 2142 | PLEC    | ####   |
| KASDSELR              | 0  | Q15149 | PLEC_HUM  | 2037 | PLEC    | ####   |
| KASDSELR              | 0  | Q15149 | PLEC_HUM  | 2037 | PLEC    | ####   |
| KEAEQEAAR             | 0  | Q15149 | PLEC_HUM  | 2277 | PLEC    | ####   |
| KELIPTEEAR            | 0  | Q15149 | PLEC_HUM  | 3925 | PLEC    | ####   |
| KESYSALMR             | 0  | Q15149 | PLEC_HUM  | 792  | PLEC    | Q15149 |
| KFAEQTLR              | 0  | Q15149 | PLEC_HUM  | 2309 | PLEC    | ####   |
| KFAEQTLR              | 0  | Q15149 | PLEC_HUM  | 2309 | PLEC    | ####   |
| KGLILK                | 0  | Q15149 | PLEC_HUM  | 4168 | PLEC    | ####   |
| KGLILK                | 0  | Q15149 | PLEC_HUM  | 4168 | PLEC    | ####   |
| KGLILK                | 0  | Q15149 | PLEC_HUM  | 4168 | PLEC    | ####   |
| KGLLSAEVAR            | 0  | Q15149 | PLEC_HUM  | 3849 | PLEC    | ####   |
| KGLLSAEVAR            | 0  | Q15149 | PLEC_HUM  | 3849 | PLEC    | ####   |

|                      |           |           |            |        |
|----------------------|-----------|-----------|------------|--------|
| KGWLYYEAGQR          | 0 Q15149  | PLEC_HUM  | 4513 PLEC  | ####   |
| KLTFR                | 0 Q15149  | PLEC_HUM  | 4019 PLEC  | ####   |
| KLTFR                | 0 Q15149  | PLEC_HUM  | 4019 PLEC  | ####   |
| KTFTK                | 0 Q15149  | PLEC_HUM  | 183 PLEC   | ####   |
| LAEEVAALEKQR         | 9 Q15149  | PLEC_HUM  | 1508 PLEC  | ####   |
| LKAEAEELLQQKELAQEQAR | 11 Q15149 | PLEC_HUM  | 2473 PLEC  | ####   |
| LKAEATEAAR           | 1 Q15149  | PLEC_HUM  | 2350 PLEC  | ####   |
| LKLSYK               | 1 Q15149  | PLEC_HUM  | 4580 PLEC  | ####   |
| LKTEAEIALK           | 1 Q15149  | PLEC_HUM  | 1986 PLEC  | ####   |
| LKTISLVIR            | 1 Q15149  | PLEC_HUM  | 1226 PLEC  | 5J1I   |
| LLPLKGAEK            | 4 Q15149  | PLEC_HUM  | 3681 PLEC  | ####   |
| MGIVGPEFKDK          | 8 Q15149  | PLEC_HUM  | 4138 PLEC  | ####   |
| MGIVGPEFKDK          | 8 Q15149  | PLEC_HUM  | 4138 PLEC  | ####   |
| M[147.04]GIVGPEFKDK  | 8 Q15149  | PLEC_HUM  | 4138 PLEC  | ####   |
| QLQLAQEAAQKR         | 10 Q15149 | PLEC_HUM  | 2182 PLEC  | ####   |
| SAEAELOQSKR          | 8 Q15149  | PLEC_HUM  | 1718 PLEC  | ####   |
| SSIAGLLLKATNEK       | 8 Q15149  | PLEC_HUM  | 2841 PLEC  | ####   |
| TLKPEEQR             | 2 Q15149  | PLEC_HUM  | 1055 PLEC  | ####   |
| TPVEVPVGGFKGR        | 10 Q15149 | PLEC_HUM  | 3384 PLEC  | ####   |
| WQLKANEALR           | 3 Q15149  | PLEC_HUM  | 1774 PLEC  | ####   |
| YLTCPKTK             | 5 Q15149  | PLEC_HUM  | 4576 PLEC  | ####   |
| AHEQALAELTR          | 10 Q15477 | SKIV2_HUM | 791 SKIV2L | ####   |
| AAPGAEFAPNKR         | 10 Q15233 | NONO_HUM  | 467 NONO   | ####   |
| DKGFGFIR             | 1 Q15233  | NONO_HUM  | 109 NONO   | 3SDE   |
| GIVEFSGKPAAR         | 7 Q15233  | NONO_HUM  | 198 NONO   | 3SDE   |
| KALDR                | 0 Q15233  | NONO_HUM  | 203 NONO   | 3SDE   |
| KLFEK                | 0 Q15233  | NONO_HUM  | 92 NONO    | 3SDE   |
| KQLELR               | 0 Q15233  | NONO_HUM  | 338 NONO   | ####   |
| KQLELR               | 0 Q15233  | NONO_HUM  | 338 NONO   | ####   |
| KQLELR               | 0 Q15233  | NONO_HUM  | 338 NONO   | ####   |
| DAVHNKLWLQR          | 5 Q15262  | PTPRK_HUM | 227 PTPRK  | ####   |
| TKCAEPMR             | 1 Q15262  | PTPRK_HUM | 385 PTPRK  | ####   |
| VTVFDLKNK            | 6 Q15269  | PWP2_HUM  | 43 PWP2    | Q15269 |
| IKMIDMPVER           | 1 Q15287  | RNPS1_HUM | 188 RNPS1  | 4A8X   |
| LGKIVDR              | 2 Q15293  | RCN1_HUM  | 86 RCN1    | Q15293 |
| LYKDDQLDDGK          | 2 Q15370  | ELOB_HUM  | 46 ELOB    | 4AJY   |
| EWKEQGSK             | 2 Q15392  | DHC24_HUM | 82 DHCR24  | Q15392 |
| ISLLKLTQGETLR        | 4 Q15392  | DHC24_HUM | 367 DHCR24 | Q15392 |
| AVMISAIEKQK          | 8 Q15393  | SF3B3_HUM | 137 SF3B3  | Q15393 |
| AKNEPVGK             | 1 Q15424  | SAFB1_HUM | 483 SAFB   | ####   |
| NIVDKTASFVAR         | 4 Q15459  | SF3A1_HUM | 55 SF3A1   | ####   |
| KLAQDVRAK            | 0 Q15669  | RHOH_HUM  | 138 RHOH   | ####   |
| ILQAGFKR             | 6 Q15691  | MARE1_HUM | 83 MAPRE1  | 2R8U   |
| KAMGYQPLVTMDDAMER    | 0 Q15738  | NSDHL_HUM | 345 NSDHL  | Q15738 |
| VNYIGTKNVIETCK       | 6 Q15738  | NSDHL_HUM | 126 NSDHL  | Q15738 |
| VKEKEAILK            | 3 Q9P0V9  | SEP10_HUM | 377 10-Sep | ####   |
| KVTLGTQPTVLR         | 0 Q16531  | DDB1_HUM  | 628 DDB1   | 3EI3   |

|               |   |        |          |     |           |          |
|---------------|---|--------|----------|-----|-----------|----------|
| SGKVAFR       | 2 | Q16658 | FSCN1_HU | 220 | FSCN1     | 3LLP     |
| EIAQDFKTDLR   | 6 | Q16695 | H31T_HUN | 80  | HIST3H3   | 3A6N     |
| KLPFQR        | 0 | Q16695 | H31T_HUN | 65  | HIST3H3   | 3A6N     |
| KQLATK        | 0 | Q16695 | H31T_HUN | 19  | HIST3H3   | Q16695   |
| KQLATK        | 0 | Q16695 | H31T_HUN | 19  | HIST3H3   | Q16695   |
| KQLATK        | 0 | Q16695 | H31T_HUN | 19  | HIST3H3   | Q16695   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695_Q |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| YQKSTELLIR    | 2 | Q16695 | H31T_HUN | 57  | HIST3H3   | 3A6N     |
| YQKSTELLIR    | 2 | Q16695 | H31T_HUN | 57  | HIST3H3   | 3A6N     |
| YQKSTELLIR    | 2 | Q16695 | H31T_HUN | 57  | HIST3H3   | 3A6N     |
| KTESHK        | 0 | Q16777 | H2A2C_HU | 120 | HIST2H2AC | Q16777   |
| YQKSTELLIR    | 2 | Q16695 | H31T_HUN | 57  | HIST3H3   | 3A6N     |
| AVTKYTSSK     | 3 | Q93079 | H2B1H_HU | 121 | HIST1H2BH | Q93079   |
| EIAQDFKTDLR   | 6 | Q16695 | H31T_HUN | 80  | HIST3H3   | 3A6N     |
| HAVSEGTKAVTK  | 7 | Q93079 | H2B1H_HU | 117 | HIST1H2BH | Q93079   |
| KLPFQR        | 0 | Q16695 | H31T_HUN | 65  | HIST3H3   | 3A6N     |
| KQLATK        | 0 | Q16695 | H31T_HUN | 19  | HIST3H3   | Q16695   |
| LAHYNKR       | 5 | Q93079 | H2B1H_HU | 86  | HIST1H2BH | Q93079   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| YQKSTELLIR    | 2 | Q16695 | H31T_HUN | 57  | HIST3H3   | 3A6N     |
| YQKSTELLIR    | 2 | Q16695 | H31T_HUN | 57  | HIST3H3   | 3A6N     |
| YQKSTELLIR    | 2 | Q16695 | H31T_HUN | 57  | HIST3H3   | 3A6N     |
| NDEELNKLLGK   | 6 | Q96KK5 | H2A1H_HU | 96  | HIST1H2AH | Q96KK5   |
| NDEELNKLLGK   | 6 | Q96KK5 | H2A1H_HU | 96  | HIST1H2AH | Q96KK5   |
| NDEELNKLLGK   | 6 | Q96KK5 | H2A1H_HU | 96  | HIST1H2AH | Q96KK5   |
| NDEELNKLLGK   | 6 | Q96KK5 | H2A1H_HU | 96  | HIST1H2AH | Q96KK5   |
| TKQTAR        | 1 | Q16695 | H31T_HUN | 5   | HIST3H3   | Q16695   |
| KQLYNIYAK     | 0 | Q16740 | CLPP_HUM | 203 | CLPP      | 1TG6     |
| KQLYNIYAK     | 0 | Q16740 | CLPP_HUM | 203 | CLPP      | 1TG6     |
| TGKLGPGRLR    | 2 | Q16762 | THTR_HUN | 24  | TST       | Q16762   |
| AVGEKVVR      | 4 | Q16795 | NDUA9_HL | 189 | NDUFA9    | 5XTB     |
| ADVKGGLTQYEGK | 3 | Q16851 | UGPA_HUM | 291 | UGP2      | ####     |
| ADVKGGLTQYEGK | 3 | Q16851 | UGPA_HUM | 291 | UGP2      | 3R3I     |
| ADVKGGLTQYEGK | 3 | Q16851 | UGPA_HUM | 291 | UGP2      | 3R3I     |
| INKESLLPVAK   | 2 | Q16851 | UGPA_HUM | 198 | UGP2      | 3R3I     |
| INKESLLPVAK   | 2 | Q16851 | UGPA_HUM | 198 | UGP2      | 3R3I     |
| LGSSFTKVQDYLR | 6 | Q16851 | UGPA_HUM | 438 | UGP2      | 3R3I     |
| IKATNNK       | 1 | Q16881 | TRXR1_HU | 291 | TXNRD1    | 3QFA     |
| INEKTGK       | 3 | Q16881 | TRXR1_HU | 462 | TXNRD1    | 3QFA     |
| KIGLETVGVK    | 0 | Q16881 | TRXR1_HU | 449 | TXNRD1    | 3QFA     |

|                          |          |          |              |           |
|--------------------------|----------|----------|--------------|-----------|
| NYGWKVEETVK              | 4 Q16881 | TRXR1_HU | 239 TXNRD1   | 3QFA      |
| AKEELEK                  | 1 Q16891 | MIC60_HU | 299 IMMT     | ####      |
| KIEEVR                   | 0 Q16891 | MIC60_HU | 467 IMMT     | ####      |
| KSAQWR                   | 0 Q16891 | MIC60_HU | 270 IMMT     | ####      |
| TVEGALKER                | 6 Q16891 | MIC60_HU | 282 IMMT     | ####      |
| LKVTELK                  | 1 Q1KMD3 | HNRL2_HU | 7 HNRNPUL2   | ####      |
| YGGQPLFSEKFPTLWSGAR      | 9 Q1KMD3 | HNRL2_HU | 273 HNRNPUL2 | Q1KMD3    |
| KLDLISELR                | 0 Q2M389 | WASC4_HU | 586 WASHC4   | Q2M389    |
| KGGAGGK                  | 0 Q53EL6 | PDCD4_HU | 115 PDCD4    | Q53EL6_Q5 |
| IKIAPPER                 | 1 Q562R1 | ACTBL_HU | 329 ACTBL2   | Q562R1    |
| IKIAPPER                 | 1 Q562R1 | ACTBL_HU | 329 ACTBL2   | Q562R1    |
| NIYKEAYR                 | 3 Q5BJE1 | CC178_HU | 500 CCDC178  | Q5BJE1_Q5 |
| KTSLR                    | 0 Q5BKZ1 | ZN326_HU | 367 ZNF326   | ####      |
| IIQKVFAFR                | 3 Q5T4S7 | UBR4_HU  | 3820 UBR4    | ####      |
| EEPLAAKEALGHLSLAEVGTFFI  | 6 Q5VST9 | OBSCN_HU | 5519 OBSCN   | ####      |
| QVFVCGNDSKAK             | 9 Q687X5 | STE4_HU  | 161 STEAP4   | ####      |
| LYLGKNR                  | 4 Q6EMK4 | VASN_HU  | 133 VASN     | Q6EMK4    |
| IISKEGIPGLYR             | 3 Q6NUK1 | SCMC1_HU | 437 SLC25A24 | Q6NUK1    |
| ILKHEGLGAFYK             | 2 Q6NUK1 | SCMC1_HU | 336 SLC25A24 | Q6NUK1    |
| KILALR                   | 0 Q6P1N0 | C2D1A_HU | 861 CC2D1A   | ####      |
| LFSQDECAKIEAR            | 8 Q6P6C2 | ALKB5_HU | 102 ALKBH5   | 407X      |
| KSLQLASQR                | 0 Q6PGP7 | TTC37_HU | 1425 TTC37   | ####      |
| IKEEAKK                  | 5 Q6PIY5 | CA228_HU | 122 C1orf228 | ####      |
| KDCSETLATFVK             | 0 Q6PJF5 | RHDF2_HU | 514 RHBDP2   | ####      |
| GTQDKTTMTSFTNEDLLR       | 4 Q6UVK1 | CSPG4_HU | 953 CSPG4    | ####      |
| GTQDKTTM[147.04]VTSFTNEI | 4 Q6UVK1 | CSPG4_HU | 953 CSPG4    | ####      |
| KGNLQLQGTR               | 0 Q6UVK1 | CSPG4_HU | 831 CSPG4    | ####      |
| KGNLQLQGTR               | 0 Q6UVK1 | CSPG4_HU | 831 CSPG4    | ####      |
| DGDPLEKLNWVR             | 6 Q6UWB1 | IL27A_HU | 364 IL27A    | ####      |
| AEGIEKSYSQSILLDLTDNR     | 5 Q6YHK3 | CD109_HU | 858 CD109    | Q6YHK3    |
| EKALSFMR                 | 1 Q6YHK3 | CD109_HU | 952 CD109    | Q6YHK3    |
| IKLYWSK                  | 1 Q6YHK3 | CD109_HU | 560 CD109    | Q6YHK3    |
| IKLYWSK                  | 1 Q6YHK3 | CD109_HU | 560 CD109    | Q6YHK3    |
| IKLYWSK                  | 1 Q6YHK3 | CD109_HU | 560 CD109    | Q6YHK3    |
| IPVQLVFKNK               | 7 Q6YHK3 | CD109_HU | 556 CD109    | Q6YHK3    |
| IPVQLVFKNK               | 7 Q6YHK3 | CD109_HU | 556 CD109    | Q6YHK3    |
| KQLTDNLK                 | 0 Q6YHK3 | CD109_HU | 943 CD109    | Q6YHK3    |
| LQSTLKTLSFSFPNTVTGSR     | 5 Q6YHK3 | CD109_HU | 878 CD109    | Q6YHK3    |
| TRDENIKVGSPFELVVSNGK     | 6 Q6YHK3 | CD109_HU | 478 CD109    | ####      |
| TSLNLIKDPK               | 7 Q6YHK3 | CD109_HU | 169 CD109    | Q6YHK3    |
| TYIQLKTR                 | 5 Q6YHK3 | CD109_HU | 471 CD109    | Q6YHK3    |
| TYIQLKTR                 | 5 Q6YHK3 | CD109_HU | 471 CD109    | Q6YHK3    |
| VKAEPSEK                 | 1 Q6YHK3 | CD109_HU | 567 CD109    | Q6YHK3    |
| YTYGKPVK                 | 4 Q6YHK3 | CD109_HU | 258 CD109    | Q6YHK3    |
| KKVSSTDPRPR              | 0 Q6ZSZ5 | ARHG1_HU | 742 ARHGEF18 | ####      |
| SEGGKTPVAR               | 4 Q70UQ0 | IKIP_HU  | 28 IKBIP     | Q70UQ0_C  |
| HGKYMCCCLLYR             | 2 Q71U36 | TBA1A_HU | 311 TUBA1A   | 5JCO      |

|                         |   |        |           |       |           |          |
|-------------------------|---|--------|-----------|-------|-----------|----------|
| TTFVSKDISR              | 5 | Q7KYR7 | BT2A1_HU  | 101   | BTN2A1    | Q7KYR7_Q |
| LKLYLPK                 | 1 | Q7KZF4 | SND1_HUN  | 541   | SND1      | 3BDL     |
| LKLYLPK                 | 1 | Q7KZF4 | SND1_HUN  | 541   | SND1      | 3BDL     |
| LKLYLPK                 | 1 | Q7KZF4 | SND1_HUN  | 541   | SND1      | 3BDL     |
| LKLYLPK                 | 1 | Q7KZF4 | SND1_HUN  | 541   | SND1      | 3BDL     |
| LKLYLPK                 | 1 | Q7KZF4 | SND1_HUN  | 541   | SND1      | 3BDL     |
| LKLYLPK                 | 1 | Q7KZF4 | SND1_HUN  | 541   | SND1      | 3BDL     |
| KVSMDNR                 | 0 | Q7L1Q6 | BZW1_HU   | 208   | BZW1      | Q7L1Q6   |
| ELKGLHR                 | 2 | Q7LC44 | ARC_HUM   | 62    | ARC       | ####     |
| KLDDSYSEAVR             | 0 | Q86UP2 | KTN1_HUN  | 1240  | KTN1      | Q86UP2   |
| DLFTCTIKR               | 7 | Q86VP6 | CAND1_HU  | 574   | CAND1     | 1U6G     |
| ISLKFNK                 | 3 | Q86Y13 | DZIP3_HUN | 376   | DZIP3     | ####     |
| EKVQWGVFVPR             | 1 | Q8IWA0 | WDR75_HU  | 628   | WDR75     | ####     |
| QGKGSR                  | 2 | Q8IYB4 | PEX5R_HU  | 33    | PEX5L     | Q8IYB4_Q |
| KVNELR                  | 0 | Q8IZP2 | ST134_HU  | 5     | ST13P4    | ####     |
| LAILYAKR                | 6 | Q8IZP2 | ST134_HU  | 149   | ST13P4    | Q8IZP2   |
| LAILYAKR                | 6 | Q8IZP2 | ST134_HU  | 149   | ST13P4    | Q8IZP2   |
| AVTKYTSSK               | 3 | Q8N257 | H2B3B_HU  | 121   | HIST3H2BB | Q8N257   |
| KESYSIYVYK              | 0 | Q8N257 | H2B3B_HU  | 35    | HIST3H2BB | Q8N257   |
| LAHYNKR                 | 5 | Q8N257 | H2B3B_HU  | 86    | HIST3H2BB | Q8N257   |
| KGNYAER                 | 0 | Q96KK5 | H2A1H_HU  | 37    | HIST1H2AH | Q96KK5   |
| SQIDELADKFNR            | 9 | Q8N3U4 | STAG2_HU  | 664   | STAG2     | 4PJW     |
| KDDSVGYR                | 0 | Q8N766 | EMC1_HUN  | 413   | EMC1      | Q8N766   |
| DGSLSDKR                | 6 | Q8N8Z6 | DCBD1_HU  | 246   | DCBLD1    | Q8N8Z6   |
| DGSLSDKR                | 6 | Q8N8Z6 | DCBD1_HU  | 246   | DCBLD1    | Q8N8Z6   |
| AKVEFNIR                | 1 | Q8NC51 | PAIRB_HU  | 303   | SERBP1    | Q8NC51   |
| KGFVLHK                 | 0 | Q8NC51 | PAIRB_HU  | 321   | SERBP1    | ####     |
| ELSTKYLTM[147.04]K      | 4 | Q8NDH2 | CC168_HU  | 1465  | CCDC168   | ####     |
| SKAIAK                  | 1 | Q8NEY8 | PPHLN_HU  | 292   | PPHLN1    | ####     |
| LQNLQDAAKDM[147.04]K    | 8 | Q8NF91 | SYNE1_HU  | 5632  | SYNE1     | ####     |
| KM[147.04]HIQSAVSKMNPGE | 9 | Q8NFC6 | BD1L1_HU  | 1215  | BOD1L1    | ####     |
| QTMLCPEMKIK             | 8 | Q8TAL5 | CI043_HUN | 234   | C9orf43   | ####     |
| FKDTAYCATFR             | 1 | Q8TED0 | UTP15_HU  | 80    | UTP15     | Q8TED0   |
| IERKIATISLESK           | 3 | Q8TEK3 | DOT1L_HU  | 1203  | DOT1L     | ####     |
| AAKQGDITLVSGM[147.04]K  | 2 | Q8TEM1 | PO210_HU  | 201   | NUP210    | ####     |
| KASPPSGLWSPAYASH        | 0 | Q8TEM1 | PO210_HU  | 1872  | NUP210    | ####     |
| NFWQGVKSK               | 6 | Q8TEQ6 | GEMI5_HU  | 426   | GEMIN5    | 5H3U     |
| QEAFWRKEK               | 6 | Q8TF01 | PNISR_HU  | 429   | PNISR     | ####     |
| KVAMVLK                 | 0 | Q8WWY8 | LIPH_HUM  | 126   | LIPH      | ####     |
| KQIQLR                  | 0 | Q8WXF1 | PSPC1_HU  | 346   | PSPC1     | ####     |
| LLNDQCKNFNDWFSNIK       | 6 | Q8WXH0 | SYNE2_HU  | 1845  | SYNE2     | ####     |
| VPEAPKEVVPEK            | 5 | Q8WZ42 | TITIN_HUN | 11457 | TTN       | ####     |
| LLTTDQKSEIR             | 6 | Q92466 | DDB2_HUN  | 309   | DDB2      | 4.00E+54 |
| LDDLSTGKLNLSQVR         | 8 | Q92499 | DDX1_HUN  | 358   | DDX1      | Q92499   |
| AQEIKTK                 | 4 | Q92598 | HS105_HU  | 786   | HSPH1     | ####     |
| KLVAIR                  | 0 | Q92621 | NU205_HU  | 975   | NUP205    | Q92621   |
| KLVAIR                  | 0 | Q92621 | NU205_HU  | 975   | NUP205    | Q92621   |

|                         |           |           |               |          |
|-------------------------|-----------|-----------|---------------|----------|
| NKLLQCLHAK              | 1 Q92621  | NU205_HU  | 1271 NUP205   | Q92621   |
| VAKIQQGALELLR           | 2 Q92621  | NU205_HU  | 1565 NUP205   | Q92621   |
| VKVDVLR                 | 1 Q92667  | AKAP1_HU  | 803 AKAP1     | Q92667   |
| VTFSQDPTTVALCISKEGRPPAR | 15 Q92692 | NECT2_HU  | 186 NECTIN2   | ####     |
| LIDFLESGKTNLR           | 8 Q92841  | DDX17_HU  | 313 DDX17     | Q92841   |
| SGKAPILIATDVASR         | 2 Q92841  | DDX17_HU  | 468 DDX17     | Q92841   |
| LKDYQR                  | 1 Q92888  | ARHG1_HL  | 616 ARHGEF1   | 3ODW     |
| KLVNTINPGAR             | 0 Q92900  | RENT1_HU  | 929 UPF1      | ####     |
| GGETIKQLQER             | 5 Q92945  | FUBP2_HU  | 257 KHSRP     | 2JVZ     |
| SVSLTGAPESVQKAK         | 12 Q92945 | FUBP2_HU  | 203 KHSRP     | Q92945   |
| DLLQFFKPR               | 6 Q93009  | UBP7_HUN  | 869 USP7      | 5FWI     |
| VWFIKVR                 | 4 Q93050  | VPP1_HUN  | 296 ATP6V0A1  | Q93050   |
| AVTKYTSSK               | 3 Q93079  | H2B1H_HU  | 121 HIST1H2BH | Q93079   |
| AVTKYTSSK               | 3 Q93079  | H2B1H_HU  | 121 HIST1H2BH | Q93079   |
| AVTKYTSSK               | 3 Q93079  | H2B1H_HU  | 121 HIST1H2BH | Q93079   |
| AVTKYTSSK               | 3 Q93079  | H2B1H_HU  | 121 HIST1H2BH | Q93079   |
| HAVSEGTKAVTK            | 7 Q93079  | H2B1H_HU  | 117 HIST1H2BH | Q93079   |
| KESYSVYVYK              | 0 Q93079  | H2B1H_HU  | 35 HIST1H2BH  | Q93079   |
| LAHYNKR                 | 5 Q93079  | H2B1H_HU  | 86 HIST1H2BH  | Q93079   |
| SAPAPKK                 | 5 Q93079  | H2B1H_HU  | 12 HIST1H2BH  | Q93079   |
| KESYSVYVYK              | 0 Q93079  | H2B1H_HU  | 35 HIST1H2BH  | Q93079   |
| KGNYAER                 | 0 Q96KK5  | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5   |
| KGNYAER                 | 0 Q96KK5  | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5   |
| KGNYAER                 | 0 Q96KK5  | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5   |
| KGNYAER                 | 0 Q96KK5  | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5   |
| KGNYAER                 | 0 Q96KK5  | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5   |
| KGNYAER                 | 0 Q96KK5  | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5   |
| KGNYAER                 | 0 Q96KK5  | H2A1H_HU  | 37 HIST1H2AH  | Q96KK5   |
| NDEELNKLLGK             | 6 Q96KK5  | H2A1H_HU  | 96 HIST1H2AH  | Q96KK5   |
| CLAKAYVR                | 3 Q969P0  | IGSF8_HUN | 409 IGSF8     | ####     |
| YLGSYSGKVELR            | 7 Q969P0  | IGSF8_HUN | 143 IGSF8     | Q969P0   |
| GGETIKSISQQSGAR         | 5 Q96AE4  | FUBP1_HU  | 400 FUBP1     | 1J4W     |
| EANQAPKSKSGSRPR         | 8 Q96AG4  | LRC59_HUI | 228 LRRC59    | Q96AG4_Q |
| NKLQQLPADFGR            | 1 Q96AG4  | LRC59_HUI | 73 LRRC59     | Q96AG4   |
| AEVLKNR                 | 4 Q96BR5  | COA7_HUN  | 211 COA7      | Q96BR5   |
| AEVLKNR                 | 4 Q96BR5  | COA7_HUN  | 211 COA7      | Q96BR5   |
| LSKFDSER                | 2 Q96CW1  | AP2M1_HL  | 256 AP2M1     | Q96CW1   |
| LSKFDSER                | 2 Q96CW1  | AP2M1_HL  | 256 AP2M1     | Q96CW1   |
| IFTLKPVR                | 4 Q96EE3  | SEH1_HUN  | 251 SEH1L     | Q96EE3   |
| LQKLLESDYFR             | 2 Q96HE7  | ERO1A_HU  | 67 ERO1A      | 3AHQ     |
| FNKIVHSSMTR             | 2 Q96HS1  | PGAM5_HL  | 144 PGAM5     | 5MUF     |
| LASLGLKFNK              | 6 Q96HS1  | PGAM5_HL  | 141 PGAM5     | 5MUF     |
| GGETIKQLQER             | 5 Q96I24  | FUBP3_HU  | 186 FUBP3     | Q96I24   |
| DGLALGMGQGLKAWPR        | 11 Q96J84 | KIRR1_HUN | 67 KIRREL1    | Q96J84   |
| WLYPVDKR                | 6 Q96KA5  | CLP1L_HUN | 517 CLPTM1L   | Q96KA5   |
| KGNYAER                 | 0 Q96KK5  | H2A1H_HU  | 37 HIST1H2AH  | ####     |
| NDEELNKLLGK             | 6 Q96KK5  | H2A1H_HU  | 96 HIST1H2AH  | Q96KK5   |
| NDEELNKLLGK             | 6 Q96KK5  | H2A1H_HU  | 96 HIST1H2AH  | ####     |

|                     |    |        |          |      |          |          |
|---------------------|----|--------|----------|------|----------|----------|
| SFTPVFLGSALKNK      | 11 | Q96RP9 | EFGM_HU  | 302  | GFM1     | Q96RP9   |
| IQKLVLAGR           | 2  | Q96S59 | RANB9_HU | 412  | RANBP9   | ####     |
| VVKYWPEK            | 2  | Q96T88 | UHRF1_HU | 563  | UHRF1    | 2PB7     |
| KLAPTCK             | 0  | Q96TA1 | NIBL1_HU | 507  | FAM129B  | ####     |
| KVPLDER             | 0  | Q96TA1 | NIBL1_HU | 62   | FAM129B  | ####     |
| GKSATVCER           | 1  | Q99470 | SDF2_HU  | 75   | SDF2     | Q99470   |
| TSDLGKSFK           | 5  | Q99523 | SORT_HU  | 294  | SORT1    | 6EHO     |
| GTVNSKLR            | 5  | Q99615 | DNJC7_HU | 306  | DNAJC7   | Q99615   |
| AYGFSCDGEGLVKFAR    | 12 | Q99622 | C10_HU   | 80   | C12orf57 | ####     |
| AAQNISKTIATSQNR     | 6  | Q99623 | PHB2_HU  | 262  | PHB2     | Q99623_Q |
| AKQEQR              | 1  | Q99623 | PHB2_HU  | 218  | PHB2     | Q99623   |
| AQFLVEKAK           | 6  | Q99623 | PHB2_HU  | 216  | PHB2     | ####     |
| GSDSLIKGK           | 6  | Q99623 | PHB2_HU  | 296  | PHB2     | Q99623_Q |
| GSDSLIKGK           | 6  | Q99623 | PHB2_HU  | 296  | PHB2     | ####     |
| GSDSLIKGK           | 6  | Q99623 | PHB2_HU  | 296  | PHB2     | ####     |
| MLGEALSKNPGYIK      | 7  | Q99623 | PHB2_HU  | 244  | PHB2     | ####     |
| SVVAKFNASQLITQR     | 4  | Q99623 | PHB2_HU  | 147  | PHB2     | Q99623   |
| SVVAKFNASQLITQR     | 4  | Q99623 | PHB2_HU  | 147  | PHB2     | Q99623   |
| GKFGR               | 1  | Q99714 | HCD2_HU  | 81   | HSD17B10 | 2023     |
| KDPVKK              | 0  | Q99729 | ROAA_HU  | 149  | HNRNPAB  | Q99729   |
| VLDPKK              | 4  | Q99729 | ROAA_HU  | 142  | HNRNPAB  | Q99729   |
| GKATISNDGATILK      | 1  | Q99832 | TCPH_HU  | 55   | CCT7     | Q99832   |
| VPEEDLKR            | 6  | Q99832 | TCPH_HU  | 320  | CCT7     | Q99832   |
| VPEEDLKR            | 6  | Q99832 | TCPH_HU  | 320  | CCT7     | Q99832   |
| VPEEDLKR            | 6  | Q99832 | TCPH_HU  | 320  | CCT7     | Q99832   |
| VQGGALEDSQLVAGVAFKK | 17 | Q99832 | TCPH_HU  | 217  | CCT7     | Q99832   |
| VEDLTFTSPFCLQVKR    | 14 | Q99873 | ANM1_HU  | 266  | PRMT1    | Q99873   |
| KDAHSTLLSK          | 0  | Q9BPW8 | NIPS1_HU | 56   | NIPSNAP1 | ####     |
| KVMEYENR            | 0  | Q9BPX6 | MICU1_HU | 110  | MICU1    | 4NSC     |
| STGKVVLK            | 3  | Q9BQA9 | CQ062_HU | 77   | C17orf62 | Q9BQA9   |
| VELGEKPLR           | 5  | Q9BSJ8 | ESYT1_HU | 189  | ESYT1    | Q9BSJ8   |
| TTWAIKHAASNPSK      | 5  | Q9BUJ2 | HNRL1_HU | 440  | HNRNPUL1 | ####     |
| DFAPPGQQKR          | 8  | Q9BVC6 | TM109_HU | 46   | TMEM109  | ####     |
| VSKNYR              | 2  | Q9BW27 | NUP85_HU | 103  | NUP85    | Q9BW27   |
| KGLIEVK             | 0  | Q9BWD1 | THIC_HU  | 211  | ACAT2    | ####     |
| DEKLIK              | 2  | Q9BXP5 | SRRT_HU  | 604  | SRRT     | Q9BXP5   |
| YNDYKLDFR           | 4  | Q9BXP5 | SRRT_HU  | 176  | SRRT     | ####     |
| TLTQKLR             | 4  | Q9BYG3 | MK67I_HU | 158  | NIFK     | ####     |
| MCTVIKR             | 5  | Q9BZE4 | NOG1_HU  | 142  | GTPBP4   | Q9BZE4   |
| KWTVVHAGAR          | 0  | Q9BZM4 | ULBP3_HU | 158  | ULBP3    | 1KCG     |
| AIKFLSTK            | 2  | Q9BZZ5 | API5_HU  | 153  | API5     | 3U0R     |
| SCKAPLYDLAAHEDK     | 2  | Q9GZL7 | WDR12_HU | 376  | WDR12    | Q9GZL7   |
| KMNALFEGR           | 0  | Q9H307 | PININ_HU | 262  | PNN      | ####     |
| KM[147.04]NALFEGR   | 0  | Q9H307 | PININ_HU | 262  | PNN      | ####     |
| KQEFLEK             | 0  | Q9H444 | CHM4B_HU | 39   | CHMP4B   | 4ABM     |
| FLKLVPDLAIVQR       | 2  | Q9H583 | HEAT1_HU | 1643 | HEATR1   | ####     |
| EILQDKDGLNQR        | 5  | Q9H6R4 | NOL6_HU  | 192  | NOL6     | Q9H6R4   |

|                      |           |           |             |          |
|----------------------|-----------|-----------|-------------|----------|
| LLPTKNNVR            | 4 Q9H6R4  | NOL6_HUN  | 271 NOL6    | Q9H6R4   |
| TFVSGACDASSKLWDIR    | 11 Q9HAV0 | GBB4_HUN  | 209 GNB4    | ####     |
| VFAAEALLKR           | 8 Q9HC52  | CBX8_HUN  | 18 CBX8     | 5EQ0     |
| AQLETALKWR           | 7 Q9HCE1  | MOV10_HI  | 332 MOV10   | Q9HCE1   |
| YCITKLDR             | 4 Q9HCE1  | MOV10_HI  | 846 MOV10   | Q9HCE1   |
| GNFAGAKLPR           | 6 Q9HCU4  | CELR2_HUI | 2183 CELSR2 | Q9HCU4   |
| VGSALLDTANKR         | 10 Q9HCU4 | CELR2_HUI | 2121 CELSR2 | Q9HCU4   |
| VGSALLDTANKR         | 10 Q9HCU4 | CELR2_HUI | 2121 CELSR2 | Q9HCU4   |
| GLFEVNPWKR           | 8 Q9HDC9  | APMAP_HI  | 179 APMAP   | Q9HDC9   |
| ATGKLIQGR            | 3 Q9NPJ3  | ACO13_HU  | 127 ACOT13  | 3F50     |
| ITLVSAAPGKVICEMK     | 9 Q9NPJ3  | ACO13_HU  | 37 ACOT13   | 3F50     |
| GVTFLFPIQAKTFHHVYSGK | 10 Q9NR30 | DDX21_HU  | 215 DDX21   | ####     |
| SQNKGGQK             | 3 Q9NR30  | DDX21_HU  | 771 DDX21   | ####     |
| STYEQVDLIGKK         | 10 Q9NR30 | DDX21_HU  | 402 DDX21   | Q9NR30   |
| SYKPVFWSPSSR         | 2 Q9NSE4  | SYIM_HUM  | 241 IARS2   | Q9NSE4   |
| KGIAWWTDK            | 0 Q9NV96  | CC50A_HU  | 202 TMEM30A | Q9NV96   |
| KSDLHPTLPAGR         | 0 Q9NV96  | CC50A_HU  | 279 TMEM30A | ####     |
| KQEAESAVR            | 0 Q9NVH1  | DJC11_HUI | 435 DNAJC11 | ####     |
| AKAAR                | 2 Q9NVI7  | ATD3A_HU  | 60 ATAD3A   | ####     |
| AKAER                | 1 Q9NVI7  | ATD3A_HU  | 246 ATAD3A  | ####     |
| AQYQDKLAR            | 5 Q9NVI7  | ATD3A_HU  | 183 ATAD3A  | ####     |
| AQYQDKLAR            | 5 Q9NVI7  | ATD3A_HU  | 183 ATAD3A  | ####     |
| KTLSEETR             | 0 Q9NVI7  | ATD3A_HU  | 165 ATAD3A  | ####     |
| LKAAEHR              | 1 Q9NVI7  | ATD3A_HU  | 262 ATAD3A  | ####     |
| AKAAR                | 2 Q9NVI7  | ATD3A_HU  | 60 ATAD3A   | ####     |
| YVASSSKDGSVR         | 6 Q9NVX2  | NLE1_HUM  | 224 NLE1    | Q9NVX2   |
| AEVEQVELPDGKKR       | 12 Q9NW13 | RBM28_HI  | 666 RBM28   | ####     |
| EKLCFLDK             | 1 Q9NZ01  | TECR_HUM  | 16 TECR     | 2DZJ     |
| TKDGGQILPVPNVVVR     | 1 Q9P258  | RCC2_HUM  | 320 RCC2    | 5GWN     |
| LWTEGEKR             | 6 Q9P273  | TEN3_HUM  | 2655 TENM3  | Q9P273   |
| AQDGFIFSKHEHTDTFNFR  | 9 Q9P2B2  | FPRP_HUM  | 492 PTGFRN  | Q9P2B2   |
| VVDTKSGEANVR         | 4 Q9P2B2  | FPRP_HUM  | 435 PTGFRN  | ####     |
| VVDTKSGEANVR         | 4 Q9P2B2  | FPRP_HUM  | 435 PTGFRN  | ####     |
| AEGAQNQAKK           | 8 Q9P2E9  | RRBP1_HU  | 300 RRBP1   | Q9P2E9_Q |
| AEGAQNQGKK           | 8 Q9P2E9  | RRBP1_HU  | 270 RRBP1   | ####     |
| AEGAQNQGKK           | 8 Q9P2E9  | RRBP1_HU  | 270 RRBP1   | ####     |
| EKDTVK               | 1 Q9P2E9  | RRBP1_HU  | 1385 RRBP1  | Q9P2E9   |
| KAEGAQNQGK           | 0 Q9P2E9  | RRBP1_HU  | 261 RRBP1   | ####     |
| KAEGAQNQGK           | 0 Q9P2E9  | RRBP1_HU  | 261 RRBP1   | ####     |
| KQLVAR               | 0 Q9P2E9  | RRBP1_HU  | 746 RRBP1   | ####     |
| KVEGAQNQGK           | 0 Q9P2E9  | RRBP1_HU  | 301 RRBP1   | ####     |
| AKQAATMSEVEWR        | 1 Q9UHB9  | SRP68_HUI | 288 SRP68   | Q9UHB9   |
| DAGLKQAPASR          | 4 Q9UHD8  | SEPT9_HUI | 262 9-Sep   | ####     |
| AGLFIDKGVK           | 6 Q9UHN6  | TMEM2_HI  | 733 TMEM2   | ####     |
| LTEKTVFPLADVSR       | 3 Q9UHN6  | TMEM2_HI  | 1262 TMEM2  | Q9UHN6   |
| VIDQDTAKILESER       | 7 Q9UHN6  | TMEM2_HI  | 278 TMEM2   | ####     |
| HMVMQKLLR            | 5 Q9UHX1  | PUF60_HU  | 454 PUF60   | Q9UHX1   |



|                      |           |           |              |           |
|----------------------|-----------|-----------|--------------|-----------|
| EAGGAFGKR            | 7 Q9UII2  | ATIF1_HUM | 49 ATPIF1    | Q9UII2_Q9 |
| EAGGAFGKR            | 7 Q9UII2  | ATIF1_HUM | 49 ATPIF1    | Q9UII2    |
| TDKGWSFLLGK          | 2 Q9UIQ6  | LCAP_HUM  | 872 LNPEP    | ####      |
| KIYSTLAGTR           | 0 Q9UJS0  | CMC2_HUM  | 235 SLC25A13 | 4P5W      |
| LSLDKVFR             | 4 Q9UJZ1  | STML2_HUM | 145 STOML2   | Q9UJZ1_Q9 |
| SDVETIFSKYGR         | 8 Q9UKM9  | RALY_HUM  | 44 RALY      | 1WF1      |
| ILTGGADKNVVVFDK      | 7 Q9UMS4  | PRP19_HUM | 244 PRPF19   | 4LG8      |
| KYVIYIER             | 0 Q9UNX3  | RL26L_HUM | 77 RPL26L1   | Q9UNX3    |
| SFHNELLTQLEQKVELDSR  | 12 Q9UQB8 | BAIP2_HUM | 108 BAIAP2   | ####      |
| LEEKQK               | 3 Q9UQE7  | SMC3_HUM  | 340 SMC3     | ####      |
| AAKDVFNK             | 2 Q9Y277  | VDAC3_HUM | 15 VDAC3     | Q9Y277    |
| LTLDTIFVPNTGKK       | 12 Q9Y277 | VDAC3_HUM | 109 VDAC3    | Q9Y277    |
| VDKSAADGPR           | 2 Q9Y285  | SYFA_HUM  | 117 FARSA    | 3L4G      |
| KGLYMANDLK           | 0 Q9Y2Q3  | GSTK1_HUM | 62 GSTK1     | 3RPP      |
| KGLYM[147.04]ANDLK   | 0 Q9Y2Q3  | GSTK1_HUM | 62 GSTK1     | 3RPP      |
| AAPAGKTSSVFEDPVISK   | 5 Q9Y2R9  | RT07_HUM  | 81 MRPS7     | Q9Y2R9    |
| EGLDSAKR             | 6 Q9Y2Z4  | SYYM_HUM  | 367 YARS2    | 2PID      |
| QGELNKGR             | 5 Q9Y305  | ACOT9_HUM | 237 ACOT9    | Q9Y305    |
| LEDILESINSIKSR       | 11 Q9Y3A6 | TMED5_HUM | 164 TMED5    | ####      |
| INVYKR               | 4 Q9Y3C1  | NOP16_HUM | 156 NOP16    | Q9Y3C1    |
| FQSEKAAGSVSK         | 4 Q9Y3D6  | FIS1_HUM  | 25 FIS1      | 1PC2      |
| INKNCWR              | 2 Q9Y3I0  | RTCB_HUM  | 17 RTCB      | Q9Y3I0    |
| AYQHKVGNIIDTMITDAFLK | 4 Q9Y3Z3  | SAMH1_HUM | 377 SAMHD1   | 5A00      |
| ALGDLISATKAAAGK      | 9 Q9Y490  | TLN1_HUM  | 2099 TLN1    | ####      |
| DLQEVKAAAR           | 5 Q9Y490  | TLN1_HUM  | 1068 TLN1    | ####      |
| RLQAAGNAVKR          | 9 Q9Y490  | TLN1_HUM  | 2464 TLN1    | ####      |
| TVKAVEDEATK          | 2 Q9Y490  | TLN1_HUM  | 2133 TLN1    | ####      |
| FKSYCSNLVR           | 1 Q9Y5B9  | SP16H_HUM | 280 SUPT16H  | 5E5B      |
| KKVEFLK              | 0 Q9Y5B9  | SP16H_HUM | 80 SUPT16H   | 5E5B      |
| IQKYSEGEIR           | 2 Q9Y5K5  | UCHL5_HUM | 210 UCHL5    | 4UEL      |
| LVCYNNKITASYEDR      | 6 Q9Y624  | JAM1_HUM  | 78 F11R      | 1NBQ      |
| VEWKFDQGDTR          | 3 Q9Y624  | JAM1_HUM  | 63 F11R      | 1NBQ      |
| VTFLPTGITFKSVTR      | 10 Q9Y624 | JAM1_HUM  | 97 F11R      | 1NBQ      |
| VTFLPTGITFKSVTR      | 10 Q9Y624 | JAM1_HUM  | 97 F11R      | 1NBQ      |
| AAPDITGHR            | 8 Q9Y639  | NPTN_HUM  | 244 NPTN     | ####      |
| QVSGQLLEERKK         | 10 Q9Y6D9 | MD1L1_HUM | 385 MAD1L1   | ####      |
| NYAQVFNKLR           | 7 Q9Y6E2  | BZW2_HUM  | 117 BZW2     | Q9Y6E2    |
| DGSPLDDKDER          | 7 Q9Y6N7  | ROBO1_HUM | 214 ROBO1    | 5OPE      |
| GGKLMITYTR           | 2 Q9Y6N7  | ROBO1_HUM | 224 ROBO1    | 5OPE      |
| GGKLM[147.04]ITYTR   | 2 Q9Y6N7  | ROBO1_HUM | 224 ROBO1    | 5OPE      |
| YAKLGDTR             | 2 Q9Y6N7  | ROBO1_HUM | 516 ROBO1    | Q9Y6N7    |
| ATDADTGKNAEVEYR      | 7 Q9Y6N8  | CAD10_HUM | 300 CDH10    | ####      |

| pdbA_type | pepB                      | positionB | accessionB | uniprotB  | modposB |
|-----------|---------------------------|-----------|------------|-----------|---------|
| Phyre     | EVVEAHVDQKNK              | 9         | A0A0B4J2C  | A0A0B4J2C | 233     |
|           | GVEVTVGHEQEEGGWPYAGTAEAIK | 14        | A0A0B4J2C  | A0A0B4J2C | 203     |
|           | NNQESDCVSKKK              | 10        | A6NDG6     | PGP_HUM   | 301     |
|           | HSPKVETTDPCVPPK           | 3         | A6NHR9     | SMHD1_HL  | 1976    |
| Phyre     | DAVTYTEHAKR               | 9         | P62805     | H4_HUM    | 78      |
|           | KNCPHVVVGTPGR             | 0         | O00148     | DX39A_HU  | 162     |
| Phyre     | NSKQQLSAEELDAQLDAYNAR     | 2         | Q86V81     | THOC4_HU  | 235     |
| Structure | KGCVITISGR                | 0         | O00154     | BACH_HUM  | 286     |
| Structure | FPKTLFATEDALEVR           | 2         | O00159     | MYO1C_HL  | 721     |
| Structure | SDWKVVR                   | 3         | O00159     | MYO1C_HL  | 285     |
| Structure | SLASKDVESPSWR             | 4         | O00159     | MYO1C_HL  | 404     |
| Structure | KYEAFQR                   | 0         | O00159     | MYO1C_HL  | 667     |
| Phyre     | MKDTDSEEEIR               | 1         | P0DP23     | CALM1_HL  | 78      |
| Structure | AIYDTPCIQAESEKWQQALK      | 13        | O00232     | PSD12_HU  | 262     |
| Structure | KFYGPEGPGYGVFAGR          | 0         | O00264     | PGRC1_HU  | 105     |
| Structure | FSAYIKNSNPALNDNLEK        | 5         | O00299     | CLIC1_HUM | 119     |
| Phyre     | SKISVNDFIK                | 1         | P10515     | ODP2_HUM  | 473     |
| Structure | VIPVKLGIIGVVNR            | 4         | O00429     | DNM1L_HL  | 238     |
| Phyre     | VVFAADGILWPKR             | 12        | O00469     | PLOD2_HU  | 148     |
|           | DGITAGKAALR               | 6         | O00481     | BT3A1_HU  | 108     |
|           | DLINLAKK                  | 6         | P22087     | FBRL_HUM  | 205     |
|           | YPASTVQILGAEKALFR         | 12        | O00567     | NOP56_HU  | 333     |
| Structure | KQYPISLVLPATR             | 0         | O00571     | DDX3X_HU  | 264     |
| Structure | GLDISNVKHVINFDLPSDIEEYVHR | 7         | O00571     | DDX3X_HU  | 511     |
| Docking   | ATFNPAQDKCGIR             | 8         | O00592     | PODXL_HU  | 394     |
| Modeller  | LASVPGSQTVVVKEITIHTK      | 12        | O00592     | PODXL_HU  | 411     |
| Modeller  | ATFNPAQDKCGIR             | 8         | O00592     | PODXL_HU  | 394     |
| Modeller  | ATFNPAQDKCGIR             | 8         | O00592     | PODXL_HU  | 394     |
| Modeller  | LASVPGSQTVVVKEITIHTK      | 12        | O00592     | PODXL_HU  | 411     |
| Structure | STHIPYRDSKLTR             | 9         | O14782     | KIF3C_HUM | 321     |
| Modeller  | YFLDKTLTSR                | 4         | O14874     | BCKD_HUM  | 192     |
|           | AYPHVFTKGIPNVLR           | 7         | O14949     | QCR8_HUM  | 33      |
|           | AKSLLHCFQCCGAK            | 1         | O14975     | S27A2_HUI | 141     |
|           | FSSCIDMGKELLAR            | 8         | O15020     | SPTN2_HUI | 1971    |
| Modeller  | DLVLSGDLGSLYAMTQDKVFR     | 17        | O15031     | PLXB2_HUI | 460     |
| Modeller  | RDLVLSGDLGSLYAMTQDKVFR    | 18        | O15031     | PLXB2_HUI | 460     |
| Modeller  | VYLTPDGTSSSEYDSILVEINKR   | 20        | O15031     | PLXB2_HUI | 438     |
| Modeller  | FCDNSSAIQGKEVR            | 10        | O15067     | PUR4_HUM  | 279     |
| Phyre     | TWKPTLVILR                | 2         | O15143     | ARC1B_HU  | 87      |
| Phyre     | NYEIKNEADR                | 4         | O15145     | ARPC3_HU  | 61      |
| Phyre     | GSKFYGPAGPYGIFAGR         | 2         | O15173     | PGRC2_HU  | 135     |
| Phyre     | SEGKSMFAGVPTMR            | 3         | O15260     | SURF4_HUI | 139     |
|           | LGVVFEKEKDR               | 6         | O15357     | SHIP2_HUM | 383     |
|           | VADWTGATYQDKR             | 11        | O15371     | EIF3D_HUM | 53      |
|           | QGLTKDAHNALLDIQSSGR       | 4         | Q99613     | EIF3C_HUM | 627     |
| Phyre     | LFKPPQPPAR                | 2         | O15372     | EIF3H_HUM | 306     |

|           |                           |    |        |           |     |
|-----------|---------------------------|----|--------|-----------|-----|
| Structure | ELKEIQYGIR                | 2  | O15382 | BCAT2_HU  | 377 |
| Structure | LGGNYGPTVLVQQEALKR        | 16 | O15382 | BCAT2_HU  | 246 |
| Structure | KTFSHELSDFGLESTAGEIPVVAIR | 0  | P30101 | PDIA3_HUI | 305 |
| Structure | FEDCSSAKTILK              | 7  | O43143 | DHX15_HU  | 230 |
| Structure | LQLPVWEYKDR               | 8  | O43143 | DHX15_HU  | 143 |
| Structure | IVSKDLTNSHFFLDFQK         | 3  | O43159 | RRP8_HUN  | 417 |
| Structure | NSLKELWLVIHGR             | 3  | O43169 | CYB5B_HU  | 35  |
| Structure | DGVIEASINHEKGYVQSK        | 11 | O43242 | PSMD3_HL  | 455 |
| Structure | EAGVEMGDEDDLSTPNEKLLGHLVK | 17 | P14868 | SYDC_HUN  | 374 |
|           | EFNEEGALSVLQQFKESDLSHVQNK | 14 | O43390 | HNRPR_HU  | 84  |
| Structure | KANPDLPIIR                | 0  | O43678 | NDUA2_HL  | 46  |
| Structure | NDGAAILAAVSSIAQKIR        | 15 | P28331 | NDUS1_HU  | 499 |
| Phyre     | EAILAIHKEAQR              | 7  | O43707 | ACTN4_HU  | 592 |
| Phyre     | AIMTYVSSFYHAFSGAQKAETAANR | 17 | O43707 | ACTN4_HU  | 273 |
| Phyre     | ICKVLAVNQENEHLMEDYEK      | 2  | O43707 | ACTN4_HU  | 283 |
| Structure | KTFTAWCNSHLR              | 0  | O43707 | ACTN4_HU  | 54  |
| Structure | DLLDPAWEKQQR              | 9  | O43707 | ACTN4_HU  | 50  |
| Structure | KAGTQIENIDEDFR            | 0  | O43707 | ACTN4_HU  | 66  |
| Structure | KAGTQIENIDEDFRDGLK        | 0  | O43707 | ACTN4_HU  | 66  |
| Phyre     | VHKINNVNK                 | 2  | O43707 | ACTN4_HU  | 108 |
| Structure | IKIIAPPERK                | 1  | P68032 | ACTC_HUN  | 330 |
| Structure | AAAYSKLGNAGAVQDCER        | 5  | O43765 | SGTA_HUN  | 137 |
| Modeller  | KYGTCPHGGYGLGLER          | 0  | O43776 | SYNC_HUN  | 507 |
| Phyre     | GAEVNQVKEQLLQSNPVLEAFGNAK | 7  | O43795 | MYO1B_HL  | 139 |
|           | LKEDVLEQR                 | 1  | O43818 | U3IP2_HU  | 113 |
|           | KLLDLVQQSCNYK             | 0  | P55769 | NH2L1_HU  | 21  |
| Structure | KLDLFANVVHVK              | 0  | O43837 | IDH3B_HUI | 135 |
| Phyre     | LGKIVSK                   | 2  | O43852 | CALU_HUN  | 75  |
| Phyre     | TFDQLTPEESKER             | 10 | O43852 | CALU_HUN  | 70  |
| Structure | LYQLSKAGK                 | 5  | O43865 | SAHH2_HU  | 267 |
| Structure | YKQDVYLLPK                | 1  | O43865 | SAHH2_HU  | 478 |
|           | LLTQGFTNWNKR              | 10 | O60264 | SMCA5_HL  | 847 |
| Phyre     | FNLETEWKNNYPR             | 7  | O60313 | OPA1_HUN  | 579 |
|           | KLIDTFGIR                 | 0  | O60353 | FZD6_HUN  | 108 |
| Phyre     | VM[147.04]LGETNPADSKPGTIR | 11 | O60361 | NDK8_HUN  | 85  |
| Phyre     | IGYSSPLTSDQSSKIK          | 14 | O60488 | ACSL4_HUI | 354 |
| Phyre     | SDQSYVISFVVPNQKR          | 14 | O60488 | ACSL4_HUI | 621 |
|           | IYDRKFILLECK              | 5  | O60516 | 4EBP3_HUI | 43  |
| Structure | KEAAWAITNATSGGTPEQIR      | 0  | O60684 | IMA7_HUN  | 396 |
| Structure | DSDSKLVENCVCLLR           | 4  | O60716 | CTND1_HU  | 574 |
| Structure | LLPGELAKHAVSEGTK          | 8  | O60814 | H2B1K_HU  | 109 |
| Structure | VLKQVHPDTGISSK            | 2  | O60814 | H2B1K_HU  | 47  |
|           | SAPAPKK                   | 5  | O60814 | H2B1K_HU  | 12  |
| Structure | LLPGELAKHAVSEGTK          | 8  | O60814 | H2B1K_HU  | 109 |
|           | AVTKAQK                   | 3  | O60814 | H2B1K_HU  | 21  |
| Phyre     | AVTKYTSK                  | 3  | O60814 | H2B1K_HU  | 121 |
|           | LLPGELAKHAVSEGTK          | 8  | O60814 | H2B1K_HU  | 109 |

|           |                               |           |           |      |
|-----------|-------------------------------|-----------|-----------|------|
| Structure | DAVTYTEHAKR                   | 9 P62805  | H4_HUMAI  | 78   |
| Phyre     | AVTKYTSAK                     | 3 O60814  | H2B1K_HU  | 121  |
| Phyre     | VAIVGGSGSGKSTIVR              | 10 O75027 | ABCB7_HU  | 511  |
|           | VGEKPVEVISLSR                 | 3 O75054  | IGSF3_HUN | 191  |
|           | ENKDLACFYTTK                  | 2 O75165  | DJC13_HUI | 8    |
| Structure | LKSIAFPSIGSGR                 | 1 O75367  | H2AY_HUN  | 307  |
|           | APLKIFAQDGEGQR                | 3 O75369  | FLNB_HUN  | 681  |
|           | DNKDGSCSAEYIPFAPGDYDVNITYGGAH | 2 O75369  | FLNB_HUN  | 1379 |
|           | VKVEPAVDTSR                   | 1 O75369  | FLNB_HUN  | 1221 |
|           | GAGIGGLGITVEGPSESKINCR        | 17 O75369 | FLNB_HUN  | 1372 |
|           | VLQSFTVDSSKAGLAPLEVR          | 10 O75369 | FLNB_HUN  | 1449 |
| Modeller  | DILADLIPKEQAR                 | 8 O75390  | CISY_HUM  | 43   |
|           | GFSIPECQKLLPK                 | 8 O75390  | CISY_HUM  | 103  |
| Phyre     | GEALSALDSKANNLSSLSK           | 9 O75396  | SC22B_HUI | 169  |
| Phyre     | DLQQYQSQAQQLFR                | 9 O75396  | SC22B_HUI | 38   |
|           | YSALAKLSEK                    | 5 O75400  | PR40A_HU  | 433  |
| Structure | KEITGIGPSTTTETETIAK           | 0 O75436  | VP26A_HU  | 214  |
| Phyre     | NDVAHKQLSAFGEYVAEILPK         | 5 O75489  | NDUS3_HU  | 56   |
|           | DFENSMNQVKLLK                 | 9 O75521  | ECI2_HUM  | 51   |
| Structure | QITDKAR                       | 4 O75533  | SF3B1_HUI | 522  |
|           | ETGVIEKLLTSYGFIQCSE           | 6 O75534  | CSDE1_HUI | 32   |
| Structure | SLVQEMVGSFGKR                 | 11 O75643 | U520_HUN  | 557  |
| Structure | EEEVTGPVIAPLFPQKR             | 15 O75643 | U520_HUN  | 2059 |
| Structure | EEEVTGPVIAPLFPQKR             | 15 O75643 | U520_HUN  | 2059 |
| Structure | YAQAGFEGFKTLNR                | 9 O75643  | U520_HUN  | 479  |
|           | GDSAPATAKENAAAPSPVR           | 8 O75781  | PALM_HUN  | 109  |
|           | KIEDLIK                       | 0 O75935  | DCTN3_HU  | 60   |
| Phyre     | FNALKVPVPEDK                  | 4 O75947  | ATP5H_HU  | 78   |
| Phyre     | SCAEWVSLSKAR                  | 9 O75947  | ATP5H_HU  | 109  |
| Phyre     | SCAEWVSLSKAR                  | 9 O75947  | ATP5H_HU  | 109  |
| Phyre     | YTAQVDAEEKEDVK                | 9 O75947  | ATP5H_HU  | 95   |
| Phyre     | LKQMFGNADMNTFPTFK             | 1 P18859  | ATP5J_HUI | 79   |
| Phyre     | QASIQHIQNAIDTEKSQQALVQK       | 14 P24539 | AT5F1_HUI | 154  |
| Phyre     | SCAEWVSLSKAR                  | 9 O75947  | ATP5H_HU  | 109  |
| Docking   | LTGVSISQVNHKPLR               | 11 O75955 | FLOT1_HUI | 422  |
|           | KAAYDIEVNTR                   | 0 O75955  | FLOT1_HUI | 220  |
|           | LTGVSISQVNHKPLR               | 11 O75955 | FLOT1_HUI | 422  |
|           | TDKELIATVR                    | 2 Q14254  | FLOT2_HUI | 280  |
|           | LAEAEKSQLIM[147.04]QAEAEASVR  | 5 O75955  | FLOT1_HUI | 302  |
|           | IVNSAQTGSFKQLTVK              | 10 O75964 | ATP5L_HUI | 66   |
|           | LGSKWPVFELK                   | 3 O76024  | WFS1_HUN  | 836  |
|           | EASDLQQLWKQNP                 | 10 O76094 | SRP72_HUI | 475  |
| Phyre     | VKLTNAEGVEFK                  | 1 O76094  | SRP72_HUI | 287  |
| Structure | EEEEESKQPGVSEQQR              | 6 O94776  | MTA2_HUI  | 71   |
| Phyre     | SIRPDNMSEYSKQMQR              | 11 Q13547 | HDAC1_HU  | 89   |
|           | GDASGLKR                      | 6 O94826  | TOM70_HL  | 78   |
| Phyre     | YVKALFR                       | 2 O94826  | TOM70_HL  | 188  |

|           |                               |    |        |          |     |
|-----------|-------------------------------|----|--------|----------|-----|
| Structure | SKWLAGDVPAAR                  | 1  | O94906 | PRP6_HUN | 618 |
| Phyre     | SKWLAGDVPAAR                  | 1  | O94906 | PRP6_HUN | 618 |
| Structure | HSTGDTKVPFCLQSCVKPLK          | 6  | O94925 | GLSK_HUN | 279 |
| Modeller  | YGKATIEGYYQK                  | 2  | O95394 | AGM1_HUI | 177 |
|           | NPQQQESLKHATR                 | 8  | O95816 | BAG2_HUN | 111 |
|           | NIENSDKAIK                    | 6  | O95816 | BAG2_HUN | 186 |
| Phyre     | GAGSKTLQQNAESR                | 4  | O95816 | BAG2_HUN | 200 |
| Structure | KVVQLDVR                      | 0  | O95831 | AIFM1_HU | 232 |
| Structure | SLEKISR                       | 3  | O95831 | AIFM1_HU | 295 |
| Structure | SNIWVAGDAACFYDIKLGR           | 15 | O95831 | AIFM1_HU | 446 |
|           | ELWFSDDPNVTKTLR               | 11 | O95831 | AIFM1_HU | 189 |
| Structure | AGAEVKSR                      | 5  | O95831 | AIFM1_HU | 278 |
| Structure | AGAEVKSR                      | 5  | O95831 | AIFM1_HU | 278 |
| Structure | ELWFSDDPNVTKTLR               | 11 | O95831 | AIFM1_HU | 189 |
| Structure | FIIPNVVKYSPNCK                | 7  | P00338 | LDHA_HUN | 126 |
| Structure | NVNIFKFIIPNVVK                | 5  | P00338 | LDHA_HUN | 118 |
| Structure | EVHKQVVESAYEVIK               | 3  | P00338 | LDHA_HUN | 232 |
| Structure | LKKSADTLWGIQK                 | 2  | P00338 | LDHA_HUN | 318 |
| Structure | QVVESAYEVIK                   | 10 | P00338 | LDHA_HUN | 243 |
| Structure | DQLIYNLLKEEQTPQNK             | 8  | P00338 | LDHA_HUN | 14  |
| Structure | YISPDQLADLYKSF                | 11 | P06733 | ENOA_HUN | 281 |
| Structure | MVVESAYEVIK                   | 10 | P07195 | LDHB_HUN | 244 |
| Structure | ALASLMTYKCAVVDVPFGGAK         | 8  | P00367 | DHE3_HUN | 171 |
| Structure | ALASLM[147.04]TYKCAVVDVPFGGAK | 8  | P00367 | DHE3_HUN | 171 |
| Structure | ISGASEKDIVHSGLAYTMER          | 6  | P00367 | DHE3_HUN | 503 |
| Structure | STPAITLESPIKYPLR              | 12 | P00387 | NB5R3_HU | 42  |
| Structure | FKLWYTLDR                     | 1  | P00387 | NB5R3_HU | 234 |
|           | VLQKLGADAVGMSTVPEVIVAR        | 3  | P00491 | PNPH_HUN | 211 |
| Structure | DDNGKPYVLPSVR                 | 4  | P00505 | AATM_HUI | 73  |
| Structure | YYDPKTCGFDFTGAVEDISK          | 4  | P00505 | AATM_HUI | 185 |
| Structure | DVFLPKPTWGNHTPIFR             | 5  | P00505 | AATM_HUI | 159 |
| Structure | KQWLQEVK                      | 0  | P00505 | AATM_HUI | 338 |
| Structure | ASAELALGENSEVLKSGR            | 14 | P00505 | AATM_HUI | 122 |
| Structure | KAEAQIAAKNLDK                 | 8  | P00505 | AATM_HUI | 90  |
| Structure | YYDPKTCGFDFTGAVEDISK          | 4  | P00505 | AATM_HUI | 185 |
| Structure | GKSPSDCCHNQCAAGCTGPR          | 1  | P00533 | EGFR_HUN | 226 |
|           | VLGSGAFGTVYKGLWIPEGEK         | 11 | P00533 | EGFR_HUN | 728 |
| Structure | ASLSKLGDVYVNDAFGTAHR          | 4  | P00558 | PGK1_HUN | 156 |
| Structure | DCVGPEVEKACANPAAGSVILLENLR    | 8  | P00558 | PGK1_HUN | 106 |
| Structure | AAVPSIKFCLDNQAK               | 6  | P00558 | PGK1_HUN | 48  |
| Structure | ELNYFAKALESPPERPFLAILGGAK     | 6  | P00558 | PGK1_HUN | 199 |
| Structure | IKAAPSIK                      | 1  | P00558 | PGK1_HUN | 41  |
| Structure | LTLDKLDVK                     | 4  | P00558 | PGK1_HUN | 11  |
| Structure | LTLDKLDVKGK                   | 8  | P00558 | PGK1_HUN | 15  |
| Structure | IKAAPSIK                      | 1  | P00558 | PGK1_HUN | 41  |
| Structure | LTLDKLDVK                     | 4  | P00558 | PGK1_HUN | 11  |
| Structure | GCITIIGGGDTATCCAkwntEDK       | 16 | P00558 | PGK1_HUN | 382 |

|           |                                  |           |          |     |
|-----------|----------------------------------|-----------|----------|-----|
| Structure | DCVGPEVEKACANPAAGSVILLENLR       | 8 P00558  | PGK1_HUM | 106 |
| Phyre     | FHVEEEGKGK                       | 7 P00558  | PGK1_HUM | 131 |
| Structure | GCITIIGGGDTATCCAKWNTEDK          | 16 P00558 | PGK1_HUM | 382 |
| Structure | KELNYFAK                         | 0 P00558  | PGK1_HUM | 192 |
| Structure | SLLGKDVFLK                       | 4 P00558  | PGK1_HUM | 91  |
| Structure | VDFNVPMKNNQITNNQR                | 7 P00558  | PGK1_HUM | 30  |
| Structure | KYAEAVTR                         | 0 P00558  | PGK1_HUM | 323 |
| Structure | LTLDKLDVK                        | 4 P00558  | PGK1_HUM | 11  |
| Structure | GCITIIGGGDTATCCAKWNTEDK          | 16 P00558 | PGK1_HUM | 382 |
| Phyre     | FHVEEEGKGK                       | 7 P00558  | PGK1_HUM | 131 |
| Docking   | KGVPVK                           | 0 P00966  | ASSY_HUM | 229 |
|           | EGAKYVSHGATGK                    | 3 P00966  | ASSY_HUM | 112 |
| Structure | GYDQSAYDGKDYIALNEDLR             | 9 P10321  | 1C07_HUM | 145 |
|           | LKDLEALLNSKEAALSTALSEK           | 10 P02545 | LMNA_HUI | 144 |
|           | LKDLEALLNSK                      | 1 P02545  | LMNA_HUI | 135 |
| Phyre     | ASSHSSQTQGGGSVTKK                | 15 P02545 | LMNA_HUI | 417 |
| Phyre     | EVSGIKAAYEAELGDAR                | 5 P02545  | LMNA_HUI | 78  |
| Phyre     | VAVEEVDEEGKFVR                   | 10 P02545 | LMNA_HUI | 450 |
|           | LQEKEDLQELNDR                    | 3 P02545  | LMNA_HUI | 32  |
|           | MQQQQLDEYQELLDIKLALDM[147.04]EIH | 14 P02545 | LMNA_HUI | 366 |
|           | EVSGIKAAYEAELGDAR                | 5 P02545  | LMNA_HUI | 78  |
|           | LQLELSKVR                        | 6 P02545  | LMNA_HUI | 108 |
|           | LQTMKEELDFQK                     | 4 P02545  | LMNA_HUI | 201 |
|           | GQVAKLEAALGEAK                   | 4 P02545  | LMNA_HUI | 171 |
|           | GQVAKLEAALGEAKK                  | 13 P02545 | LMNA_HUI | 180 |
|           | LQEKEDLQELNDR                    | 3 P02545  | LMNA_HUI | 32  |
|           | KEGDLIAAQAR                      | 0 P02545  | LMNA_HUI | 123 |
|           | EVSGIKAAYEAELGDAR                | 5 P02545  | LMNA_HUI | 78  |
|           | LVEIDNGKQR                       | 7 P02545  | LMNA_HUI | 233 |
|           | LQLELSKVR                        | 6 P02545  | LMNA_HUI | 108 |
|           | AQHEDQVEQYKK                     | 10 P02545 | LMNA_HUI | 260 |
|           | LQEKEDLQELNDR                    | 3 P02545  | LMNA_HUI | 32  |
|           | LQTM[147.04]KEELDFQK             | 4 P02545  | LMNA_HUI | 201 |
|           | LVEIDNGKQR                       | 7 P02545  | LMNA_HUI | 233 |
|           | TYSAKLDNAR                       | 4 P02545  | LMNA_HUI | 270 |
| Structure | AATVTGKLVHANFGTK                 | 6 P02786  | TFR1_HUM | 231 |
| Structure | ADIKEMGLSLQWLYSAR                | 3 P02786  | TFR1_HUM | 633 |
| Structure | ADIKEMGLSLQWLYSAR                | 3 P02786  | TFR1_HUM | 633 |
| Structure | AVLGTSNFKVSASPLLYTIEK            | 8 P02786  | TFR1_HUM | 495 |
| Structure | HPVTGQFLYQDSNWASKVEK             | 16 P02786 | TFR1_HUM | 531 |
| Structure | IPELNKVAR                        | 5 P02786  | TFR1_HUM | 585 |
| Structure | LFGNMEGDCPSDWKTDSTCR             | 13 P02786 | TFR1_HUM | 358 |
| Structure | LFGNM[147.04]EGDCPSDWKTDSTCR     | 13 P02786 | TFR1_HUM | 358 |
| Structure | LVHANFGTKK                       | 8 P02786  | TFR1_HUM | 240 |
| Structure | LVYLVENPGGYVAYSKAATVTGK          | 15 P02786 | TFR1_HUM | 224 |
| Structure | VEYHFLSPYVSPKESPF                | 12 P02786 | TFR1_HUM | 693 |
| Structure | LVYLVENPGGYVAYSKAATVTGK          | 15 P02786 | TFR1_HUM | 224 |

|           |                                  |           |          |     |
|-----------|----------------------------------|-----------|----------|-----|
| Structure | LDSTDFTGTIKLLNENSYVPR            | 10 P02786 | TFR1_HUM | 145 |
| Structure | EFKLSK                           | 2 P02786  | TFR1_HUM | 177 |
| Structure | EIKILNIFGVIK                     | 2 P02786  | TFR1_HUM | 385 |
| Structure | ILNIFGVIKGFVEPDHYVVGAQR          | 8 P02786  | TFR1_HUM | 394 |
| Structure | LAQMFSDMVLKDGFAQPSR              | 10 P02786 | TFR1_HUM | 439 |
| Structure | LAQMFSDM[147.04]VLKDGFAQPSR      | 10 P02786 | TFR1_HUM | 439 |
| Structure | LAQM[147.04]FSDMVLKDGFAQPSR      | 10 P02786 | TFR1_HUM | 439 |
| Structure | LAQM[147.04]FSDM[147.04]VLKDGFAQ | 10 P02786 | TFR1_HUM | 439 |
| Structure | LDSTDFTGTIKLLNENSYVPR            | 10 P02786 | TFR1_HUM | 145 |
| Structure | LTTDFGNAEKTDR                    | 9 P02786  | TFR1_HUM | 665 |
| Structure | LAQMFSDMVLKDGFAQPSR              | 10 P02786 | TFR1_HUM | 439 |
| Structure | LDSTDFTGTIKLLNENSYVPR            | 10 P02786 | TFR1_HUM | 145 |
| Structure | LYWDDLKR                         | 6 P02786  | TFR1_HUM | 128 |
| Structure | TMQNVKHPVTGQFLYQDSNWASK          | 5 P02786  | TFR1_HUM | 514 |
| Structure | TM[147.04]QNVKHPVTGQFLYQDSNW/    | 5 P02786  | TFR1_HUM | 514 |
| Structure | AAAEKLFGNMEGDCPSDWK              | 4 P02786  | TFR1_HUM | 344 |
| Structure | EAGSQKDENLALYVENQFR              | 5 P02786  | TFR1_HUM | 161 |
| Structure | EFKLSK                           | 2 P02786  | TFR1_HUM | 177 |
| Structure | ILNIFGVIKGFVEPDHYVVGAQR          | 8 P02786  | TFR1_HUM | 394 |
| Structure | LSKVWR                           | 2 P02786  | TFR1_HUM | 180 |
| Structure | LTTDFGNAEKTDR                    | 9 P02786  | TFR1_HUM | 665 |
| Structure | LAQMFSDMVLKDGFAQPSR              | 10 P02786 | TFR1_HUM | 439 |
| Structure | LAQM[147.04]FSDMVLKDGFAQPSR      | 10 P02786 | TFR1_HUM | 439 |
| Structure | LYWDDLKR                         | 6 P02786  | TFR1_HUM | 128 |
| Structure | LDSTDFTGTIKLLNENSYVPR            | 10 P02786 | TFR1_HUM | 145 |
| Structure | TM[147.04]QNVKHPVTGQFLYQDSNW/    | 5 P02786  | TFR1_HUM | 514 |
| Structure | HPVTGQFLYQDSNWASKVEK             | 16 P02786 | TFR1_HUM | 531 |
| Structure | AAAEVAGQFVIKLTHDVELNLDYER        | 11 P02786 | TFR1_HUM | 600 |
| Structure | VEYHFLSPYVSPKESPR                | 12 P02786 | TFR1_HUM | 693 |
| Structure | VSASPLLYTLIEKTMQNVK              | 12 P02786 | TFR1_HUM | 508 |
| Structure | LVHANFGTKK                       | 8 P02786  | TFR1_HUM | 240 |
| Structure | VEYHFLSPYVSPKESPR                | 12 P02786 | TFR1_HUM | 693 |
| Structure | LDSTDFTGTIKLLNENSYVPR            | 10 P02786 | TFR1_HUM | 145 |
| Structure | LTTDFGNAEKTDR                    | 9 P02786  | TFR1_HUM | 665 |
| Structure | TMQNVKHPVTGQFLYQDSNWASK          | 5 P02786  | TFR1_HUM | 514 |
| Structure | VSASPLLYTLIEKTMQNVK              | 12 P02786 | TFR1_HUM | 508 |
| Structure | AAAEKLFGNMEGDCPSDWK              | 4 P02786  | TFR1_HUM | 344 |
| Structure | AAAEKLFGNMEGDCPSDWK              | 4 P02786  | TFR1_HUM | 344 |
| Structure | AAAEKLFGNMEGDCPSDWK              | 4 P02786  | TFR1_HUM | 344 |
| Structure | AAAEKLFGNM[147.04]EGDCPSDWK      | 4 P02786  | TFR1_HUM | 344 |
| Structure | DSAQNSVIIVDKNGR                  | 11 P02786 | TFR1_HUM | 205 |
| Structure | LVYLVENPGGYVAYSKAATVTGK          | 15 P02786 | TFR1_HUM | 224 |
| Structure | TMQNVKHPVTGQFLYQDSNWASK          | 5 P02786  | TFR1_HUM | 514 |
| Structure | LVYLVENPGGYVAYSKAATVTGK          | 15 P02786 | TFR1_HUM | 224 |
| Structure | VEYHFLSPYVSPKESPR                | 12 P02786 | TFR1_HUM | 693 |
| Structure | AGLQVYNKCWK                      | 7 P13987  | CD59_HUM | 63  |
| Structure | EFKLSK                           | 2 P02786  | TFR1_HUM | 177 |

|           |                               |           |          |     |
|-----------|-------------------------------|-----------|----------|-----|
| Structure | LTTDFGNAEKTDR                 | 9 P02786  | TFR1_HUM | 665 |
| Phyre     | DPASDQMQRHWKEQR               | 10 P04040 | CATA_HUM | 16  |
| Phyre     | AAQKADVLTTGAGNPVGDK           | 3 P04040  | CATA_HUM | 23  |
| Phyre     | GILAADESTGSIKR                | 13 P04075 | ALDOA_HU | 42  |
| Phyre     | GILAADESTGSIKR                | 13 P04075 | ALDOA_HU | 42  |
| Phyre     | VDKGVVPLAGTNGETTTQGLDGLSER    | 2 P04075  | ALDOA_HU | 111 |
| Phyre     | GILAADESTGSIKR                | 13 P04075 | ALDOA_HU | 42  |
| Phyre     | VDKGVVPLAGTDGETTTQGLDGLSER    | 2 P09972  | ALDOC_HU | 111 |
| Structure | AAMKGLGTDEDTLIEILASR          | 3 P04083  | ANXA1_HU | 128 |
| Structure | AAYLQETGKPLDETLK              | 8 P04083  | ANXA1_HU | 90  |
| Structure | DLAKDITSDTSGDFR               | 3 P04083  | ANXA1_HU | 166 |
| Structure | KGTDVNVFNTILTTR               | 0 P04083  | ANXA1_HU | 214 |
| Structure | DFGSFDKFK                     | 6 P04179  | SODM_HU  | 130 |
| Structure | YDNSLKIISNASCTTNCLAPLAK       | 5 P04406  | G3P_HUM  | 145 |
| Structure | WGDAGAEEYVVESTGVFTTMEKAGAHLQ  | 20 P04406 | G3P_HUM  | 107 |
| Structure | DPSKIK                        | 3 P04406  | G3P_HUM  | 84  |
| Structure | TVDGPSGKLWR                   | 7 P04406  | G3P_HUM  | 194 |
| Structure | WGDAGAEEYVVESTGVFTTMEKAGAHLQ  | 20 P04406 | G3P_HUM  | 107 |
| Structure | YDNSLKIISNASCTTNCLAPLAK       | 5 P04406  | G3P_HUM  | 145 |
| Structure | WGDAGAEEYVVESTGVFTTMEKAGAHLQ  | 20 P04406 | G3P_HUM  | 107 |
| Structure | YDDIKK                        | 4 P04406  | G3P_HUM  | 259 |
| Structure | AVGKVIPELNGK                  | 3 P04406  | G3P_HUM  | 219 |
| Structure | GALQNIIPASTGAAKAVGK           | 14 P04406 | G3P_HUM  | 215 |
| Structure | LEKPAKYDDIK                   | 5 P04406  | G3P_HUM  | 254 |
| Structure | LEKPAKYDDIK                   | 5 P04406  | G3P_HUM  | 254 |
| Structure | TVDGPSGKLWR                   | 7 P04406  | G3P_HUM  | 194 |
| Structure | WGDAGAEEYVVESTGVFTTMEKAGAHLQ  | 20 P04406 | G3P_HUM  | 107 |
| Structure | YDNSLKIISNASCTTNCLAPLAK       | 5 P04406  | G3P_HUM  | 145 |
| Structure | FHGTVKAENGK                   | 5 P04406  | G3P_HUM  | 61  |
| Structure | TVDGPSGKLWR                   | 7 P04406  | G3P_HUM  | 194 |
| Structure | AVGKVIPELNGK                  | 3 P04406  | G3P_HUM  | 219 |
| Structure | GALQNIIPASTGAAKAVGK           | 14 P04406 | G3P_HUM  | 215 |
| Structure | TVDGPSGKLWR                   | 7 P04406  | G3P_HUM  | 194 |
| Structure | VVKQASEGPLK                   | 2 P04406  | G3P_HUM  | 263 |
| Structure | SSKGQIIGNFQAFDEDTGLPAHAR      | 2 Q14126  | DSG2_HUM | 406 |
| Unknown   | VSEMQKLDQVK                   | 5 P04843  | RPN1_HUM | 553 |
| Unknown   | ELVLKSAVEAER                  | 4 P04843  | RPN1_HUM | 564 |
| Unknown   | VSEM[147.04]QKLDQVK           | 5 P04843  | RPN1_HUM | 553 |
| Unknown   | VSEMQKLDQVK                   | 5 P04843  | RPN1_HUM | 553 |
| Unknown   | VSEM[147.04]QKLDQVK           | 5 P04843  | RPN1_HUM | 553 |
| Unknown   | ELVLKSAVEAER                  | 4 P04843  | RPN1_HUM | 564 |
| Unknown   | KDTYIENEK                     | 0 P04843  | RPN1_HUM | 579 |
|           | DVPAYSQDTEFKVHYENNSPFLTITSMTR | 10 P04843 | RPN1_HUM | 215 |
| Unknown   | QELVTIKIDHILDAL               | 5 P04843  | RPN1_HUM | 599 |
|           | GKQGGK                        | 1 P04908  | H2A1B_HU | 6   |
| Structure | NDEELNKLLGR                   | 6 P04908  | H2A1B_HU | 96  |
| Structure | DAVTYTEHAKR                   | 9 P62805  | H4_HUMAI | 78  |



|           |                             |    |        |           |     |
|-----------|-----------------------------|----|--------|-----------|-----|
| Structure | TVTAMDVVYALKR               | 11 | P62805 | H4_HUMAI  | 92  |
| Structure | GVLKVFLENVIR                | 3  | P62805 | H4_HUMAI  | 60  |
| Structure | KTVTAMDVVYALKR              | 12 | P62805 | H4_HUMAI  | 92  |
| Structure | TVTAMDVVYALKR               | 11 | P62805 | H4_HUMAI  | 92  |
| Structure | TVTAM[147.04]DVVYALKR       | 11 | P62805 | H4_HUMAI  | 92  |
| Phyre     | AVTKYTSSK                   | 3  | P62807 | H2B1C_HU  | 121 |
| Phyre     | TKQTAR                      | 1  | P68431 | H31_HUMAI | 5   |
| Structure | VTIAQGGVLPNIQAVLLPKK        | 18 | P04908 | H2A1B_HU  | 119 |
| Structure | YQKSTELLIR                  | 2  | Q16695 | H31T_HUN  | 57  |
| Phyre     | YQKSTELLIR                  | 2  | Q16695 | H31T_HUN  | 57  |
| Structure | EIAQDFKTDLR                 | 6  | Q16695 | H31T_HUN  | 80  |
| Structure | RVTIMPKDIQLAR               | 6  | Q16695 | H31T_HUN  | 123 |
| Structure | VTIMPKDIQLAR                | 5  | Q16695 | H31T_HUN  | 123 |
| Structure | VTIM[147.04]PKDIQLAR        | 5  | Q16695 | H31T_HUN  | 123 |
| Phyre     | TKQTAR                      | 1  | Q16695 | H31T_HUN  | 5   |
| Structure | VTIAQGGVLPNIQAVLLPKK        | 18 | P04908 | H2A1B_HU  | 119 |
| Structure | KESYSVYVYK                  | 0  | Q93079 | H2B1H_HU  | 35  |
| Structure | LAHYNKR                     | 5  | Q93079 | H2B1H_HU  | 86  |
| Structure | LLLPGEAKHAVSEGTK            | 8  | Q93079 | H2B1H_HU  | 109 |
| Phyre     | KGNYAER                     | 0  | Q96KK5 | H2A1H_HU  | 37  |
| Phyre     | NDEELNKLLGR                 | 6  | P04908 | H2A1B_HU  | 96  |
| Structure | LLGKVITIAQGGVLPNIQAVLLPK    | 3  | Q96KK5 | H2A1H_HU  | 100 |
|           | SLAGQSGQGKPR                | 9  | P04920 | B3A2_HUN  | 893 |
| Phyre     | AVAGDASESALLKCIELCCGSVK     | 12 | P05023 | AT1A1_HU  | 458 |
| Phyre     | IISANGCKVDNSSLTGESEPTQR     | 7  | P05023 | AT1A1_HU  | 212 |
| Phyre     | IVEIPFNSTNKYQLSIHK          | 10 | P05023 | AT1A1_HU  | 487 |
| Phyre     | ILAAQGCKVDNSSLTGESEPTQR     | 7  | P20648 | ATP4A_HU  | 223 |
| Phyre     | TEISFRPNPKSYEAYVLNIVR       | 10 | P05026 | AT1B1_HU  | 96  |
| Phyre     | DEKDKVGNVEYFGLGNSPGFPLQYYPY | 5  | P05026 | AT1B1_HU  | 223 |
| Phyre     | IECKAYGENIGYSEK             | 3  | P05026 | AT1B1_HU  | 277 |
| Phyre     | IECKAYGENIGYSEKDR           | 3  | P05026 | AT1B1_HU  | 277 |
| Phyre     | DFLAGGVAAAISKTAVERIER       | 12 | P05141 | ADT2_HUN  | 23  |
| Phyre     | DFLAGGVAAAISKTAVERIER       | 12 | P05141 | ADT2_HUN  | 23  |
| Phyre     | IPKEQGVLSFWR                | 2  | P05141 | ADT2_HUN  | 63  |
| Phyre     | KGTDIMYTGTLDCWR             | 0  | P05141 | ADT2_HUN  | 245 |
| Phyre     | KGTDIM[147.04]YTGTLDCWR     | 0  | P05141 | ADT2_HUN  | 245 |
| Phyre     | LAADVGKAGAER                | 6  | P05141 | ADT2_HUN  | 147 |
| Phyre     | LLLQVQHASKQITADK            | 9  | P05141 | ADT2_HUN  | 43  |
| Phyre     | DFLAGGVAAAISKTAVERIER       | 12 | P05141 | ADT2_HUN  | 23  |
| Phyre     | AFFKGAWSNVLR                | 3  | P05141 | ADT2_HUN  | 272 |
| Phyre     | DFLAGGVAAAISKTAVERIER       | 12 | P05141 | ADT2_HUN  | 23  |
| Phyre     | IPKEQGVLSFWR                | 2  | P05141 | ADT2_HUN  | 63  |
| Phyre     | KGTDIMYTGTLDCWR             | 0  | P05141 | ADT2_HUN  | 245 |
| Phyre     | KGTDIM[147.04]YTGTLDCWR     | 0  | P05141 | ADT2_HUN  | 245 |
| Phyre     | LLLQVQHASKQITADK            | 9  | P05141 | ADT2_HUN  | 43  |
| Phyre     | VKLLLQVQHASK                | 1  | P05141 | ADT2_HUN  | 33  |
| Phyre     | DFLAGGVAAAISKTAVERIER       | 12 | P05141 | ADT2_HUN  | 23  |

|           |                             |    |        |          |     |
|-----------|-----------------------------|----|--------|----------|-----|
| Phyre     | YFPTQALNFAFKDK              | 11 | P05141 | ADT2_HUN | 92  |
| Phyre     | DFLAGGVAAAISKTAVER          | 12 | P05141 | ADT2_HUN | 23  |
| Phyre     | DFLAGGVAAAISKTAVER          | 12 | P05141 | ADT2_HUN | 23  |
| Phyre     | DFLAGGVAAAISKTAVER          | 12 | P05141 | ADT2_HUN | 23  |
| Phyre     | YFPTQALNFAFKDK              | 11 | P05141 | ADT2_HUN | 92  |
| Phyre     | YFPTQALNFAFKDK              | 11 | P05141 | ADT2_HUN | 92  |
| Phyre     | LAADVKGSGTER                | 6  | P12236 | ADT3_HUN | 147 |
| Structure | AYTVLLYGNPGYVLKDGARPDVTESEG | 15 | P05187 | PPB1_HUN | 424 |
| Structure | TYNVDKHVPDSGATATAYLCGVK     | 5  | P05187 | PPB1_HUN | 109 |
| Structure | TYNVDKHVPDSGATATAYLCGVK     | 5  | P05187 | PPB1_HUN | 109 |
| Unknown   | AGLNCSTENMPIKINLIAPPR       | 12 | P05198 | IF2A_HUM | 226 |
| Unknown   | GVFNVMQEPKVVTDTDETAR        | 9  | P05198 | IF2A_HUM | 276 |
| Unknown   | SKTVYSILR                   | 1  | P05198 | IF2A_HUM | 106 |
| Structure | GGSVLVTCSTCDQPKLLGIETPLPK   | 15 | P05362 | ICAM1_HU | 56  |
|           | AQLLLKATPEDNGR              | 5  | P05362 | ICAM1_HU | 359 |
|           | LKLEPHEGLLR                 | 1  | P08195 | 4F2_HUM  | 615 |
| Structure | YVASYLLAALGGNSSPSAKDIK      | 18 | P05387 | RLA2_HUN | 21  |
| Phyre     | GNVGFVFTKEDLTEIR            | 8  | P05388 | RLA0_HUN | 92  |
| Phyre     | GNVGFVFTKEDLTEIR            | 8  | P05388 | RLA0_HUN | 92  |
| Phyre     | GHLENNPALEKLLPHIR           | 10 | P05388 | RLA0_HUN | 77  |
| Structure | LKPEDITQIQPQQLVLR           | 1  | P05556 | ITB1_HUM | 107 |
| Phyre     | LKPEDITQIQPQQLVLR           | 1  | P05556 | ITB1_HUM | 107 |
| Phyre     | SGEPQFTTLKF                 | 9  | P05556 | ITB1_HUM | 134 |
| Structure | TVMPYISTTPAKLR              | 11 | P05556 | ITB1_HUM | 202 |
| Structure | TVMPYISTTPAKLR              | 11 | P05556 | ITB1_HUM | 202 |
| Phyre     | DWSHYFKIIEDLR               | 6  | P05783 | K1C18_HU | 131 |
| Phyre     | RLESKIR                     | 4  | P05783 | K1C18_HU | 111 |
| Phyre     | VVSETNDTKVLR                | 8  | P05783 | K1C18_HU | 426 |
|           | DWSHYFKIIEDLR               | 6  | P05783 | K1C18_HU | 131 |
|           | LESKIR                      | 3  | P05783 | K1C18_HU | 111 |
|           | RLESKIR                     | 4  | P05783 | K1C18_HU | 111 |
|           | DWSHYFKIIEDLR               | 6  | P05783 | K1C18_HU | 131 |
|           | KVIDDTNITR                  | 0  | P05783 | K1C18_HU | 187 |
|           | LQLETEIEALKEELLFMK          | 10 | P05783 | K1C18_HU | 207 |
|           | LQLETEIEALKEELLFM[147.04]K  | 10 | P05783 | K1C18_HU | 207 |
|           | KVIDDTNITR                  | 0  | P05783 | K1C18_HU | 187 |
|           | NLKASLENSLR                 | 2  | P05783 | K1C18_HU | 317 |
|           | QAQYEALLNIKVK               | 11 | P05783 | K1C18_HU | 370 |
|           | VKLEAEIATYR                 | 1  | P05783 | K1C18_HU | 372 |
| Phyre     | EHLEKK                      | 4  | P05783 | K1C18_HU | 118 |
| Docking   | LESKIR                      | 3  | P05783 | K1C18_HU | 111 |
| Phyre     | RLESKIR                     | 4  | P05783 | K1C18_HU | 111 |
|           | GGMGSGGLATGIAGGLAGMGGIQNEKE | 25 | P05783 | K1C18_HU | 81  |
|           | NLKASLENSLR                 | 2  | P05783 | K1C18_HU | 317 |
|           | VKLEAEIATYR                 | 1  | P05783 | K1C18_HU | 372 |
|           | SQDLAKIM[147.04]ADIR        | 5  | P05783 | K1C18_HU | 247 |
|           | GGMGSGGLATGIAGGLAGMGGIQNEKE | 25 | P05783 | K1C18_HU | 81  |

|       |                               |    |        |           |     |
|-------|-------------------------------|----|--------|-----------|-----|
|       | VVSETNDTKVLR                  | 8  | P05783 | K1C18_HUI | 426 |
|       | KVIDDTNITR                    | 0  | P05783 | K1C18_HUI | 187 |
|       | LESKIR                        | 3  | P05783 | K1C18_HUI | 111 |
| Phyre | WSLLQQQKTAR                   | 7  | P05787 | K2C8_HUN  | 130 |
| Phyre | KVIDDTNITR                    | 0  | P05783 | K1C18_HUI | 187 |
| Phyre | VKYETELAMR                    | 1  | P05783 | K1C18_HUI | 167 |
|       | KLLEGEESR                     | 0  | P05787 | K2C8_HUN  | 393 |
|       | MLETKWSLLQQQK                 | 4  | P05787 | K2C8_HUN  | 122 |
|       | M[147.04]LETKWSLLQQQK         | 4  | P05787 | K2C8_HUN  | 122 |
|       | TKTEISEMNR                    | 1  | P05787 | K2C8_HUN  | 304 |
|       | WSLLQQQKTAR                   | 7  | P05787 | K2C8_HUN  | 130 |
| Phyre | DWSHYFKIIEDLR                 | 6  | P05783 | K1C18_HUI | 131 |
| Phyre | KVIDDTNITR                    | 0  | P05783 | K1C18_HUI | 187 |
| Phyre | NLKASLENSLR                   | 2  | P05783 | K1C18_HUI | 317 |
| Phyre | SQDLAKIMADIR                  | 5  | P05783 | K1C18_HUI | 247 |
| Phyre | VKLEAEIATYR                   | 1  | P05783 | K1C18_HUI | 372 |
| Phyre | VVSETNDTKVLR                  | 8  | P05783 | K1C18_HUI | 426 |
|       | TKTEISEM[147.04]NR            | 1  | P05787 | K2C8_HUN  | 304 |
|       | SLDMDSIIAEVKAQYEDIANR         | 11 | P05787 | K2C8_HUN  | 264 |
|       | DANAKLSELEAALQR               | 4  | P05787 | K2C8_HUN  | 352 |
|       | LKLEAELGNMQGLVEDFK            | 1  | P05787 | K2C8_HUN  | 160 |
|       | LQAEIEGLKGQR                  | 8  | P05787 | K2C8_HUN  | 325 |
|       | NKYEDEINKR                    | 1  | P05787 | K2C8_HUN  | 178 |
|       | NKYEDEINKR                    | 8  | P05787 | K2C8_HUN  | 185 |
|       | SLDMDSIIAEVKAQYEDIANR         | 11 | P05787 | K2C8_HUN  | 264 |
|       | TKTEISEMNR                    | 1  | P05787 | K2C8_HUN  | 304 |
|       | TKTEISEM[147.04]NR            | 1  | P05787 | K2C8_HUN  | 304 |
|       | YEELQSLAGKHGDDLRL             | 9  | P05787 | K2C8_HUN  | 295 |
| Phyre | FLEQQNKM[147.04]LETK          | 6  | P05787 | K2C8_HUN  | 117 |
| Phyre | WSLLQQQKTAR                   | 7  | P05787 | K2C8_HUN  | 130 |
| Phyre | GLQAQIASSGLTVEVDAPKSQDLAK     | 18 | P05783 | K1C18_HUI | 241 |
| Phyre | LLEDGEDFNLGDALDSSNSMQTIQKTTTR | 24 | P05783 | K1C18_HUI | 407 |
| Phyre | LLEDGEDFNLGDALDSSNSMQTIQKTTTR | 24 | P05783 | K1C18_HUI | 407 |
|       | DANAKLSELEAALQR               | 4  | P05787 | K2C8_HUN  | 352 |
|       | DVDEAYMKNKVELESR              | 8  | P05787 | K2C8_HUN  | 207 |
|       | LQAEIEGLKGQR                  | 8  | P05787 | K2C8_HUN  | 325 |
|       | SLDMDSIIAEVKAQYEDIANR         | 11 | P05787 | K2C8_HUN  | 264 |
| Phyre | FLEQQNKM[147.04]LETK          | 6  | P05787 | K2C8_HUN  | 117 |
| Phyre | WSLLQQQKTAR                   | 7  | P05787 | K2C8_HUN  | 130 |
|       | SLDMDSIIAEVKAQYEDIANR         | 11 | P05787 | K2C8_HUN  | 264 |
|       | TLNNKFASFIDK                  | 4  | P05787 | K2C8_HUN  | 101 |
|       | KVIDDTNITR                    | 0  | P05783 | K1C18_HUI | 187 |
|       | NLKASLENSLR                   | 2  | P05783 | K1C18_HUI | 317 |
|       | SQDLAKIMADIR                  | 5  | P05783 | K1C18_HUI | 247 |
| Phyre | VVSETNDTKVLR                  | 8  | P05783 | K1C18_HUI | 426 |
| Phyre | GLQAQIASSGLTVEVDAPKSQDLAK     | 18 | P05783 | K1C18_HUI | 241 |
| Phyre | SQDLAKIMADIR                  | 5  | P05783 | K1C18_HUI | 247 |

|       |                           |           |           |      |
|-------|---------------------------|-----------|-----------|------|
| Phyre | VKLEAEIATYR               | 1 P05783  | K1C18_HUI | 372  |
|       | TLNNKFASFDK               | 4 P05787  | K2C8_HUN  | 101  |
|       | KVIDDTNITR                | 0 P05783  | K1C18_HUI | 187  |
|       | VKLEAEIATYR               | 1 P05783  | K1C18_HUI | 372  |
|       | MLETKWSLLQQQK             | 4 P05787  | K2C8_HUN  | 122  |
|       | SLDMDSIIAEVKAQYEDIANR     | 11 P05787 | K2C8_HUN  | 264  |
|       | TLNNKFASFDK               | 4 P05787  | K2C8_HUN  | 101  |
|       | KVIDDTNITR                | 0 P05783  | K1C18_HUI | 187  |
| Phyre | VVSETNDTKVLR              | 8 P05783  | K1C18_HUI | 426  |
|       | LLQDSVDFSLADAINTEFKNTR    | 18 P08670 | VIME_HUN  | 97   |
|       | QAKQESTEYR                | 2 P08670  | VIME_HUN  | 313  |
|       | SKFADLSEANR               | 1 P08670  | VIME_HUN  | 294  |
|       | KVESLQEEIAFLK             | 0 P08670  | VIME_HUN  | 223  |
|       | VVSETNDTKVLR              | 8 P05783  | K1C18_HUI | 426  |
|       | KVIDDTNITR                | 0 P05783  | K1C18_HUI | 187  |
|       | LLETKWTLLQEQK             | 4 P08729  | K2C7_HUN  | 122  |
| Phyre | LLETKWTLLQEQK             | 4 P08729  | K2C7_HUN  | 122  |
|       | WTLLQEQKSAK               | 7 P08729  | K2C7_HUN  | 130  |
|       | AKLEAAIAEAEER             | 1 P08729  | K2C7_HUN  | 331  |
|       | AKQEELEAALQR              | 1 P08729  | K2C7_HUN  | 353  |
|       | LQAEIDNIKNQR              | 8 P08729  | K2C7_HUN  | 326  |
|       | GLQAQIASSGLTVEVDAPKSQDLAK | 18 P05783 | K1C18_HUI | 241  |
|       | AKLEAAIAEAEER             | 1 P08729  | K2C7_HUN  | 331  |
|       | LQAEIDNIKNQR              | 8 P08729  | K2C7_HUN  | 326  |
| Phyre | KGPPQVR                   | 0 P05783  | K1C18_HUI | 119  |
|       | YLEGTSCIAGVLVPAKDQPGR     | 15 P58107 | EPIPL_HUN | 2234 |
|       | AEAESMYQIKYEELQSLAGK      | 9 P05787  | K2C8_HUN  | 285  |
|       | LQAEIEGLKGQR              | 8 P05787  | K2C8_HUN  | 325  |
|       | SRAEAESMYQIKYEELQSLAGK    | 11 P05787 | K2C8_HUN  | 285  |
|       | TKTEISEM[147.04]NR        | 1 P05787  | K2C8_HUN  | 304  |
|       | KLLEGESR                  | 0 P05787  | K2C8_HUN  | 393  |
|       | LQAEIEGLKGQR              | 8 P05787  | K2C8_HUN  | 325  |
| Phyre | SYKVSTSGPR                | 2 P05787  | K2C8_HUN  | 11   |
| Phyre | TKTEISEMNR                | 1 P05787  | K2C8_HUN  | 304  |
| Phyre | TKTEISEM[147.04]NR        | 1 P05787  | K2C8_HUN  | 304  |
| Phyre | AVVVKK                    | 4 P05787  | K2C8_HUN  | 464  |
|       | DGKLVSESSDVLPK            | 2 P05787  | K2C8_HUN  | 472  |
|       | KLLEGESR                  | 0 P05787  | K2C8_HUN  | 393  |
|       | MLETKWSLLQQQK             | 4 P05787  | K2C8_HUN  | 122  |
|       | SYKVSTSGPR                | 2 P05787  | K2C8_HUN  | 11   |
|       | TKTEISEMNR                | 1 P05787  | K2C8_HUN  | 304  |
|       | TLNNKFASFDK               | 4 P05787  | K2C8_HUN  | 101  |
|       | VTQKSYK                   | 3 P05787  | K2C8_HUN  | 8    |
| Phyre | WSLLQQQKTAR               | 7 P05787  | K2C8_HUN  | 130  |
|       | MLETKWSLLQQQK             | 4 P05787  | K2C8_HUN  | 122  |
|       | SLDMDSIIAEVKAQYEDIANR     | 11 P05787 | K2C8_HUN  | 264  |
|       | TQEKEQIKTLNNK             | 7 P05787  | K2C8_HUN  | 96   |

|         |                        |    |        |          |     |
|---------|------------------------|----|--------|----------|-----|
| Phyre   | EQIKTLNNK              | 3  | P05787 | K2C8_HUN | 96  |
| Phyre   | MLETKWSLLQQQK          | 4  | P05787 | K2C8_HUN | 122 |
| Phyre   | M[147.04]LETKWSLLQQQK  | 4  | P05787 | K2C8_HUN | 122 |
| Phyre   | TQEKEQIKTLNNK          | 7  | P05787 | K2C8_HUN | 96  |
| Docking | GELAIKDANAK            | 5  | P05787 | K2C8_HUN | 347 |
| Phyre   | LQAEIEGLKGQR           | 8  | P05787 | K2C8_HUN | 325 |
| Phyre   | SLDMDSIIAEVKAQYEDIANR  | 11 | P05787 | K2C8_HUN | 264 |
| Phyre   | TKTEISEMNR             | 1  | P05787 | K2C8_HUN | 304 |
| Phyre   | TKTEISEM[147.04]NR     | 1  | P05787 | K2C8_HUN | 304 |
| Phyre   | YEELQSLAGKHGDDLRL      | 9  | P05787 | K2C8_HUN | 295 |
|         | DGKLVSSESDVLPK         | 2  | P05787 | K2C8_HUN | 472 |
| Phyre   | AEAESMYQIKYEELQSLAGK   | 9  | P05787 | K2C8_HUN | 285 |
| Phyre   | DGKLVSSESDVLPK         | 2  | P05787 | K2C8_HUN | 472 |
| Phyre   | FASFIDKVR              | 6  | P05787 | K2C8_HUN | 108 |
| Phyre   | FLEQQNKMLETK           | 6  | P05787 | K2C8_HUN | 117 |
| Phyre   | GELAIKDANAK            | 5  | P05787 | K2C8_HUN | 347 |
| Docking | KLLEGEESR              | 0  | P05787 | K2C8_HUN | 393 |
| Phyre   | LKLEAELGNMQGLVEDFK     | 1  | P05787 | K2C8_HUN | 160 |
| Phyre   | LQAEIEGLKGQR           | 8  | P05787 | K2C8_HUN | 325 |
| Phyre   | SLDMDSIIAEVKAQYEDIANR  | 11 | P05787 | K2C8_HUN | 264 |
| Phyre   | SRAEAESMYQIKYEELQSLAGK | 11 | P05787 | K2C8_HUN | 285 |
| Phyre   | SYKVSTSGPR             | 2  | P05787 | K2C8_HUN | 11  |
| Phyre   | TKTEISEMNR             | 1  | P05787 | K2C8_HUN | 304 |
| Phyre   | TKTEISEM[147.04]NR     | 1  | P05787 | K2C8_HUN | 304 |
| Phyre   | TLNNKFASFIDK           | 4  | P05787 | K2C8_HUN | 101 |
| Phyre   | WSLLQQQKTAR            | 7  | P05787 | K2C8_HUN | 130 |
| Phyre   | YEELQSLAGKHGDDLRL      | 9  | P05787 | K2C8_HUN | 295 |
| Phyre   | DGKLVSSESDVLPK         | 2  | P05787 | K2C8_HUN | 472 |
| Phyre   | DVDEAYMNKVELESR        | 8  | P05787 | K2C8_HUN | 207 |
| Docking | LQAEIEGLKGQR           | 8  | P05787 | K2C8_HUN | 325 |
| Phyre   | SLDMDSIIAEVKAQYEDIANR  | 11 | P05787 | K2C8_HUN | 264 |
|         | GELAIKDANAK            | 5  | P05787 | K2C8_HUN | 347 |
|         | LQAEIEGLKGQR           | 8  | P05787 | K2C8_HUN | 325 |
|         | MLETKWSLLQQQK          | 4  | P05787 | K2C8_HUN | 122 |
|         | M[147.04]LETKWSLLQQQK  | 4  | P05787 | K2C8_HUN | 122 |
|         | SYKVSTSGPR             | 2  | P05787 | K2C8_HUN | 11  |
|         | TKTEISEMNR             | 1  | P05787 | K2C8_HUN | 304 |
|         | TKTEISEM[147.04]NR     | 1  | P05787 | K2C8_HUN | 304 |
|         | WSLLQQQKTAR            | 7  | P05787 | K2C8_HUN | 130 |
|         | YEELQSLAGKHGDDLRL      | 9  | P05787 | K2C8_HUN | 295 |
| Phyre   | AEAESMYQIKYEELQSLAGK   | 9  | P05787 | K2C8_HUN | 285 |
| Phyre   | LQAEIEGLKGQR           | 8  | P05787 | K2C8_HUN | 325 |
| Phyre   | SLDMDSIIAEVKAQYEDIANR  | 11 | P05787 | K2C8_HUN | 264 |
| Phyre   | WSLLQQQKTAR            | 7  | P05787 | K2C8_HUN | 130 |
| Phyre   | YEELQSLAGKHGDDLRL      | 9  | P05787 | K2C8_HUN | 295 |
| Phyre   | LQAEIEGLKGQR           | 8  | P05787 | K2C8_HUN | 325 |
| Phyre   | SLDMDSIIAEVKAQYEDIANR  | 11 | P05787 | K2C8_HUN | 264 |

|           |                        |           |          |     |
|-----------|------------------------|-----------|----------|-----|
| Phyre     | TKTEISEMNR             | 1 P05787  | K2C8_HUN | 304 |
| Phyre     | YEELQSLAGKHGDDL        | 9 P05787  | K2C8_HUN | 295 |
| Phyre     | SLDMDSIIAEVKAQYEDIANR  | 11 P05787 | K2C8_HUN | 264 |
| Phyre     | AEAESMYQIKYEELQSLAGK   | 9 P05787  | K2C8_HUN | 285 |
| Phyre     | KLLEGESR               | 0 P05787  | K2C8_HUN | 393 |
| Phyre     | SLDMDSIIAEVKAQYEDIANR  | 11 P05787 | K2C8_HUN | 264 |
| Phyre     | SRAEAESMYQIKYEELQSLAGK | 11 P05787 | K2C8_HUN | 285 |
| Phyre     | TLNNKFASFIDK           | 4 P05787  | K2C8_HUN | 101 |
|           | FLEQQNKMLETK           | 6 P05787  | K2C8_HUN | 117 |
|           | KLLEGESR               | 0 P05787  | K2C8_HUN | 393 |
|           | M[147.04]LETKWSLLQQQK  | 4 P05787  | K2C8_HUN | 122 |
|           | SYKVSTSGPR             | 2 P05787  | K2C8_HUN | 11  |
|           | VTQKSYK                | 3 P05787  | K2C8_HUN | 8   |
|           | WSLLQQQKTAR            | 7 P05787  | K2C8_HUN | 130 |
| Phyre     | FLEQQNKMLETK           | 6 P05787  | K2C8_HUN | 117 |
| Phyre     | FLEQQNKM[147.04]LETK   | 6 P05787  | K2C8_HUN | 117 |
| Docking   | WSLLQQQKTAR            | 7 P05787  | K2C8_HUN | 130 |
| Structure | LQAEIEGLKGQR           | 8 P05787  | K2C8_HUN | 325 |
|           | TLNNKFASFIDK           | 4 P05787  | K2C8_HUN | 101 |
| Phyre     | KVESLQEEIAFLK          | 0 P08670  | VIME_HUN | 223 |
| Phyre     | SKFADLSEANR            | 1 P08670  | VIME_HUN | 294 |
| Structure | DANAKLSELEAALQR        | 4 P05787  | K2C8_HUN | 352 |
| Phyre     | KVESLQEEIAFLK          | 0 P08670  | VIME_HUN | 223 |
|           | LQAEIEGLKGQR           | 8 P05787  | K2C8_HUN | 325 |
|           | AEAESMYQIKYEELQSLAGK   | 9 P05787  | K2C8_HUN | 285 |
|           | LQAEIEGLKGQR           | 8 P05787  | K2C8_HUN | 325 |
|           | M[147.04]LETKWSLLQQQK  | 4 P05787  | K2C8_HUN | 122 |
|           | SLDMDSIIAEVKAQYEDIANR  | 11 P05787 | K2C8_HUN | 264 |
|           | SRAEAESMYQIKYEELQSLAGK | 11 P05787 | K2C8_HUN | 285 |
|           | SKFADLSEANR            | 1 P08670  | VIME_HUN | 294 |
|           | TKTEISEMNR             | 1 P05787  | K2C8_HUN | 304 |
|           | TLNNKFASFIDK           | 4 P05787  | K2C8_HUN | 101 |
| Phyre     | FLEQQNKILLAELEQLK      | 6 P08670  | VIME_HUN | 129 |
| Phyre     | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN | 97  |
| Phyre     | SLDMDSIIAEVKAQYEDIANR  | 11 P05787 | K2C8_HUN | 264 |
| Phyre     | AEAEAWYQTKFETLQAQAGK   | 9 P08729  | K2C7_HUN | 286 |
| Phyre     | AEAEAWYQTKFETLQAQAGK   | 9 P08729  | K2C7_HUN | 286 |
|           | LLETKWTLLEQK           | 4 P08729  | K2C7_HUN | 122 |
| Phyre     | LQAEIDNIKNQR           | 8 P08729  | K2C7_HUN | 326 |
| Phyre     | LQAEIEGLKGQR           | 8 P05787  | K2C8_HUN | 325 |
| Phyre     | TKTEISEMNR             | 1 P05787  | K2C8_HUN | 304 |
| Phyre     | LQAEIDNIKNQR           | 8 P08729  | K2C7_HUN | 326 |
|           | AEAEAWYQTKFETLQAQAGK   | 9 P08729  | K2C7_HUN | 286 |
|           | LLETKWTLLEQK           | 4 P08729  | K2C7_HUN | 122 |
| Phyre     | AEAEAWYQTKFETLQAQAGK   | 9 P08729  | K2C7_HUN | 286 |
|           | YEELQSLAGKHGDDL        | 9 P05787  | K2C8_HUN | 295 |
| Phyre     | AYRAQKNLDFEDPYEDAESR   | 5 Q96IW2  | SHD_HUM  | 38  |

|           |                            |    |        |           |     |
|-----------|----------------------------|----|--------|-----------|-----|
| Structure | SNDPKSQNHHPGWLMR           | 4  | P06213 | INSR_HUM  | 571 |
| Phyre     | EGNDLYHEMIESGVINLKDATSK    | 17 | P06576 | ATPB_HUN  | 259 |
| Phyre     | VVDLLAPYAKGGK              | 9  | P06576 | ATPB_HUN  | 198 |
| Phyre     | VYKEVK                     | 2  | P24539 | AT5F1_HUI | 191 |
| Phyre     | LVPLKETIK                  | 4  | P06576 | ATPB_HUN  | 485 |
| Phyre     | GYLDKLEPSK                 | 4  | P25705 | ATPA_HUN  | 498 |
| Phyre     | ADKLAEHSS                  | 2  | P06576 | ATPB_HUN  | 522 |
| Phyre     | ADKLAEHSS                  | 2  | P06576 | ATPB_HUN  | 522 |
| Phyre     | ADKLAEHSS                  | 2  | P06576 | ATPB_HUN  | 522 |
| Phyre     | ADKLAEHSS                  | 2  | P06576 | ATPB_HUN  | 522 |
| Phyre     | STVAQLVKR                  | 7  | P25705 | ATPA_HUN  | 261 |
| Phyre     | VVDALGNAIDGKGPIGSK         | 11 | P25705 | ATPA_HUN  | 161 |
| Phyre     | IGEKYVDMSVK                | 3  | P48047 | ATPO_HUN  | 192 |
| Phyre     | IGEKYVDM[147.04]SVK        | 3  | P48047 | ATPO_HUN  | 192 |
| Phyre     | GQKVLDSGAPIKIPVGPETLGR     | 2  | P06576 | ATPB_HUN  | 124 |
| Structure | ELTIGSKLQDAEIAR            | 6  | P06703 | S10A6_HUI | 47  |
| Structure | FTASAGIQVVGDDLTVTNPKR      | 19 | P06733 | ENOA_HUN  | 326 |
| Structure | YISPDQLADLYKFSIK           | 11 | P06733 | ENOA_HUN  | 281 |
| Structure | GVSKAVEHINK                | 3  | P06733 | ENOA_HUN  | 64  |
| Structure | TAIGKAGYTDK                | 4  | P06733 | ENOA_HUN  | 233 |
| Structure | YM[147.04]GKGVS            | 3  | P06733 | ENOA_HUN  | 60  |
| Structure | YISPDQLADLYKFSIK           | 11 | P06733 | ENOA_HUN  | 281 |
| Structure | FTASAGIQVVGDDLTVTNPKR      | 19 | P06733 | ENOA_HUN  | 326 |
| Structure | SGKYDLDFK                  | 2  | P06733 | ENOA_HUN  | 256 |
| Structure | YISPDQLADLYKFSIK           | 11 | P06733 | ENOA_HUN  | 281 |
| Structure | AVEHINKTIAPALVSK           | 6  | P06733 | ENOA_HUN  | 71  |
| Structure | GNPTVEVDLFTSKGLFR          | 12 | P06733 | ENOA_HUN  | 28  |
| Structure | DNDKTR                     | 3  | P06733 | ENOA_HUN  | 54  |
| Structure | TAIGKAGYTDK                | 4  | P06733 | ENOA_HUN  | 233 |
| Structure | YGKDATNVGDEGGFAPNILENK     | 2  | P06733 | ENOA_HUN  | 202 |
| Structure | YM[147.04]GKGVS            | 3  | P06733 | ENOA_HUN  | 60  |
| Structure | YISPDQLADLYKFSIK           | 11 | P06733 | ENOA_HUN  | 281 |
| Structure | IGAENVYHNLKNVIK            | 9  | P06733 | ENOA_HUN  | 193 |
| Structure | YGKDATNVGDEGGFAPNILENK     | 2  | P06733 | ENOA_HUN  | 202 |
| Structure | FTASAGIQVVGDDLTVTNPKR      | 19 | P06733 | ENOA_HUN  | 326 |
| Structure | GVSKAVEHINK                | 3  | P06733 | ENOA_HUN  | 64  |
| Structure | IDKLMIMDGTENK              | 2  | P06733 | ENOA_HUN  | 92  |
| Structure | LNVTEQEKIDK                | 7  | P06733 | ENOA_HUN  | 89  |
| Structure | LNVTEQEKIDKLMIMDGTENK      | 7  | P06733 | ENOA_HUN  | 89  |
| Structure | SKFGANAILGVSLAVCK          | 1  | P06733 | ENOA_HUN  | 105 |
| Structure | DATNVGDEGGFAPNILENKEGLELLK | 18 | P06733 | ENOA_HUN  | 221 |
| Structure | TAIGKAGYTDK                | 4  | P06733 | ENOA_HUN  | 233 |
| Structure | TAIGKAGYTDK                | 4  | P06733 | ENOA_HUN  | 233 |
| Structure | YGKDATNVGDEGGFAPNILENK     | 2  | P06733 | ENOA_HUN  | 202 |
| Structure | FYEAFSKNLK                 | 6  | P08238 | HS90B_HU  | 435 |
| Phyre     | YISPDQLADLYKFSIK           | 11 | P06733 | ENOA_HUN  | 281 |
| Structure | VKEFGIDPQNMFEFWDWVGGR      | 1  | P06744 | G6PI_HUM  | 254 |

|           |                              |           |           |     |
|-----------|------------------------------|-----------|-----------|-----|
| Structure | ELQAAGKSPEDLER               | 6 P06744  | G6PI_HUM  | 454 |
| Structure | DPQFQKLQQWYR                 | 5 P06744  | G6PI_HUM  | 12  |
| Structure | M[147.04]LVDLAKSR            | 6 P06744  | G6PI_HUM  | 73  |
|           | FINYVKNCFR                   | 5 P06748  | NPM_HUM   | 273 |
|           | TPKGPSSVEDIK                 | 2 P06748  | NPM_HUM   | 239 |
|           | VEAKFINYVK                   | 3 P06748  | NPM_HUM   | 267 |
|           | TPKGPSSVEDIK                 | 2 P06748  | NPM_HUM   | 239 |
|           | VEAKFINYVK                   | 3 P06748  | NPM_HUM   | 267 |
|           | SNQNGKDSKPSSTPR              | 8 P06748  | NPM_HUM   | 215 |
|           | SNQNGKDSKPSSTPR              | 5 P06748  | NPM_HUM   | 212 |
|           | MQASIEKGGSLPK                | 6 P06748  | NPM_HUM   | 257 |
|           | FINYVKNCFR                   | 5 P06748  | NPM_HUM   | 273 |
|           | VEAKFINYVK                   | 3 P06748  | NPM_HUM   | 267 |
|           | TPKGPSSVEDIK                 | 2 P06748  | NPM_HUM   | 239 |
|           | AKM[147.04]QASIEK            | 1 P06748  | NPM_HUM   | 250 |
|           | TPKGPSSVEDIK                 | 2 P06748  | NPM_HUM   | 239 |
|           | SAPGGGSKVPQK                 | 7 P06748  | NPM_HUM   | 150 |
|           | VEAKFINYVK                   | 3 P06748  | NPM_HUM   | 267 |
|           | AKM[147.04]QASIEK            | 1 P06748  | NPM_HUM   | 250 |
|           | DSKPSSTPR                    | 2 P06748  | NPM_HUM   | 215 |
|           | DTPAKNAQK                    | 4 P06748  | NPM_HUM   | 202 |
|           | FINYVKNCFR                   | 5 P06748  | NPM_HUM   | 273 |
|           | SNQNGKDSKPSSTPR              | 8 P06748  | NPM_HUM   | 215 |
|           | TPKGPSSVEDIK                 | 2 P06748  | NPM_HUM   | 239 |
|           | FINYVKNCFR                   | 5 P06748  | NPM_HUM   | 273 |
|           | FINYVKNCFR                   | 5 P06748  | NPM_HUM   | 273 |
|           | MQASIEKGGSLPK                | 6 P06748  | NPM_HUM   | 257 |
|           | M[147.04]QASIEKGGSLPK        | 6 P06748  | NPM_HUM   | 257 |
| Structure | TVSLGAGAKDELHIVEAEAMNYEGSPIK | 8 P06748  | NPM_HUM   | 54  |
|           | MQASIEKGGSLPK                | 6 P06748  | NPM_HUM   | 257 |
|           | M[147.04]QASIEKGGSLPK        | 6 P06748  | NPM_HUM   | 257 |
|           | TPKGPSSVEDIK                 | 2 P06748  | NPM_HUM   | 239 |
| Phyre     | LATALQKLEEA EK               | 6 P06753  | TPM3_HUM  | 113 |
| Phyre     | LEEAEKAADESER                | 5 P06753  | TPM3_HUM  | 119 |
| Phyre     | KLVIIEGDLER                  | 0 P06753  | TPM3_HUM  | 169 |
| Phyre     | LKEAETR                      | 1 P06753  | TPM3_HUM  | 234 |
| Phyre     | IKIIAPPER                    | 1 P68032  | ACTC_HUM  | 330 |
| Phyre     | IKIIAPPER                    | 1 Q562R1  | ACTBL_HUI | 329 |
| Structure | EPVGTCFLQDGT KTVEYAPCR       | 12 P06756 | ITAV_HUM  | 165 |
| Structure | QVVCDLGNPMKAGTQLLAGLR        | 10 P06756 | ITAV_HUM  | 718 |
| Structure | EPVGTCFLQDGT KTVEYAPCR       | 12 P06756 | ITAV_HUM  | 165 |
| Phyre     | QVVCDLGNPMKAGTQLLAGLR        | 10 P06756 | ITAV_HUM  | 718 |
| Phyre     | DVELLYPVKEK                  | 8 P07099  | HYEP_HUM  | 286 |
| Structure | NVNVFKFIIPQIVK               | 5 P07195  | LDHB_HUM  | 119 |
| Structure | SLADELALVDVLEDK LK           | 14 P07195 | LDHB_HUM  | 58  |
| Structure | EVHKMVVESAYEVIK              | 3 P07195  | LDHB_HUM  | 233 |
| Structure | MVVESAYEVIK LK               | 10 P07195 | LDHB_HUM  | 244 |



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| Structure | KSADTLWDIQK                  | 0 P07195  | LDHB_HUN  | 319 |
| Structure | KSNFAEALAAHK                 | 0 P07237  | PDIA1_HUI | 31  |
| Structure | NGDTASPKEYTAGR               | 7 P07237  | PDIA1_HUI | 114 |
| Structure | NNFEGEVTKENLLDFIK            | 8 P07237  | PDIA1_HUI | 222 |
| Structure | SVSDYDGKLSNFK                | 7 P07237  | PDIA1_HUI | 271 |
| Structure | LAKVDATEESDLAQYGV            | 2 P07237  | PDIA1_HUI | 81  |
| Structure | ENLLDFIKHNQLPLVIEFTEQTAPK    | 7 P07237  | PDIA1_HUI | 230 |
| Structure | NNFEGEVTKENLLDFIK            | 8 P07237  | PDIA1_HUI | 222 |
| Structure | ASMKGLGTDEDSLIEIICSR         | 3 P07355  | ANXA2_HU  | 119 |
| Structure | KEVKGDLENAFLNLVQCIQNKPLYFADR | 0 P07355  | ANXA2_HU  | 246 |
| Structure | YKSYSPYDMLESIR               | 1 P07355  | ANXA2_HU  | 233 |
| Structure | TKGVDEVITIVNILTNR            | 1 P07355  | ANXA2_HU  | 49  |
| Structure | DLYDAGVKR                    | 7 P07355  | ANXA2_HU  | 204 |
| Structure | EVKGDLENAFLNLVQCIQNKPLYFADR  | 2 P07355  | ANXA2_HU  | 249 |
| Structure | KLMVALAK                     | 0 P07355  | ANXA2_HU  | 169 |
| Structure | KLM[147.04]VALAK             | 0 P07355  | ANXA2_HU  | 169 |
| Structure | DLYDAGVKR                    | 7 P07355  | ANXA2_HU  | 204 |
| Structure | TDLEKDIISDTSGDFR             | 4 P07355  | ANXA2_HU  | 157 |
| Structure | TDLEKDIISDTSGDFR             | 4 P07355  | ANXA2_HU  | 157 |
| Structure | YGKSLYYYIQQDTK               | 2 P07355  | ANXA2_HU  | 313 |
| Structure | LSLEGDHSTPPSAYGSVKAYTNFDAER  | 17 P07355 | ANXA2_HU  | 28  |
| Structure | SVPHLQKVFD                   | 6 P07355  | ANXA2_HU  | 227 |
| Structure | YKSYSPYDMLESIR               | 1 P07355  | ANXA2_HU  | 233 |
| Structure | SVPHLQKVFD                   | 6 P07355  | ANXA2_HU  | 227 |
| Structure | YKSYSPYDMLESIR               | 1 P07355  | ANXA2_HU  | 233 |
| Structure | YKSYSPYDM[147.04]LESIR       | 1 P07355  | ANXA2_HU  | 233 |
| Structure | TDLEKDIISDTSGDFR             | 4 P07355  | ANXA2_HU  | 157 |
| Structure | TDLEKDIISDTSGDFR             | 4 P07355  | ANXA2_HU  | 157 |
|           | SEVDMLKIR                    | 6 P07355  | ANXA2_HU  | 302 |
| Structure | ISVYYNEATGGKYVPR             | 11 P07437 | TBB5_HUN  | 58  |
| Structure | MSMKEVDEQMLNVQNK             | 3 P07437  | TBB5_HUN  | 324 |
| Structure | TFVNITPAEVGVLVGKDR           | 15 P07737 | PROF1_HU  | 54  |
| Structure | TFVNITPAEVGVLVGKDR           | 15 P07737 | PROF1_HU  | 54  |
| Structure | SSFYVNGTLGGQKCSVIR           | 13 P07737 | PROF1_HU  | 70  |
| Structure | SSFYVNGTLGGQKCSVIR           | 13 P07737 | PROF1_HU  | 70  |
| Structure | KDLYANTVLSGGTTMYPGIADR       | 0 P60709  | ACTB_HUN  | 291 |
| Phyre     | KLTWVFNGLVDGWDDPR            | 0 P07814  | SYEP_HUM  | 437 |
| Phyre     | KLTWVFNGLVDGWDDPR            | 0 P07814  | SYEP_HUM  | 437 |
|           | EVAKHPK                      | 3 P07814  | SYEP_HUM  | 532 |
| Phyre     | LNLENKDYKK                   | 8 P07814  | SYEP_HUM  | 602 |
|           | DQVDIAVQELLQLKAQYK           | 13 P07814 | SYEP_HUM  | 939 |
| Phyre     | SVVNMEWDKIWAFNK              | 8 P07814  | SYEP_HUM  | 491 |
| Structure | DNSTMGYMAAKK                 | 10 P07900 | HS90A_HU  | 631 |
| Structure | DNSTM[147.04]GYM[147.04]AAKK | 10 P07900 | HS90A_HU  | 631 |
| Structure | VEKVVVSNR                    | 2 P07900  | HS90A_HU  | 585 |
| Phyre     | ADLINNLGTIAKSGTK             | 11 P07900 | HS90A_HU  | 112 |
| Structure | CLELFTELAEDKENYKK            | 11 P07900 | HS90A_HU  | 431 |

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|-----------|--------------------------------|----|--------|-----------|-----|
| Structure | FYEQFSKNIK                     | 6  | P07900 | HS90A_HU  | 443 |
| Phyre     | TKPIWTR                        | 1  | P07900 | HS90A_HU  | 294 |
| Structure | FYEQFSKNIK                     | 6  | P07900 | HS90A_HU  | 443 |
| Structure | FYEQFSKNIK                     | 6  | P07900 | HS90A_HU  | 443 |
| Structure | VEKVVVSNR                      | 2  | P07900 | HS90A_HU  | 585 |
| Phyre     | FYEQFSKNIK                     | 6  | P07900 | HS90A_HU  | 443 |
| Phyre     | LDSGKELHINLIPNK                | 4  | P07900 | HS90A_HU  | 74  |
| Phyre     | FYEQFSKNIK                     | 6  | P07900 | HS90A_HU  | 443 |
| Structure | FYEAFSKNLK                     | 6  | P08238 | HS90B_HU  | 435 |
| Phyre     | FYEQFSKNIK                     | 6  | P07900 | HS90A_HU  | 443 |
| Structure | FYEQFSKNIK                     | 6  | P07900 | HS90A_HU  | 443 |
| Structure | KHLEINPDHSIETLR                | 0  | P07900 | HS90A_HU  | 632 |
| Structure | KHLEINPDHPIVETLR               | 0  | P08238 | HS90B_HU  | 624 |
| Structure | RAPFDLFENKK                    | 9  | P08238 | HS90B_HU  | 347 |
| Structure | LILEQMOKDPQALSEHLK             | 7  | P31948 | STIP1_HUN | 513 |
| Docking   | AVVPSKR                        | 5  | P07910 | HNRPC_HU  | 157 |
|           | KELTQIK                        | 0  | P07910 | HNRPC_HU  | 198 |
|           | SGFNSKSGQR                     | 5  | P07910 | HNRPC_HU  | 176 |
|           | KELTQIK                        | 0  | P07910 | HNRPC_HU  | 198 |
|           | LKGDDLQAIK                     | 1  | P07910 | HNRPC_HU  | 189 |
|           | KELTQIK                        | 0  | P07910 | HNRPC_HU  | 198 |
|           | LKGDDLQAIK                     | 1  | P07910 | HNRPC_HU  | 189 |
|           | QKVDSLLENLEK                   | 1  | P07910 | HNRPC_HU  | 206 |
|           | SGFNSKSGQR                     | 5  | P07910 | HNRPC_HU  | 176 |
|           | IVGCSVHKGFAFVQYVNER            | 7  | P07910 | HNRPC_HU  | 50  |
| Structure | YGKIVGCSVHK                    | 2  | P07910 | HNRPC_HU  | 42  |
|           | YGKIVGCSVHK                    | 2  | P07910 | HNRPC_HU  | 42  |
| Structure | SSGPYGGGGQYFAKPR               | 13 | P09651 | ROA1_HUN  | 350 |
| Structure | IKAAMPR                        | 1  | P07954 | FUMH_HUI  | 263 |
| Structure | SKEFAQIIK                      | 1  | P07954 | FUMH_HUI  | 223 |
| Structure | THTQDAVPLTLGQEFSGYVQQVKYAMTR   | 22 | P07954 | FUMH_HUI  | 256 |
| Structure | IKAAMPR                        | 1  | P07954 | FUMH_HUI  | 263 |
| Structure | IKAAM[147.04]PR                | 1  | P07954 | FUMH_HUI  | 263 |
| Structure | IEYDTFGELKVPNDK                | 9  | P07954 | FUMH_HUI  | 61  |
| Structure | STMNFKIGGVTER                  | 5  | P07954 | FUMH_HUI  | 80  |
| Structure | IEYDTFGELKVPNDK                | 9  | P07954 | FUMH_HUI  | 61  |
| Structure | IEYDTFGELKVPNDKYYGAQTVR        | 9  | P07954 | FUMH_HUI  | 61  |
|           | IDIHSCNHEAEKLGCSASN VFAR       | 11 | P08069 | IGF1R_HUN | 812 |
| Structure | MEEVTGTKGR                     | 7  | P08069 | IGF1R_HUN | 469 |
| Structure | M[147.04]EEVTGTKGR             | 7  | P08069 | IGF1R_HUN | 469 |
| Structure | ASCESDVLHFTSTTTSKNR            | 16 | P08069 | IGF1R_HUN | 502 |
| Docking   | DLIADLKYELTGK                  | 6  | P08133 | ANXA6_HU  | 75  |
| Structure | TSFPEDTVITYKCEESFVK            | 11 | P08174 | DAF_HUM/  | 64  |
| Structure | LNSASLKQPYITQNYFPVGTVVEYECRPGY | 6  | P08174 | DAF_HUM/  | 110 |
| Phyre     | TSFPEDTVITYKCEESFVK            | 11 | P08174 | DAF_HUM/  | 64  |
| Structure | ELPAQKWWHTGALYR                | 5  | P08195 | 4F2_HUMA  | 217 |
| Structure | IGDLQAFQGHGAGNLAGLKGR          | 18 | P08195 | 4F2_HUMA  | 245 |

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|-----------|-------------------------------|-----------|----------|-----|
| Structure | DIENLKDASSFLAEWQNITK          | 5 P08195  | 4F2_HUMA | 354 |
| Structure | NQKDDVAQTDLLQIDPNFGSK         | 2 P08195  | 4F2_HUMA | 269 |
| Structure | NQKDDVAQTDLLQIDPNFGSKEDFDSLLQ | 20 P08195 | 4F2_HUMA | 287 |
| Structure | DDVAQTDLLQIDPNFGSKEDFDSLLQSAK | 17 P08195 | 4F2_HUMA | 287 |
| Structure | GENSWFSTQVDTVATKVK            | 15 P08195 | 4F2_HUMA | 329 |
| Structure | IGDLQAFQGHGAGNLAGLKGR         | 18 P08195 | 4F2_HUMA | 245 |
| Docking   | IGDLQAFQGHGAGNLAGLKGR         | 18 P08195 | 4F2_HUMA | 245 |
| Structure | EDFDSLLQSAKK                  | 10 P08195 | 4F2_HUMA | 298 |
| Structure | ELPAQKWWHTGALYR               | 5 P08195  | 4F2_HUMA | 217 |
| Structure | IGDLQAFQGHGAGNLAGLKGR         | 18 P08195 | 4F2_HUMA | 245 |
| Structure | EDFDSLLQSAKK                  | 10 P08195 | 4F2_HUMA | 298 |
| Structure | IGDLQAFQGHGAGNLAGLKGR         | 18 P08195 | 4F2_HUMA | 245 |
| Structure | IGDLQAFQGHGAGNLAGLKGR         | 18 P08195 | 4F2_HUMA | 245 |
| Structure | LKLEPHEGLLLR                  | 1 P08195  | 4F2_HUMA | 615 |
| Structure | LRENELTYYCCKK                 | 11 P13987 | CD59_HUN | 90  |
| Phyre     | LKLEPHEGLLLR                  | 1 P08195  | 4F2_HUMA | 615 |
| Structure | LKLEPHEGLLLR                  | 1 P08195  | 4F2_HUMA | 615 |
| Phyre     | IGDLQAFQGHGAGNLAGLKGR         | 18 P08195 | 4F2_HUMA | 245 |
| Phyre     | LKLEPHEGLLLR                  | 1 P08195  | 4F2_HUMA | 615 |
| Structure | IDGSANLKSQDDRDK               | 7 P54709  | AT1B3_HU | 259 |
| Phyre     | LKLEPHEGLLLR                  | 1 P08195  | 4F2_HUMA | 615 |
| Structure | ALVFQPVAEKDKQTDFEHR           | 10 P08237 | PFKAM_HL | 727 |
| Phyre     | ELISNASDALDKIR                | 11 P08238 | HS90B_HU | 53  |
| Phyre     | FYEAFSKNLK                    | 6 P08238  | HS90B_HU | 435 |
| Phyre     | VEKVTISNR                     | 2 P08238  | HS90B_HU | 577 |
| Phyre     | ADLINNLGTIAKSGTK              | 11 P08238 | HS90B_HU | 107 |
| Structure | SLVSVTKEGLELPEDEEEKK          | 6 P08238  | HS90B_HU | 538 |
| Structure | CLELFSELAEDKENYKK             | 11 P08238 | HS90B_HU | 423 |
| Structure | FYEAFSKNLK                    | 6 P08238  | HS90B_HU | 435 |
| Structure | GFEVVMTEPIDEYCVQQLKEFDGK      | 19 P08238 | HS90B_HU | 526 |
| Phyre     | KHLEINPDHPIVETLR              | 0 P08238  | HS90B_HU | 624 |
| Phyre     | RAPFDLFENKK                   | 9 P08238  | HS90B_HU | 347 |
| Structure | SIYYITGESKEQVANSAFVER         | 9 P08238  | HS90B_HU | 491 |
| Phyre     | EKYIDQEELNK                   | 1 P08238  | HS90B_HU | 275 |
| Phyre     | IKEKYIDQEELNK                 | 3 P08238  | HS90B_HU | 275 |
| Phyre     | YESLTDPSKLD SGKELK            | 13 P08238 | HS90B_HU | 69  |
| Phyre     | DNSTMGYMMAKK                  | 10 P08238 | HS90B_HU | 623 |
| Phyre     | FYEAFSKNLK                    | 6 P08238  | HS90B_HU | 435 |
| Phyre     | KHLEINPDHPIVETLR              | 0 P08238  | HS90B_HU | 624 |
| Phyre     | FYEAFSKNLK                    | 6 P08238  | HS90B_HU | 435 |
| Phyre     | KHLEINPDHPIVETLR              | 0 P08238  | HS90B_HU | 624 |
| Phyre     | VEKVTISNR                     | 2 P08238  | HS90B_HU | 577 |
| Phyre     | VEKVTISNR                     | 2 P08238  | HS90B_HU | 577 |
| Structure | ILKVIR                        | 2 P08238  | HS90B_HU | 402 |
| Structure | FYEAFSKNLK                    | 6 P08238  | HS90B_HU | 435 |
| Phyre     | ETQKSIYYITGESK                | 3 P08238  | HS90B_HU | 481 |
| Phyre     | GTKVILHLK                     | 2 P08238  | HS90B_HU | 180 |

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|-----------|------------------------|-----------|-----------|-----|
| Phyre     | TKPIWTR                | 1 P08238  | HS90B_HU  | 286 |
| Phyre     | FENLCKIMK              | 5 P08238  | HS90B_HU  | 565 |
| Phyre     | KVEKVTISNR             | 3 P08238  | HS90B_HU  | 577 |
| Structure | SIYYITGESKEQVANSAFVER  | 9 P08238  | HS90B_HU  | 491 |
| Phyre     | APFDLFENKK             | 8 P08238  | HS90B_HU  | 347 |
| Structure | YIDQEELNKTPIWTR        | 8 P08238  | HS90B_HU  | 284 |
| Docking   | QKAEADKNDK             | 1 P08238  | HS90B_HU  | 641 |
| Phyre     | KFYEAFSKNLK            | 7 P08238  | HS90B_HU  | 435 |
| Phyre     | EKYIDQEELNK            | 1 P08238  | HS90B_HU  | 275 |
| Phyre     | YESLTDPSKLDSGKELK      | 13 P08238 | HS90B_HU  | 69  |
| Phyre     | FENLCKIMK              | 5 P08238  | HS90B_HU  | 565 |
| Phyre     | ELKIDIIPNPQER          | 2 P08238  | HS90B_HU  | 72  |
| Structure | DYTKAMDVYQK            | 3 P31948  | STIP1_HUN | 446 |
| Structure | LILEQMQRDPQALSEHLK     | 7 P31948  | STIP1_HUN | 513 |
| Phyre     | FYEAFSKNLK             | 6 P08238  | HS90B_HU  | 435 |
| Phyre     | FYEAFSKNLK             | 6 P08238  | HS90B_HU  | 435 |
| Phyre     | FYEAFSKNLK             | 6 P08238  | HS90B_HU  | 435 |
| Phyre     | KTSDFNFLAQEGCTK        | 0 Q9UHD1  | CHRD1_HU  | 198 |
| Structure | GQAFVIFKELGSSTNALR     | 7 P08579  | RU2B_HUN  | 57  |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN  | 97  |
|           | LQDEIQNMKEEMAR         | 8 P08670  | VIME_HUN  | 373 |
|           | LQDEIQNMKEEM[147.04]AR | 8 P08670  | VIME_HUN  | 373 |
|           | LQDEIQNM[147.04]KEEMAR | 8 P08670  | VIME_HUN  | 373 |
|           | SKFADLSEAANR           | 1 P08670  | VIME_HUN  | 294 |
|           | TNEKVELQELNDR          | 3 P08670  | VIME_HUN  | 104 |
|           | LQDEIQNMKEEMAR         | 8 P08670  | VIME_HUN  | 373 |
|           | ETNLDSLPLVDTHSKR       | 14 P08670 | VIME_HUN  | 439 |
|           | FLEQQNKILLAELEQLK      | 6 P08670  | VIME_HUN  | 129 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN  | 97  |
|           | FANYIDKVR              | 6 P08670  | VIME_HUN  | 120 |
|           | FLEQQNKILLAELEQLK      | 6 P08670  | VIME_HUN  | 129 |
|           | ILLAELEQLKGQ GK        | 9 P08670  | VIME_HUN  | 139 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN  | 97  |
|           | SKFADLSEAANR           | 1 P08670  | VIME_HUN  | 294 |
|           | TLLIKTVETR             | 4 P08670  | VIME_HUN  | 445 |
|           | TNEKVELQELNDR          | 3 P08670  | VIME_HUN  | 104 |
|           | ETNLDSLPLVDTHSKR       | 14 P08670 | VIME_HUN  | 439 |
|           | FANYIDKVR              | 6 P08670  | VIME_HUN  | 120 |
|           | GQGKSR                 | 3 P08670  | VIME_HUN  | 143 |
|           | ETNLDSLPLVDTHSKR       | 14 P08670 | VIME_HUN  | 439 |
|           | FLEQQNKILLAELEQLK      | 6 P08670  | VIME_HUN  | 129 |
| Structure | ILLAELEQLKGQ GK        | 9 P08670  | VIME_HUN  | 139 |
|           | ETNLDSLPLVDTHSKR       | 14 P08670 | VIME_HUN  | 439 |
|           | FANYIDKVR              | 6 P08670  | VIME_HUN  | 120 |
|           | FLEQQNKILLAELEQLK      | 6 P08670  | VIME_HUN  | 129 |
|           | ILLAELEQLKGQ GK        | 9 P08670  | VIME_HUN  | 139 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN  | 97  |

|           |                        |           |          |     |
|-----------|------------------------|-----------|----------|-----|
| Structure | QQYESVAAKNLQEAEEWYK    | 8 P08670  | VIME_HUN | 282 |
|           | SKFADLSEANR            | 1 P08670  | VIME_HUN | 294 |
|           | TLLIKTVETR             | 4 P08670  | VIME_HUN | 445 |
|           | TNEKVELQELNDR          | 3 P08670  | VIME_HUN | 104 |
|           | KVESLQEEIAFLK          | 0 P08670  | VIME_HUN | 223 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN | 97  |
|           | QVQSLTCEVDALKGTNESLER  | 12 P08670 | VIME_HUN | 334 |
|           | ETNLDSLPLVDTHSKR       | 14 P08670 | VIME_HUN | 439 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN | 97  |
|           | TNEKVELQELNDR          | 3 P08670  | VIME_HUN | 104 |
|           | LQDEIQNMKEEMAR         | 8 P08670  | VIME_HUN | 373 |
|           | LQDEIQNMKEEM[147.04]AR | 8 P08670  | VIME_HUN | 373 |
|           | SKFADLSEANR            | 1 P08670  | VIME_HUN | 294 |
|           | LQDEIQNMKEEMAR         | 8 P08670  | VIME_HUN | 373 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN | 97  |
| Structure | KVESLQEEIAFLK          | 0 P08670  | VIME_HUN | 223 |
|           | ETNLDSLPLVDTHSKR       | 14 P08670 | VIME_HUN | 439 |
|           | FLEQQNKILLAELEQLK      | 6 P08670  | VIME_HUN | 129 |
|           | KVESLQEEIAFLK          | 0 P08670  | VIME_HUN | 223 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN | 97  |
|           | LQDEIQNMKEEMAR         | 8 P08670  | VIME_HUN | 373 |
|           | LQDEIQNMKEEM[147.04]AR | 8 P08670  | VIME_HUN | 373 |
|           | LQDEIQNM[147.04]KEEMAR | 8 P08670  | VIME_HUN | 373 |
|           | NLQEAEEWYKSK           | 9 P08670  | VIME_HUN | 292 |
|           | QAKQESTEYRR            | 2 P08670  | VIME_HUN | 313 |
|           | QQYESVAAKNLQEAEEWYK    | 8 P08670  | VIME_HUN | 282 |
|           | SKFADLSEANR            | 1 P08670  | VIME_HUN | 294 |
|           | TNEKVELQELNDR          | 3 P08670  | VIME_HUN | 104 |
|           | ETNLDSLPLVDTHSKR       | 14 P08670 | VIME_HUN | 439 |
|           | FLEQQNKILLAELEQLK      | 6 P08670  | VIME_HUN | 129 |
| Phyre     | ILLAELEQLKGQ GK        | 9 P08670  | VIME_HUN | 139 |
|           | KVESLQEEIAFLK          | 0 P08670  | VIME_HUN | 223 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN | 97  |
|           | LQDEIQNMKEEMAR         | 8 P08670  | VIME_HUN | 373 |
|           | SKFADLSEANR            | 1 P08670  | VIME_HUN | 294 |
|           | TLLIKTVETR             | 4 P08670  | VIME_HUN | 445 |
|           | TNEKVELQELNDR          | 3 P08670  | VIME_HUN | 104 |
|           | ETNLDSLPLVDTHSKR       | 14 P08670 | VIME_HUN | 439 |
|           | FLEQQNKILLAELEQLK      | 6 P08670  | VIME_HUN | 129 |
|           | LLQDSVDFSLADAINTEFKNTR | 18 P08670 | VIME_HUN | 97  |
|           | QQYESVAAKNLQEAEEWYK    | 8 P08670  | VIME_HUN | 282 |
|           | KVESLQEEIAFLK          | 0 P08670  | VIME_HUN | 223 |
|           | AEAEAWYQTKFETLQAQAGK   | 9 P08729  | K2C7_HUN | 286 |
|           | LLETKWTLQEQK           | 4 P08729  | K2C7_HUN | 122 |
|           | LQAEIDNIKNQR           | 8 P08729  | K2C7_HUN | 326 |
| Structure | ILLAELEQLKGQ GK        | 9 P08670  | VIME_HUN | 139 |
|           | GISIKLQEEER            | 4 P08708  | RS17_HUM | 72  |

|           |                           |           |          |      |
|-----------|---------------------------|-----------|----------|------|
| Structure | LGNDFHTNKR                | 8 P08708  | RS17_HUM | 32   |
| Structure | AVLKFAAATGATPIAGR         | 3 P08865  | RSSA_HUM | 89   |
| Phyre     | LQAEIDNIKNQR              | 8 P08729  | K2C7_HUM | 326  |
| Phyre     | AKLEAAIAEAEER             | 1 P08729  | K2C7_HUM | 331  |
|           | LLETKWTLQEQK              | 4 P08729  | K2C7_HUM | 122  |
| Phyre     | AKQEELEAALQR              | 1 P08729  | K2C7_HUM | 353  |
| Phyre     | LQAEIDNIKNQR              | 8 P08729  | K2C7_HUM | 326  |
|           | VELEAKVDALNDEINFLR        | 5 P08729  | K2C7_HUM | 214  |
|           | VELEAKVDALNDEINFLR        | 5 P08729  | K2C7_HUM | 214  |
| Phyre     | AEAEAWYQTKFETLQAQAGK      | 9 P08729  | K2C7_HUM | 286  |
| Phyre     | AKLEAAIAEAEER             | 1 P08729  | K2C7_HUM | 331  |
| Phyre     | AQYEEMAKCSR               | 7 P08729  | K2C7_HUM | 273  |
| Phyre     | FLEQQNKLLET               | 6 P08729  | K2C7_HUM | 117  |
| Phyre     | LQAEIDNIKNQR              | 8 P08729  | K2C7_HUM | 326  |
| Phyre     | AKLEAAIAEAEER             | 1 P08729  | K2C7_HUM | 331  |
| Docking   | LQAEIDNIKNQR              | 8 P08729  | K2C7_HUM | 326  |
|           | SELTGKFEK                 | 5 P08758  | ANXA5_HU | 76   |
| Structure | FNAHGDANTIVCNSKDGGAWGTEQR | 14 P09382 | LEG1_HUM | 64   |
| Structure | FNAHGDANTIVCNSKDGGAWGTEQR | 14 P09382 | LEG1_HUM | 64   |
| Structure | IKGEHPGLSIGDVAK           | 1 P09429  | HMGB1_HI | 114  |
| Structure | GKMSSYAFFVQTCR            | 1 P09429  | HMGB1_HI | 12   |
| Structure | KHPDASVNFSEFSK            | 0 P09429  | HMGB1_HI | 30   |
| Structure | KHPDASVNFSEFSK            | 0 P09429  | HMGB1_HI | 30   |
| Phyre     | AIKELEEWYAR               | 2 P09496  | CLCA_HUM | 141  |
|           | SVLISLKQAPLVH             | 6 P09496  | CLCA_HUM | 242  |
| Phyre     | KQEAWEK                   | 6 P09496  | CLCA_HUM | 136  |
|           | IAAYLFKGNNR               | 6 Q00610  | CLH1_HUM | 1516 |
| Phyre     | EVCFACVDGKEFR             | 9 Q00610  | CLH1_HUM | 1264 |
|           | DSLYKDAMQYASESK           | 4 Q00610  | CLH1_HUM | 1535 |
|           | DSLYKDAM[147.04]QYASESK   | 4 Q00610  | CLH1_HUM | 1535 |
|           | MYDAAKLLYNNVSNFGR         | 5 Q00610  | CLH1_HUM | 1215 |
|           | LLPGEAKHAVSEGK            | 8 Q93079  | H2B1H_HU | 109  |
|           | SVLMSLKQTPLSR             | 6 P09497  | CLCB_HUM | 223  |
|           | SVLM[147.04]SLKQTPLSR     | 6 P09497  | CLCB_HUM | 223  |
| Structure | SEEQLKEEGIEYK             | 5 P09622  | DLDH_HUM | 410  |
| Structure | AKTNADTDGMVK              | 1 P09622  | DLDH_HUM | 430  |
| Structure | AKTNADTDGM[147.04]VK      | 1 P09622  | DLDH_HUM | 430  |
| Structure | RPFTKNLGLEELGIELDPR       | 4 P09622  | DLDH_HUM | 320  |
|           | DPNTR                     | 4 P09651  | ROA1_HUM | 52   |
| Structure | KLFIGGLSFETTDESLR         | 0 P09651  | ROA1_HUM | 15   |
| Phyre     | SSGPYGGGGQYFAKPR          | 13 P09651 | ROA1_HUM | 350  |
| Phyre     | SSGPYGGGGQYFAKPR          | 13 P09651 | ROA1_HUM | 350  |
| Structure | KLFIGGLSFETTDESLR         | 0 P09651  | ROA1_HUM | 15   |
|           | KLFIGGLSFETTDESLR         | 0 P09651  | ROA1_HUM | 15   |
|           | SSGPYGGGGQYFAKPR          | 13 P09651 | ROA1_HUM | 350  |
| Structure | KLFIGGLSFETTDESLR         | 0 P09651  | ROA1_HUM | 15   |
| Phyre     | SSGPYGGGGQYFAKPR          | 13 P09651 | ROA1_HUM | 350  |

|           |                               |    |        |           |      |
|-----------|-------------------------------|----|--------|-----------|------|
| Structure | SSGPYGGGGQYFAKPR              | 13 | P09651 | ROA1_HUN  | 350  |
| Structure | SSGPYGGGGQYFAKPR              | 13 | P09651 | ROA1_HUN  | 350  |
|           | SSGPYGGGGQYFAKPR              | 13 | P09651 | ROA1_HUN  | 350  |
|           | GEIIAKQGGGGGGGSPVPIER         | 5  | P52272 | HNRPM_HI  | 388  |
| Phyre     | SSGPYGGGGQYFAKPR              | 13 | P09651 | ROA1_HUN  | 350  |
|           | NQSQGYNQWQQGQFWGQKPWSQHYF     | 17 | Q00839 | HNRPU_HL  | 814  |
| Phyre     | SSGPYGGGGQYFAKPR              | 13 | P09651 | ROA1_HUN  | 350  |
|           | GGPSPGDVEAIKNAIANASTLAEVER    | 11 | P09661 | RU2A_HUN  | 205  |
|           | TLGDFAAEYAKSNR                | 10 | P09874 | PARP1_HU  | 119  |
| Structure | VGTVIGSNKLEQMPSK              | 8  | P09874 | PARP1_HU  | 600  |
| Structure | VGTVIGSNKLEQMPSKEDIAEHFMK     | 8  | P09874 | PARP1_HU  | 600  |
| Structure | MECEPIDCEEGWALLKCGGK          | 15 | P09914 | IFIT1_HUM | 151  |
| Phyre     | AVTKYTSSK                     | 3  | Q93079 | H2B1H_HU  | 121  |
| Phyre     | MVQEAEKYKADEVQR               | 6  | P0DMV8 | HS71A_HU  | 524  |
| Phyre     | M[147.04]VQEAEKYKADEVQR       | 6  | P0DMV8 | HS71A_HU  | 524  |
| Phyre     | MVQEAEKYKADEVQR               | 6  | P0DMV8 | HS71A_HU  | 524  |
| Phyre     | M[147.04]VQEAEKYKADEVQR       | 6  | P0DMV8 | HS71A_HU  | 524  |
| Structure | STLEPVEKALR                   | 7  | P0DMV8 | HS71A_HU  | 319  |
| Phyre     | ITITNDKGR                     | 6  | P0DMV8 | HS71A_HU  | 507  |
| Phyre     | MVQEAEKYKADEVQR               | 6  | P0DMV8 | HS71A_HU  | 524  |
| Structure | KFGDPVVQSDMK                  | 0  | P0DMV8 | HS71A_HU  | 77   |
| Structure | EAFSLFDKDGDTITTKELGTVMR       | 16 | P0DP23 | CALM1_HL  | 31   |
| Structure | GYDQSAYDGKDIALNEDLR           | 9  | P10321 | 1C07_HUN  | 145  |
| Structure | GYDQSAYDGKDIALNEDLR           | 9  | P10321 | 1C07_HUN  | 145  |
| Modeller  | AASGEAKPKAK                   | 8  | P10412 | H14_HUM   | 119  |
| Modeller  | AAKPKTAKPKAAKPK               | 12 | P10412 | H14_HUM   | 210  |
| Modeller  | KASGPPVSELITK                 | 0  | P10412 | H14_HUM   | 34   |
| Unknown   | SKISVNDFIIK                   | 1  | P10515 | ODP2_HUN  | 473  |
|           | AWTSKSGSPLSPSIQSR             | 4  | P10586 | PTPRF_HUI | 994  |
|           | ADEARPNTIDFGKDDQHFTVTGLHKGTTY | 24 | P10586 | PTPRF_HUI | 884  |
|           | DDQHFTVTGLHKGTTYIFR           | 11 | P10586 | PTPRF_HUI | 884  |
|           | FTLTGLKPDTTYDIKVR             | 14 | P10586 | PTPRF_HUI | 987  |
|           | ADEARPNTIDFGKDDQHFTVTGLHK     | 12 | P10586 | PTPRF_HUI | 872  |
| Structure | VKCDQYWPAPR                   | 1  | P10586 | PTPRF_HUI | 1459 |
|           | FTLTGLKPDTTYDIK               | 6  | P10586 | PTPRF_HUI | 979  |
|           | FTLTGLKPDTTYDIK               | 6  | P10586 | PTPRF_HUI | 979  |
| Phyre     | DDQHFTVTGLHKGTTYIFR           | 11 | P10586 | PTPRF_HUI | 884  |
| Structure | MIKPFHSLSEK                   | 2  | P10599 | THIO_HUM  | 39   |
| Modeller  | VGEFSGANKEKLEATINELV          | 10 | P10599 | THIO_HUM  | 96   |
| Phyre     | QKLFQEDDEIPLYLK               | 1  | P14406 | CX7A2_HU  | 33   |
| Structure | LKVGLQVVAVK                   | 1  | P10809 | CH60_HUN  | 292  |
| Structure | GYISPYFINTSKGQK               | 11 | P10809 | CH60_HUN  | 233  |
| Structure | TVIIEQSWGSPKVTK               | 11 | P10809 | CH60_HUN  | 72   |
| Structure | DKYKNIGAK                     | 3  | P10809 | CH60_HUN  | 91   |
| Structure | ISKGANPVEIR                   | 2  | P10809 | CH60_HUN  | 133  |
| Structure | DKYKNIGAK                     | 3  | P10809 | CH60_HUN  | 91   |
| Structure | DVKFGADAR                     | 2  | P10809 | CH60_HUN  | 31   |

|           |                          |           |          |     |
|-----------|--------------------------|-----------|----------|-----|
| Structure | ISKGANPVEIR              | 2 P10809  | CH60_HUN | 133 |
| Structure | SIAKEGF EK               | 3 P10809  | CH60_HUN | 125 |
| Structure | CIPALDSLTPANEDQKIGIEI IK | 15 P10809 | CH60_HUN | 462 |
| Structure | DKYKNIGAK                | 3 P10809  | CH60_HUN | 91  |
| Structure | IGIEI IKR                | 6 P10809  | CH60_HUN | 469 |
| Structure | TLKIPAMTI AK             | 2 P10809  | CH60_HUN | 473 |
| Structure | TLKIPAM[147.04]TI AK     | 2 P10809  | CH60_HUN | 473 |
| Structure | KPLVIIAEDVDGEALSTLV LNR  | 0 P10809  | CH60_HUN | 269 |
| Structure | DGKTLNDELEIIEGMK         | 2 P10809  | CH60_HUN | 205 |
| Structure | ISKGANPVEIR              | 2 P10809  | CH60_HUN | 133 |
| Structure | TLKIPAMTI AK             | 2 P10809  | CH60_HUN | 473 |
| Structure | TLKIPAM[147.04]TI AK     | 2 P10809  | CH60_HUN | 473 |
| Structure | ISKGANPVEIR              | 2 P10809  | CH60_HUN | 133 |
| Structure | TLKIPAMTI AK             | 2 P10809  | CH60_HUN | 473 |
| Structure | TLKIPAM[147.04]TI AK     | 2 P10809  | CH60_HUN | 473 |
| Structure | EIGNIISDAMKK             | 10 P10809 | CH60_HUN | 191 |
| Structure | GQKCEFQDAYVLLSEK         | 2 P10809  | CH60_HUN | 236 |
| Structure | GVMLAVDAVIAELKK          | 13 P10809 | CH60_HUN | 156 |
| Structure | GVM[147.04]LAVDAVIAELKK  | 13 P10809 | CH60_HUN | 156 |
| Structure | GYISPYFINTSKGQK          | 11 P10809 | CH60_HUN | 233 |
| Structure | IQEII EQLDVTTSEYEKEK     | 16 P10809 | CH60_HUN | 387 |
| Structure | IQEII EQLDVTTSEYEKEKLNER | 16 P10809 | CH60_HUN | 387 |
| Structure | TLNDELEIIEGMKFDR         | 12 P10809 | CH60_HUN | 218 |
| Structure | DGVTVAKSIDLK             | 6 P10809  | CH60_HUN | 82  |
| Structure | GYISPYFINTSKGQK          | 11 P10809 | CH60_HUN | 233 |
| Structure | TVIIEQSWGSPKVTK          | 11 P10809 | CH60_HUN | 72  |
| Structure | VGEVIVTKDDAMLLK          | 7 P10809  | CH60_HUN | 352 |
| Structure | DKYKNIGAK                | 3 P10809  | CH60_HUN | 91  |
| Structure | ISKGANPVEIR              | 2 P10809  | CH60_HUN | 133 |
| Structure | TLKIPAMTI AK             | 2 P10809  | CH60_HUN | 473 |
| Structure | DKYKNIGAK                | 3 P10809  | CH60_HUN | 91  |
| Structure | DVKFGADAR                | 2 P10809  | CH60_HUN | 31  |
| Structure | CIPALDSLTPANEDQKIGIEI IK | 15 P10809 | CH60_HUN | 462 |
| Structure | TLKIPAMTI AK             | 2 P10809  | CH60_HUN | 473 |
| Structure | GQKCEFQDAYVLLSEK         | 2 P10809  | CH60_HUN | 236 |
| Structure | GYISPYFINTSKGQK          | 11 P10809 | CH60_HUN | 233 |
| Structure | GYISPYFINTSKGQK          | 11 P10809 | CH60_HUN | 233 |
| Structure | TVIIEQSWGSPKVTK          | 11 P10809 | CH60_HUN | 72  |
| Structure | TVIIEQSWGSPKVTK          | 11 P10809 | CH60_HUN | 72  |
| Structure | ALMLQGVDLLADAVAVTMGPKGR  | 20 P10809 | CH60_HUN | 58  |
| Structure | GVMLAVDAVIAELKK          | 13 P10809 | CH60_HUN | 156 |
| Structure | GYISPYFINTSKGQK          | 11 P10809 | CH60_HUN | 233 |
| Structure | DKYKNIGAK                | 3 P10809  | CH60_HUN | 91  |
| Structure | DVKFGADAR                | 2 P10809  | CH60_HUN | 31  |
| Structure | ISKGANPVEIR              | 2 P10809  | CH60_HUN | 133 |
| Structure | SIAKEGF EK               | 3 P10809  | CH60_HUN | 125 |
| Structure | SIDLKDK                  | 4 P10809  | CH60_HUN | 87  |



|           |                                |    |        |           |     |
|-----------|--------------------------------|----|--------|-----------|-----|
| Structure | YKNIGAK                        | 1  | P10809 | CH60_HUN  | 91  |
|           | KPLVIIAEDVDGEALSTLVLR          | 0  | P10809 | CH60_HUN  | 269 |
| Structure | VGDKVLLPEYGGTK                 | 3  | P61604 | CH10_HUN  | 70  |
| Phyre     | KISSIQSIVPALEIANAHR            | 0  | P10809 | CH60_HUN  | 250 |
| Structure | AVQKLR                         | 3  | P11021 | BIP_HUMA  | 287 |
| Structure | KSQIFSTASDNQPTVTIK             | 0  | P11021 | BIP_HUMA  | 447 |
| Structure | KSDIDEIVLVGGSTR                | 0  | P11021 | BIP_HUMA  | 353 |
| Structure | KKELEEIVQPIISK                 | 0  | P11021 | BIP_HUMA  | 620 |
| Structure | KSQIFSTASDNQPTVTIK             | 0  | P11021 | BIP_HUMA  | 447 |
| Structure | NKITITNDQNR                    | 1  | P11021 | BIP_HUMA  | 523 |
| Structure | NKITITNDQNR                    | 1  | P11021 | BIP_HUMA  | 523 |
| Structure | IINEPTAAAIAYGLDKR              | 15 | P11021 | BIP_HUMA  | 213 |
| Structure | IPKIQQLVK                      | 2  | P11021 | BIP_HUMA  | 370 |
| Structure | AVQKLR                         | 3  | P11021 | BIP_HUMA  | 287 |
| Structure | NKITITNDQNR                    | 1  | P11021 | BIP_HUMA  | 523 |
| Structure | GTLDPVEKALR                    | 7  | P11142 | HSP7C_HU  | 319 |
| Structure | FDDAVVQSDMKHWPFMVVNDAGRPK      | 10 | P11142 | HSP7C_HU  | 88  |
| Structure | LIGDAAKNQVAM[147.04]NPTNTVFDAR | 6  | P11142 | HSP7C_HU  | 56  |
| Structure | MVNHFIAEFKR                    | 9  | P11142 | HSP7C_HU  | 246 |
| Structure | M[147.04]VNHFIAEFKR            | 9  | P11142 | HSP7C_HU  | 246 |
| Structure | FDDAVVQSDMKHWPFMVVNDAGRPK      | 10 | P11142 | HSP7C_HU  | 88  |
| Structure | GTLDPVEKALR                    | 7  | P11142 | HSP7C_HU  | 319 |
| Phyre     | LSKEDIER                       | 2  | P11142 | HSP7C_HU  | 512 |
| Phyre     | IINEPTAAAIAYGLDKK              | 15 | P11142 | HSP7C_HU  | 187 |
| Phyre     | ITITNDKGR                      | 6  | P11142 | HSP7C_HU  | 507 |
| Structure | IINEPTAAAIAYGLDKK              | 15 | P11142 | HSP7C_HU  | 187 |
|           | ITITNDKGR                      | 6  | P11142 | HSP7C_HU  | 507 |
| Phyre     | LIGDAAKNQVAMNPTNTVFDAR         | 6  | P11142 | HSP7C_HU  | 56  |
| Structure | AEQWNVNVVETSAKTR               | 13 | P11233 | RALA_HUN  | 159 |
|           | VVESTKDLGR                     | 5  | P11277 | SPTB1_HUI | 981 |
| Structure | SDPDPKAPANK                    | 5  | P11310 | ACADM_HI  | 212 |
| Structure | AEEVATFFAKM[147.04]LDHEYTTK    | 9  | P11387 | TOP1_HUN  | 262 |
| Modeller  | NGYGAKLCNIFSTK                 | 5  | P11388 | TOP2A_HU  | 168 |
| Structure | LHGGKDSASPR                    | 4  | P11388 | TOP2A_HU  | 798 |
| Structure | KQSEPFKATPEEK                  | 7  | P11413 | G6PD_HUN  | 89  |
| Phyre     | IIAQKIYGADDIELLPEAQHK          | 4  | P11586 | C1TC_HUN  | 832 |
| Phyre     | IIAQKIYGADDIELLPEAQHK          | 4  | P11586 | C1TC_HUN  | 832 |
| Modeller  | EEAGKLDFCDGHSPAVTITFVCPSER     | 4  | P11717 | MPRI_HUN  | 271 |
| Modeller  | HAEPEQNWAEVDGSQTETEEK          | 19 | P11717 | MPRI_HUN  | 511 |
| Phyre     | KEFSPFGTITSAK                  | 0  | P11940 | PABP1_HU  | 312 |
| Phyre     | YQGVNLYVKNLDDGIDDER            | 8  | P11940 | PABP1_HU  | 299 |
| Phyre     | AKEFTNVYIK                     | 1  | P11940 | PABP1_HU  | 188 |
| Structure | AIEKMNGMMLLNR                  | 3  | P11940 | PABP1_HU  | 157 |
| Structure | AIEKMNGM[147.04]LLNDR          | 3  | P11940 | PABP1_HU  | 157 |
| Structure | AIEKM[147.04]NGMMLLNR          | 3  | P11940 | PABP1_HU  | 157 |
| Structure | AIEKM[147.04]NGM[147.04]LLNDR  | 3  | P11940 | PABP1_HU  | 157 |
| Phyre     | AKEFTNVYIK                     | 1  | P11940 | PABP1_HU  | 188 |

|           |                         |           |          |     |
|-----------|-------------------------|-----------|----------|-----|
| Structure | KSGVGNIFIKNLDK          | 9 P11940  | PABP1_HU | 104 |
| Structure | NLDKSIDNK               | 3 P11940  | PABP1_HU | 108 |
| Structure | SGVGNIFIKNLDK           | 8 P11940  | PABP1_HU | 104 |
| Phyre     | YQGVNLYVKNLDDGIDDER     | 8 P11940  | PABP1_HU | 299 |
| Phyre     | YQGVNLYVKNLDDGIDDERLR   | 8 P11940  | PABP1_HU | 299 |
|           | ILKCAGNEDIITLR          | 2 P12004  | PCNA_HUN | 80  |
| Structure | ILKCAGNEDIITLR          | 2 P12004  | PCNA_HUN | 80  |
| Structure | ILKCAGNEDIITLR          | 2 P12004  | PCNA_HUN | 80  |
|           | LKAQLGPDESK             | 1 P12081  | SYHC_HUN | 42  |
| Phyre     | DFLAGGIAAAISKTAVER      | 12 P12236 | ADT3_HUN | 23  |
| Phyre     | AFFKGAWSNVLR            | 3 P12236  | ADT3_HUN | 272 |
| Phyre     | DFLAGGIAAAISKTAVER      | 12 P12236 | ADT3_HUN | 23  |
| Phyre     | IPKEQGVLSFWR            | 2 P12236  | ADT3_HUN | 63  |
| Phyre     | KGADIMYTGTVDCWR         | 0 P12236  | ADT3_HUN | 245 |
| Phyre     | KGADIM[147.04]YTGTVDCWR | 0 P12236  | ADT3_HUN | 245 |
| Docking   | LAADVKGSGTER            | 6 P12236  | ADT3_HUN | 147 |
| Phyre     | LLLQVQHASKQIAADK        | 9 P12236  | ADT3_HUN | 43  |
| Phyre     | DFLAGGIAAAISKTAVER      | 12 P12236 | ADT3_HUN | 23  |
| Phyre     | DFLAGGIAAAISKTAVER      | 12 P12236 | ADT3_HUN | 23  |
| Phyre     | LPEASQSPLVLKQAVR        | 11 Q13330 | MTA1_HUN | 527 |
| Phyre     | KGADIMYTGTVDCWR         | 0 P12236  | ADT3_HUN | 245 |
|           | KYEQGFITDPVVLSPK        | 0 P12268  | IMDH2_HU | 109 |
|           | YFSEADKIK               | 6 P12268  | IMDH2_HU | 436 |
| Structure | DKYPNLQVIGGNVVTAQAQK    | 1 P12268  | IMDH2_HU | 293 |
| Phyre     | ICDQWDNLGALTQKR         | 13 P12814 | ACTN1_HU | 492 |
| Docking   | VHKISNVNK               | 2 P12814  | ACTN1_HU | 89  |
| Phyre     | VHKISNVNK               | 2 P12814  | ACTN1_HU | 89  |
|           | FTVPMLKEACR             | 6 P12956  | XRCC6_HU | 582 |
|           | IAAYKSILQER             | 4 P13010  | XRCC5_HU | 265 |
| Phyre     | KMPFTEK                 | 0 P12956  | XRCC6_HU | 445 |
| Structure | YGSDIVPFSKVDEEQMK       | 9 P13010  | XRCC5_HU | 325 |
| Structure | IAAYKSILQER             | 4 P13010  | XRCC5_HU | 265 |
| Phyre     | EKASWSSLSMDEK           | 1 P13073  | COX41_HU | 67  |
| Phyre     | VFSGLVSTGLKVR           | 10 P13639 | EF2_HUMA | 426 |
| Phyre     | FAAKGEGQLGPAER          | 3 P13639  | EF2_HUMA | 239 |
| Phyre     | FAAKGEGQLGPAER          | 3 P13639  | EF2_HUMA | 239 |
| Phyre     | ETVSEESNVCLSKSPNK       | 13 P13639 | EF2_HUMA | 594 |
| Phyre     | EDLYLKPIQR              | 5 P13639  | EF2_HUMA | 445 |
| Phyre     | EDLYLKPIQR              | 5 P13639  | EF2_HUMA | 445 |
| Phyre     | VFSGLVSTGLKVR           | 10 P13639 | EF2_HUMA | 426 |
| Phyre     | FAAKGEGQLGPAER          | 3 P13639  | EF2_HUMA | 239 |
| Phyre     | FSKSATSPEGK             | 2 P13639  | EF2_HUMA | 275 |
| Phyre     | KVEDMM[147.04]K         | 0 P13639  | EF2_HUMA | 252 |
| Phyre     | KVEDM[147.04]MK         | 0 P13639  | EF2_HUMA | 252 |
| Phyre     | KVEDM[147.04]M[147.04]K | 0 P13639  | EF2_HUMA | 252 |
| Phyre     | LIEKLDIK                | 3 P13639  | EF2_HUMA | 318 |
| Phyre     | VAVEAKNPADLPK           | 5 P13639  | EF2_HUMA | 512 |

|           |                              |           |           |      |
|-----------|------------------------------|-----------|-----------|------|
|           | FAAKGEGQLGPAER               | 3 P13639  | EF2_HUMA  | 239  |
|           | LIEKLDIK                     | 3 P13639  | EF2_HUMA  | 318  |
|           | QFAEMYVAKFAAK                | 8 P13639  | EF2_HUMA  | 235  |
|           | QFAEM[147.04]YVAKFAAK        | 8 P13639  | EF2_HUMA  | 235  |
|           | FAAKGEGQLGPAER               | 3 P13639  | EF2_HUMA  | 239  |
|           | FSKSATSPEGK                  | 2 P13639  | EF2_HUMA  | 275  |
|           | LIEKLDIK                     | 3 P13639  | EF2_HUMA  | 318  |
|           | QFAEMYVAKFAAK                | 8 P13639  | EF2_HUMA  | 235  |
|           | LIEKLDIK                     | 3 P13639  | EF2_HUMA  | 318  |
|           | FAAKGEGQLGPAER               | 3 P13639  | EF2_HUMA  | 239  |
|           | LIEKLDIK                     | 3 P13639  | EF2_HUMA  | 318  |
| Phyre     | FAAKGEGQLGPAER               | 3 P13639  | EF2_HUMA  | 239  |
| Phyre     | QFAEMYVAKFAAK                | 8 P13639  | EF2_HUMA  | 235  |
| Phyre     | QFAEM[147.04]YVAKFAAK        | 8 P13639  | EF2_HUMA  | 235  |
| Phyre     | FAAKGEGQLGPAER               | 3 P13639  | EF2_HUMA  | 239  |
| Phyre     | LIEKLDIK                     | 3 P13639  | EF2_HUMA  | 318  |
| Phyre     | QFAEMYVAKFAAK                | 8 P13639  | EF2_HUMA  | 235  |
| Phyre     | DLEEDHACIPIKK                | 11 P13639 | EF2_HUMA  | 571  |
| Phyre     | KEDLYLKPIQR                  | 0 P13639  | EF2_HUMA  | 439  |
| Phyre     | KEDLYLKPIQR                  | 6 P13639  | EF2_HUMA  | 445  |
| Structure | EKYGIVDYMIEQSGPPSK           | 1 P13667  | PDIA4_HUI | 272  |
| Phyre     | FLKVSQGQLVVMQPEK             | 2 P13667  | PDIA4_HUI | 349  |
| Phyre     | YKVEGFPTIYFAPSGDK            | 1 P13667  | PDIA4_HUI | 596  |
| Phyre     | FQSKYEPR                     | 3 P13667  | PDIA4_HUI | 366  |
| Structure | IDINMSGFNETDDLKR             | 14 P13797 | PLST_HUM  | 335  |
| Phyre     | KLENCNYAVELGK                | 0 P13797  | PLST_HUM  | 459  |
| Structure | LGGEVSCLVAGTKCDK             | 12 P13804 | ETFA_HUM  | 59   |
|           | LANQFAIYKPVTDFFLQLVDAGK      | 8 P42704  | LPPRC_HUI | 1252 |
| Phyre     | YEFSNKGADVFLALAR             | 5 P13807  | GYS1_HUN  | 337  |
|           | LLCGKETMVTSTTEPSR            | 4 P14314  | GLU2B_HU  | 487  |
|           | LLCGKETM[147.04]VTSTTEPSR    | 4 P14314  | GLU2B_HU  | 487  |
|           | NKFEEAER                     | 1 P14314  | GLU2B_HU  | 376  |
| iTasser   | KLIELQAGK                    | 0 P14314  | GLU2B_HU  | 158  |
| Structure | TATESFASDPILYRPVAVALDTKGPEIR | 22 P14618 | KPYM_HUN  | 115  |
| Structure | KASDVHEVR                    | 0 P14618  | KPYM_HUN  | 247  |
| Structure | NICKVVEVGSK                  | 3 P14618  | KPYM_HUN  | 166  |
| Structure | NIKIISK                      | 2 P14618  | KPYM_HUN  | 266  |
| Structure | LNFSHGTHEYHAETIKNVR          | 15 P14618 | KPYM_HUN  | 89   |
| Structure | GATLKITLDNAYMEK              | 4 P14618  | KPYM_HUN  | 141  |
| Structure | GIFPVLCCKDPVQEAWAEDVDLR      | 7 P14618  | KPYM_HUN  | 475  |
| Structure | LNFSHGTHEYHAETIKNVR          | 15 P14618 | KPYM_HUN  | 89   |
| Phyre     | VFITDDFHDMMMPKYLNFBK         | 12 P14625 | ENPL_HUN  | 428  |
| Structure | ELISNASDALDKIR               | 11 P14625 | ENPL_HUN  | 114  |
| Phyre     | QDKIYFMAGSSR                 | 2 P14625  | ENPL_HUN  | 537  |
|           | FQNVAKEGVK                   | 5 P14625  | ENPL_HUN  | 593  |
| Phyre     | QDKIYFMAGSSR                 | 2 P14625  | ENPL_HUN  | 537  |
| Phyre     | AQAYQTGKDISTNYYASQK          | 7 P14625  | ENPL_HUN  | 671  |

|           |                                  |           |           |      |
|-----------|----------------------------------|-----------|-----------|------|
| Phyre     | ELISNASDALDKIR                   | 11 P14625 | ENPL_HUN  | 114  |
| Phyre     | NLGTIAKSGTSEFLNK                 | 6 P14625  | ENPL_HUN  | 168  |
| Phyre     | VFITDDFHDMMMPKYLNFVK             | 12 P14625 | ENPL_HUN  | 428  |
| Phyre     | AQAYQTGKDISTNYYASQK              | 7 P14625  | ENPL_HUN  | 671  |
| Phyre     | KSDYIK                           | 0 P14625  | ENPL_HUN  | 405  |
| Phyre     | VFITDDFHDMMMPKYLNFVK             | 12 P14625 | ENPL_HUN  | 428  |
| Phyre     | AQAYQTGKDISTNYYASQK              | 7 P14625  | ENPL_HUN  | 671  |
| Phyre     | DISTNYYASQKK                     | 10 P14625 | ENPL_HUN  | 682  |
| Phyre     | SGYLLPDTKAYGDR                   | 8 P14625  | ENPL_HUN  | 733  |
| Phyre     | IADDKYNDFWKEFGTNIK               | 11 P14625 | ENPL_HUN  | 486  |
| Phyre     | SGYLLPDTKAYGDR                   | 8 P14625  | ENPL_HUN  | 733  |
| Phyre     | EELVKNLGTIAK                     | 4 P14625  | ENPL_HUN  | 161  |
| Phyre     | ELISNASDALDKIR                   | 11 P14625 | ENPL_HUN  | 114  |
| Phyre     | VFITDDFHDMMMPKYLNFVK             | 12 P14625 | ENPL_HUN  | 428  |
| Phyre     | AQAYQTGKDISTNYYASQK              | 7 P14625  | ENPL_HUN  | 671  |
| Phyre     | IEKAVVSQR                        | 2 P14625  | ENPL_HUN  | 633  |
| Phyre     | IMKAQAYQTGK                      | 2 P14625  | ENPL_HUN  | 663  |
| Phyre     | IM[147.04]KAQAYQTGK              | 2 P14625  | ENPL_HUN  | 663  |
| Phyre     | SGYLLPDTKAYGDR                   | 8 P14625  | ENPL_HUN  | 733  |
| Phyre     | KTLDMIK                          | 0 P14625  | ENPL_HUN  | 467  |
| Structure | KYSQFINFPIYVWSSK                 | 0 P14625  | ENPL_HUN  | 270  |
| Structure | EVNAVDSEHEKNVMNDAWR              | 10 P14735 | IDE_HUMA  | 192  |
| Structure | GWVNTLVGGQKEGAR                  | 10 P14735 | IDE_HUMA  | 364  |
| Structure | EVNAVDSEHEKNVMNDAWR              | 10 P14735 | IDE_HUMA  | 192  |
| Structure | IVPIKDIR                         | 4 P14735  | IDE_HUMA  | 308  |
| Structure | NPNGPYPYTLKLCFSTAQHAS            | 10 P14866 | HNRPL_HU  | 579  |
| Structure | FSTPEQAANKR                      | 8 P14866  | HNRPL_HU  | 493  |
| Phyre     | FSTPEQAANKR                      | 8 P14866  | HNRPL_HU  | 493  |
| Structure | YEEENFYLEPYLKEVIR                | 12 P14927 | QCR7_HUN  | 96   |
| Structure | NLVVIPKSVTPER                    | 6 P15121  | ALDR_HUN  | 263  |
| Structure | MPILGLGTWKSPPGQVTEAVK            | 9 P15121  | ALDR_HUN  | 22   |
| Phyre     | TIAIGKVLK                        | 5 P15170  | ERF3A_HUI | 490  |
| Phyre     | TIAIGKVLK                        | 5 P15170  | ERF3A_HUI | 490  |
| Phyre     | TIAIGKVLK                        | 5 P15170  | ERF3A_HUI | 490  |
| Structure | QISGFGKK                         | 6 P15529  | MCP_HUM   | 244  |
| Phyre     | AEDKEWMPVTK                      | 3 P15880  | RS2_HUMA  | 58   |
|           | QM[147.04]GQPCDAYQKR             | 10 P15924 | DESP_HUN  | 140  |
|           | IQESKNQCTQVVQER                  | 4 P15924  | DESP_HUN  | 1802 |
|           | SLLATMKTELQK                     | 6 P15924  | DESP_HUN  | 829  |
|           | LLEAASVSSKGLPSPYNMSSAPGSR        | 9 P15924  | DESP_HUN  | 2811 |
|           | LLEAASVSSKGLPSPYNM[147.04]SSAPG: | 9 P15924  | DESP_HUN  | 2811 |
|           | QQIQNDLNQWKQYSR                  | 10 P15924 | DESP_HUN  | 1868 |
|           | LQAEIKR                          | 5 P15924  | DESP_HUN  | 1907 |
|           | RVEEDIQQQKATGSEVSQR              | 9 P15924  | DESP_HUN  | 1434 |
| Structure | GLVGIEFKEK                       | 7 P15924  | DESP_HUN  | 2326 |
|           | LKNTLTQTENLR                     | 1 P15924  | DESP_HUN  | 1413 |
|           | FQNSLKELQLQK                     | 5 P15924  | DESP_HUN  | 1564 |

|           |                               |           |           |     |
|-----------|-------------------------------|-----------|-----------|-----|
| Structure | YVQKGEYR                      | 3 P16070  | CD44_HUN  | 158 |
| Structure | ALKSCSPELQQK                  | 2 P16152  | CBR1_HUN  | 148 |
| Structure | ALKSCSPELQQK                  | 2 P16152  | CBR1_HUN  | 148 |
| Modeller  | KATGPPVSELITK                 | 0 P16401  | H15_HUM   | 37  |
| Modeller  | KAASGEAKPK                    | 0 P16401  | H15_HUM   | 113 |
| Modeller  | KALAAGGYDVEK                  | 0 P16401  | H15_HUM   | 67  |
| Modeller  | GTGASGSFKLNK                  | 8 P16401  | H15_HUM   | 109 |
| Modeller  | NGLSLAALKK                    | 8 P16401  | H15_HUM   | 66  |
| Modeller  | GTGASGSFKLNKK                 | 11 P16403 | H12_HUM   | 109 |
| Modeller  | KASGPPVSELITK                 | 0 P16403  | H12_HUM   | 34  |
| Modeller  | KALAAAGYDVEK                  | 0 P16403  | H12_HUM   | 64  |
| Modeller  | SGVSLAALKK                    | 8 P16403  | H12_HUM   | 63  |
|           | ALAAAGYDVEKNNSR               | 10 P16403 | H12_HUM   | 75  |
| Modeller  | GTLVQTKGTGASGSFK              | 6 P16403  | H12_HUM   | 97  |
| Modeller  | SGVSLAALKK                    | 8 P16403  | H12_HUM   | 63  |
| Modeller  | GTLVQTKGTGASGSFK              | 6 P16403  | H12_HUM   | 97  |
| Modeller  | KASGPPVSELITK                 | 0 P16403  | H12_HUM   | 34  |
| Structure | SGVSLAALKK                    | 8 P16403  | H12_HUM   | 63  |
| Structure | INKGVATNWLR                   | 2 P16435  | NCPR_HUN  | 487 |
| Phyre     | IGIFGQDEDVTSKFTGR             | 12 P16615 | AT2A2_HU  | 650 |
| Phyre     | NYLEPGKECVQPATK               | 6 P16615  | AT2A2_HU  | 995 |
| Phyre     | LTSIKSTTLR                    | 4 P16615  | AT2A2_HU  | 169 |
|           | IGIFGQDEDVTSKFTGR             | 12 P16615 | AT2A2_HU  | 650 |
| Phyre     | ITLVNKNQAIIKL                 | 5 P17301  | ITA2_HUM  | 671 |
| Phyre     | IFSGPSSEQFGYAVQQFINPKGNWLLVGS | 20 P17301 | ITA2_HUM  | 59  |
| Structure | EIKAIASIPTR                   | 2 P17301  | ITA2_HUM  | 330 |
| Structure | VVFNLNTYKTK                   | 8 P17301  | ITA2_HUM  | 230 |
| Structure | AALVYSDDKLER                  | 8 P17342  | ANPRC_HU  | 208 |
| Structure | STCIYGGAPKGPQIR               | 9 P17844  | DDX5_HUN  | 207 |
| Phyre     | NVIFQPVAEKK                   | 10 Q01813 | PFKAP_HUI | 736 |
| Structure | TLPKGQLESIVENIR               | 3 P17858  | PFKAL_HUI | 474 |
| Structure | EKFENLGIQPPK                  | 1 P17980  | PRS6A_HUI | 211 |
| Phyre     | SLLVIPNTLAVNAAQDSTDLVAKLR     | 22 P17987 | TCPA_HUN  | 466 |
| Phyre     | SLKFATEAAITILR                | 2 P17987  | TCPA_HUN  | 515 |
| Phyre     | SLLVIPNTLAVNAAQDSTDLVAKLR     | 22 P17987 | TCPA_HUN  | 466 |
| Phyre     | ANEVISKLYAVHQEGNK             | 6 P50990  | TCPQ_HUN  | 466 |
| Phyre     | TSLGPKGM[147.04]DK            | 5 P50991  | TCPD_HUN  | 55  |
| Phyre     | SLKFATEAAITILR                | 2 P17987  | TCPA_HUN  | 515 |
| Phyre     | STLGPKGMDK                    | 5 P78371  | TCPB_HUN  | 46  |
| Phyre     | STLGPKGM[147.04]DK            | 5 P78371  | TCPB_HUN  | 46  |
| Phyre     | SNLPAKAIGHR                   | 5 P18077  | RL35A_HUI | 95  |
|           | THQKFVIATSTK                  | 3 Q02878  | RL6_HUM   | 192 |
| Phyre     | KDALHLLVFTDDVPHIALDGK         | 0 P18084  | ITB5_HUM  | 267 |
| Phyre     | KDALHLLVFTDDVPHIALDGK         | 0 P18084  | ITB5_HUM  | 267 |
| Phyre     | SLGTKLAEEMR                   | 4 P18084  | ITB5_HUM  | 163 |
| Phyre     | KVLQLLR                       | 0 P18124  | RL7_HUM   | 107 |
| Phyre     | FKEANNFLWPFK                  | 1 P18124  | RL7_HUM   | 202 |

|           |                                |           |          |     |
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| Phyre     | GINGVSPKVR                     | 7 P18124  | RL7_HUMA | 104 |
| Phyre     | KAGNFYVPAEPK                   | 0 P18124  | RL7_HUMA | 77  |
| Structure | EAVKAASDELSK                   | 3 P18206  | VINC_HUM | 784 |
|           | KSAEFLHMLKNAESNAELK            | 10 P18621 | RL17_HUM | 96  |
| Phyre     | ETAQAIKGMHIR                   | 6 P18621  | RL17_HUM | 37  |
| Structure | YADLTEDQLPSCESLKDTIAR          | 15 P18669 | PGAM1_HI | 157 |
| Structure | FSGWYDADLSPAGHEEAKR            | 17 P18669 | PGAM1_HI | 39  |
| Structure | HYGGTLGLNKAETAAK               | 9 P18669  | PGAM1_HI | 100 |
| Structure | HYGGTLGLNKAETAAK               | 9 P18669  | PGAM1_HI | 100 |
| Structure | DKVAELENSEFR                   | 1 P19256  | LFA3_HUM | 62  |
|           | AAVTPGKK                       | 6 P19338  | NUCL_HUN | 87  |
|           | VAVATPAKK                      | 7 P19338  | NUCL_HUN | 79  |
| Structure | KFGYVDFESAEDLEK                | 0 P19338  | NUCL_HUN | 348 |
| Structure | TGISDVFAKNDLAVVDVR             | 8 P19338  | NUCL_HUN | 333 |
| Phyre     | GGKNSTWSGESK                   | 2 P19338  | NUCL_HUN | 477 |
| Phyre     | TLLAKNLPYK                     | 4 P19338  | NUCL_HUN | 398 |
| Phyre     | EAMEDGEIDGNKVTLDWAKPK          | 18 P19338 | NUCL_HUN | 646 |
|           | KAAATPAKK                      | 0 P19338  | NUCL_HUN | 88  |
|           | KAAATPAK                       | 0 P19338  | NUCL_HUN | 88  |
| Structure | KFGYVDFESAEDLEK                | 0 P19338  | NUCL_HUN | 348 |
| Structure | SKGIAYIEFK                     | 1 P19338  | NUCL_HUN | 429 |
| Structure | TLLAKNLPYK                     | 4 P19338  | NUCL_HUN | 398 |
| Structure | KFGYVDFESAEDLEK                | 0 P19338  | NUCL_HUN | 348 |
| Phyre     | GGKNSTWSGESK                   | 2 P19338  | NUCL_HUN | 477 |
| Structure | KFGYVDFESAEDLEK                | 0 P19338  | NUCL_HUN | 348 |
| Structure | TLLAKNLPYK                     | 4 P19338  | NUCL_HUN | 398 |
| Phyre     | GLSEDTEETLKESFDGFSVR           | 11 P19338 | NUCL_HUN | 589 |
| Phyre     | TLLAKNLPYK                     | 4 P19338  | NUCL_HUN | 398 |
| Phyre     | ETGSSKGFGFVDFNSEEDAK           | 5 P19338  | NUCL_HUN | 610 |
| Phyre     | GGKNSTWSGESK                   | 2 P19338  | NUCL_HUN | 477 |
| Structure | KFGYVDFESAEDLEK                | 0 P19338  | NUCL_HUN | 348 |
| Structure | SAPELKTGISDVFAK                | 5 P19338  | NUCL_HUN | 324 |
| Structure | SISLYTGEKGQNQDYR               | 9 P19338  | NUCL_HUN | 467 |
| Phyre     | SKGYAFIEFASFEDAK               | 1 P19338  | NUCL_HUN | 523 |
| Docking   | TLLAKNLPYK                     | 4 P19338  | NUCL_HUN | 398 |
| Structure | KFGYVDFESAEDLEK                | 0 P19338  | NUCL_HUN | 348 |
| Phyre     | ETGSSKGFGFVDFNSEEDAK           | 5 P19338  | NUCL_HUN | 610 |
| Phyre     | TLFVKGLSEDTEETLK               | 4 P19338  | NUCL_HUN | 577 |
| Structure | DTPENNPDPFDFTPENYKR            | 18 P19404 | NDUV2_HI | 61  |
| Phyre     | DLIKDLK                        | 3 P50995  | ANX11_HU | 252 |
|           | LQFSLKK                        | 5 P20290  | BTF3_HUM | 93  |
| Structure | LTDKTVIGCSGFHGDCLTLTK          | 3 P20618  | PSB1_HUM | 77  |
| Structure | LVKDVFISSAER                   | 2 P20618  | PSB1_HUM | 204 |
| Structure | EVLEKQPVLSQTEAR                | 4 P28070  | PSB4_HUM | 201 |
|           | AGGSASAMLQPLLDNQVGFKNMQNVEH    | 19 P20618 | PSB1_HUM | 184 |
|           | AGGSASAMLQPLLDNQVGFKNM[147.04] | 19 P20618 | PSB1_HUM | 184 |
|           | AGGSASAM[147.04]LQPLLDNQVGFKNI | 19 P20618 | PSB1_HUM | 184 |

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|-----------|--------------------------------|----|--------|----------|------|
| Structure | LDFLRPYTVPNKK                  | 11 | Q99436 | PSB7_HUM | 237  |
| Phyre     | TCDLVGEKGK                     | 7  | P20645 | MPRD_HUI | 38   |
| Phyre     | GGDEYDNHCGKEQR                 | 10 | P20645 | MPRD_HUI | 134  |
| Docking   | ELTGLKALYETELADAR              | 5  | P20700 | LMNB1_HL | 79   |
|           | AEHDQLLLNYAKK                  | 11 | P20700 | LMNB1_HL | 123  |
| Structure | VILKNSQGEEVAQR                 | 3  | P20700 | LMNB1_HL | 532  |
|           | KLLEGEEER                      | 0  | P20700 | LMNB1_HL | 379  |
|           | LAVYIDKVR                      | 6  | P20700 | LMNB1_HL | 49   |
|           | KLLEGEEER                      | 0  | P20700 | LMNB1_HL | 379  |
|           | GLGLSKAYVGQK                   | 5  | P21333 | FLNA_HUM | 2569 |
|           | NDNDTFTVKYTPR                  | 8  | P21333 | FLNA_HUM | 837  |
|           | VDVGKDQEFTVKSK                 | 11 | P21333 | FLNA_HUM | 994  |
|           | VKVEPSHDASK                    | 1  | P21333 | FLNA_HUM | 865  |
|           | AYVGQKSSFTVDCSK                | 5  | P21333 | FLNA_HUM | 2575 |
| Structure | MKVIYPAVEGR                    | 1  | P21589 | 5NTD_HUN | 536  |
| Structure | VTQSNFAVGKYKTDEFQLHTNVNDGTEFGI | 10 | P21796 | VDAC1_HU | 174  |
| Structure | DVFTKGYGFGLIK                  | 4  | P21796 | VDAC1_HU | 20   |
| Structure | LTFDSSFSPNTGKK                 | 12 | P21796 | VDAC1_HU | 109  |
| Structure | NVNAGGHKLGLGLEFQA              | 7  | P21796 | VDAC1_HU | 274  |
| Structure | YQIDPDACFSAKVNNSLIGLGYTQTLKPG  | 11 | P21796 | VDAC1_HU | 236  |
| Structure | NVNAGGHKLGLGLEFQA              | 7  | P21796 | VDAC1_HU | 274  |
| Structure | SENGLEFTSSGSANTETTKVTGSLETK    | 18 | P21796 | VDAC1_HU | 53   |
| Structure | TKSENGLEFTSSGSANTETTKVTGSLETK  | 20 | P21796 | VDAC1_HU | 53   |
| Structure | LTFDSSFSPNTGKK                 | 12 | P21796 | VDAC1_HU | 109  |
| Structure | DVFTKGYGFGLIK                  | 4  | P21796 | VDAC1_HU | 20   |
| Phyre     | ETLKAIHYALNCCGLAGGVEQFISDICPK  | 3  | P21926 | CD9_HUM/ | 144  |
| Phyre     | DTYNKLLK                       | 4  | P21926 | CD9_HUM/ | 131  |
| Phyre     | ETLKAIHYALNCCGLAGGVEQFISDICPK  | 3  | P21926 | CD9_HUM/ | 144  |
| Phyre     | EVQEFYKDTYNK                   | 6  | P21926 | CD9_HUM/ | 126  |
| Phyre     | KDVLETFTVK                     | 0  | P21926 | CD9_HUM/ | 170  |
| Phyre     | SSKASLSLEGEAEAEASSPKGK         | 20 | Q09666 | AHNK_HUM | 5765 |
| Structure | KGTVLLADNVICPGAPDFLAHVR        | 0  | P21964 | COMT_HUI | 212  |
|           | NLVPGESVYGEKR                  | 11 | P22087 | FBRL_HUM | 121  |
| Structure | VSISEGDDKIEYR                  | 8  | P22087 | FBRL_HUM | 131  |
|           | GNQSGKNVMVEPHR                 | 5  | P22087 | FBRL_HUM | 84   |
| Phyre     | VLPEKLGVDLDAQTWR               | 4  | P22102 | PUR2_HUM | 697  |
| Structure | SAGVQCFGPTAEAAQLESSKR          | 19 | P22102 | PUR2_HUM | 107  |
|           | KNFEWVAER                      | 0  | P22234 | PUR6_HUM | 247  |
| Docking   | IATGSFLKR                      | 7  | P22234 | PUR6_HUM | 110  |
| Structure | KNFEWVAER                      | 0  | P22234 | PUR6_HUM | 247  |
| Structure | EVYELLDSPGKVLLQSK              | 10 | P22234 | PUR6_HUM | 30   |
| Structure | TKEVYELLDSPGKVLLQSK            | 12 | P22234 | PUR6_HUM | 30   |
| Structure | V TSAHKGPDETLR                 | 5  | P22234 | PUR6_HUM | 304  |
| Structure | VVVLMSGSTDLGHCEKIK             | 15 | P22234 | PUR6_HUM | 283  |
| Unknown   | DLKEVTPEGLQMVK                 | 2  | P22234 | PUR6_HUM | 235  |
| Structure | VELLLKSESQCR                   | 5  | P22234 | PUR6_HUM | 261  |
| Structure | GIKLVVADTR                     | 2  | P22314 | UBA1_HUM | 185  |

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| Structure | TFIAIKPDGVQR              | 5 P22392  | NDKB_HUM | 12  |
| Structure | VMLGETNPADSKPGTIR         | 11 P22392 | NDKB_HUM | 100 |
| Structure | VM[147.04]LGETNPADSKPGTIR | 11 P22392 | NDKB_HUM | 100 |
| Structure | VMLGETNPADSKPGTIR         | 11 P22392 | NDKB_HUM | 100 |
| Structure | VMLGETNPADSKPGTIR         | 11 P22392 | NDKB_HUM | 100 |
| Structure | VMLGETNPADSKPGTIR         | 11 P22392 | NDKB_HUM | 100 |
| Phyre     | TATEKPGPAEAAR             | 4 P22570  | ADRO_HUM | 287 |
| Structure | EESGKPGAHVTVK             | 4 P22626  | ROA2_HUM | 104 |
| Structure | KLFIGGLSFETTEESLR         | 0 P22626  | ROA2_HUM | 22  |
| Structure | NYYEQWGKLTDCVVMR          | 7 P22626  | ROA2_HUM | 46  |
| Structure | NYYEQWGKLTDCVVM[147.04]R  | 7 P22626  | ROA2_HUM | 46  |
| Structure | VVEPKR                    | 4 P22626  | ROA2_HUM | 94  |
| Structure | KLFIGGLSFETTEESLR         | 0 P22626  | ROA2_HUM | 22  |
| Structure | EESGKPGAHVTVK             | 4 P22626  | ROA2_HUM | 104 |
| Structure | IVLQKYHTINGHNAEVR         | 4 P22626  | ROA2_HUM | 173 |
| Structure | KLFIGGLSFETTEESLR         | 0 P22626  | ROA2_HUM | 22  |
| Structure | NYYEQWGKLTDCVVMR          | 7 P22626  | ROA2_HUM | 46  |
| Structure | NYYEQWGKLTDCVVM[147.04]R  | 7 P22626  | ROA2_HUM | 46  |
| Structure | VVEPKR                    | 4 P22626  | ROA2_HUM | 94  |
| Docking   | KLFIGGLSFETTEESLR         | 0 P22626  | ROA2_HUM | 22  |
| Structure | EESGKPGAHVTVK             | 4 P22626  | ROA2_HUM | 104 |
| Structure | EESGKPGAHVTVK             | 4 P22626  | ROA2_HUM | 104 |
| Structure | EKEQFR                    | 1 P22626  | ROA2_HUM | 17  |
| Structure | KLFIGGLSFETTEESLR         | 0 P22626  | ROA2_HUM | 22  |
| Docking   | VVEPKR                    | 4 P22626  | ROA2_HUM | 94  |
| Structure | AAYNQVKTIAQGNLSNTDVQAAK   | 6 P22695  | QCR2_HUM | 359 |
| Structure | GGLGLSGAKANYR             | 8 P22695  | QCR2_HUM | 250 |
| Structure | GGLGLSGAKANYR             | 8 P22695  | QCR2_HUM | 250 |
| Structure | LFVGNLPADITEDEFKR         | 15 P23246 | SFPQ_HUM | 314 |
| Structure | YGEPGEVFINKGK             | 10 P23246 | SFPQ_HUM | 330 |
| Structure | GIVEFASKPAAR              | 7 P23246  | SFPQ_HUM | 421 |
| Structure | LAQKNPMYQK                | 3 P23246  | SFPQ_HUM | 466 |
| Structure | LAQKNPM[147.04]YQK        | 3 P23246  | SFPQ_HUM | 466 |
| Structure | GFGFIKLESR                | 5 P23246  | SFPQ_HUM | 338 |
| Structure | GIVEFASKPAAR              | 7 P23246  | SFPQ_HUM | 421 |
| Phyre     | RPGEKTYTQR                | 4 P23246  | SFPQ_HUM | 291 |
| Structure | GIVEFASKPAAR              | 7 P23246  | SFPQ_HUM | 421 |
| Structure | GIVEFASKPAAR              | 7 P23246  | SFPQ_HUM | 421 |
| Structure | LFVGNLPADITEDEFKR         | 15 P23246 | SFPQ_HUM | 314 |
| Structure | ALIEMEKQQQDQVDR           | 6 Q15233  | NONO_HUM | 279 |
| Structure | EKLEMEMEAAR               | 1 Q15233  | NONO_HUM | 295 |
| Structure | SEEKSDSEGFK               | 3 P23246  | SFPQ_HUM | 271 |
| Structure | VIFGLFGKTVPK              | 7 P23284  | PPIB_HUM | 67  |
| Structure | DKPLKDVIIADCGK            | 1 P23284  | PPIB_HUM | 192 |
|           | GDGTGGKSIYGER             | 6 P23284  | PPIB_HUM | 116 |
| Structure | TVDNFVALATGEKGFYK         | 12 P23284 | PPIB_HUM | 84  |
| Structure | TVPKTVDNFVALATGEK         | 3 P23284  | PPIB_HUM | 71  |



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| Structure | VIKDFM[147.04]IQGGDFTR     | 2 P23284  | PPIB_HUM  | 98  |
| Structure | VIFGLFGKTVPK               | 7 P23284  | PPIB_HUM  | 67  |
| Structure | DTNGSQFFITTVKTAWL DGK      | 12 P23284 | PPIB_HUM  | 158 |
| Structure | DKPLKDVIIADCGK             | 4 P23284  | PPIB_HUM  | 195 |
| Structure | GDGTGGKSIYGER              | 6 P23284  | PPIB_HUM  | 116 |
| Structure | IEVEKPFAIAKE               | 10 P23284 | PPIB_HUM  | 215 |
| Structure | IEVEKPFAIAKE               | 4 P23284  | PPIB_HUM  | 209 |
| Structure | TVDNFVALATGEKGFYK          | 12 P23284 | PPIB_HUM  | 84  |
|           | GDGTGGKSIYGER              | 6 P23284  | PPIB_HUM  | 116 |
|           | GDGTGGKSIYGER              | 6 P23284  | PPIB_HUM  | 116 |
| Structure | KDYTSGAMLTGELK             | 0 P23381  | SYWC_HUM  | 418 |
| Structure | SLKAGNASKDEIDSAVK          | 2 P23381  | SYWC_HUM  | 27  |
| Structure | KPFYLYTGR                  | 0 P23381  | SYWC_HUM  | 154 |
| Structure | FGFPEGSVELYAEKVATR         | 13 P23396 | RS3_HUM   | 90  |
| Structure | TQNVLG EKGR                | 7 P23396  | RS3_HUM   | 62  |
| Phyre     | YKLLGGLAVR                 | 1 P23396  | RS3_HUM   | 108 |
| Structure | FGFPEGSVELYAEKVATR         | 13 P23396 | RS3_HUM   | 90  |
| Phyre     | FIMESGAKGCEVVVSGK          | 7 P23396  | RS3_HUM   | 132 |
| Phyre     | FGFPEGSVELYAEKVATR         | 13 P23396 | RS3_HUM   | 90  |
| Structure | YKLLGGLAVR                 | 1 P23396  | RS3_HUM   | 108 |
| Phyre     | FVNVVPTFGKK                | 9 P62861  | RS30_HUM  | 51  |
| Phyre     | YKLLGGLAVR                 | 1 P23396  | RS3_HUM   | 108 |
| Phyre     | YKLLGGLAVR                 | 1 P23396  | RS3_HUM   | 108 |
| Structure | KSSTPEEVK                  | 0 P23528  | COF1_HUM  | 22  |
| Structure | VFNDMKVR                   | 5 P23528  | COF1_HUM  | 19  |
| Structure | VFNDMKVR                   | 5 P23528  | COF1_HUM  | 19  |
| Phyre     | DQKLSLDDR                  | 2 P23763  | VAMP1_HUM | 61  |
| Phyre     | LAQYESKK                   | 6 P24534  | EF1B_HUM  | 129 |
| Phyre     | LAQYESKK                   | 6 P24534  | EF1B_HUM  | 129 |
| Phyre     | SIQADGLVWGSSKLVPVGYGIK     | 12 P24534 | EF1B_HUM  | 176 |
| Phyre     | STVAQLVKR                  | 7 P25705  | ATPA_HUM  | 261 |
| Phyre     | VVDALGNAIDGKGPIGSK         | 11 P25705 | ATPA_HUM  | 161 |
| Structure | TPIGSFLGSLSLPATKLGSIQGAIEK | 16 P24752 | THIL_HUM  | 66  |
| Structure | GSTPYGGVKLEDLIVK           | 8 P24752  | THIL_HUM  | 174 |
| Structure | GSTPYGGVKLEDLIVK           | 8 P24752  | THIL_HUM  | 174 |
| Structure | VDFSKVPK                   | 4 P24752  | THIL_HUM  | 263 |
| Structure | GSTPYGGVKLEDLIVK           | 8 P24752  | THIL_HUM  | 174 |
| Phyre     | IIPVLTQESATYIAEEYSR        | 2 P25205  | MCM3_HUM  | 579 |
|           | GLGKGGAK                   | 3 P62805  | H4_HUM    | 13  |
| Phyre     | ADGKISEQSDAK               | 3 P25705  | ATPA_HUM  | 531 |
| Phyre     | ADGKISEQSDAK               | 3 P25705  | ATPA_HUM  | 531 |
| Docking   | GPIGSKTR                   | 5 P25705  | ATPA_HUM  | 167 |
| Phyre     | VGLKAPGIIPR                | 3 P25705  | ATPA_HUM  | 175 |
| Phyre     | ITKFENAFLSHVVSQHQALLGTIR   | 2 P25705  | ATPA_HUM  | 506 |
|           | LVSLIGSKTIPTQR             | 7 P25786  | PSA1_HUM  | 115 |
| Structure | KLAQQYYLVYQEPIPTAQLVQR     | 0 P25787  | PSA2_HUM  | 92  |
| Structure | KLAQQYYLVYQEPIPTAQLVQR     | 0 P25787  | PSA2_HUM  | 92  |

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| Structure | KLAQQYYLVYQEPIPTAQLVQR     | 0 P25787  | PSA2_HUM  | 92  |
| Phyre     | LKQIEEQTK                  | 1 P26038  | MOES_HUI  | 352 |
| Structure | LTPKIGFPWSEIR              | 3 P26038  | MOES_HUI  | 237 |
| Structure | AKFYPEDVSEELIQDITQR        | 1 P26038  | MOES_HUI  | 83  |
| Structure | AKFYPEDVSEELIQDITQR        | 1 P26038  | MOES_HUI  | 83  |
| Phyre     | LKEYR                      | 1 P26373  | RL13_HUM  | 118 |
| Phyre     | SKLILFPR                   | 1 P26373  | RL13_HUM  | 123 |
| Phyre     | NKSTESLQANVQR              | 1 P26373  | RL13_HUM  | 105 |
| Phyre     | SKLILFPR                   | 1 P26373  | RL13_HUM  | 123 |
| Phyre     | AKEAAEQDVEK                | 1 P26373  | RL13_HUM  | 200 |
| Phyre     | KGDSSAEELK                 | 0 P26373  | RL13_HUM  | 136 |
| Phyre     | NKSTESLQANVQR              | 1 P26373  | RL13_HUM  | 105 |
| Phyre     | SKLILFPR                   | 1 P26373  | RL13_HUM  | 123 |
|           | SKLILFPR                   | 1 P26373  | RL13_HUM  | 123 |
| Structure | GMPGFSTSKK                 | 8 P26440  | IVD_HUMA  | 238 |
| Structure | SELKELLTR                  | 3 P26447  | S10A4_HUI | 35  |
| Structure | TDEAAFQKLMSNLDSNR          | 7 P26447  | S10A4_HUI | 57  |
| Structure | TDEAAFQKLMSNLDSNR          | 7 P26447  | S10A4_HUI | 57  |
| Structure | TDEAAFQKLMSNLDSNR          | 7 P26447  | S10A4_HUI | 57  |
| Unknown   | KLPIDVTEGEVISLGLPFGK       | 0 P26599  | PTBP1_HUI | 65  |
| Structure | IITFTKNNQFQALLQYADPVSAQHAK | 5 P26599  | PTBP1_HUI | 218 |
|           | ITLSKHQNVQLPR              | 4 P26599  | PTBP1_HUI | 410 |
| Structure | IITFTKNNQFQALLQYADPVSAQHAK | 5 P26599  | PTBP1_HUI | 218 |
|           | ITLSKHQNVQLPR              | 4 P26599  | PTBP1_HUI | 410 |
|           | ITLSKHQNVQLPR              | 4 P26599  | PTBP1_HUI | 410 |
| Structure | IDFSKLTSLNVK               | 4 P26599  | PTBP1_HUI | 259 |
| Structure | IITFTKNNQFQALLQYADPVSAQHAK | 5 P26599  | PTBP1_HUI | 218 |
| Structure | IITFTKNNQFQALLQYADPVSAQHAK | 5 P26599  | PTBP1_HUI | 218 |
| Phyre     | ILNEKVNTPTTTVYR            | 4 P26639  | SYTC_HUM  | 243 |
| Phyre     | ILNEKVNTPTTTVYR            | 4 P26639  | SYTC_HUM  | 243 |
|           | EEKQKPQAER                 | 2 P26641  | EF1G_HUM  | 241 |
|           | KFAETQPK                   | 0 P26641  | EF1G_HUM  | 220 |
|           | AVLGEVKLCEK                | 6 P26641  | EF1G_HUM  | 208 |
| Structure | ILGLLDAYLKTR               | 9 P26641  | EF1G_HUM  | 147 |
|           | KLVIPSELGYGER              | 0 P26885  | FKBP2_HUI | 103 |
| Structure | YMKVSCGK                   | 3 P27635  | RL10_HUM  | 78  |
| Phyre     | INKMLSCAGADR               | 2 P27635  | RL10_HUM  | 101 |
| Phyre     | INKM[147.04]LSCAGADR       | 2 P27635  | RL10_HUM  | 101 |
| Phyre     | LIPDGCGVKYIPNR             | 8 P27635  | RL10_HUM  | 198 |
| Docking   | GPLDKWR                    | 4 P27635  | RL10_HUM  | 208 |
| Phyre     | LIPDGCGVKYIPNR             | 8 P27635  | RL10_HUM  | 198 |
| Phyre     | GAFGKPQGTVAR               | 4 P27635  | RL10_HUM  | 121 |
| Phyre     | FNADEFEDMVAEKR             | 12 P27635 | RL10_HUM  | 188 |
| Structure | FYGDEEKDKGLQTSQDAR         | 6 P27797  | CALR_HUM  | 62  |
| Phyre     | IKDPDASKPEDWDER            | 1 P27797  | CALR_HUM  | 209 |
| Structure | KVHVIFNYK                  | 0 P27797  | CALR_HUM  | 143 |
| Structure | KVHVIFNYK                  | 0 P27797  | CALR_HUM  | 143 |

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| Phyre     | LLSKTPELNLDQFHDK                 | 3 P27824  | CALX_HUM  | 170 |
|           | GTLSGWILSKAK                     | 9 P27824  | CALX_HUM  | 87  |
| Phyre     | LNKPFLFDTKPLIVQYEVNFQNGIECGGAY   | 9 P27824  | CALX_HUM  | 144 |
|           | VSSDNVADLHEKYSGSTP               | 11 P28074 | PSB5_HUM  | 257 |
| Phyre     | NEKGLLTYTSWEDALSR                | 2 P28331  | NDUS1_HU  | 311 |
| Structure | ESWHGKPLPK                       | 5 P29401  | TKT_HUMA  | 260 |
| Structure | GITGVEDKESWHGKPLPK               | 13 P29401 | TKT_HUMA  | 260 |
| Structure | GITGVEDKESWHGKPLPK               | 7 P29401  | TKT_HUMA  | 254 |
| Structure | MPSLPSYKVGDK                     | 7 P29401  | TKT_HUMA  | 310 |
| Structure | M[147.04]PSLPSYKVGDK             | 7 P29401  | TKT_HUMA  | 310 |
| Structure | NSTFSEIFKK                       | 8 P29401  | TKT_HUMA  | 352 |
| Structure | KAYGQALAK                        | 0 P29401  | TKT_HUMA  | 319 |
| Structure | AVELAANTKGICFIR                  | 8 P29401  | TKT_HUMA  | 465 |
| Structure | KAYGQALAK                        | 0 P29401  | TKT_HUMA  | 319 |
| Structure | KAYGQALAK                        | 0 P29401  | TKT_HUMA  | 319 |
| Structure | SGKPAELLK                        | 2 P29401  | TKT_HUMA  | 597 |
| Structure | KLILDSAR                         | 0 P29401  | TKT_HUMA  | 543 |
| Structure | AVELAANTKGICFIR                  | 8 P29401  | TKT_HUMA  | 465 |
|           | GVVQELQQAISKLEAR                 | 11 P29692 | EF1D_HUM  | 107 |
| Structure | DGDFENVPYTGAVKVGAIQR             | 14 P30040 | ERP29_HUI | 137 |
| Structure | WLKGQGVYLGMPGCLPVYDALAGEFIR      | 2 P30040  | ERP29_HUI | 146 |
| Structure | GVFTKELPSGK                      | 4 P30041  | PRDX6_HU  | 209 |
| Structure | DINAYNCEEPTEKLPFIIDDR            | 12 P30041 | PRDX6_HU  | 97  |
| Structure | GVFTKELPSGK                      | 4 P30041  | PRDX6_HU  | 209 |
|           | AHKAEGK                          | 2 P30044  | PRDX5_HU  | 142 |
| Structure | ATGDWKGLR                        | 5 P30050  | RL12_HUM  | 54  |
| Structure | VGDDIAKATGDWK                    | 6 P30050  | RL12_HUM  | 48  |
| Phyre     | TFEEDPAVGAIVLTGGDKAFAAGADIK      | 17 P30084 | ECHM_HUI  | 92  |
| Phyre     | TFEEDPAVGAIVLTGGDKAFAAGADIK      | 17 P30084 | ECHM_HUI  | 92  |
| Structure | APVAGTCYQAEWDDYVPKLYEQLSGK       | 17 P30086 | PEBP1_HUI | 179 |
| Structure | NAKGSNYWR                        | 2 P30101  | PDIA3_HUI | 274 |
| Structure | NAKGSNYWR                        | 2 P30101  | PDIA3_HUI | 274 |
| Structure | GFPTIYFSPANKK                    | 11 P30101 | PDIA3_HUI | 460 |
| Structure | YGVSGYPTLKIFR                    | 9 P30101  | PDIA3_HUI | 104 |
| Structure | FLDAGHKLNFASVR                   | 6 P30101  | PDIA3_HUI | 296 |
| Structure | GFPTIYFSPANKK                    | 11 P30101 | PDIA3_HUI | 460 |
| Structure | NAKGSNYWR                        | 2 P30101  | PDIA3_HUI | 274 |
| Structure | ADVVPKTAENFR                     | 5 P30405  | PPIF_HUM  | 73  |
| Structure | ALCTGEKGFGYK                     | 6 P30405  | PPIF_HUM  | 86  |
| Structure | SGTVDPQELQKALTTMGFR              | 10 P30626 | SORCN_HU  | 127 |
| Modeller  | LSMQKSMQNHA AVFR                 | 4 P31040  | SDHA_HUM  | 517 |
| Structure | LSM[147.04]QKSM[147.04]QNHA AVFR | 4 P31040  | SDHA_HUM  | 517 |
| Structure | EAVKHIGYDDSSK                    | 3 P31153  | METK2_HU  | 88  |
| Structure | AAVDYQKVVR                       | 6 P31153  | METK2_HU  | 81  |
| Structure | EAVKHIGYDDSSK                    | 3 P31153  | METK2_HU  | 88  |
| Structure | EAVKHIGYDDSSK                    | 3 P31153  | METK2_HU  | 88  |
| Structure | AVVPAKYLDEDTIYHLQPSGR            | 5 P31153  | METK2_HU  | 234 |

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| Structure | KVDSKSLFHYP                      | 4 P31327  | CPSM_HUN  | 1486 |
| Structure | LPMNKEWPSNLDLR                   | 4 P31327  | CPSM_HUN  | 831  |
| Structure | LPM[147.04]NKEWPSNLDLR           | 4 P31327  | CPSM_HUN  | 831  |
| Structure | IEFEGQPVDFVDPNKQNLIAEVSTK        | 14 P31327 | CPSM_HUN  | 197  |
| Structure | GTMLGKIEFEGQPVDFVDPNK            | 5 P31327  | CPSM_HUN  | 182  |
| Structure | AEQPDGLILGMGGQTALNCGVELFKR       | 24 P31327 | CPSM_HUN  | 522  |
| Structure | VMIGENVDEKHLPTLDHPIIPADYVAIK     | 9 P31327  | CPSM_HUN  | 1291 |
| Structure | VM[147.04]IGENVDEKHLPTLDHPIIPADY | 9 P31327  | CPSM_HUN  | 1291 |
| Structure | EPLFGISTGNLITGLAAGAKTYK          | 19 P31327 | CPSM_HUN  | 307  |
| Structure | LPMNKEWPSNLDLR                   | 4 P31327  | CPSM_HUN  | 831  |
| Structure | LPM[147.04]NKEWPSNLDLR           | 4 P31327  | CPSM_HUN  | 831  |
| Structure | AEQPDGLILGMGGQTALNCGVELFKR       | 24 P31327 | CPSM_HUN  | 522  |
| Structure | AIDDNMSLDEIEKLTYIDKWFLYK         | 12 P31327 | CPSM_HUN  | 869  |
| Phyre     | ETLMDLSTKAFAMTNQILVEK            | 8 P31327  | CPSM_HUN  | 612  |
| Structure | IGSSMKSVGEVMAIGR                 | 5 P31327  | CPSM_HUN  | 793  |
| Structure | IGSSM[147.04]KSVGEVMAIGR         | 5 P31327  | CPSM_HUN  | 793  |
| Structure | LPMNKEWPSNLDLR                   | 4 P31327  | CPSM_HUN  | 831  |
| Structure | LPM[147.04]NKEWPSNLDLR           | 4 P31327  | CPSM_HUN  | 831  |
| Structure | DGSIDLVINLPNNNTKVFHDNYVIR        | 15 P31327 | CPSM_HUN  | 1444 |
| Structure | KELSEPSSTR                       | 0 P31327  | CPSM_HUN  | 841  |
| Structure | LPMNKEWPSNLDLR                   | 4 P31327  | CPSM_HUN  | 831  |
| Structure | LPM[147.04]NKEWPSNLDLR           | 4 P31327  | CPSM_HUN  | 831  |
| Structure | VAQAPWKAVNTLNLEALEFAK            | 6 P31327  | CPSM_HUN  | 1107 |
| Structure | TLKGLNSESMTETLKR                 | 2 P31327  | CPSM_HUN  | 892  |
| Structure | EPLFGISTGNLITGLAAGAKTYK          | 19 P31327 | CPSM_HUN  | 307  |
| Structure | EPLFGISTGNLITGLAAGAKTYK          | 19 P31327 | CPSM_HUN  | 307  |
| Structure | LPMNKEWPSNLDLR                   | 4 P31327  | CPSM_HUN  | 831  |
| Structure | TLKGLNSESMTETLKR                 | 2 P31327  | CPSM_HUN  | 892  |
| Structure | TAVDSGIPLLTNFQVTKLFAEAVQK        | 16 P31327 | CPSM_HUN  | 1471 |
| Structure | VAQAPWKAVNTLNLEALEFAK            | 6 P31327  | CPSM_HUN  | 1107 |
| Structure | VISSIEQKTER                      | 7 P31946  | 1433B_HUI | 70   |
| Structure | VISSIEQKTER                      | 7 P31946  | 1433B_HUI | 70   |
| Structure | NLLSVAYKNVVGAR                   | 7 P31946  | 1433B_HUI | 51   |
| Phyre     | DCEECIQLEPTFIKGYTR               | 13 P31948 | STIP1_HUN | 429  |
| Phyre     | LAYINPDALALEEKNKGNECFQK          | 12 P31948 | STIP1_HUN | 364  |
| Phyre     | LAYINPDALALEEKNKGNECFQK          | 12 P31948 | STIP1_HUN | 364  |
| Phyre     | AYEDGCKTVDLKPDWGK                | 6 P31948  | STIP1_HUN | 63   |
| Phyre     | TYEEGLKHEANNPQLK                 | 6 P31948  | STIP1_HUN | 100  |
| Structure | ELGNDAYKK                        | 7 P31948  | STIP1_HUN | 237  |
| Phyre     | TVDLKPDPWGKGYSR                  | 9 P31948  | STIP1_HUN | 73   |
| Phyre     | TVDLKPDPWGKGYSR                  | 9 P31948  | STIP1_HUN | 73   |
|           | LMAEGAPKWPK                      | 7 P32004  | L1CAM_HL  | 137  |
| Phyre     | LMAEGAPKWPK                      | 7 P32004  | L1CAM_HL  | 137  |
|           | LM[147.04]AEGAPKWPK              | 7 P32004  | L1CAM_HL  | 137  |
| Phyre     | VSWSPAEDHNAPIEKYDIEFEDK          | 14 P32004 | L1CAM_HL  | 647  |
| Phyre     | VTAINKYGPGEPSPVSETVVTPEAAPEKNP   | 5 P32004  | L1CAM_HL  | 694  |
| Phyre     | HAYYVTVEAAPYWLHKPQSHLYGPGETAI    | 15 P32004 | L1CAM_HL  | 338  |

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| Phyre     | LVVFPTDDISLKCEASGKPEVQFR        | 11 P32004 | L1CAM_HU | 56  |
| Structure | EVKLSDYK                        | 2 P32119  | PRDX2_HU | 29  |
| Structure | GLFIIDGKGVLR                    | 7 P32119  | PRDX2_HU | 135 |
| Structure | IGKPAPDFKATAVVDGAFK             | 8 P32119  | PRDX2_HU | 16  |
| Structure | KEGGLGPLNIPLADVTR               | 0 P32119  | PRDX2_HU | 92  |
| Structure | GLFIIDGKGVLR                    | 7 P32119  | PRDX2_HU | 135 |
| Structure | IGKPAPDFK                       | 2 P32119  | PRDX2_HU | 10  |
| Structure | IGHPAPNFKATAVMPDGQFK            | 8 Q06830  | PRDX1_HU | 16  |
| Structure | TIAQDYGVKKADEGISFR              | 9 Q06830  | PRDX1_HU | 120 |
| Structure | KEGGLGPLNIPLADVTR               | 0 P32119  | PRDX2_HU | 92  |
| Structure | IFKGCNIENACYPLGICAER            | 2 P32320  | CDD_HUM  | 51  |
| Phyre     | NFLGEKYIR                       | 5 P32969  | RL9_HUM  | 121 |
| Structure | TICSHVQNMKGVTLGFR               | 10 P32969 | RL9_HUM  | 82  |
| Structure | VDKWWGNR                        | 2 P32969  | RL9_HUM  | 59  |
| Phyre     | KFLDGIYVSEK                     | 0 P32969  | RL9_HUM  | 174 |
| Structure | TILSNQTVDIPENVDTLKGR            | 18 P32969 | RL9_HUM  | 21  |
| Structure | KFAYLGR                         | 0 P40429  | RL13A_HU | 134 |
| Phyre     | KFLDGIYVSEK                     | 0 P32969  | RL9_HUM  | 174 |
|           | KLFVQDLATR                      | 0 P33176  | KINH_HUM | 801 |
|           | KSAEIDSDDTGGSAQK                | 0 P33176  | KINH_HUM | 813 |
|           | LKEAVR                          | 1 P33176  | KINH_HUM | 903 |
| Structure | SGLAAKHFDIVGAGVIDEDYR           | 5 P33316  | DUT_HUM  | 179 |
|           | SGLAAKHFDIVGAGVIDEDYR           | 5 P33316  | DUT_HUM  | 179 |
|           | GQSDIAITKDMFEEALR               | 8 P33991  | MCM4_HU  | 837 |
| Phyre     | VELLKELSR                       | 4 P33991  | MCM4_HU  | 450 |
| Phyre     | KPDIYER                         | 0 P33991  | MCM4_HU  | 455 |
| Docking   | TPALKYQQLFEDIR                  | 4 P33991  | MCM4_HU  | 819 |
| Phyre     | TSVLAAANPIESQWNPCK              | 16 P33991 | MCM4_HU  | 627 |
| Phyre     | TSVLAAANPIESQWNPCK              | 16 P33991 | MCM4_HU  | 627 |
| Modeller  | YSEGYPGKR                       | 7 P34897  | GLYM_HUM | 103 |
| Modeller  | VIPSPFKHADIVTTTTTHK             | 6 P34897  | GLYM_HUM | 269 |
| Docking   | LNPKTGLIDYNQLALTAR              | 3 P34897  | GLYM_HUM | 200 |
| Modeller  | VLELVSITANKNTCPGDR              | 10 P34897 | GLYM_HUM | 409 |
| Modeller  | VLELVSITANKNTCPGDR              | 10 P34897 | GLYM_HUM | 409 |
| Modeller  | SFLKDKSETSQR                    | 4 P34897  | GLYM_HUM | 474 |
| Modeller  | YSEGYPGKR                       | 7 P34897  | GLYM_HUM | 103 |
| Modeller  | LNPKTGLIDYNQLALTAR              | 3 P34897  | GLYM_HUM | 200 |
| Modeller  | LQDFKSFLK                       | 4 P34897  | GLYM_HUM | 469 |
| Modeller  | SFLKDKSETSQR                    | 4 P34897  | GLYM_HUM | 474 |
| Modeller  | VLELVSITANKNTCPGDR              | 10 P34897 | GLYM_HUM | 409 |
| Phyre     | NHAAPFSKVLTFYR                  | 7 P34932  | HSP74_HU | 430 |
| Structure | QQIMQLKIMTNR                    | 6 P35052  | GPC1_HUM | 461 |
| Structure | DVQDFWISLPGTLCSEKMASTASDDR      | 16 P35052 | GPC1_HUM | 404 |
| Docking   | FVVEKAEQKK                      | 4 P35232  | PHB_HUM  | 202 |
| Phyre     | FVVEKAEQKK                      | 4 P35232  | PHB_HUM  | 202 |
| Phyre     | NVPVITGSKDLQNVNITLR             | 8 P35232  | PHB_HUM  | 83  |
| Phyre     | AAIISAEGDSKAAELIANSLATAGDGLIELR | 10 P35232 | PHB_HUM  | 219 |

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| Phyre     | KAAIISAEGDSK                    | 0 P35232  | PHB_HUM/  | 208  |
|           | FVVEKAEQQK                      | 4 P35232  | PHB_HUM/  | 202  |
|           | FVVEKAEQQK                      | 4 P35232  | PHB_HUM/  | 202  |
| Phyre     | AAQNISKTIATSQNR                 | 6 Q99623  | PHB2_HUN  | 262  |
| Phyre     | AAQNISKTIATSQNR                 | 6 Q99623  | PHB2_HUN  | 262  |
| Phyre     | VLPSITTEILKSVVAR                | 10 P35232 | PHB_HUM/  | 128  |
| Phyre     | VLPSITTEILKSVVAR                | 10 P35232 | PHB_HUM/  | 128  |
| Phyre     | FALACNASDKIIEPIQSR              | 9 P35250  | RFC2_HUN  | 176  |
| Phyre     | VCKTFQMAEYLK                    | 2 P35250  | RFC2_HUN  | 304  |
|           | KYTEITATYFQGVR                  | 0 P35573  | GDE_HUM/  | 511  |
| Phyre     | EKQLAAENR                       | 1 P35579  | MYH9_HUI  | 860  |
|           | ALEEAMEQKAELER                  | 8 P35579  | MYH9_HUI  | 1492 |
| Phyre     | EQLAKLMATLR                     | 4 P35579  | MYH9_HUI  | 656  |
| Phyre     | VIQYLAYVASSHKSK                 | 12 P35579 | MYH9_HUI  | 199  |
|           | TQLEELEDELQATEDAKLR             | 16 P35579 | MYH9_HUI  | 1555 |
|           | ALEEAMEQKAELER                  | 8 P35579  | MYH9_HUI  | 1492 |
|           | ALEEAM[147.04]EQKAELER          | 8 P35579  | MYH9_HUI  | 1492 |
|           | VTTEAKLK                        | 5 P35579  | MYH9_HUI  | 972  |
|           | KFDQLLAEEK                      | 0 P35579  | MYH9_HUI  | 1445 |
| Phyre     | NTDQASMPDNTAAQKVSHLLGINVTDF     | 14 P35579 | MYH9_HUI  | 373  |
| Phyre     | NTDQASM[147.04]PDNTAAQKVSHLLGI  | 14 P35579 | MYH9_HUI  | 373  |
| Phyre     | VISGVLQLGNIVFKK                 | 13 P35579 | MYH9_HUI  | 355  |
|           | AKQTLENER                       | 1 P35579  | MYH9_HUI  | 1219 |
|           | KVEAQLQELQVK                    | 0 P35579  | MYH9_HUI  | 1249 |
|           | LQEMEGTVKSK                     | 8 P35579  | MYH9_HUI  | 1802 |
| Structure | FVAELWKDVDR                     | 6 P35580  | MYH10_HL  | 620  |
| Structure | SSEHINEGETAMLVCKSESVPVTDWAW'    | 15 P35613 | BASI_HUM  | 243  |
| Structure | TEFKVSDDDQWGEYSCVFLPEPMGTANIC   | 3 P35613  | BASI_HUM  | 191  |
| Structure | TEFKVSDDDQWGEYSCVFLPEPM[147.04] | 3 P35613  | BASI_HUM  | 191  |
| Structure | GGVVLKEDALPGQK                  | 5 P35613  | BASI_HUM  | 179  |
| Structure | SSEHINEGETAMLVCKSESVPVTDWAW'    | 15 P35613 | BASI_HUM  | 243  |
| Structure | SSEHINEGETAM[147.04]LVCKSESVPV' | 15 P35613 | BASI_HUM  | 243  |
| Structure | WLKGGVVLK                       | 2 P35613  | BASI_HUM  | 173  |
| Structure | SSEHINEGETAMLVCKSESVPVTDWAW'    | 15 P35613 | BASI_HUM  | 243  |
|           | LKGEATVSFDDPPSAK                | 1 P35637  | FUS_HUM/  | 334  |
|           | LKGEATVSFDDPPSAK                | 1 P35637  | FUS_HUM/  | 334  |
|           | KTGQPMINLYTDR                   | 0 P35637  | FUS_HUM/  | 316  |
|           | KTGQPM[147.04]INLYTDR           | 0 P35637  | FUS_HUM/  | 316  |
| Phyre     | ANAEKTSGSNVK                    | 4 P56381  | ATP5E_HUI | 37   |
| Phyre     | EAVLLLLK                        | 6 P36578  | RL4_HUMA  | 172  |
| Phyre     | TKEAVLLLLK                      | 1 P36578  | RL4_HUMA  | 165  |
| Phyre     | KLDELYGTWR                      | 0 P36578  | RL4_HUMA  | 259  |
| Phyre     | NVTLPVAFKAPIRPDIVNFVHTNLR       | 8 P36578  | RL4_HUMA  | 29   |
| Phyre     | SDEKAAVAGK                      | 3 P36578  | RL4_HUMA  | 368  |
| Phyre     | KLDELYGTWR                      | 0 P36578  | RL4_HUMA  | 259  |
| Phyre     | LNILKLAPGGHVGR                  | 4 P36578  | RL4_HUMA  | 239  |
| Phyre     | MFAPTKTWR                       | 5 P36578  | RL4_HUMA  | 106  |

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| Phyre     | M[147.04]FAPTKTWR             | 5 P36578  | RL4_HUMA  | 106 |
| Phyre     | KTVGVEPAADGK                  | 0 P46779  | RL28_HUM  | 47  |
| Phyre     | AGGKILTFDQLALDSPK             | 3 Q07020  | RL18_HUM  | 119 |
| Phyre     | AGGKILTFDQLALDSPK             | 3 Q07020  | RL18_HUM  | 119 |
| Phyre     | VQEVPKLK                      | 5 Q07020  | RL18_HUM  | 97  |
| Modeller  | ILKSPEIQR                     | 2 P36578  | RL4_HUMA  | 294 |
| Phyre     | IVSGEAEVSEVTPENLQDFVGKPVFTVER | 21 P36776 | LONM_HUI  | 748 |
| Phyre     | LSSDVLTLLIKQYCR               | 10 P36776 | LONM_HUI  | 701 |
|           | EFELSKLQQR                    | 5 P36776  | LONM_HUI  | 374 |
|           | VVDNPIYLSDMGAALTGAESHELQDVLEE | 33 P36776 | LONM_HUI  | 357 |
|           | EFELSKLQQR                    | 5 P36776  | LONM_HUI  | 374 |
|           | KYLLQEQLK                     | 0 P36776  | LONM_HUI  | 393 |
| Phyre     | KYLLQEQLK                     | 0 P36776  | LONM_HUI  | 393 |
|           | VVDNPIYLSDMGAALTGAESHELQDVLEE | 33 P36776 | LONM_HUI  | 357 |
| Phyre     | LSSDVLTLLIKQYCR               | 10 P36776 | LONM_HUI  | 701 |
| Structure | INQDPQVMLAPLISIALKVSQQLQR     | 17 P36871 | PGM1_HUI  | 545 |
| Structure | TIVLQESIGKGR                  | 9 P36897  | TGFR1_HU  | 213 |
|           | DQEKEYEPQHR                   | 3 P36941  | TNR3_HUN  | 48  |
| Unknown   | TSGSVYITLKK                   | 9 P37108  | SRP14_HUI | 31  |
| Unknown   | TSGSVYITLKK                   | 9 P37108  | SRP14_HUI | 31  |
| Structure | SVTKIYNYYK                    | 3 P37837  | TALDO_HU  | 219 |
| Structure | LIELYKEAGISK                  | 5 P37837  | TALDO_HU  | 130 |
| Structure | TGVVTDGVKHSMPFCEIAVEEAVR      | 8 P38117  | ETFB_HUM  | 35  |
| Structure | EKVDLVLLGK                    | 1 P38117  | ETFB_HUM  | 116 |
|           | DDGYSTKDSYSSR                 | 6 P38159  | RBMX_HUI  | 217 |
| Structure | GFAFVTFESPADAKDAAR            | 13 P38159 | RBMX_HUI  | 63  |
| Docking   | DKGTGR                        | 1 P38646  | GRP75_HU  | 537 |
| Phyre     | KSQVFSTAADGQTQVEIK            | 0 P38646  | GRP75_HU  | 468 |
| Phyre     | NTTIPTKK                      | 6 P38646  | GRP75_HU  | 467 |
| Structure | ETGVDLTCKDNMALQR              | 7 P38646  | GRP75_HU  | 300 |
| Structure | MPKVQQTVQDLFGR                | 2 P38646  | GRP75_HU  | 394 |
| Phyre     | NAEKYAEEDR                    | 3 P38646  | GRP75_HU  | 567 |
| Phyre     | NAEKYAEEDRR                   | 3 P38646  | GRP75_HU  | 567 |
| Phyre     | KDSETGENIR                    | 0 P38646  | GRP75_HU  | 625 |
| Structure | QAVTNPNTFYATKR                | 13 P38646 | GRP75_HU  | 121 |
| Structure | AMQDAEVSKSDIGEVLVGGMTR        | 8 P38646  | GRP75_HU  | 377 |
| Structure | AM[147.04]QDAEVSKSDIGEVLVGGMT | 8 P38646  | GRP75_HU  | 377 |
| Structure | TIAPCQKAMQDAEVSK              | 6 P38646  | GRP75_HU  | 368 |
| Structure | ETAENYLGHTAKNAVITVPAYFNDSQR   | 11 P38646 | GRP75_HU  | 187 |
| Structure | VINEPTAAALAYGLDKSEDK          | 15 P38646 | GRP75_HU  | 234 |
| Structure | EANFTVSSMHGDMPPQKER           | 15 P38919 | IF4A3_HUN | 314 |
| Structure | GIYAYGF EKPSAIQQR             | 8 P38919  | IF4A3_HUN | 60  |
| Structure | FKQESTVATER                   | 1 Q9H307  | PININ_HUN | 157 |
| Structure | GGAGVGSMTKIYGGR               | 9 P39019  | RS19_HUM  | 77  |
| Phyre     | LLEPVLLGKER                   | 9 P62249  | RS16_HUM  | 60  |
| Unknown   | IAGQVAAANKK                   | 9 P39019  | RS19_HUM  | 143 |
| Phyre     | SLLVQTKR                      | 6 P39023  | RL3_HUMA  | 356 |

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| Phyre     | FIDTTSKFGHGR                  | 6 P39023  | RL3_HUMA  | 373  |
| Phyre     | LIKNNASTDYDLSDK               | 2 P39023  | RL3_HUMA  | 300  |
| Phyre     | QLEKDFSSMK                    | 3 P39023  | RL3_HUMA  | 148  |
| Phyre     | IYKIGQGYLIK                   | 2 P39023  | RL3_HUMA  | 286  |
|           | IYKIGQGYLIK                   | 2 P39023  | RL3_HUMA  | 286  |
| Structure | GLKYQEGGVESAFHK               | 2 P40121  | CAPG_HUN  | 115  |
| Structure | MAAYTDEGGKDGPEFTFTTPK         | 9 P40189  | IL6RB_HUN | 601  |
| Structure | M[147.04]AAYTDEGGKDGPEFTFTTPK | 9 P40189  | IL6RB_HUN | 601  |
|           | SLKEEGVQR                     | 2 P40222  | TXLNA_HU  | 256  |
| Phyre     | GIDPFSLDALSKEGIVALR           | 11 P40227 | TCPZ_HUM  | 307  |
| Phyre     | FTFIEKCNNPR                   | 5 P40227  | TCPZ_HUM  | 365  |
| Phyre     | GFVVINQKGIDPFSLDALSK          | 7 P40227  | TCPZ_HUM  | 295  |
| Phyre     | AVDDGVNTFKVLTR                | 9 P50990  | TCPQ_HUN  | 400  |
| Phyre     | AVDDGVNTFKVLTR                | 9 P50990  | TCPQ_HUN  | 400  |
| Phyre     | LAAIVAKQVLLGR                 | 6 P40429  | RL13A_HUI | 25   |
| Phyre     | MVVPAAALKVVR                  | 7 P40429  | RL13A_HUI | 125  |
| Phyre     | LAAIVAKQVLLGR                 | 6 P40429  | RL13A_HUI | 25   |
| Phyre     | LKVFDGIPPPYDK                 | 1 P40429  | RL13A_HUI | 103  |
| Phyre     | LAAIVAKQVLLGR                 | 6 P40429  | RL13A_HUI | 25   |
| Phyre     | KLSSAMSAAK                    | 0 P40925  | MDHC_HU   | 239  |
| Phyre     | KLSSAM[147.04]SAAK            | 0 P40925  | MDHC_HU   | 239  |
| Structure | AAVKGYLGPEQLPDCLK             | 3 P40926  | MDHM_HL   | 78   |
| Structure | LTLYDIAHTPGVAADLSHIETKAAVK    | 21 P40926 | MDHM_HL   | 74   |
| Structure | TIIP LISQCTPKVDFPQDQLTALTGR   | 11 P40926 | MDHM_HL   | 215  |
| Structure | ASIKKGEDFVK                   | 3 P40926  | MDHM_HL   | 328  |
| Structure | AAVKGYLGPEQLPDCLK             | 3 P40926  | MDHM_HL   | 78   |
| Structure | GVLGPEQLPDCLKGCDVVVIPAGVPR    | 12 P40926 | MDHM_HL   | 91   |
| Structure | VNVPVIGGHAGKTIIP LISQCTPK     | 11 P40926 | MDHM_HL   | 203  |
| Structure | IQEAGTEVVAK                   | 9 P40926  | MDHM_HL   | 239  |
| Structure | MISDAIPELKASIK                | 9 P40926  | MDHM_HL   | 324  |
| Structure | M[147.04]ISDAIPELKASIK        | 9 P40926  | MDHM_HL   | 324  |
| Structure | IQEAGTEVVAK                   | 9 P40926  | MDHM_HL   | 239  |
| Structure | IQEAGTEVVAK                   | 9 P40926  | MDHM_HL   | 239  |
| Structure | KPGMTR                        | 0 P40926  | MDHM_HL   | 105  |
| Phyre     | FVDLYGAQKIVDR                 | 8 P40939  | ECHA_HUN  | 728  |
| Phyre     | GLYPAPLKIIDVVK                | 7 P40939  | ECHA_HUN  | 303  |
| Phyre     | GLYPAPLKIIDVVK                | 7 P40939  | ECHA_HUN  | 303  |
| Docking   | GLYPAPLKIIDVVK                | 7 P40939  | ECHA_HUN  | 303  |
| Phyre     | FAKEFVDAR                     | 2 P41221  | WNT5A_HI  | 194  |
| Phyre     | LSALYKLESDYEILER              | 5 P41252  | SYIC_HUM, | 268  |
| Phyre     | KDSLPCVPDASGCFTEVTDFAGQYVK    | 0 P41252  | SYIC_HUM, | 344  |
| Phyre     | TQLKGSELEITLTR                | 3 P41252  | SYIC_HUM, | 1061 |
| Phyre     | DADKSIIR                      | 3 P41252  | SYIC_HUM, | 375  |
| Phyre     | LSALYKLESDYEILER              | 5 P41252  | SYIC_HUM, | 268  |
|           | KDSLPCVPDASGCFTEVTDFAGQYVK    | 0 P41252  | SYIC_HUM, | 344  |
| Structure | KNICQFLVEIGLAK                | 0 P41567  | EIF1_HUM, | 91   |
| Structure | DADVQNFVSFISKDSIQK            | 12 P42126 | ECI1_HUM, | 283  |



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| Structure | KATASR                          | 0 P42126  | ECI1_HUM  | 260  |
|           | VTGNFKHASPILPITEFSDIPR          | 5 P42167  | LAP2B_HUI | 303  |
| Modeller  | LANQFAIYKPVTDFFLQLVDAGK         | 8 P42704  | LPPRC_HUI | 1252 |
| Structure | DFTATDLSEFAAKAALSAGK            | 12 P42765 | THIM_HUN  | 38   |
| Phyre     | QLDDLKVELSQLR                   | 5 P42766  | RL35_HUM  | 25   |
| Phyre     | VLTVINQQTQKENLR                 | 9 P42766  | RL35_HUM  | 66   |
| Phyre     | QLDDLKVELSQLR                   | 5 P42766  | RL35_HUM  | 25   |
|           | KTSSFLDQR                       | 0 P42892  | ECE1_HUM  | 401  |
| Phyre     | EVKYFSFPGELLMR                  | 2 P43003  | EAA1_HUN  | 79   |
| Phyre     | NM[147.04]FPPNLVEACFKQFK        | 12 P43003 | EAA1_HUN  | 188  |
| Phyre     | TNYEKR                          | 4 P43003  | EAA1_HUN  | 196  |
|           | TNYEKR                          | 4 P43003  | EAA1_HUN  | 196  |
| Phyre     | EVTVPVFYPTTEKVVLEVEPVGMLK       | 11 P43121 | MUC18_HL  | 251  |
| Phyre     | EVTVPVFYPTTEKVVLEVEPVGMLK       | 11 P43121 | MUC18_HL  | 251  |
| Phyre     | EVTVPVFYPTTEKVVLEVEPVGM[147.04] | 11 P43121 | MUC18_HL  | 251  |
| Phyre     | APEEPNIQVNPLGIPVNSKEPEEVATCVGR  | 18 P43121 | MUC18_HL  | 153  |
| Phyre     | APEEPNIQVNPLGIPVNSKEPEEVATCVGR  | 18 P43121 | MUC18_HL  | 153  |
|           | TGFYCKLCSLFYTNEEVAK             | 5 P43243  | MATR3_HL  | 804  |
|           | IGPYQPNVPVGIDYVIPKTGFYCK        | 17 P43243 | MATR3_HL  | 798  |
| Phyre     | LTFDITTFSPNTGKK                 | 12 P45880 | VDAC2_HU  | 120  |
| Phyre     | SCSGVEFSTSGSSNTDTGKVTGTLET      | 18 P45880 | VDAC2_HU  | 64   |
| Phyre     | YKWCEYGLTFTEK                   | 1 P45880  | VDAC2_HU  | 74   |
| Phyre     | DIFNKGFGFLVK                    | 4 P45880  | VDAC2_HU  | 31   |
| Phyre     | SCSGVEFSTSGSSNTDTGKVTGTLET      | 18 P45880 | VDAC2_HU  | 64   |
| Phyre     | SINAGGHKVGLEALEA                | 7 P45880  | VDAC2_HU  | 285  |
| Phyre     | YQLDPTASISAKVNNSSLIGVGYTQTLRPG  | 11 P45880 | VDAC2_HU  | 247  |
| Phyre     | DIFNKGFGFLVK                    | 4 P45880  | VDAC2_HU  | 31   |
| Modeller  | ELNLSFCEIKR                     | 9 P46060  | RAGP1_HU  | 306  |
| Modeller  | VINLNDNTFTEKGAVAMAETLK          | 11 P46060 | RAGP1_HU  | 251  |
| Phyre     | KDLAIYYSYGDFLLGK                | 0 P46087  | NOP2_HUN  | 272  |
| Phyre     | TTTGNKVFGALK                    | 5 P46777  | RL5_HUMA  | 158  |
| Phyre     | KHIMGQNVADYMR                   | 0 P46777  | RL5_HUMA  | 197  |
| Phyre     | KHIM[147.04]GQNVADYMR           | 0 P46777  | RL5_HUMA  | 197  |
| Phyre     | KHIM[147.04]GQNVADYM[147.04]R   | 0 P46777  | RL5_HUMA  | 197  |
| Phyre     | LVIQDKNK                        | 5 P46777  | RL5_HUMA  | 41   |
| Phyre     | EGKTDYYAR                       | 2 P46777  | RL5_HUMA  | 27   |
| Phyre     | VKENDQK                         | 1 P46778  | RL21_HUM  | 110  |
|           | KPATSYVR                        | 0 P46779  | RL28_HUM  | 72   |
|           | KTVGVEPAADGK                    | 0 P46779  | RL28_HUM  | 47   |
|           | NCSSFLIKR                       | 7 P46779  | RL28_HUM  | 19   |
|           | KPATSYVR                        | 0 P46779  | RL28_HUM  | 72   |
|           | NKQTYSTEPNNLK                   | 1 P46779  | RL28_HUM  | 22   |
|           | KPATSYVR                        | 0 P46779  | RL28_HUM  | 72   |
| Structure | KTYVTPR                         | 0 P46781  | RS9_HUMA  | 11   |
| Structure | LDSQKHIDFSLR                    | 4 P46781  | RS9_HUMA  | 155  |
| Structure | KQVVNIPSFIVR                    | 0 P46781  | RS9_HUMA  | 139  |
| Structure | LDQELKLIGEYGLR                  | 5 P46781  | RS9_HUMA  | 30   |

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| Structure | RPFEKSR                       | 4 P46781  | RS9_HUMA  | 22   |
| Structure | ELLTLDEKDPR                   | 7 P46781  | RS9_HUMA  | 66   |
| Structure | KTYVTPR                       | 0 P46781  | RS9_HUMA  | 11   |
| Phyre     | THFGGGKTTGFGMIYDSL DYAK       | 6 P62847  | RS24_HUM  | 68   |
| Structure | KAQCPIVER                     | 0 P46782  | RS5_HUMA  | 63   |
| Structure | YAKYLPHSAGR                   | 2 P46782  | RS5_HUMA  | 47   |
| Unknown   | TIAECLADELINA AAKGSSNSYAIK    | 14 P46782 | RS5_HUMA  | 182  |
| Unknown   | TIAECLADELINA AAKGSSNSYAIK    | 14 P46782 | RS5_HUMA  | 182  |
|           | KLTELGTVDPK                   | 0 P46940  | IQGA1_HU  | 1465 |
|           | ATFYGEQVDYYKSYIK              | 11 P46940 | IQGA1_HU  | 1528 |
|           | MHQARKR                       | 5 P46940  | IQGA1_HU  | 823  |
|           | LFKTALQEEIK                   | 2 P46940  | IQGA1_HU  | 1027 |
|           | NKDQGTIEDYVEGLR               | 1 P60660  | MYL6_HUN  | 81   |
| Phyre     | YKATGLHFR                     | 1 P46940  | IQGA1_HU  | 104  |
|           | NLGSIAKMLQHAASNK              | 6 P46940  | IQGA1_HU  | 1230 |
|           | SLNIKTDPVDIYK                 | 4 P46940  | IQGA1_HU  | 1088 |
| Phyre     | SPWSNKYDP PLEDGAM[147.04]PSAR | 5 P47756  | CAPZB_HU  | 78   |
| Phyre     | SPWSNKYDP PLEDGAMPSAR         | 5 P47756  | CAPZB_HU  | 78   |
| Phyre     | SPWSNKYDP PLEDGAM[147.04]PSAR | 5 P47756  | CAPZB_HU  | 78   |
| Phyre     | KLEVEANNAFDQYR                | 0 P47756  | CAPZB_HU  | 95   |
| Phyre     | SPWSNKYDP PLEDGAMPSAR         | 5 P47756  | CAPZB_HU  | 78   |
| Phyre     | SPWSNKYDP PLEDGAM[147.04]PSAR | 5 P47756  | CAPZB_HU  | 78   |
| Structure | DYQDNKADVILK                  | 5 P47813  | IF1AX_HUN | 88   |
| Phyre     | GEELKGHNTLPSPWR               | 4 P47897  | SYQ_HUMA  | 366  |
| Structure | LVMEDGKMDPVAYR                | 6 P47897  | SYQ_HUMA  | 412  |
| Structure | LVM[147.04]EDGKMDPVAYR        | 6 P47897  | SYQ_HUMA  | 412  |
| Structure | TDFKEEPEPGFKR                 | 11 P47897 | SYQ_HUMA  | 628  |
| Structure | KILQLVATGAVR                  | 0 P47897  | SYQ_HUMA  | 498  |
| Structure | TQKEIEQEA AVELSQLR            | 2 P47985  | UCRI_HUM  | 182  |
| Structure | TQKEIEQEA AVELSQLR            | 2 P47985  | UCRI_HUM  | 182  |
|           | GEVPCTVTSASPLEEATLSELKTVLK    | 21 P48047 | ATPO_HUN  | 158  |
| Phyre     | LEAKTDPSILGGMIVR              | 3 P48047  | ATPO_HUN  | 176  |
| Phyre     | NYCNIQVTKVTQVDGNSPVR          | 8 P48444  | COPD_HUN  | 485  |
| Structure | LEDTKLIK                      | 4 P48643  | TCPE_HUM  | 223  |
|           | DSKTSSAEVTIQNVIK              | 2 P48960  | CD97_HUN  | 290  |
| Phyre     | LSYNTASNKTR                   | 8 P49207  | RL34_HUM  | 19   |
| Phyre     | AQAQSQKAK                     | 6 P49207  | RL34_HUM  | 115  |
| Phyre     | LSYNTASNKTR                   | 8 P49207  | RL34_HUM  | 19   |
| Phyre     | NKWFFQK                       | 1 P61353  | RL27_HUM  | 128  |
| Docking   | NKPYPVR                       | 1 P49257  | LMAN1_HL  | 197  |
| Docking   | YVSSLTEEISKR                  | 10 P49257 | LMAN1_HL  | 372  |
|           | KRKPEEESPR                    | 0 P49321  | NASP_HUN  | 719  |
| Phyre     | GLKPSTIIPLMKK                 | 12 P49327 | FAS_HUMA  | 786  |
| Structure | GVQKLVLTSR                    | 3 P49327  | FAS_HUMA  | 1911 |
| Phyre     | DGVVRPLKCTVFHGAQVEDAFR        | 7 P49327  | FAS_HUMA  | 1827 |
| Phyre     | DIMLATGKLSPDAIPGK             | 7 P49327  | FAS_HUMA  | 1582 |
| Phyre     | DIM[147.04]LATGKLSPDAIPGK     | 7 P49327  | FAS_HUMA  | 1582 |

|           |                            |    |        |          |      |
|-----------|----------------------------|----|--------|----------|------|
| Phyre     | GVDLVLSLAEEKLQASVR         | 12 | P49327 | FAS_HUMA | 1752 |
| Phyre     | DGVVRPLKCTVFHGAQVEDAFR     | 7  | P49327 | FAS_HUMA | 1827 |
| Phyre     | DIMLATGKLSPPAIPGK          | 7  | P49327 | FAS_HUMA | 1582 |
| Phyre     | VFTTVGSAEKR                | 9  | P49327 | FAS_HUMA | 1704 |
|           | KYEEIDNAPEER               | 0  | P49411 | EFTU_HUN | 91   |
| Phyre     | IVAVTGAEQAQKALR            | 10 | P49588 | SYAC_HUN | 762  |
| Phyre     | KCLSVMEAK                  | 0  | P49588 | SYAC_HUN | 772  |
| Phyre     | KCLSV[147.04]EAK           | 0  | P49588 | SYAC_HUN | 772  |
| Phyre     | AVYTQDCPLAAAKAIQGLR        | 12 | P49588 | SYAC_HUN | 677  |
| Structure | YKYGYEIPVDMCLK             | 1  | P60900 | PSA6_HUN | 104  |
|           | LNLYELKEGR                 | 6  | P49720 | PSB3_HUN | 77   |
| Phyre     | IQESPGKVAAGR               | 6  | P49736 | MCM2_HU  | 384  |
| Structure | KGIVNEQFLLQR               | 0  | P49748 | ACADV_HU | 556  |
| Structure | EKITAFVVER                 | 1  | P49748 | ACADV_HU | 278  |
|           | KPAKAESKSFVGMFK            | 0  | P49748 | ACADV_HU | 64   |
| Structure | TQFGEKIHNFGLIQEK           | 5  | P49748 | ACADV_HU | 372  |
| Structure | KGIVNEQFLLQR               | 0  | P49748 | ACADV_HU | 556  |
|           | SVYFKPSLTPSGEFR            | 4  | P49790 | NU153_HU | 384  |
|           | FKLQDVADSK                 | 1  | P49792 | RBP2_HUN | 2424 |
|           | LYEAKYDLAK                 | 5  | P49792 | RBP2_HUN | 40   |
|           | ESPCGKIAVAVLEETTR          | 5  | P49792 | RBP2_HUN | 2466 |
| Structure | TKEILLK                    | 1  | P49821 | NDUV1_HL | 66   |
| Structure | ELFVQSEIFPLETPAFAIKEQGFR   | 18 | P49915 | GUAA_HUN | 65   |
| Structure | GLQKEEVLLTHGDSVDK          | 3  | P49915 | GUAA_HUN | 145  |
| Phyre     | NPYYGGESASITPLEDLYKR       | 18 | P50395 | GDIB_HUN | 54   |
| Phyre     | LSPKAATLAER                | 3  | P50454 | SERPH_HU | 39   |
| Phyre     | SPKLFYADHPFIFLVR           | 2  | P50454 | SERPH_HU | 380  |
| Structure | KYM[147.04]LPLDNLK         | 0  | P50570 | DYN2_HUN | 562  |
| Structure | IGQGTGGEVFKAR              | 10 | P50750 | CDK9_HUN | 35   |
|           | VPAQKATGQK                 | 4  | P50914 | RL14_HUN | 182  |
|           | APAPKASGK                  | 4  | P50914 | RL14_HUN | 209  |
|           | ATGQKAAPAK                 | 4  | P50914 | RL14_HUN | 187  |
|           | KAPAKVPAQK                 | 5  | P50914 | RL14_HUN | 177  |
|           | VPAQKATGQK                 | 4  | P50914 | RL14_HUN | 182  |
|           | APAKVPAQK                  | 4  | P50914 | RL14_HUN | 177  |
|           | VPAQKATGQK                 | 4  | P50914 | RL14_HUN | 182  |
|           | KAPAKVPAQK                 | 5  | P50914 | RL14_HUN | 177  |
|           | APAKVPAQK                  | 4  | P50914 | RL14_HUN | 177  |
| Phyre     | AVDDGVNTFKVLTR             | 9  | P50990 | TCPQ_HUN | 400  |
| Phyre     | AVDDGVNTFKVLTR             | 9  | P50990 | TCPQ_HUN | 400  |
| Phyre     | LCKTVGATALPR               | 2  | P50990 | TCPQ_HUN | 326  |
| Phyre     | RLCKTVGATALPR              | 3  | P50990 | TCPQ_HUN | 326  |
| Phyre     | AIADTGANVVVTGGKVADMALHYANK | 14 | P50990 | TCPQ_HUN | 296  |
| Phyre     | DALSDLALHFLNKMK            | 12 | P50991 | TCPD_HUN | 319  |
| Phyre     | DALSDLALHFLNKM[147.04]K    | 12 | P50991 | TCPD_HUN | 319  |
| Phyre     | FSNISAAKAVADAIR            | 7  | P50991 | TCPD_HUN | 42   |
| Phyre     | GKGAYQDR                   | 1  | P50991 | TCPD_HUN | 21   |

|           |                                |           |           |      |
|-----------|--------------------------------|-----------|-----------|------|
| Phyre     | KLGGTIDDCELVEGLVLTQK           | 0 P50991  | TCPD_HUN  | 213  |
| Phyre     | AYILNLVKQIK                    | 7 P50991  | TCPD_HUN  | 288  |
| Phyre     | DALSDLALHFLNKMK                | 12 P50991 | TCPD_HUN  | 319  |
| Phyre     | VDNIIKAAPR                     | 5 P78371  | TCPB_HUN  | 522  |
|           | VDNIIKAAPR                     | 5 P78371  | TCPB_HUN  | 522  |
| Phyre     | VAEIEHAEKEK                    | 8 P78371  | TCPB_HUN  | 272  |
| Phyre     | AYILNLVKQIK                    | 7 P50991  | TCPD_HUN  | 288  |
|           | AYKAEFK                        | 2 P50995  | ANX11_HU  | 315  |
| Phyre     | ESTEGSPLGEVVEQGTR              | 4 P51398  | RT29_HUN  | 218  |
| Phyre     | KAYLPQELLGK                    | 0 P51398  | RT29_HUN  | 321  |
|           | KEKAQDR                        | 0 P51532  | SMCA4_HL  | 1602 |
|           | GGNIGAKWTIDLK                  | 6 P51659  | DHB4_HUN  | 663  |
| Structure | GGKAVANYDSVEEGEK               | 2 P51659  | DHB4_HUN  | 68   |
| Phyre     | KLFIGGLSFETDDSLR               | 0 P51991  | ROA3_HUN  | 36   |
| Phyre     | MLKDKFNECGHVLADIK              | 2 P52272  | HNRPM_HI  | 670  |
|           | GEIIAKQGGGGGGGSPGIER           | 5 P52272  | HNRPM_HI  | 388  |
| Phyre     | GCGVVKFESPEVAER                | 5 P52272  | HNRPM_HI  | 698  |
| Phyre     | GCGVVKFESPEVAER                | 5 P52272  | HNRPM_HI  | 698  |
| Structure | GSYSIKSR                       | 5 P52565  | GDIR1_HUI | 178  |
| Phyre     | GLPYKATENDIYNFFSPLNPVR         | 4 P52597  | HNRPF_HU  | 299  |
|           | LLKPYTGSK                      | 2 P52701  | MSH6_HUI  | 149  |
| Structure | TQANDYFKAK                     | 7 P53041  | PPP5_HUM  | 40   |
| Structure | LLQDHPWLLSQNLVVKPDQLIKR        | 21 P53396 | ACLY_HUM  | 64   |
| Structure | AQKLLVGVDK                     | 2 P53396  | ACLY_HUM  | 151  |
| Structure | LGQEATVGKATGFLK                | 8 P53396  | ACLY_HUM  | 97   |
| Phyre     | LLELGPKEVAQQTR                 | 6 P53621  | COPA_HUN  | 1134 |
| Phyre     | VLTIDPTEFKFK                   | 9 P53621  | COPA_HUN  | 598  |
|           | DDNMFQIGKMR                    | 8 P53999  | TCP4_HUN  | 68   |
|           | KGISLNPEQWSQLK                 | 0 P53999  | TCP4_HUN  | 101  |
| Structure | KGISLNPEQWSQLK                 | 0 P53999  | TCP4_HUN  | 101  |
| Structure | KGISLNPEQWSQLK                 | 0 P53999  | TCP4_HUN  | 101  |
| Structure | KGISLNPEQWSQLK                 | 0 P53999  | TCP4_HUN  | 101  |
| Structure | EYWMDPEGEMKPGR                 | 10 P53999 | TCP4_HUN  | 97   |
| Structure | KGISLNPEQWSQLK                 | 0 P53999  | TCP4_HUN  | 101  |
|           | ALSSSKQSSSR                    | 5 P53999  | TCP4_HUN  | 53   |
| Docking   | KAGAEVVK                       | 0 P54577  | SYYC_HUM  | 147  |
| Structure | KIFTFAEK                       | 0 P54577  | SYYC_HUM  | 190  |
| Structure | FFYKEK                         | 3 P54578  | UBP14_HU  | 334  |
| Phyre     | IDCVSKNEDIPNAVYPHNGMIDLK       | 5 P54709  | AT1B3_HU  | 194  |
| Phyre     | VMFKITAR                       | 3 P54709  | AT1B3_HU  | 274  |
| Phyre     | IDCVSKNEDIPNAVYPHNGM[147.04]IC | 5 P54709  | AT1B3_HU  | 194  |
| Phyre     | IDCVSKNEDIPNAVYPHNGMIDLK       | 5 P54709  | AT1B3_HU  | 194  |
| Phyre     | IDCVSKNEDIPNAVYPHNGM[147.04]IC | 5 P54709  | AT1B3_HU  | 194  |
| Phyre     | IDGSANLKSQDDR                  | 7 P54709  | AT1B3_HU  | 259  |
| Phyre     | IDGSANLKSQDDRDK                | 7 P54709  | AT1B3_HU  | 259  |
| Phyre     | EVTVECKIDGSANLK                | 6 P54709  | AT1B3_HU  | 251  |
| Phyre     | IDCVSKNEDIPNAVYPHNGMIDLK       | 5 P54709  | AT1B3_HU  | 194  |

|           |                              |    |        |           |      |
|-----------|------------------------------|----|--------|-----------|------|
| Phyre     | SQDDRDKFLGR                  | 6  | P54709 | AT1B3_HU  | 266  |
| Phyre     | SQDDRDKFLGR                  | 6  | P54709 | AT1B3_HU  | 266  |
| Phyre     | SDPTSYAGYIEDLKK              | 13 | P54709 | AT1B3_HU  | 111  |
|           | NAKFYPVTR                    | 2  | P54851 | EMP2_HUN  | 129  |
| Phyre     | EFLEDTCVQYVQKHISAENTK        | 12 | Q9UNN8 | EPCR_HUN  | 192  |
|           | LIDIFYPGDQQSVTFGTKSR         | 17 | P54886 | P5CS_HUM  | 300  |
| Structure | LSLSTSKLNSLAIGLR             | 6  | P54886 | P5CS_HUM  | 432  |
| Structure | FASYLTFSPSEVKSLR             | 12 | P54886 | P5CS_HUM  | 662  |
| Structure | KGDIFLVR                     | 0  | P55072 | TERA_HUN  | 148  |
| Structure | IVSQLLTLMMDGLKQR             | 12 | P55072 | TERA_HUN  | 336  |
| Structure | LDQLIYIPLPDEKSR              | 12 | P55072 | TERA_HUN  | 651  |
| Structure | KYEMFAQTLQQSR                | 0  | P55072 | TERA_HUN  | 754  |
| Structure | KYEMFAQTLQQSR                | 0  | P55072 | TERA_HUN  | 754  |
| Structure | KYEM[147.04]FAQTLQQSR        | 0  | P55072 | TERA_HUN  | 754  |
| Structure | LDQLIYIPLPDEKSR              | 12 | P55072 | TERA_HUN  | 651  |
|           | AQPAVNGKLGVPNGR              | 7  | P55199 | ELL_HUMA  | 355  |
| Phyre     | KYAVLYQPLFDK                 | 0  | P55209 | NP1L1_HU  | 105  |
| Phyre     | YAVLYQPLFDKR                 | 10 | P55209 | NP1L1_HU  | 116  |
|           | VLIGENKAER                   | 7  | P55265 | DSRAD_HU  | 798  |
|           | KILAAIIMK                    | 0  | P55265 | DSRAD_HU  | 867  |
| Structure | AWKADR                       | 2  | P55809 | SCOT1_HU  | 214  |
| Modeller  | SAKPGDDVR                    | 2  | P55809 | SCOT1_HU  | 296  |
| Modeller  | YGDLANWMIPGKMVK              | 11 | P55809 | SCOT1_HU  | 418  |
| Phyre     | IFEQKDR                      | 4  | P55884 | EIF3B_HUN | 734  |
| Phyre     | IKDMDLWEQQEEER               | 1  | Q14152 | EIF3A_HUN | 720  |
| Structure | AGMFVSKFFGGYVPEMVLTDPDDQR    | 6  | P56192 | SYMC_HUN  | 663  |
|           | QHNSCTTENKNEPCGAR            | 9  | P56199 | ITA1_HUM  | 563  |
|           | KVIQDCEDENIQR                | 0  | P56199 | ITA1_HUM  | 292  |
|           | ATTGYDPYPYGGEKLALFQAIGK      | 12 | P58107 | EPIPL_HUN | 130  |
|           | DPFSGKQVSVFQAMK              | 5  | P58107 | EPIPL_HUN | 1018 |
|           | LEHGQATAKDVGSLASVQR          | 8  | P58107 | EPIPL_HUN | 594  |
|           | FVDPNTQEKVSUR                | 8  | P58107 | EPIPL_HUN | 2062 |
| Phyre     | SSKELLLQPVITSR               | 2  | P59998 | ARPC4_HU  | 44   |
| Structure | GWLKSNVSDAVAQSTR             | 3  | P60174 | TPIS_HUM  | 231  |
| Structure | VVLAYEPVWAIGTGKTATPQQAQEVHEK | 14 | P60174 | TPIS_HUM  | 212  |
| Structure | TATPQQAQEVHEKLR              | 12 | P60174 | TPIS_HUM  | 225  |
| Phyre     | QVLKDLVK                     | 3  | P60228 | EIF3E_HUN | 275  |
| Phyre     | SQM[147.04]LAMNIEKK          | 9  | P60228 | EIF3E_HUN | 424  |
| Phyre     | KYLELSKNGTEPESFHK            | 6  | Q504Q3 | PAN2_HUN  | 1155 |
| Phyre     | MQKGDPPQVYEELFSYSCPK         | 2  | Q9Y262 | EIF3L_HUN | 403  |
| Phyre     | MQKGDPPQVYEELFSYSCPK         | 2  | Q9Y262 | EIF3L_HUN | 403  |
|           | SPSKAAR                      | 3  | P60468 | SC61B_HUI | 20   |
| Phyre     | SDEMNVKVLDFEHFLPMLQTVAK      | 6  | P60660 | MYL6_HUN  | 63   |
| Phyre     | ALGQNPTNAEVLKVLGNPK          | 12 | P60660 | MYL6_HUN  | 50   |
| Structure | VAPEEHPVLLTEAPLNPKANR        | 17 | P60709 | ACTB_HUN  | 113  |
| Structure | VAPEEHPVLLTEAPLNPKANR        | 17 | P60709 | ACTB_HUN  | 113  |
| Structure | KDLYANTVLSGGTMMYPGIADR       | 0  | P60709 | ACTB_HUN  | 291  |

|           |                                |           |           |     |
|-----------|--------------------------------|-----------|-----------|-----|
| Structure | KDLYANTVLSGGTTM[147.04]YPGIADR | 0 P60709  | ACTB_HUN  | 291 |
| Structure | KDLYANTVLSGGTTMYPGIADR         | 0 P60709  | ACTB_HUN  | 291 |
| Structure | KDLYANTVLSGGTTM[147.04]YPGIADR | 0 P60709  | ACTB_HUN  | 291 |
| Structure | KDLYANTVLSGGTTMYPGIADR         | 0 P60709  | ACTB_HUN  | 291 |
| Structure | KDLYANTVLSGGTTM[147.04]YPGIADR | 0 P60709  | ACTB_HUN  | 291 |
| Structure | KDLYANTVLSGGTTMYPGIADR         | 0 P60709  | ACTB_HUN  | 291 |
| Structure | KDLYANTVLSGGTTMYPGIADR         | 0 P60709  | ACTB_HUN  | 291 |
| Structure | GILTLKYPIEHGIVTNWDDMEK         | 5 P60709  | ACTB_HUN  | 68  |
| Structure | HQGVMVGMGQKDSYVGDEAQS          | 10 P60709 | ACTB_HUN  | 50  |
| Structure | HQGVM[147.04]VGMGQKDSYVGDEAQ   | 10 P60709 | ACTB_HUN  | 50  |
| Structure | GILTLKYPIEHGIITNWDDMEK         | 5 P68032  | ACTC_HUN  | 70  |
| Structure | GILTLKYPIEHGIITNWDDM[147.04]EK | 5 P68032  | ACTC_HUN  | 70  |
| Structure | DLTDYLMKILTER                  | 7 Q562R1  | ACTBL_HUI | 192 |
| Structure | GFKDQIYDIFQK                   | 2 P60842  | IF4A1_HUN | 193 |
| Structure | GIYAYGFEPKPSAIQQR              | 8 P60842  | IF4A1_HUN | 54  |
| Structure | KGVAINMVTEEDKR                 | 0 P60842  | IF4A1_HUN | 369 |
| Structure | GFKDQIYDIFQK                   | 2 P60842  | IF4A1_HUN | 193 |
| Structure | GFKDQIYEIFQK                   | 2 Q14240  | IF4A2_HUN | 194 |
| Structure | IM[147.04]KDLDQCR              | 2 P60903  | S10AA_HU  | 57  |
| Phyre     | IFYDMKVR                       | 5 P60981  | DEST_HUN  | 19  |
| Structure | IKLQLWDTAGQER                  | 1 P61006  | RAB8A_HU  | 58  |
| Phyre     | IYQNIQDGSLDLNAAESGVQHKPSAPQGC  | 21 P61106 | RAB14_HU  | 193 |
| Phyre     | DKDNFWMTR                      | 1 P61160  | ARP2_HUN  | 368 |
|           | EKLCYVGYNIEQEQK                | 1 P61160  | ARP2_HUN  | 219 |
| Phyre     | ACYLSINPQKDETLETEK             | 9 P61163  | ACTZ_HUN  | 230 |
| Phyre     | ACYLSINPQKDETLETEK             | 9 P61163  | ACTZ_HUN  | 230 |
| Structure | LWFKTNTK                       | 3 P61201  | CSN2_HUN  | 150 |
| Modeller  | AAKGTVGSILDR                   | 2 P61221  | ABCE1_HU  | 181 |
| Modeller  | ILAGKQKPNLGK                   | 4 P61221  | ABCE1_HU  | 126 |
| Modeller  | STALKILAGK                     | 4 P61221  | ABCE1_HU  | 121 |
| Structure | KTSYAQHQQVR                    | 0 P61247  | RS3A_HUN  | 152 |
| Structure | TQGTKIASDGLK                   | 4 P61247  | RS3A_HUN  | 56  |
| Docking   | AKLVSK                         | 1 P61289  | PSME3_HU  | 188 |
| Phyre     | LLIEKCNTVK                     | 4 P61289  | PSME3_HU  | 132 |
| Phyre     | ITSEAEDLVANFFPKK               | 14 P61289 | PSME3_HU  | 36  |
| Phyre     | NKWFFQK                        | 1 P61353  | RL27_HUM  | 128 |
| Phyre     | AVIVKNIDDGTSRPPYSHALVAGIDR     | 4 P61353  | RL27_HUM  | 27  |
| Structure | SQGKVLQATVVAVGSGSK             | 3 P61604  | CH10_HUN  | 40  |
| Structure | GKGGEIQPVSVK                   | 1 P61604  | CH10_HUN  | 56  |
| Structure | VLQATVVAVGSGSKGK               | 13 P61604 | CH10_HUN  | 54  |
| Structure | DGDILGKYVD                     | 6 P61604  | CH10_HUN  | 99  |
| Structure | GGEIQPVSVKVGDK                 | 9 P61604  | CH10_HUN  | 66  |
| Structure | GKGGEIQPVSVKVGDK               | 11 P61604 | CH10_HUN  | 66  |
| Structure | SAAETVTKGGIM[147.04]LPEK       | 7 P61604  | CH10_HUN  | 28  |
| Structure | VGDKVLLPEYGGTK                 | 3 P61604  | CH10_HUN  | 70  |
| Structure | VVLDDKDYFLFR                   | 5 P61604  | CH10_HUN  | 86  |
| Structure | VLLPEYGGTKVVLDDKDYFLFR         | 9 P61604  | CH10_HUN  | 80  |

|           |                          |    |        |           |     |
|-----------|--------------------------|----|--------|-----------|-----|
| Structure | VLLPEYGGTKVVLDDDKDYFLFR  | 9  | P61604 | CH10_HUM  | 80  |
| Structure | SAAETVTKGGIMLPEK         | 7  | P61604 | CH10_HUM  | 28  |
| Structure | SAAETVTKGGIM[147.04]LPEK | 7  | P61604 | CH10_HUM  | 28  |
| Structure | VLLPEYGGTKVVLDDDKDYFLFR  | 9  | P61604 | CH10_HUM  | 80  |
| Structure | VVLDDDKDYFLFR            | 5  | P61604 | CH10_HUM  | 86  |
| Structure | SAAETVTKGGIMLPEK         | 7  | P61604 | CH10_HUM  | 28  |
| Structure | SAAETVTKGGIM[147.04]LPEK | 7  | P61604 | CH10_HUM  | 28  |
| Structure | VNHVTL SQPKIVK           | 9  | P61769 | B2MG_HUI  | 111 |
|           | VNHVTL SQPKIVK           | 9  | P61769 | B2MG_HUI  | 111 |
| Structure | HESGASIKIDEPLEGSEDR      | 7  | P61978 | HNRPK_HU  | 422 |
| Phyre     | HESGASIKIDEPLEGSEDR      | 7  | P61978 | HNRPK_HU  | 422 |
| Phyre     | LLIHQSLAGGIIGVKGAK       | 14 | P61978 | HNRPK_HU  | 163 |
| Phyre     | NAGAVIGKGGK              | 7  | P61978 | HNRPK_HU  | 60  |
| Phyre     | ENTQTTIKLFQECCPHSTDR     | 7  | P61978 | HNRPK_HU  | 179 |
| Structure | VISSIEQKTSADGNEK         | 7  | P61981 | 1433G_HU  | 69  |
| Structure | VISSIEQKTSADGNEK         | 7  | P61981 | 1433G_HU  | 69  |
| Structure | ELNITAAKEIEVGGGR         | 7  | P62081 | RS7_HUMA  | 49  |
| Structure | FSGKHVVFIQR              | 3  | P62081 | RS7_HUMA  | 90  |
| Structure | LIKVHLDK                 | 2  | P62081 | RS7_HUMA  | 155 |
| Structure | LWKTFDTCFNCLPIAAIVDEK    | 2  | P62136 | PP1A_HUM  | 150 |
| Structure | AGKIVVNLTGR              | 2  | P62244 | RS15A_HUI | 60  |
| Structure | DLEKWQNNLLPSR            | 3  | P62244 | RS15A_HUI | 88  |
| Structure | MNVLADALKSINNAEK         | 8  | P62244 | RS15A_HUI | 12  |
| Structure | LNKCGVISPR               | 2  | P62244 | RS15A_HUI | 71  |
| Structure | VEEIAASKCR               | 7  | Q02543 | RL18A_HUI | 136 |
| Structure | VKGGGHVAQIYAIR           | 1  | P62249 | RS16_HUM  | 73  |
| Structure | EIKDILIQYDR              | 2  | P62249 | RS16_HUM  | 109 |
| Structure | QSISKALVAYYQK            | 4  | P62249 | RS16_HUM  | 90  |
| Unknown   | LLEPVLLGKER              | 9  | P62249 | RS16_HUM  | 60  |
| Structure | NLLSVAYKNVIGAR           | 7  | P62258 | 1433E_HUI | 50  |
| Structure | NLLSVAYKNVIGAR           | 7  | P62258 | 1433E_HUI | 50  |
| Phyre     | KGHAVGDIPGVR             | 0  | P62266 | RS23_HUM  | 108 |
| Phyre     | VANVSLLALYKGK            | 10 | P62266 | RS23_HUM  | 135 |
|           | KGHAVGDIPGVR             | 0  | P62266 | RS23_HUM  | 108 |
| Structure | QYKIPDWFLNR              | 2  | P62269 | RS18_HUM  | 78  |
| Structure | KGLTPSQIGVILR            | 0  | P62277 | RS13_HUM  | 43  |
| Structure | SKGLAPDLPEDLYHLIK        | 1  | P62277 | RS13_HUM  | 78  |
| Structure | LTSDDVKEQIYK             | 6  | P62277 | RS13_HUM  | 34  |
| Structure | MHAPGKGLSQSALPYR         | 5  | P62277 | RS13_HUM  | 9   |
| Structure | SKGLAPDLPEDLYHLIK        | 1  | P62277 | RS13_HUM  | 78  |
| Structure | SVPTWLKLTSDDVK           | 6  | P62277 | RS13_HUM  | 27  |
| Structure | FVTGNKILR                | 5  | P62277 | RS13_HUM  | 70  |
| Structure | KGLTPSQIGVILR            | 0  | P62277 | RS13_HUM  | 43  |
| Structure | FVTGNKILR                | 5  | P62277 | RS13_HUM  | 70  |
| Structure | MHAPGKGLSQSALPYR         | 5  | P62277 | RS13_HUM  | 9   |
| Structure | YYKNIGLGFK               | 2  | P62280 | RS11_HUM  | 38  |
| Structure | EAIEGTYIDKK              | 9  | P62280 | RS11_HUM  | 58  |

|           |                         |           |           |     |
|-----------|-------------------------|-----------|-----------|-----|
| Phyre     | FVKWPR                  | 2 P62424  | RL7A_HUM  | 56  |
| Phyre     | HWGGNVLGPKSVAR          | 9 P62424  | RL7A_HUM  | 245 |
| Phyre     | LKVPPAINQFTQALDR        | 1 P62424  | RL7A_HUM  | 75  |
| Phyre     | TCTTVAFTQVNSEDKGALAK    | 14 P62424 | RL7A_HUM  | 212 |
| Phyre     | LKVPPAINQFTQALDR        | 1 P62424  | RL7A_HUM  | 75  |
| Phyre     | HWGGNVLGPKSVAR          | 9 P62424  | RL7A_HUM  | 245 |
| Phyre     | AMELLKVS                | 5 Q9Y3U8  | RL36_HUM  | 62  |
| Phyre     | HWGGNVLGPKSVAR          | 9 P62424  | RL7A_HUM  | 245 |
| Phyre     | KMGVPYCIK               | 0 P62424  | RL7A_HUM  | 176 |
| Phyre     | LKVPPAINQFTQALDR        | 1 P62424  | RL7A_HUM  | 75  |
| Phyre     | HWGGNVLGPKSVAR          | 9 P62424  | RL7A_HUM  | 245 |
| Phyre     | LKVPPAINQFTQALDR        | 1 P62424  | RL7A_HUM  | 75  |
| Phyre     | AGVNTVTTLVENKK          | 12 P62424 | RL7A_HUM  | 150 |
| Structure | TIKAQIWDTAGQER          | 2 P62491  | RB11A_HU  | 61  |
| Structure | TIKAQIWDTAGQER          | 2 P62491  | RB11A_HU  | 61  |
| Structure | LIYDTKGR                | 5 P62701  | RS4X_HUM  | 106 |
| Structure | KIFVGTK                 | 0 P62701  | RS4X_HUM  | 128 |
| Structure | TDITYPAGFMDVISIDKTGENFR | 16 P62701 | RS4X_HUM  | 94  |
| Structure | LIYDTKGR                | 5 P62701  | RS4X_HUM  | 106 |
| Structure | GNKPWISLPR              | 2 P62701  | RS4X_HUM  | 233 |
| Phyre     | GILTLKYPIEHGIITNWDDMEK  | 5 P62736  | ACTA_HUM  | 70  |
| Phyre     | KIEDNNTLVFIVDVK         | 0 P62750  | RL23A_HUI | 89  |
| Phyre     | LYDIDVAKVNTLIRPDGEK     | 7 P62750  | RL23A_HUI | 123 |
| Structure | DAVTYTEHAKR             | 9 P62805  | H4_HUMAI  | 78  |
| Structure | DNIQGITKPAIR            | 7 P62805  | H4_HUMAI  | 32  |
| Structure | KTVTAMDVVYALK           | 0 P62805  | H4_HUMAI  | 80  |
| Structure | KTVTAMDVVYALKR          | 12 P62805 | H4_HUMAI  | 92  |
| Structure | KTVTAM[147.04]DVVYALK   | 0 P62805  | H4_HUMAI  | 80  |
| Structure | TVTAMDVVYALKR           | 11 P62805 | H4_HUMAI  | 92  |
| Structure | TVTAM[147.04]DVVYALKR   | 11 P62805 | H4_HUMAI  | 92  |
| Structure | GVLKVFLENVIR            | 3 P62805  | H4_HUMAI  | 60  |
| Phyre     | GGKGLGK                 | 2 P62805  | H4_HUMAI  | 9   |
| Phyre     | GLGKGGAK                | 3 P62805  | H4_HUMAI  | 13  |
| Structure | GVLKVFLENVIR            | 3 P62805  | H4_HUMAI  | 60  |
| Structure | KTVTAMDVVYALKR          | 12 P62805 | H4_HUMAI  | 92  |
| Structure | TVTAMDVVYALKR           | 11 P62805 | H4_HUMAI  | 92  |
| Structure | TVTAMDVVYALKR           | 11 P62805 | H4_HUMAI  | 92  |
| Structure | TVTAM[147.04]DVVYALKR   | 11 P62805 | H4_HUMAI  | 92  |
| Structure | TKQTAR                  | 1 P68431  | H31_HUM/  | 5   |
| Structure | VTIMPKDIQLAR            | 5 P68431  | H31_HUM/  | 123 |
| Structure | VTIM[147.04]PKDIQLAR    | 5 P68431  | H31_HUM/  | 123 |
| Structure | EIAQDFKTDLR             | 6 Q16695  | H31T_HUN  | 80  |
| Structure | VTIMPKDIQLAR            | 5 Q16695  | H31T_HUN  | 123 |
| Structure | VTIM[147.04]PKDIQLAR    | 5 Q16695  | H31T_HUN  | 123 |
| Structure | GVLKVFLENVIR            | 3 P62805  | H4_HUMAI  | 60  |
| Structure | KTVTAMDVVYALK           | 0 P62805  | H4_HUMAI  | 80  |
| Structure | KTVTAM[147.04]DVVYALK   | 0 P62805  | H4_HUMAI  | 80  |



|           |                         |    |        |          |     |
|-----------|-------------------------|----|--------|----------|-----|
| Structure | TVTAMDVVYALKR           | 11 | P62805 | H4_HUMAI | 92  |
| Phyre     | EIAQDFKTDLR             | 6  | Q16695 | H31T_HUN | 80  |
| Structure | KTVTAMDVVYALK           | 0  | P62805 | H4_HUMAI | 80  |
| Structure | YQKSTELLIR              | 2  | Q16695 | H31T_HUN | 57  |
| Phyre     | DAVTYTEHAKR             | 9  | P62805 | H4_HUMAI | 78  |
| Phyre     | GVLKVFLNVIR             | 3  | P62805 | H4_HUMAI | 60  |
| Structure | GVLKVFLNVIR             | 3  | P62805 | H4_HUMAI | 60  |
| Structure | GVLKVFLNVIR             | 3  | P62805 | H4_HUMAI | 60  |
| Structure | DAVTYTEHAKR             | 9  | P62805 | H4_HUMAI | 78  |
| Structure | TVTAMDVVYALKR           | 11 | P62805 | H4_HUMAI | 92  |
| Phyre     | DAVTYTEHAKR             | 9  | P62805 | H4_HUMAI | 78  |
| Phyre     | KTVTAMDVVYALK           | 0  | P62805 | H4_HUMAI | 80  |
| Phyre     | DAVTYTEHAKR             | 9  | P62805 | H4_HUMAI | 78  |
| Structure | LLLPGELAKHAVSEGK        | 8  | Q93079 | H2B1H_HU | 109 |
| Phyre     | AVTKYTSSK               | 3  | Q93079 | H2B1H_HU | 121 |
| Phyre     | HAVSEGKAVTK             | 7  | Q93079 | H2B1H_HU | 117 |
| Phyre     | DAVTYTEHAKR             | 9  | P62805 | H4_HUMAI | 78  |
| Phyre     | DAVTYTEHAKR             | 9  | P62805 | H4_HUMAI | 78  |
| Phyre     | KTVTAMDVVYALK           | 0  | P62805 | H4_HUMAI | 80  |
| Phyre     | TVTAMDVVYALKR           | 11 | P62805 | H4_HUMAI | 92  |
| Structure | LLLPGELAKHAVSEGK        | 8  | Q93079 | H2B1H_HU | 109 |
| Phyre     | DAVTYTEHAKR             | 9  | P62805 | H4_HUMAI | 78  |
| Phyre     | KTVTAMDVVYALK           | 0  | P62805 | H4_HUMAI | 80  |
| Phyre     | KTVTAMDVVYALKR          | 12 | P62805 | H4_HUMAI | 92  |
| Phyre     | TVTAMDVVYALKR           | 11 | P62805 | H4_HUMAI | 92  |
| Structure | LLLPGELAKHAVSEGK        | 8  | Q93079 | H2B1H_HU | 109 |
| Phyre     | DAVTYTEHAKR             | 9  | P62805 | H4_HUMAI | 78  |
| Phyre     | KTVTAMDVVYALK           | 0  | P62805 | H4_HUMAI | 80  |
| Phyre     | TVTAMDVVYALKR           | 11 | P62805 | H4_HUMAI | 92  |
| Phyre     | GVLKVFLNVIR             | 3  | P62805 | H4_HUMAI | 60  |
| Phyre     | KTVTAMDVVYALKR          | 12 | P62805 | H4_HUMAI | 92  |
| Phyre     | TVTAMDVVYALKR           | 11 | P62805 | H4_HUMAI | 92  |
| Phyre     | TVTAM[147.04]DVVYALKR   | 11 | P62805 | H4_HUMAI | 92  |
|           | AVTKYTSSK               | 3  | P62807 | H2B1C_HU | 121 |
| Structure | KNLQYYDISAK             | 0  | P62826 | RAN_HUM. | 142 |
| Structure | VTYKNVPNWHR             | 3  | P62826 | RAN_HUM. | 99  |
| Structure | KYVATLGVEVHPLVFHTNR     | 0  | P62826 | RAN_HUM. | 38  |
| Structure | VTYKNVPNWHR             | 3  | P62826 | RAN_HUM. | 99  |
| Structure | AKSIVFHR                | 1  | P62826 | RAN_HUM. | 134 |
| Structure | FNVWDTAGQEKFGGLR        | 10 | P62826 | RAN_HUM. | 71  |
| Structure | KKNLQYYDISAK            | 0  | P62826 | RAN_HUM. | 141 |
| Structure | KKNLQYYDISAK            | 1  | P62826 | RAN_HUM. | 142 |
| Structure | THFGGGKTTGFGMIYDSL DYAK | 6  | P62847 | RS24_HUM | 68  |
| Phyre     | DISEASVFDAYVLPKLYVK     | 14 | P62854 | RS26_HUM | 66  |
| Structure | VQPIKLAR                | 4  | P62857 | RS28_HUM | 10  |
| Phyre     | VTKVLGR                 | 2  | P62857 | RS28_HUM | 16  |
| Structure | FVNVVPTFGKK             | 9  | P62861 | RS30_HUM | 51  |

|           |                        |           |           |     |
|-----------|------------------------|-----------|-----------|-----|
| Phyre     | KACGDSTLTQITAGLDPVGR   | 0 P62879  | GBB2_HUN  | 23  |
| Structure | AKLVILANNCPALR         | 1 P62888  | RL30_HUM  | 44  |
| Structure | KSLESINSR              | 0 P62888  | RL30_HUM  | 9   |
| Structure | AKLVILANNCPALR         | 1 P62888  | RL30_HUM  | 44  |
| Phyre     | LNKAVWAK               | 2 P62899  | RL31_HUM  | 70  |
| Phyre     | LNKAVWAK               | 2 P62899  | RL31_HUM  | 70  |
| Phyre     | KYDAFLASESLIKQIPR      | 12 P62906 | RL10A_HUI | 118 |
| Phyre     | KVLCLAVAVGHVK          | 0 P62906  | RL10A_HUI | 161 |
| Phyre     | KYDAFLASESLIKQIPR      | 12 P62906 | RL10A_HUI | 118 |
| Phyre     | ILGPGLNKAGK            | 7 P62906  | RL10A_HUI | 130 |
| Phyre     | KYDAFLASESLIK          | 0 P62906  | RL10A_HUI | 106 |
|           | ILGPGLNKAGK            | 7 P62906  | RL10A_HUI | 130 |
| Phyre     | KFLVHNVK               | 0 P62910  | RL32_HUM  | 76  |
| Phyre     | SYCAEIAHNVSSKNR        | 12 P62910 | RL32_HUM  | 106 |
| Structure | VLEQLTGQTPVFSKAR       | 13 P62913 | RL11_HUM  | 52  |
| Phyre     | GAPLAKVVFR             | 5 P62917  | RL8_HUMA  | 60  |
| Phyre     | GAPLAKVVFR             | 5 P62917  | RL8_HUMA  | 60  |
| Phyre     | IDKPILK                | 2 P62917  | RL8_HUMA  | 177 |
| Structure | HNGTGGKSIYGEK          | 6 P62937  | PPIA_HUM  | 76  |
| Structure | VSFELFADKVPK           | 8 P62937  | PPIA_HUM  | 28  |
| Structure | VSFELFADKVPKTAENFR     | 11 P62937 | PPIA_HUM  | 31  |
| Structure | HNGTGGKSIYGEK          | 6 P62937  | PPIA_HUM  | 76  |
| Structure | VSFELFADKVPK           | 8 P62937  | PPIA_HUM  | 28  |
| Structure | HNGTGGKSIYGEK          | 6 P62937  | PPIA_HUM  | 76  |
| Structure | HNGTGGKSIYGEKFEDENFILK | 6 P62937  | PPIA_HUM  | 76  |
| Unknown   | VSFELFADKVPKTAENFR     | 11 P62937 | PPIA_HUM  | 31  |
| Structure | VKEGMNIVEAMER          | 1 P62937  | PPIA_HUM  | 133 |
| Structure | VKEGM[147.04]NIVEAMER  | 1 P62937  | PPIA_HUM  | 133 |
| Structure | TLSDYNIQESTLHLVLR      | 8 P62987  | RL40_HUM  | 63  |
| Structure | TLSDYNIQESTLHLVLR      | 8 P62987  | RL40_HUM  | 63  |
| Structure | TLTGKTITLEVEPSDTIENVK  | 4 P62987  | RL40_HUM  | 11  |
| Structure | IQDKEGIPPDQQR          | 3 P62987  | RL40_HUM  | 33  |
| Structure | TLSDYNIQESTLHLVLR      | 8 P62987  | RL40_HUM  | 63  |
| Structure | IQDKEGIPPDQQR          | 3 P62987  | RL40_HUM  | 33  |
| Phyre     | LIFAGKQLEDGR           | 5 P62987  | RL40_HUM  | 48  |
| Structure | LIFAGKQLEDGR           | 5 P62987  | RL40_HUM  | 48  |
| Structure | LIFAGKQLEDGR           | 5 P62987  | RL40_HUM  | 48  |
| Structure | LLPGELAKHAVSEGTK       | 8 Q93079  | H2B1H_HU  | 109 |
| Structure | VVSSIEQKTEGAEK         | 7 P63104  | 1433Z_HUI | 68  |
| Structure | AKLAEQAER              | 1 P63104  | 1433Z_HUI | 11  |
| Structure | VVSSIEQKTEGAEK         | 7 P63104  | 1433Z_HUI | 68  |
| Structure | VVSSIEQKTEGAEK         | 7 P63104  | 1433Z_HUI | 68  |
| Structure | VVSSIEQKTEGAEEK        | 13 P63104 | 1433Z_HUI | 74  |
| Structure | NLLSVAYKNVVGAR         | 7 P63104  | 1433Z_HUI | 49  |
| Structure | VIGQDSSEIHFKVK         | 11 P63165 | SUMO1_HI  | 37  |
| Structure | FSPNSSNPPIIVSCGWDKLVK  | 16 P63244 | RACK1_HU  | 172 |
| Structure | KGTPWEGGLFK            | 0 P63279  | UBC9_HUN  | 49  |

|           |                                |           |           |     |
|-----------|--------------------------------|-----------|-----------|-----|
| Phyre     | GAEEANVTGPGGVPVQGSKYAADR       | 18 P67809 | YBOX1_HU  | 137 |
| Phyre     | KLVILEGELER                    | 0 P67936  | TPM4_HUM  | 132 |
| Phyre     | IKIIAPPER                      | 1 P68032  | ACTC_HUM  | 330 |
| Phyre     | GILTLKYPIEHGIITNWDDMEK         | 5 P68032  | ACTC_HUM  | 70  |
| Phyre     | GILTLKYPIEHGIITNWDDMEK         | 5 P68032  | ACTC_HUM  | 70  |
| Phyre     | GILTLKYPIEHGIITNWDDMEK         | 5 P68032  | ACTC_HUM  | 70  |
| Phyre     | GILTLKYPIEHGIITNWDDMEK         | 5 P68032  | ACTC_HUM  | 70  |
| Phyre     | GILTLKYPIEHGIITNWDDMEK         | 5 P68032  | ACTC_HUM  | 70  |
| Phyre     | DSYVGDEAQSKR                   | 10 P68032 | ACTC_HUM  | 63  |
| Phyre     | HQGVMVGMGQKDSYVGDEAQSK         | 10 P68032 | ACTC_HUM  | 52  |
| Phyre     | HQGVM[147.04]VGM[147.04]GQKDSY | 10 P68032 | ACTC_HUM  | 52  |
| Docking   | IKIIAPPER                      | 1 P68032  | ACTC_HUM  | 330 |
| Phyre     | MQKEITALAPSTMK                 | 2 P68032  | ACTC_HUM  | 317 |
| Phyre     | MQKEITALAPSTM[147.04]K         | 2 P68032  | ACTC_HUM  | 317 |
| Phyre     | M[147.04]QKEITALAPSTMK         | 2 P68032  | ACTC_HUM  | 317 |
| Phyre     | M[147.04]QKEITALAPSTM[147.04]K | 2 P68032  | ACTC_HUM  | 317 |
| Phyre     | FHKLQNVQIALDYL                 | 2 Q15149  | PLEC_HUM  | 236 |
| Phyre     | IEKYNVPLNR                     | 2 Q9UHB6  | LIMA1_HU  | 189 |
| Phyre     | MAKYQAAVSK                     | 2 Q9UHB6  | LIMA1_HU  | 273 |
| Structure | TKIYHPNIDEK                    | 1 P68036  | UB2L3_HU  | 73  |
|           | LPLQDVYKIGGIGTVPVGR            | 7 P68104  | EF1A1_HU  | 255 |
| Phyre     | EHALLAYTLGVKQLIVGVNK           | 11 P68104 | EF1A1_HU  | 146 |
| Phyre     | QTVAVGVKAVDK                   | 8 P68104  | EF1A1_HU  | 439 |
| Phyre     | QTVAVGVKAVDKK                  | 8 P68104  | EF1A1_HU  | 439 |
| Phyre     | VTKSAQK                        | 2 P68104  | EF1A1_HU  | 453 |
| Phyre     | KDGNASGTTLLEALDCILPPTPTDKPLR   | 25 P68104 | EF1A1_HU  | 244 |
| Docking   | LPLQDVYKIGGIGTVPVGR            | 7 P68104  | EF1A1_HU  | 255 |
| Phyre     | VETGVLPKPGMVVTFAPVNVTEVK       | 6 P68104  | EF1A1_HU  | 273 |
| Phyre     | DGNASGTTLLEALDCILPPTPTDKPLR    | 24 P68104 | EF1A1_HU  | 244 |
|           | AAGAGKVTK                      | 5 P68104  | EF1A1_HU  | 450 |
|           | LPLQDVYKIGGIGTVPVGR            | 7 P68104  | EF1A1_HU  | 255 |
| Phyre     | LPLQDVYKIGGIGTVPVGR            | 7 P68104  | EF1A1_HU  | 255 |
|           | LPLQDVYKIGGIGTVPVGR            | 7 P68104  | EF1A1_HU  | 255 |
| Phyre     | STTTGHLYKCGGIDKR               | 15 P68104 | EF1A1_HU  | 36  |
| Phyre     | DVNAAIATIKTK                   | 9 Q71U36  | TBA1A_HU  | 336 |
| Phyre     | YQKSTELLIR                     | 2 P68431  | H31_HUM/  | 57  |
| Phyre     | YQKSTELLIR                     | 2 P68431  | H31_HUM/  | 57  |
| Phyre     | KQLATKAAR                      | 5 P68431  | H31_HUM/  | 24  |
| Phyre     | KQLATK                         | 0 P68431  | H31_HUM/  | 19  |
| Phyre     | TKQTAR                         | 1 P68431  | H31_HUM/  | 5   |
| Phyre     | EIAQDFKTDLR                    | 6 P68431  | H31_HUM/  | 80  |
| Phyre     | KQLATKAAR                      | 0 P68431  | H31_HUM/  | 19  |
| Phyre     | KQLATKAAR                      | 5 P68431  | H31_HUM/  | 24  |
| Phyre     | KQLATKAAR                      | 5 P68431  | H31_HUM/  | 24  |
|           | EDLQLDKPASGVKEEWYAR            | 12 P78347 | GTF2I_HUM | 456 |
|           | EFNF EKWNAR                    | 5 P78347  | GTF2I_HUM | 353 |
|           | EDLQLDKPASGVKEEWYAR            | 12 P78347 | GTF2I_HUM | 456 |

|           |                           |           |           |      |
|-----------|---------------------------|-----------|-----------|------|
| Phyre     | VAEIEHAEKEK               | 8 P78371  | TCPB_HUM  | 272  |
| Docking   | SLHDALCVLAQTVKDSR         | 13 P78371 | TCPB_HUM  | 402  |
| Structure | NKPEWFFK                  | 1 P78417  | GSTO1_HU  | 59   |
| Structure | SLGKGSAPPGPVPEGSIR        | 3 P78417  | GSTO1_HU  | 11   |
| Structure | HEVININLKNKPEWFFK         | 8 P78417  | GSTO1_HU  | 57   |
|           | YFEGVSPKSLK               | 7 P78527  | PRKDC_HU  | 689  |
| Structure | DLLLNTMSQEEKAAYLSDPR      | 11 P78527 | PRKDC_HU  | 3825 |
|           | NVDSNNKELSAIR             | 6 P78527  | PRKDC_HU  | 357  |
|           | YFEGVSPKSLK               | 7 P78527  | PRKDC_HU  | 689  |
| Structure | NVDSNNKELSAIR             | 6 P78527  | PRKDC_HU  | 357  |
|           | DQEKLSLMYAR               | 3 P78527  | PRKDC_HU  | 2738 |
|           | KAALSALESFLK              | 0 P78527  | PRKDC_HU  | 310  |
| Structure | LMDEFKIGELFSK             | 5 P78527  | PRKDC_HU  | 148  |
| Structure | NTCTSVYTKDR               | 8 P78527  | PRKDC_HU  | 117  |
|           | TKNLSSNEAISLEEIR          | 1 P78527  | PRKDC_HU  | 838  |
| Structure | LMDEFKIGELFSK             | 5 P78527  | PRKDC_HU  | 148  |
|           | SPQEVKPGEK                | 5 P78536  | ADA17_HU  | 292  |
| Structure | NQKPEVR                   | 2 P83731  | RL24_HUM  | 97   |
| Structure | AITGASLADIMAKR            | 12 P83731 | RL24_HUM  | 93   |
| Structure | AITGASLADIM[147.04]AKR    | 12 P83731 | RL24_HUM  | 93   |
| Phyre     | MPEKVTWMR                 | 3 P84098  | RL19_HUM  | 92   |
| Phyre     | M[147.04]PEKVTWM[147.04]R | 3 P84098  | RL19_HUM  | 92   |
| Phyre     | KGTANAR                   | 0 P84098  | RL19_HUM  | 82   |
| Phyre     | KPVTVHSR                  | 0 P84098  | RL19_HUM  | 53   |
| Structure | KTGQAPGYSYTAANK           | 0 P99999  | CYC_HUM   | 40   |
| Structure | FKEQLTPSQIMSLEK           | 1 Q00059  | TFAM_HUM  | 118  |
| Structure | KIYQDAYR                  | 0 Q00059  | TFAM_HUM  | 97   |
| Structure | AEWQVYKEEISR              | 6 Q00059  | TFAM_HUM  | 111  |
| Structure | AEWQVYKEEISR              | 6 Q00059  | TFAM_HUM  | 111  |
| Phyre     | EKGSSASVLK                | 1 Q00325  | MPCP_HUM  | 295  |
| Structure | VKELQAEQEDR               | 1 Q00341  | VIGLN_HUI | 1039 |
|           | KGAVITQIR                 | 0 Q00341  | VIGLN_HUI | 1071 |
|           | KGAVITQIR                 | 0 Q00341  | VIGLN_HUI | 1071 |
|           | LKDAYGK                   | 1 Q86Y13  | DZIP3_HUM | 1061 |
| Phyre     | LEKHELIEFR                | 2 Q00610  | CLH1_HUM  | 1501 |
| Phyre     | MYDAAKLLYNNVSNFGR         | 5 Q00610  | CLH1_HUM  | 1215 |
| Phyre     | IAAYLFKGNNR               | 6 Q00610  | CLH1_HUM  | 1516 |
| Phyre     | LKLLLPWLEAR               | 1 Q00610  | CLH1_HUM  | 856  |
| Phyre     | WKQSVELCK                 | 1 Q00610  | CLH1_HUM  | 1522 |
| Phyre     | LHIIIEVGTPPTGNQPFPPK      | 17 Q00610 | CLH1_HUM  | 245  |
| Phyre     | WLKEDKLECSEELGDLVK        | 2 Q00610  | CLH1_HUM  | 453  |
| Structure | KVSQPIEGHAASFAQFK         | 0 Q00610  | CLH1_HUM  | 189  |
| Phyre     | YIQAACKTGQIK              | 6 Q00610  | CLH1_HUM  | 737  |
| Phyre     | GQFSTDELVAEVEKR           | 13 Q00610 | CLH1_HUM  | 851  |
| Phyre     | GQFSTDELVAEVEKR           | 13 Q00610 | CLH1_HUM  | 851  |
| Phyre     | LEKHELIEFR                | 2 Q00610  | CLH1_HUM  | 1501 |
| Phyre     | EAKLTDQLPLIIVCDR          | 2 Q00610  | CLH1_HUM  | 767  |

|           |                           |    |        |           |      |
|-----------|---------------------------|----|--------|-----------|------|
|           | YLQMARKK                  | 6  | Q00610 | CLH1_HUM  | 1162 |
|           | APQCLGKFIEIAAR            | 6  | Q00839 | HNRPU_HL  | 565  |
|           | GYFEYIEENKYSR             | 9  | Q00839 | HNRPU_HL  | 265  |
|           | HLYTKDIDIHEVR             | 4  | Q00839 | HNRPU_HL  | 352  |
|           | QMADTGKLNTLLQR            | 6  | Q00839 | HNRPU_HL  | 551  |
|           | QM[147.04]ADTGKLNTLLQR    | 6  | Q00839 | HNRPU_HL  | 551  |
|           | TTWVTKHAAENPGK            | 5  | Q00839 | HNRPU_HL  | 516  |
|           | DEDYKQR                   | 4  | Q00839 | HNRPU_HL  | 614  |
|           | HAAENPGKYNILGTNTIMDK      | 7  | Q00839 | HNRPU_HL  | 524  |
|           | KMCLFAGFQR                | 0  | Q00839 | HNRPU_HL  | 592  |
|           | TTWVTKHAAENPGK            | 5  | Q00839 | HNRPU_HL  | 516  |
|           | APQCLGKFIEIAAR            | 6  | Q00839 | HNRPU_HL  | 565  |
|           | DLPEHAVLKMK               | 8  | Q00839 | HNRPU_HL  | 635  |
|           | DLPEHAVLKM[147.04]K       | 8  | Q00839 | HNRPU_HL  | 635  |
|           | KAEVEGKDLPEHAVLK          | 6  | Q00839 | HNRPU_HL  | 626  |
|           | KMCLFAGFQR                | 0  | Q00839 | HNRPU_HL  | 592  |
|           | QMADTGKLNTLLQR            | 6  | Q00839 | HNRPU_HL  | 551  |
|           | APQCLGKFIEIAAR            | 6  | Q00839 | HNRPU_HL  | 565  |
|           | DLPEHAVLKMK               | 8  | Q00839 | HNRPU_HL  | 635  |
|           | DLPEHAVLKM[147.04]K       | 8  | Q00839 | HNRPU_HL  | 635  |
|           | GYFEYIEENKYSR             | 9  | Q00839 | HNRPU_HL  | 265  |
|           | HLYTKDIDIHEVR             | 4  | Q00839 | HNRPU_HL  | 352  |
|           | GYFEYIEENKYSR             | 9  | Q00839 | HNRPU_HL  | 265  |
| Phyre     | EKPYPFPIPEEYTFIQNVPLEDR   | 1  | Q00839 | HNRPU_HL  | 464  |
|           | LAEISDVWEEMKTTLK          | 11 | Q01082 | SPTB2_HUI | 1048 |
|           | NEIDNYEEDYQKMR            | 11 | Q01082 | SPTB2_HUI | 1120 |
| Phyre     | KFANSLVGQQQLQAFNTYR       | 0  | Q01082 | SPTB2_HUI | 329  |
| Structure | LQAAYAGDKADDIQR           | 8  | Q01082 | SPTB2_HUI | 1878 |
| Structure | NDSFTTCIELGKSLAR          | 11 | Q01082 | SPTB2_HUI | 1975 |
| Phyre     | LISDINKAWER               | 6  | Q01082 | SPTB2_HUI | 394  |
|           | EASLGEASKLQQFLR           | 8  | Q01082 | SPTB2_HUI | 1063 |
|           | LFDANKAELFTQSCADLDK       | 5  | Q01082 | SPTB2_HUI | 1381 |
|           | EIGQSVDEVEKLIK            | 10 | Q01082 | SPTB2_HUI | 2054 |
| Phyre     | KASAFNSWFENAEEDLTPVR      | 0  | Q13813 | SPTN1_HUI | 2099 |
|           | GVNASAQKFATDGEQYKPCDPQVIR | 7  | Q01082 | SPTB2_HUI | 593  |
| Structure | IDFYFDENPYFENKVLSK        | 13 | Q01105 | SET_HUMA  | 150  |
|           | SSQTQNKASR                | 6  | Q01105 | SET_HUMA  | 189  |
| Structure | IDFYFDENPYFENKVLSK        | 13 | Q01105 | SET_HUMA  | 150  |
| Structure | VEVTEFEDIKSGYR            | 9  | Q01105 | SET_HUMA  | 132  |
| Structure | EFHLESGBPSSKSTEIK         | 12 | Q01105 | SET_HUMA  | 167  |
| Structure | IDFYFDENPYFENKVLSK        | 13 | Q01105 | SET_HUMA  | 150  |
| Structure | LNEQASEEILKVEQK           | 10 | Q01105 | SET_HUMA  | 68   |
|           | MLAAKSADGSAPAGEGEGVTLQR   | 4  | Q01650 | LAT1_HUM  | 30   |
| Structure | NFGTKISAR                 | 4  | Q01813 | PFKAP_HUI | 688  |
| Structure | KEWSGLLEELAR              | 0  | Q01813 | PFKAP_HUI | 139  |
| Structure | AMEWITAKLK                | 7  | Q01813 | PFKAP_HUI | 700  |
| Structure | FTTDDSIKVLGISKR           | 13 | Q01813 | PFKAP_HUI | 724  |

|           |                              |           |           |      |
|-----------|------------------------------|-----------|-----------|------|
| Structure | SFAGNLNTYKR                  | 9 Q01813  | PFKAP_HUI | 395  |
| Structure | NVIFQPVAELKK                 | 10 Q01813 | PFKAP_HUI | 736  |
| Structure | VLPGKYLEEIATQMR              | 4 Q01813  | PFKAP_HUI | 486  |
| Structure | LAIKLPDDQIPK                 | 3 Q01813  | PFKAP_HUI | 400  |
|           | KLADISLGK                    | 0 Q02413  | DSG1_HUN  | 757  |
| Phyre     | VEEIAASKCR                   | 7 Q02543  | RL18A_HUI | 136  |
| Phyre     | IFAPNHVVAKSR                 | 9 Q02543  | RL18A_HUI | 41   |
| Structure | ALELDSNNEKGLFR               | 9 Q02790  | FKBP4_HUI | 354  |
| Structure | LEQSTIVKER                   | 7 Q02790  | FKBP4_HUI | 274  |
| Structure | ALELDSNNEKGLFR               | 9 Q02790  | FKBP4_HUI | 354  |
| Phyre     | AVDSQILPKIK                  | 8 Q02878  | RL6_HUMA  | 260  |
| Structure | LHGGKDAASPR                  | 4 Q02880  | TOP2B_HU  | 819  |
|           | SFSKEVEER                    | 3 Q04637  | IF4G1_HUN | 1188 |
|           | KGEQCVHTASGPR                | 0 Q04721  | NOTC2_HU  | 1353 |
| Structure | RFEELGVKFVK                  | 7 Q04760  | LGUL_HUN  | 148  |
| Structure | RFEELGVKFVK                  | 7 Q04760  | LGUL_HUN  | 148  |
| Structure | FEELGVKFVK                   | 6 Q04760  | LGUL_HUN  | 148  |
| Structure | EDLCTKTENLLGSYFPK            | 5 Q06323  | PSME1_HU  | 24   |
| Structure | GLFIIDDKGILR                 | 7 Q06830  | PRDX1_HU  | 136  |
| Structure | IGHPAPNFKATAVMPDGQFK         | 8 Q06830  | PRDX1_HU  | 16   |
| Structure | IGHPAPNFKATAVM[147.04]PDGQFK | 8 Q06830  | PRDX1_HU  | 16   |
| Structure | KQGGLGPMNIPLVSDPK            | 0 Q06830  | PRDX1_HU  | 93   |
| Modeller  | AGGKILTFDQLALDSPK            | 3 Q07020  | RL18_HUM  | 119  |
| Modeller  | LLVKLYR                      | 3 Q07020  | RL18_HUM  | 30   |
| Modeller  | TNSTFNQVVLKR                 | 10 Q07020 | RL18_HUM  | 49   |
| Modeller  | ENKTAVVVGTITDDVR             | 2 Q07020  | RL18_HUM  | 78   |
| Modeller  | AGGKILTFDQLALDSPK            | 3 Q07020  | RL18_HUM  | 119  |
| Structure | NDDGKK                       | 4 Q07021  | C1QBP_HU  | 179  |
| Structure | TLPKMSGGWELELNGTEAK          | 3 Q07021  | C1QBP_HU  | 104  |
| Structure | TLPKM[147.04]SGGWELELNGTEAK  | 3 Q07021  | C1QBP_HU  | 104  |
| Phyre     | EIQTSAKSR                    | 6 Q07065  | CKAP4_HU  | 301  |
| Phyre     | SSQHKQDLTEK                  | 4 Q07065  | CKAP4_HU  | 182  |
| Phyre     | ISEVLQKLQNEILK               | 6 Q07065  | CKAP4_HU  | 206  |
| Docking   | ELVSLKQEQQAFK                | 5 Q07065  | CKAP4_HU  | 332  |
|           | LFVKVEK                      | 3 Q07065  | CKAP4_HU  | 594  |
| Docking   | ISEVLQKLQNEILK               | 6 Q07065  | CKAP4_HU  | 206  |
| Phyre     | SINDNIAIFTEVQKR              | 13 Q07065 | CKAP4_HU  | 260  |
| Phyre     | SINDNIAIFTEVQKR              | 13 Q07065 | CKAP4_HU  | 260  |
|           | GTPGEKGPR                    | 5 Q07092  | COGA1_HL  | 864  |
| Structure | NNLASCYLKQGK                 | 8 Q07866  | KLC1_HUM  | 393  |
| Phyre     | AAMEALVVEVTKQPAIISQLDPVNER   | 11 Q08211 | DHX9_HUN  | 1116 |
| Phyre     | ILAKLPIEPR                   | 3 Q08211  | DHX9_HUN  | 857  |
|           | LDSELKELR                    | 5 Q08378  | GOGA3_HL  | 881  |
|           | KLSSETYSQAK                  | 0 Q08J23  | NSUN2_HL  | 640  |
|           | VINTGIKVWCR                  | 6 Q08J23  | NSUN2_HL  | 586  |
|           | GPDWHLKMPK                   | 6 Q09666  | AHNK_HUN  | 748  |
|           | LQGGSVSLASKK                 | 10 Q09666 | AHNK_HUN  | 5858 |

|           |                                |           |           |      |
|-----------|--------------------------------|-----------|-----------|------|
| Structure | KLVLYLMNYAK                    | 0 Q10567  | AP1B1_HU  | 67   |
| Phyre     | SVAQYTGGIKLER                  | 10 Q10713 | MPPA_HU   | 299  |
| Phyre     | YEAKYLSGIAHFLEK                | 3 Q10713  | MPPA_HU   | 103  |
| Phyre     | KVDAAELLR                      | 0 Q12769  | NU160_HU  | 1331 |
| Phyre     | LKESFLVTGSQDCTVK               | 1 Q12788  | TBL3_HUM  | 433  |
| Structure | EKGDWSQFTLWQQGR                | 1 Q12797  | ASPH_HUM  | 622  |
| Phyre     | WFEENASQSTVKVLIR               | 11 Q12905 | ILF2_HUM  | 221  |
| Phyre     | VKPAPDETSFSEALLK               | 1 Q12905  | ILF2_HUM  | 45   |
| Phyre     | VLECLASGIVMPDGSIGYDPCEKEATDAIG | 22 Q12906 | ILF3_HUM  | 297  |
| Phyre     | HAKWFQAR                       | 2 Q12906  | ILF3_HUM  | 214  |
| Phyre     | LNELLVKALER                    | 6 Q12931  | TRAP1_HU  | 699  |
| Structure | LIKFFIDQSK                     | 2 Q12931  | TRAP1_HU  | 424  |
| Structure | YTLHYKTDAPLNIR                 | 5 Q12931  | TRAP1_HU  | 332  |
| Phyre     | MQQLAKTQEER                    | 5 Q12931  | TRAP1_HU  | 629  |
|           | SIFYVPDMKPSMFDVSR              | 8 Q12931  | TRAP1_HU  | 349  |
|           | KMMADEALGSGLVSR                | 0 Q13011  | ECH1_HUM  | 231  |
| Structure | EMVECFNKISR                    | 7 Q13011  | ECH1_HUM  | 95   |
| Structure | EM[147.04]VECFNKISR            | 7 Q13011  | ECH1_HUM  | 95   |
|           | KMMADEALGSGLVSR                | 0 Q13011  | ECH1_HUM  | 231  |
| Phyre     | LKGLGAFVIDSDHLGHR              | 1 Q13057  | COASY_HU  | 379  |
| Structure | ITDIIGKEEGIGPENLR              | 6 Q13085  | ACACA_HU  | 1788 |
| Phyre     | LPNSKQSQDEPLR                  | 4 Q13148  | TADBP_HU  | 181  |
| Phyre     | AEIADKQSGK                     | 6 Q13151  | ROA0_HUM  | 133  |
| Phyre     | AVPKEDIYSGGGGGGSR              | 3 Q13151  | ROA0_HUM  | 176  |
| Phyre     | FFKGYGR                        | 2 Q13243  | SRSF5_HUM | 25   |
|           | INTKGVGGK                      | 3 Q9UN86  | G3BP2_HU  | 365  |
| Phyre     | EAELGAKAK                      | 6 Q13310  | PABP4_HU  | 186  |
|           | AASAPAKESPR                    | 6 Q13428  | TCOF_HUM  | 379  |
|           | KTGPAAQVQVGK                   | 0 Q13428  | TCOF_HUM  | 458  |
|           | KLSGDQPAAR                     | 0 Q13428  | TCOF_HUM  | 1348 |
|           | VVDTTKESSR                     | 5 Q13428  | TCOF_HUM  | 1335 |
| Phyre     | FGNCGFSGNEYKK                  | 11 Q13443 | ADAM9_HU  | 561  |
| Structure | APGDAVHKIYPSAYIK               | 7 Q13485  | SMAD4_HU  | 428  |
|           | IKQQQPNPVEQR                   | 1 Q13496  | MTM1_HU   | 546  |
|           | AYLLGKEDAAR                    | 5 Q13501  | SQSTM_HU  | 13   |
| Structure | YTPSQQGVAFNSGAKQR              | 14 Q13573 | SNW1_HU   | 193  |
| Structure | LLVGKSASVDAEK                  | 4 Q13619  | CUL4A_HU  | 465  |
| Structure | YEKPDGSPVFIAFR                 | 2 Q13740  | CD166_HU  | 60   |
| Structure | YEKPDGSPVFIAFR                 | 2 Q13740  | CD166_HU  | 60   |
| Structure | IAALQAFADQLIAAGHYAKGDISSR      | 18 Q13813 | SPTN1_HU  | 1519 |
|           | MKQVEELYHSLLELGEK              | 1 Q13813  | SPTN1_HU  | 1067 |
|           | DMDDEESWIKEK                   | 9 Q13813  | SPTN1_HU  | 1781 |
|           | DM[147.04]DDEESWIKEK           | 9 Q13813  | SPTN1_HU  | 1781 |
|           | LEAELAAHEPAIQGVLDTGKK          | 19 Q13813 | SPTN1_HU  | 1828 |
|           | DLKANESR                       | 2 Q13813  | SPTN1_HU  | 1141 |
|           | QGKLFGAAEVQR                   | 2 Q13813  | SPTN1_HU  | 250  |
|           | VNEVNQFAAKLIQEQHPHEELIK        | 9 Q13813  | SPTN1_HU  | 214  |

|           |                          |    |        |           |      |
|-----------|--------------------------|----|--------|-----------|------|
|           | QGFVPAAYVKK              | 9  | Q13813 | SPTN1_HU  | 1022 |
|           | EKLTVLSEER               | 1  | Q13813 | SPTN1_HU  | 441  |
|           | EAFINTEDKGDSLDSVEALIK    | 8  | Q13813 | SPTN1_HU  | 1473 |
| Structure | ELAFQISKEYER             | 7  | Q13838 | DX39B_HU  | 131  |
| Structure | ELAFQISKEYER             | 7  | Q13838 | DX39B_HU  | 131  |
| Structure | ELAFQISKEYER             | 7  | Q13838 | DX39B_HU  | 131  |
| Structure | FGTKGLAITFVSDENDAK       | 3  | Q13838 | DX39B_HU  | 384  |
| Structure | MFIGGLSWDTTCK            | 11 | Q14103 | HNRPD_HL  | 110  |
| Phyre     | FGEVVDCTLKLDIPITGR       | 9  | Q14103 | HNRPD_HL  | 129  |
| Structure | FGEVVDCTLKLDIPITGR       | 9  | Q14103 | HNRPD_HL  | 129  |
| Phyre     | FGEVVDCTLKLDIPITGR       | 9  | Q14103 | HNRPD_HL  | 129  |
| Structure | FGEVVDCTLKLDIPITGR       | 9  | Q14103 | HNRPD_HL  | 129  |
| Structure | SSKGQIIGNFQAFDEDTGLPAHAR | 2  | Q14126 | DSG2_HUN  | 406  |
| Structure | NPIAKIHSDLAER            | 4  | Q14126 | DSG2_HUN  | 72   |
| Structure | GNNVEKPLELR              | 5  | Q14126 | DSG2_HUN  | 141  |
| Structure | SSKGQIIGNFQAFDEDTGLPAHAR | 2  | Q14126 | DSG2_HUN  | 406  |
| Structure | LAKLPDFESR               | 2  | Q14126 | DSG2_HUN  | 451  |
|           | TKNETDEDGWTTVR           | 1  | Q14152 | EIF3A_HUN | 1369 |
|           | EAELQKVR                 | 5  | Q14152 | EIF3A_HUN | 603  |
|           | IKDMDLWEQQEEER           | 1  | Q14152 | EIF3A_HUN | 720  |
| Phyre     | SHLAKEGLYQYK             | 4  | Q14152 | EIF3A_HUN | 68   |
| Phyre     | AKELLGQGLLR              | 1  | Q99613 | EIF3C_HUN | 643  |
| Structure | YFVKDVLGCVCVNPGR         | 3  | Q14181 | DPOA2_HL  | 549  |
| Modeller  | DFPLNDLLSATELDKIR        | 14 | Q14204 | DYHC1_HU  | 352  |
| Modeller  | MKLNTQEIFDDWAR           | 1  | Q14204 | DYHC1_HU  | 692  |
| Structure | VLLKALER                 | 3  | Q14204 | DYHC1_HU  | 2239 |
| Modeller  | KEFGPVVIDYGK             | 0  | Q14204 | DYHC1_HU  | 1100 |
| Modeller  | VQSKVNLK                 | 3  | Q14204 | DYHC1_HU  | 1115 |
| Structure | ILDDDTIITTLLENLKR        | 14 | Q14204 | DYHC1_HU  | 3774 |
| Structure | VKEHINSVSAMK             | 1  | Q14204 | DYHC1_HU  | 1498 |
|           | AKTQTPPVSPAPQPTEER       | 1  | Q14247 | SRC8_HUN  | 398  |
| Phyre     | FLLDTNKS                 | 6  | Q14566 | MCM6_HU   | 197  |
| Phyre     | ESEDFIVEQYKHLR           | 10 | Q14566 | MCM6_HU   | 599  |
| Phyre     | SLKQNINLSAPIMSR          | 2  | Q14566 | MCM6_HU   | 517  |
| Phyre     | FLLDTNKS                 | 6  | Q14566 | MCM6_HU   | 197  |
| Phyre     | DGSGVTKSSWR              | 6  | Q14566 | MCM6_HU   | 611  |
|           | IKLEGIITR                | 1  | Q9UQE7 | SMC3_HUN  | 820  |
|           | EFEEKVKR                 | 7  | Q14683 | SMC1A_HL  | 798  |
|           | VKDYGCIK                 | 1  | Q14690 | RRP5_HUN  | 553  |
| Phyre     | DVQAVKAK                 | 5  | Q14690 | RRP5_HUN  | 1855 |
|           | KGGSTSSSPSR              | 0  | Q14739 | LBR_HUM   | 64   |
| Docking   | IEGEGSVLQAKLK            | 10 | Q14764 | MVP_HUM   | 745  |
| Phyre     | SFNAHQEEKQDLSK           | 8  | Q14789 | GGB1_HL   | 2597 |
|           | KLQAALINR                | 0  | Q14789 | GGB1_HL   | 994  |
|           | KEYLEKIQGAQK             | 0  | Q14789 | GGB1_HL   | 1988 |
|           | TVKALEFVQTESQK           | 2  | Q14789 | GGB1_HL   | 2043 |
|           | AKLIECGWK                | 1  | Q9NPA8 | ENY2_HUN  | 36   |



|           |                             |           |           |      |
|-----------|-----------------------------|-----------|-----------|------|
|           | KAGEQQETASR                 | 0 Q14980  | NUMA1_HI  | 925  |
|           | KAGEQQETASR                 | 0 Q14980  | NUMA1_HI  | 925  |
|           | AAVKCCPEESLK                | 3 Q14997  | PSME4_HU  | 636  |
|           | TKADSVPGTYR                 | 1 Q15004  | PAF15_HUI | 5    |
| Structure | NTEKAK                      | 3 Q15008  | PSMD6_HL  | 163  |
| Structure | KGDLLNR                     | 0 Q15008  | PSMD6_HL  | 372  |
| Structure | LWGDIFYNPKTR                | 9 Q15029  | U5S1_HUN  | 352  |
| Structure | IYADTFGDINYQEFAKR           | 15 Q15029 | U5S1_HUN  | 341  |
| Phyre     | FHEICSNLVKTR                | 9 Q15041  | AR6P1_HU  | 114  |
| Phyre     | GKCYGLHAFIVPIR              | 1 Q15067  | ACOX1_HU  | 198  |
| Phyre     | YAQVKPDGTYVKPLSNK           | 11 Q15067 | ACOX1_HU  | 267  |
| Phyre     | YAQVKPDGTYVKPLSNKLTYGTMVFVR | 16 Q15067 | ACOX1_HU  | 272  |
| Phyre     | YAQVKPDGTYVKPLSNK           | 11 Q15067 | ACOX1_HU  | 267  |
| Structure | KLDNTTAAVQELGR              | 0 Q15075  | EEA1_HUN  | 1319 |
| Phyre     | SGGYSSGKQGR                 | 7 Q15084  | PDIA6_HUI | 150  |
| Phyre     | SGGYSSGKQGR                 | 7 Q15084  | PDIA6_HUI | 150  |
|           | SGGYSSGKQGR                 | 7 Q15084  | PDIA6_HUI | 150  |
|           | KAALIEVER                   | 0 Q15149  | PLEC_HUM  | 2142 |
|           | EKMQAVQEATR                 | 1 Q15149  | PLEC_HUM  | 2452 |
| Structure | LSAEAEKVLALPEPSPAAPTLR      | 6 Q15149  | PLEC_HUM  | 1186 |
|           | LKQSAEEQAQAR                | 1 Q15149  | PLEC_HUM  | 2255 |
|           | TPVEVPVGGFKGR               | 10 Q15149 | PLEC_HUM  | 3384 |
|           | AVTGYKDPYSGK                | 5 Q15149  | PLEC_HUM  | 4152 |
|           | LLDAQSTGGIVDPSKSHR          | 15 Q15149 | PLEC_HUM  | 3285 |
|           | QELEAELAKVR                 | 8 Q15149  | PLEC_HUM  | 1896 |
|           | LAEVEAALEKQR                | 9 Q15149  | PLEC_HUM  | 1508 |
|           | QLAEAHAQAKAQAER             | 9 Q15149  | PLEC_HUM  | 1520 |
|           | AQLEPVASPAKKPK              | 11 Q15149 | PLEC_HUM  | 1439 |
|           | VLADPSDDTKGFFDPNTHENLTYR    | 9 Q15149  | PLEC_HUM  | 3647 |
|           | AKAVVQLKPR                  | 1 Q15149  | PLEC_HUM  | 926  |
|           | ELAEQELEKQR                 | 8 Q15149  | PLEC_HUM  | 1833 |
|           | INLAQKAFCGFEDPR             | 5 Q15149  | PLEC_HUM  | 4491 |
|           | LLEAAAQSTKGYSPYSVSGSGSTAGSR | 9 Q15149  | PLEC_HUM  | 4609 |
|           | SSIAGLLLKATNEK              | 8 Q15149  | PLEC_HUM  | 2841 |
|           | VQKSLAAEEEEAR               | 2 Q15149  | PLEC_HUM  | 2129 |
|           | LEEQAQHKADIEER              | 8 Q15149  | PLEC_HUM  | 2025 |
|           | QKGLVEDTLR                  | 1 Q15149  | PLEC_HUM  | 2047 |
|           | AQAQAAAEKLR                 | 8 Q15149  | PLEC_HUM  | 2274 |
|           | GYLNKDTHDQLSEPSEVR          | 4 Q15149  | PLEC_HUM  | 3968 |
| Unknown   | EAEGQLQLQLEALR              | 7 Q15149  | PLEC_HUM  | 877  |
|           | QAADAEMEKKH                 | 8 Q15149  | PLEC_HUM  | 2306 |
|           | QKAQVEQELTTLR               | 1 Q15149  | PLEC_HUM  | 2318 |
|           | AVTGYKDPYSGK                | 5 Q15149  | PLEC_HUM  | 4152 |
|           | DPYSGKLISLFQAMK             | 5 Q15149  | PLEC_HUM  | 4158 |
|           | LPVEVAYKR                   | 7 Q15149  | PLEC_HUM  | 4205 |
|           | KQITMEELVR                  | 0 Q15149  | PLEC_HUM  | 4027 |
|           | LPVEVAYKR                   | 7 Q15149  | PLEC_HUM  | 4205 |

|           |                              |    |        |          |      |
|-----------|------------------------------|----|--------|----------|------|
|           | INLAQKAFCGFEDPR              | 5  | Q15149 | PLEC_HUM | 4491 |
|           | KQITMEELVR                   | 0  | Q15149 | PLEC_HUM | 4027 |
|           | KQITM[147.04]EELVR           | 0  | Q15149 | PLEC_HUM | 4027 |
|           | WVKNHLLIK                    | 3  | Q15149 | PLEC_HUM | 191  |
|           | QLAEHAQAQAER                 | 9  | Q15149 | PLEC_HUM | 1520 |
|           | LQEDKEQMAQQLAETQGFQR         | 4  | Q15149 | PLEC_HUM | 2487 |
|           | LQLEETHQKNLLDEELQR           | 9  | Q15149 | PLEC_HUM | 2339 |
|           | LLEAAAQSTKGYSPYSVSGSGSTAGSR  | 9  | Q15149 | PLEC_HUM | 4609 |
|           | VLAEKLAAGIETR                | 4  | Q15149 | PLEC_HUM | 1975 |
| Structure | AQAEVEGLGKGVAR               | 9  | Q15149 | PLEC_HUM | 1175 |
|           | TLLQSGGCLAGIYLEDTEK          | 17 | Q15149 | PLEC_HUM | 3503 |
|           | AVTGYKDPYSGK                 | 5  | Q15149 | PLEC_HUM | 4152 |
|           | KQITMEELVR                   | 0  | Q15149 | PLEC_HUM | 4027 |
|           | AVTGYKDPYSGK                 | 5  | Q15149 | PLEC_HUM | 4152 |
|           | LQAEKAHAFAVQQK               | 5  | Q15149 | PLEC_HUM | 2189 |
|           | ASFAEKTAQLER                 | 5  | Q15149 | PLEC_HUM | 1725 |
|           | AAKGGEVYTDSEAR               | 2  | Q15149 | PLEC_HUM | 3027 |
|           | TLKPEEQR                     | 2  | Q15149 | PLEC_HUM | 1055 |
|           | DPYSGSTISLFQAMQKGLVLR        | 15 | Q15149 | PLEC_HUM | 3590 |
|           | LQAEVAQQKSLAQAEAEK           | 9  | Q15149 | PLEC_HUM | 1792 |
|           | LLEAAAQSTKGYSPYSVSGSGSTAGSR  | 9  | Q15149 | PLEC_HUM | 4609 |
|           | LQAEKAHAFAVQQK               | 5  | Q15149 | PLEC_HUM | 2189 |
|           | QQEGFKGTFPDAR                | 5  | Q15233 | NONO_HU  | 371  |
| Structure | GIVEFSGKPAAR                 | 7  | Q15233 | NONO_HU  | 198  |
| Structure | YGKAGEVFIHK                  | 2  | Q15233 | NONO_HU  | 99   |
| Structure | GIVEFSGKPAAR                 | 7  | Q15233 | NONO_HU  | 198  |
| Structure | YGKAGEVFIHK                  | 2  | Q15233 | NONO_HU  | 99   |
|           | AAPGAEFAPNKR                 | 10 | Q15233 | NONO_HU  | 467  |
|           | EKLEMEMEAAR                  | 1  | Q15233 | NONO_HU  | 295  |
|           | EKLEM[147.04]EMEAAR          | 1  | Q15233 | NONO_HU  | 295  |
|           | NGEDIPVAQTKNINHR             | 10 | Q15262 | PTPRK_HU | 244  |
|           | MTSGSWTETHAVNAPTYKLWHLDPDTEY | 17 | Q15262 | PTPRK_HU | 349  |
| Phyre     | LNESKLVQEALAVPR              | 4  | Q15269 | PWP2_HU  | 773  |
| Structure | NVTGDHIMEIFSTYK              | 3  | Q15287 | RNPS1_HU | 174  |
| Phyre     | TFDQLTPDESKER                | 10 | Q15293 | RCN1_HU  | 81   |
| Structure | EIPSHVLSKVCMYFTYK            | 8  | Q15369 | ELOC_HU  | 72   |
| Modeller  | EKLGCQDAFPEVYDK              | 1  | Q15392 | DHC24_HU | 496  |
| Modeller  | LGCQDAFPEVYDKICK             | 12 | Q15392 | DHC24_HU | 509  |
| Modeller  | YTIHSQLEHLQSKYIGTGHADTTK     | 12 | Q9BWJ5 | SF3B5_HU | 17   |
|           | VVGAKVVTNAR                  | 4  | Q15424 | SAFB1_HU | 436  |
|           | QNEINNPKFNFLNPDPYHAYYR       | 7  | Q15459 | SF3A1_HU | 80   |
|           | KLAQDVRAK                    | 0  | Q15669 | RHOH_HU  | 138  |
| Structure | MGVDKIIPVDK                  | 4  | Q15691 | MARE1_HU | 89   |
| Modeller  | DSTLGGKAFHITNDEPIFWTFLSR     | 6  | Q15738 | NSDHL_HU | 263  |
| Modeller  | GVNTVFHCASPPSSNNKELFYR       | 17 | Q15738 | NSDHL_HU | 114  |
|           | LKDSEAEELQR                  | 1  | Q16181 | SEPT7_HU | 373  |
| Structure | EATADDLIKVVEELTR             | 8  | Q16531 | DDB1_HU  | 1131 |

|           |                                 |           |           |       |
|-----------|---------------------------------|-----------|-----------|-------|
| Structure | VGKDELFALEQSCAQVVLQAANER        | 2 Q16658  | FSCN1_HUI | 250   |
| Structure | EIAQDFKTDLR                     | 6 Q16695  | H31T_HUN  | 80    |
| Structure | YQKSTELLIR                      | 2 Q16695  | H31T_HUN  | 57    |
| Phyre     | KSAPATGGVK                      | 0 Q16695  | H31T_HUN  | 28    |
| Phyre     | TKQTAR                          | 1 Q16695  | H31T_HUN  | 5     |
| Phyre     | YQKSTELLIR                      | 2 Q16695  | H31T_HUN  | 57    |
| Phyre     | KSAPATGGVK                      | 0 Q16695  | H31T_HUN  | 28    |
| Phyre     | KSTGGKAPR                       | 0 Q16695  | H31T_HUN  | 10    |
| Phyre     | STGGKAPR                        | 4 Q16695  | H31T_HUN  | 15    |
| Docking   | TKQTAR                          | 1 Q16695  | H31T_HUN  | 5     |
| Phyre     | YQKSTELLIR                      | 2 Q16695  | H31T_HUN  | 57    |
| Structure | EIAQDFKTDLR                     | 6 Q16695  | H31T_HUN  | 80    |
| Structure | VTIMPKDIQLAR                    | 5 Q16695  | H31T_HUN  | 123   |
| Structure | VTIM[147.04]PKDIQLAR            | 5 Q16695  | H31T_HUN  | 123   |
| Phyre     | YQKSTELLIR                      | 2 Q16695  | H31T_HUN  | 57    |
| Structure | DDVEPPRVM[147.04]M[147.04]DVKFR | 12 Q8WZ42 | TITIN_HUN | 26721 |
| Phyre     | EIAQDFKTDLR                     | 6 Q16695  | H31T_HUN  | 80    |
| Structure | LLLPGELAKHAVSEGTK               | 8 Q93079  | H2B1H_HU  | 109   |
| Phyre     | EIAQDFKTDLR                     | 6 Q16695  | H31T_HUN  | 80    |
| Structure | KESYSVYVYK                      | 0 Q93079  | H2B1H_HU  | 35    |
| Phyre     | HAVSEGTKAVTK                    | 7 Q93079  | H2B1H_HU  | 117   |
| Phyre     | YQKSTELLIR                      | 2 Q16695  | H31T_HUN  | 57    |
| Phyre     | AVTKYTSSK                       | 3 Q93079  | H2B1H_HU  | 121   |
| Phyre     | HAVSEGTKAVTK                    | 7 Q93079  | H2B1H_HU  | 117   |
| Phyre     | LLLPGELAKHAVSEGTK               | 8 Q93079  | H2B1H_HU  | 109   |
| Phyre     | VLKQVHPDTGISSK                  | 2 Q93079  | H2B1H_HU  | 47    |
| Structure | KESYSVYVYK                      | 0 Q93079  | H2B1H_HU  | 35    |
| Structure | QVHPDTGISSKAMGIMNSFVNDIFER      | 10 Q93079 | H2B1H_HU  | 58    |
| Structure | VLKQVHPDTGISSK                  | 2 Q93079  | H2B1H_HU  | 47    |
| Phyre     | EIAQDFKTDLR                     | 6 Q16695  | H31T_HUN  | 80    |
| Phyre     | RVTIMPKDIQLAR                   | 6 Q16695  | H31T_HUN  | 123   |
| Phyre     | VTIMPKDIQLAR                    | 5 Q16695  | H31T_HUN  | 123   |
| Phyre     | VTIM[147.04]PKDIQLAR            | 5 Q16695  | H31T_HUN  | 123   |
| Phyre     | NDEELNKLLGK                     | 6 Q96KK5  | H2A1H_HU  | 96    |
| Structure | GQATDIAIQAEIIMKLK               | 14 Q16740 | CLPP_HUM  | 200   |
| Structure | VIHVAGKETTNIIFSNCGCVR           | 6 Q9UBB4  | ATX10_HU  | 345   |
| Phyre     | ALVSTKWLAESIR                   | 5 Q16762  | THTR_HUN  | 14    |
| Structure | FIHVSHLNANIKSSSR                | 11 Q16795 | NDUA9_HL  | 175   |
|           | FLQEKGPSVDWGK                   | 4 Q16851  | UGPA_HUM  | 69    |
| Structure | LGSSFTKVQDYLR                   | 6 Q16851  | UGPA_HUM  | 438   |
| Structure | LVEIAQVPKAHVDEFK                | 8 Q16851  | UGPA_HUM  | 312   |
| Structure | LGSSFTKVQDYLR                   | 6 Q16851  | UGPA_HUM  | 438   |
| Structure | LVEIAQVPKAHVDEFK                | 8 Q16851  | UGPA_HUM  | 312   |
| Structure | LGSSFTKVQDYLR                   | 6 Q16851  | UGPA_HUM  | 438   |
| Structure | KIGLETGVVK                      | 0 Q16881  | TRXR1_HU  | 449   |
| Structure | KIGLETGVVK                      | 0 Q16881  | TRXR1_HU  | 449   |
| Structure | YLGIIPGDKEYCISSDDLFLPYCPGK      | 7 Q16881  | TRXR1_HU  | 324   |

|           |                                |    |        |          |      |
|-----------|--------------------------------|----|--------|----------|------|
| Structure | VEETVKHDWDR                    | 5  | Q16881 | TRXR1_HU | 245  |
|           | M[147.04]KSVIENAK              | 1  | Q16891 | MIC60_HU | 306  |
|           | KIEEVR                         | 0  | Q16891 | MIC60_HU | 467  |
|           | TVEGALKER                      | 6  | Q16891 | MIC60_HU | 282  |
|           | KAVDEAADALLK                   | 0  | Q16891 | MIC60_HU | 286  |
|           | GLKVDLAQR                      | 2  | Q1KMD3 | HNRL2_HU | 26   |
| Phyre     | DLLVQQASQCLSKLVQIASR           | 12 | Q1KMD3 | HNRL2_HU | 521  |
| Phyre     | SIFANVEAKLGEPSEIDQR            | 8  | Q2M389 | WASC4_HU | 302  |
| Docking   | KGGAGGK                        | 0  | Q53EL6 | PDCD4_HU | 115  |
| Phyre     | KDLYANTVLSGGSTM[147.04]YPGIADR | 0  | Q562R1 | ACTBL_HU | 292  |
| Phyre     | YQAAVSKQSSSTNYTNELK            | 6  | Q9UHB6 | LIMA1_HU | 280  |
| Docking   | NIYKEAYR                       | 3  | Q5BJE1 | CC178_HU | 500  |
|           | VVMEFLHECMVNFVK                | 12 | Q5BKZ1 | ZN326_HU | 364  |
|           | AVSNINTLLDKADR                 | 10 | Q5T4S7 | UBR4_HU  | 3745 |
|           | EEPLAAKEALGHLSLAEVGTEEFLLQK    | 6  | Q5VST9 | OBSCN_HU | 5519 |
|           | QVFVCGNDSKAK                   | 9  | Q687X5 | STEA4_HU | 161  |
| Modeller  | LLELKLQDNELR                   | 4  | Q6EMK4 | VASN_HU  | 154  |
| Phyre     | LAVGKTGQYSGIYDCAK              | 4  | Q6NUK1 | SCMC1_HU | 320  |
| Phyre     | LAVGKTGQYSGIYDCAK              | 4  | Q6NUK1 | SCMC1_HU | 320  |
|           | DAAKEALYR                      | 3  | Q6P1N0 | C2D1A_HU | 933  |
| Structure | AEKGLYNEHTVDR                  | 2  | Q6P6C2 | ALKB5_HU | 116  |
|           | GSWSGKLSSLLR                   | 5  | Q6PGP7 | TTC37_HU | 1439 |
|           | IKEEAKK                        | 5  | Q6PIY5 | CA228_HU | 122  |
|           | FCEKYELDQVLH                   | 3  | Q6PJF5 | RHDF2_HU | 848  |
|           | KDLLFGSIVAVDEPTRPIYR           | 0  | Q6UVK1 | CSPG4_HU | 1061 |
|           | KDLLFGSIVAVDEPTRPIYR           | 0  | Q6UVK1 | CSPG4_HU | 1061 |
|           | KDLLFGSIVAVDEPTRPIYR           | 0  | Q6UVK1 | CSPG4_HU | 1061 |
|           | VTGALQFGELQKQGAGGVEGAEEWWATC   | 11 | Q6UVK1 | CSPG4_HU | 714  |
|           | TIPLTPVEIQDLELATGYKVYGR        | 18 | Q6UWB1 | I27RA_HU | 203  |
| Phyre     | LQSTLKTLSFSFPNTVTGSR           | 5  | Q6YHK3 | CD109_HU | 878  |
| Phyre     | ALYKPKQEVK                     | 5  | Q6YHK3 | CD109_HU | 143  |
| Phyre     | DENIKVGSPFELVVSGNK             | 4  | Q6YHK3 | CD109_HU | 478  |
| Phyre     | IPVQLVFNK                      | 7  | Q6YHK3 | CD109_HU | 556  |
| Phyre     | TRDENIKVGSPFELVVSGNK           | 6  | Q6YHK3 | CD109_HU | 478  |
| Phyre     | GSFKTLTLPSLPLNSADEIYELR        | 3  | Q6YHK3 | CD109_HU | 86   |
| Phyre     | IVTLFSDFKPYK                   | 8  | Q6YHK3 | CD109_HU | 158  |
| Phyre     | KYQPNIDVQESIHFLESEFSR          | 0  | Q6YHK3 | CD109_HU | 1061 |
| Phyre     | TNIQVTVTGPSSPSVKFLIDTHNR       | 16 | Q6YHK3 | CD109_HU | 1219 |
|           | TRDENIKVGSPFELVVSGNK           | 6  | Q6YHK3 | CD109_HU | 478  |
| Phyre     | TYTWLKGHQK                     | 5  | Q6YHK3 | CD109_HU | 1018 |
| Phyre     | LKELSYMVVS                     | 1  | Q6YHK3 | CD109_HU | 494  |
| Phyre     | VGSPFELVVSGNKR                 | 12 | Q6YHK3 | CD109_HU | 491  |
| Phyre     | IKLYWSK                        | 1  | Q6YHK3 | CD109_HU | 560  |
| Phyre     | ALYKPKQEVK                     | 5  | Q6YHK3 | CD109_HU | 143  |
|           | KKVSSTDPRPR                    | 0  | Q6ZS25 | ARHGI_HU | 742  |
| Docking   | SEGGKTPVAR                     | 4  | Q70UQ0 | IKIP_HU  | 28   |
| Structure | GDEVVPKDVNAAIATIK              | 5  | Q71U36 | TBA1A_HU | 326  |

|           |                             |    |        |           |       |
|-----------|-----------------------------|----|--------|-----------|-------|
| Docking   | TTFVSKDISR                  | 5  | Q7KYR7 | BT2A1_HU  | 101   |
| Structure | KLRPLYDIPYMFEAR             | 0  | Q7KZF4 | SND1_HUN  | 389   |
| Structure | LEGENTQDKNK                 | 8  | Q7KZF4 | SND1_HUN  | 386   |
| Structure | LEGENTQDKNKK                | 10 | Q7KZF4 | SND1_HUN  | 388   |
| Structure | LEGENTQDKNKK                | 8  | Q7KZF4 | SND1_HUN  | 386   |
| Structure | NLPGLVQEGEPFSEEATLFTKELVLQR | 20 | Q7KZF4 | SND1_HUN  | 586   |
| Structure | VADISGDTQKAK                | 9  | Q7KZF4 | SND1_HUN  | 513   |
| Phyre     | SWINEKDINAVAASLR            | 5  | Q7L1Q6 | BZW1_HU   | 197   |
|           | ELKGLHR                     | 2  | Q7LC44 | ARC_HUM   | 62    |
| Phyre     | ELKDLLTELQK                 | 2  | Q86UP2 | KTN1_HUN  | 1231  |
| Structure | LKAADIDQEVK                 | 1  | Q86VP6 | CAND1_HU  | 577   |
|           | LGESVSLNKRYTR               | 8  | Q96P20 | NLRP3_HU  | 166   |
|           | SEQPTLVTASKDGYFK            | 10 | Q8IWA0 | WDR75_HU  | 466   |
| Docking   | QGKGSR                      | 2  | Q8IYB4 | PEX5R_HU  | 33    |
|           | AFVKMCK                     | 3  | Q8IZP2 | ST134_HU  | 14    |
| Phyre     | ASVFKVLQKPNAAIR             | 5  | Q8IZP2 | ST134_HU  | 156   |
| Phyre     | KVAAIEALNDGELQK             | 0  | Q8IZP2 | ST134_HU  | 114   |
| Phyre     | ESYSIYVYKVLK                | 8  | Q8N257 | H2B3B_HU  | 44    |
| Phyre     | VLKQVHPDTGISSK              | 2  | Q8N257 | H2B3B_HU  | 47    |
| Phyre     | KESYSIYVYK                  | 0  | Q8N257 | H2B3B_HU  | 35    |
| Phyre     | KESYSIYVYK                  | 0  | Q8N257 | H2B3B_HU  | 35    |
| Structure | NIVEKHTD TDVLEACSK          | 4  | Q8N3U4 | STAG2_HU  | 622   |
| Phyre     | FASLEFSPGSKK                | 10 | Q8N766 | EMC1_HUN  | 52    |
| Phyre     | ASHYLKTEYSK                 | 5  | Q8N8Z6 | DCBD1_HU  | 167   |
| Phyre     | TEYSKFCPAGCR                | 4  | Q8N8Z6 | DCBD1_HU  | 172   |
| Phyre     | KPNEGADGQWK                 | 0  | Q8NC51 | PAIRB_HU  | 310   |
|           | KPNEGADGQWK                 | 0  | Q8NC51 | PAIRB_HU  | 310   |
|           | ELSTKYLT M[147.04]K         | 4  | Q8NDH2 | CC168_HU  | 1465  |
|           | TKEIEQVYR                   | 1  | Q8NEY8 | PPHLN_HU  | 299   |
|           | LQNLQDAAKDM[147.04]K        | 8  | Q8NF91 | SYNE1_HU  | 5632  |
|           | KM[147.04]HIQSAVSKMNPGEK    | 9  | Q8NFC6 | BD1L1_HU  | 1215  |
|           | QTMLCPEMKIK                 | 8  | Q8TAL5 | CI043_HUN | 234   |
| Modeller  | YSQEPIKTFSR                 | 6  | Q8TED0 | UTP15_HU  | 74    |
|           | IERKIATISLESK               | 3  | Q8TEK3 | DOT1L_HU  | 1203  |
|           | IQEAVYKNVRPAEVR             | 6  | Q8TEM1 | PO210_HU  | 228   |
|           | KASPPSGLWSPAYASH            | 0  | Q8TEM1 | PO210_HU  | 1872  |
| Structure | GGGIDPTVKER                 | 8  | Q8TEQ6 | GEMI5_HU  | 282   |
|           | QEAFWRKEK                   | 6  | Q8TF01 | PNISR_HU  | 429   |
|           | GATTLIYTHASSKTR             | 12 | Q8WWY8 | LIPH_HUM  | 123   |
|           | NQELQKR                     | 5  | Q8WXF1 | PSPC1_HU  | 344   |
|           | LLNDQCKNFNDWF SNIK          | 6  | Q8WXH0 | SYNE2_HU  | 1845  |
|           | VPEAPKEVVPEK                | 5  | Q8WZ42 | TITIN_HUN | 11457 |
| Structure | YPDPNFKSCTPYELR             | 6  | Q92466 | DDB2_HUN  | 362   |
| Phyre     | SQHSGNAQVTQTKFLPNAPK        | 12 | Q92499 | DDX1_HUN  | 281   |
|           | IGTPVKVR                    | 5  | Q92598 | HS105_HU  | 703   |
| Phyre     | GQTCNVKLLHR                 | 7  | Q92621 | NU205_HU  | 1230  |
| Phyre     | NKLLQCLHAK                  | 1  | Q92621 | NU205_HU  | 1271  |

|           |                            |           |           |      |
|-----------|----------------------------|-----------|-----------|------|
| Phyre     | GQTCNVKLLHR                | 7 Q92621  | NU205_HU  | 1230 |
| Phyre     | IVSVDKQQWLLYLSNSGYLK       | 5 Q92621  | NU205_HU  | 1508 |
| Phyre     | YVDYGGYKR                  | 7 Q92667  | AKAP1_HU  | 800  |
|           | VTFSQDPTTVALCISKEGRPPAR    | 15 Q92692 | NECT2_HU  | 186  |
| Phyre     | STCIYGGAPKGPQIR            | 9 Q92841  | DDX17_HU  | 284  |
| Phyre     | LIQLMEEIMAEKENK            | 11 Q92841 | DDX17_HU  | 417  |
| Structure | FDGAEGSWFQKISSR            | 10 Q92888 | ARHG1_HU  | 510  |
|           | ESLMQFSKPR                 | 7 Q92900  | RENT1_HU  | 926  |
| Structure | AGVKMILIQDGSQNTNVDKPLR     | 3 Q92945  | FUBP2_HU  | 266  |
| Phyre     | IQQDSGCKVQISPDSSGLPER      | 7 Q92945  | FUBP2_HU  | 177  |
| Structure | LNTDPMLLQFFKSQGYR          | 11 Q93009 | UBP7_HUN  | 841  |
| Phyre     | VLQAAAKNIR                 | 6 Q93050  | VPP1_HUN  | 288  |
| Phyre     | ESYSVYVYKVLK               | 8 Q93079  | H2B1H_HU  | 44   |
| Phyre     | KESYSVYVYKVLK              | 9 Q93079  | H2B1H_HU  | 44   |
| Phyre     | LLLPGELAKHAVSEGTK          | 8 Q93079  | H2B1H_HU  | 109  |
| Phyre     | VLKQVHPDTGISSK             | 2 Q93079  | H2B1H_HU  | 47   |
| Phyre     | ESYSVYVYKVLK               | 8 Q93079  | H2B1H_HU  | 44   |
| Phyre     | VLKQVHPDTGISSK             | 2 Q93079  | H2B1H_HU  | 47   |
| Phyre     | KESYSVYVYK                 | 0 Q93079  | H2B1H_HU  | 35   |
| Phyre     | KAVTKAQK                   | 4 Q93079  | H2B1H_HU  | 21   |
| Phyre     | NDEELNKLLGK                | 6 Q96KK5  | H2A1H_HU  | 96   |
| Phyre     | ESYSVYVYKVLK               | 8 Q93079  | H2B1H_HU  | 44   |
| Phyre     | KESYSVYVYK                 | 0 Q93079  | H2B1H_HU  | 35   |
| Phyre     | KESYSVYVYKVLK              | 9 Q93079  | H2B1H_HU  | 44   |
| Phyre     | LAHYNKR                    | 5 Q93079  | H2B1H_HU  | 86   |
| Phyre     | QVHPDTGISSKAMGIMNSFVNDIFER | 10 Q93079 | H2B1H_HU  | 58   |
| Phyre     | SRKESYSVYVYK               | 2 Q93079  | H2B1H_HU  | 35   |
| Phyre     | LLLPGELAKHAVSEGTK          | 8 Q93079  | H2B1H_HU  | 109  |
|           | HIAMEKVASR                 | 5 Q969P0  | IGSF8_HUN | 383  |
| Phyre     | TSTQKHTHLAVSFGR            | 4 Q969P0  | IGSF8_HUN | 194  |
| Structure | NPPPNADPNMKLFTIR           | 10 Q96AE4 | FUBP1_HU  | 425  |
| Docking   | EANQAPKSKSGSRPR            | 8 Q96AG4  | LRC59_HUI | 228  |
| Phyre     | LVNLQHLDLLNNKLVTLPVSFAQLK  | 12 Q96AG4 | LRC59_HUI | 96   |
| Phyre     | AQQLHKEQQK                 | 5 Q96BR5  | COA7_HUN  | 219  |
| Phyre     | M[147.04]YKLGDVVDKDEAK     | 2 Q96BR5  | COA7_HUN  | 195  |
| Phyre     | SYLSGMPECKFGMNDK           | 9 Q96CW1  | AP2M1_HL  | 213  |
| Phyre     | YLKVFEPK                   | 2 Q96CW1  | AP2M1_HL  | 405  |
| Phyre     | KELTSSGGPTK                | 0 Q96EE3  | SEH1_HUN  | 255  |
| Structure | ISTSVKELENFR               | 5 Q96HE7  | ERO1A_HU  | 455  |
| Structure | HSQYHVDGSLEKDR             | 11 Q96HS1 | PGAM5_HL  | 116  |
| Structure | HSQYHVDGSLEKDR             | 11 Q96HS1 | PGAM5_HL  | 116  |
| Phyre     | ITGDAFKVQQAR               | 6 Q96I24  | FUBP3_HU  | 220  |
| Phyre     | DGTQQEGAVASTELLKDGR        | 15 Q96J84 | KIRR1_HUN | 174  |
| Phyre     | VNEFGESYEKATR              | 10 Q96KA5 | CLP1L_HUN | 530  |
|           | KGNYAER                    | 0 Q96KK5  | H2A1H_HU  | 37   |
| Phyre     | LLGKVITIAQGGVLPNIQAVLLPK   | 3 Q96KK5  | H2A1H_HU  | 100  |
|           | NDEELNKLLGK                | 6 Q96KK5  | H2A1H_HU  | 96   |

|           |                            |           |           |      |
|-----------|----------------------------|-----------|-----------|------|
| Phyre     | YNVPFLTfINKLDR             | 10 Q96RP9 | EFGM_HUM  | 175  |
|           | STDQTVLEELASIKNR           | 13 Q96S59 | RANB9_HU  | 405  |
| Structure | NSKYAPAEGNR                | 2 Q96T88  | UHRF1_HU  | 546  |
|           | AFILPKAEVCVR               | 5 Q96TA1  | NIBL1_HUM | 330  |
|           | KYDYDSSSVR                 | 0 Q96TA1  | NIBL1_HUM | 479  |
| Phyre     | GTPIKCGQPIR                | 4 Q99470  | SDF2_HUM  | 87   |
| Structure | NFGGKWEEIHK                | 4 Q99523  | SORT_HUM  | 248  |
| Phyre     | LDDTYIKAYLR                | 6 Q99615  | DNJC7_HU  | 329  |
|           | LVKSYEAQDPEIASLSGK         | 2 Q99622  | C10_HUM   | 86   |
| Docking   | AAQNISKTIATSQNR            | 6 Q99623  | PHB2_HUM  | 262  |
| Phyre     | ISSPTGSKDLQMVNISLR         | 7 Q99623  | PHB2_HUM  | 97   |
|           | AAQNISKTIATSQNR            | 6 Q99623  | PHB2_HUM  | 262  |
| Docking   | GSDSLIKGK                  | 6 Q99623  | PHB2_HUM  | 296  |
|           | MLGEALSKNPGYIK             | 7 Q99623  | PHB2_HUM  | 244  |
|           | NPGYIKLR                   | 5 Q99623  | PHB2_HUM  | 250  |
|           | IVQAEGEAEEAAKMLGEALSK      | 11 Q99623 | PHB2_HUM  | 236  |
| Phyre     | EYTAAVEAKQVAQQAQR          | 8 Q99623  | PHB2_HUM  | 200  |
| Phyre     | ISSPTGSKDLQMVNISLR         | 7 Q99623  | PHB2_HUM  | 97   |
| Structure | LGNNCVFAPADVTSEKDVQTALALAK | 15 Q99714 | HCD2_HUM  | 69   |
| Phyre     | FGEVVDCTIKMDPNTGR          | 9 Q99729  | ROAA_HUM  | 101  |
| Phyre     | FGEVVDCTIKMDPNTGR          | 9 Q99729  | ROAA_HUM  | 101  |
| Phyre     | VVLSKLPIGDVATQYFADR        | 4 Q99832  | TCPH_HUM  | 292  |
| Phyre     | ATISNDGATILKLLDVVHPAAK     | 11 Q99832 | TCPH_HUM  | 67   |
| Phyre     | VVLSKLPIGDVATQYFADR        | 4 Q99832  | TCPH_HUM  | 292  |
| Phyre     | YNFFTGCPKAK                | 8 Q99832  | TCPH_HUM  | 366  |
| Phyre     | VVLSKLPIGDVATQYFADR        | 4 Q99832  | TCPH_HUM  | 292  |
| Phyre     | DVAIKEPLVDVDPKQLVTNACLIK   | 14 Q99873 | ANM1_HU   | 233  |
|           | SLFVHKVDPR                 | 5 Q9BPW8  | NIPS1_HUM | 51   |
| Structure | AYSTPDKIFR                 | 6 Q9BPX6  | MICU1_HU  | 126  |
| Unknown   | KLLTLFR                    | 0 Q9BQA9  | CQ062_HU  | 88   |
| Phyre     | ELPAWVSFPDVEKAEWLNK        | 12 Q9BSJ8 | ESYT1_HUM | 138  |
|           | KAIVICPTDEDLKDR            | 0 Q9BUJ2  | HNRL1_HU  | 527  |
|           | DFAPPGQQKR                 | 8 Q9BVC6  | TM109_HU  | 46   |
| Phyre     | IDEELTGKSR                 | 7 Q9BW27  | NUP85_HU  | 92   |
|           | KGLIEVK                    | 0 Q9BWD1  | THIC_HUM  | 211  |
| Phyre     | VLDKLLLYLR                 | 3 Q9BXP5  | SRRT_HUM  | 611  |
|           | ESLSEEEAQKMGR              | 9 Q9BXP5  | SRRT_HUM  | 687  |
|           | TESISKTNR                  | 5 Q9BYG3  | MK67I_HU  | 198  |
| Phyre     | QKQSLEYLEQVR               | 1 Q9BZE4  | NOG1_HUM  | 145  |
| Structure | KFLLFDSNNR                 | 0 Q9BZM4  | ULBP3_HU  | 148  |
| Structure | LKTLPDEVLTk                | 1 Q9BZZ5  | API5_HUM  | 160  |
| Modeller  | STLTGNKVFNCISYSPLCK        | 6 Q9GZL7  | WDR12_HU  | 298  |
|           | TKPHLFYIPGR                | 1 Q9H307  | PININ_HUM | 238  |
|           | TKPHLFYIPGR                | 1 Q9H307  | PININ_HUM | 238  |
| Structure | KIEQELTAAG                 | 0 Q9H444  | CHM4B_HU  | 46   |
|           | VVESGGPEILKGLEER           | 10 Q9H583 | HEAT1_HU  | 1544 |
| Phyre     | VPLHQVPYAVKGCGR            | 10 Q9H6R4 | NOL6_HUM  | 149  |

|           |                          |           |           |      |
|-----------|--------------------------|-----------|-----------|------|
| Phyre     | EILQDKDGLNQR             | 5 Q9H6R4  | NOL6_HUN  | 192  |
|           | KACNDATLVQITSNMDSVGR     | 0 Q9HAV0  | GBB4_HUN  | 23   |
| Structure | GWSQKYSTWEPEENILDAR      | 4 Q9HC52  | CBX8_HUN  | 38   |
| Phyre     | LLTYNSLYKK               | 8 Q9HCE1  | MOV10_HI  | 714  |
| Phyre     | GLDDIKDLK                | 5 Q9HCE1  | MOV10_HI  | 858  |
| Modeller  | ALDKPVTVQFR              | 3 Q9HCU4  | CELR2_HUI | 2300 |
| Modeller  | FGLPAAAPCPKGSFGTAVR      | 10 Q9HCU4 | CELR2_HUI | 2001 |
| Modeller  | TLAGLLPHNYDPDKR          | 13 Q9HCU4 | CELR2_HUI | 2267 |
| Phyre     | EVKLLLSSETPIEGK          | 2 Q9HDC9  | APMAP_HI  | 183  |
| Structure | ITLVSAAPGKVICEM[147.04]K | 9 Q9NPJ3  | ACO13_HU  | 37   |
| Structure | ITLVSAAPGKVICEMK         | 9 Q9NPJ3  | ACO13_HU  | 37   |
|           | GVTFLFPIQAKTFHHVYSGK     | 10 Q9NR30 | DDX21_HU  | 215  |
|           | SGGGNKSNR                | 5 Q9NR30  | DDX21_HU  | 764  |
| Phyre     | GVTFLFPIQAKTFHHVYSGK     | 10 Q9NR30 | DDX21_HU  | 215  |
| Phyre     | ASKQWFINITDIK            | 2 Q9NSE4  | SYIM_HUN  | 479  |
| Phyre     | KSDLHPTLPAGR             | 0 Q9NV96  | CC50A_HU  | 279  |
|           | KSDLHPTLPAGR             | 0 Q9NV96  | CC50A_HU  | 279  |
|           | NLKVLYQFR                | 2 Q9NVH1  | DJC11_HUI | 526  |
|           | AAKAAR                   | 2 Q9NVI7  | ATD3A_HU  | 60   |
|           | AKAER                    | 1 Q9NVI7  | ATD3A_HU  | 246  |
|           | AQYQDKLAR                | 5 Q9NVI7  | ATD3A_HU  | 183  |
|           | YEDQLKQQQLLNEENLR        | 5 Q9NVI7  | ATD3A_HU  | 194  |
|           | AQYQDKLAR                | 5 Q9NVI7  | ATD3A_HU  | 183  |
|           | LKAAEHR                  | 1 Q9NVI7  | ATD3A_HU  | 262  |
|           | AKAAAR                   | 1 Q9P2D3  | HTR5B_HU  | 2048 |
| Modeller  | KLASGCKNGQILLWDPSTGK     | 0 Q9NVX2  | NLE1_HUN  | 170  |
|           | AEVEQVELPDGKKR           | 12 Q9NW13 | RBM28_HI  | 666  |
| Structure | NLFTKTHPQWYPAR           | 4 Q9NZ01  | TECR_HUN  | 38   |
| Structure | ESTMYPKAVQDLCGWR         | 6 Q9P258  | RCC2_HUN  | 422  |
| Phyre     | VYSKSGSWTVIYR            | 3 Q9P273  | TEN3_HUN  | 2219 |
| Phyre     | TTEEDRGNYYCVVSAWTKQR     | 17 Q9P2B2 | FPRP_HUN  | 522  |
|           | AQDGDIFISKEHTDTFNFR      | 9 Q9P2B2  | FPRP_HUN  | 492  |
|           | GNYYCVVSAWTKQR           | 11 Q9P2B2 | FPRP_HUN  | 522  |
| Docking   | AEGAQNQAKK               | 8 Q9P2E9  | RRBP1_HU  | 300  |
|           | KAEGAQNQGKK              | 9 Q9P2E9  | RRBP1_HU  | 270  |
|           | KVEGAQNQGKK              | 9 Q9P2E9  | RRBP1_HU  | 310  |
| Phyre     | LQELLKTTQEQLAR           | 5 Q9P2E9  | RRBP1_HU  | 1375 |
|           | KAEGAQNQGKK              | 9 Q9P2E9  | RRBP1_HU  | 270  |
|           | KVEGAQNQGK               | 0 Q9P2E9  | RRBP1_HU  | 301  |
|           | AAAGEAKVK                | 6 Q9P2E9  | RRBP1_HU  | 743  |
|           | KAEGAQNQGKK              | 9 Q9P2E9  | RRBP1_HU  | 270  |
| Modeller  | SGGTEGLLAEKLEALITQTR     | 10 Q9UHB9 | SRP68_HUI | 277  |
|           | NEKAPVDFGYVGIDSILEQMR    | 2 Q9UHD8  | SEPT9_HUI | 271  |
|           | GINQKAAFPQYQPVVMLEK      | 4 Q9UHN6  | TMEM2_HI  | 1028 |
| Phyre     | SYLPVQFQSPDKAETQR        | 11 Q9UHN6 | TMEM2_HI  | 1220 |
|           | SYLPVQFQSPDKAETQR        | 11 Q9UHN6 | TMEM2_HI  | 1220 |
| Phyre     | KQESTVMVLR               | 0 Q9UHX1  | PUF60_HU  | 458  |



|           |                             |    |        |           |      |
|-----------|-----------------------------|----|--------|-----------|------|
| Docking   | EAGGAFGKR                   | 7  | Q9UII2 | ATIF1_HUM | 49   |
| Phyre     | IQKELER                     | 2  | Q9UII2 | ATIF1_HUM | 90   |
|           | TDKGWSFLLGK                 | 2  | Q9UIQ6 | LCAP_HUM  | 872  |
| Structure | KDVEVTKEEFVLAAQK            | 0  | Q9UJS0 | CMC2_HUM  | 245  |
| Docking   | LSLDKVFR                    | 4  | Q9UJZ1 | STML2_HU  | 145  |
| Structure | VFIGNLNTAIVKK               | 11 | Q9UKM9 | RALY_HUM  | 34   |
| Structure | KVTSVVFHPSQDLVFSASPDATIR    | 0  | Q9UMS4 | PRP19_HU  | 266  |
| Phyre     | KDDEVQVVR                   | 0  | Q9UNX3 | RL26L_HUM | 51   |
|           | SFHNELLTQLEQKVELDSR         | 12 | Q9UQB8 | BAIP2_HUM | 108  |
|           | IKLEGIITR                   | 1  | Q9UQE7 | SMC3_HUM  | 820  |
| Phyre     | NFSAGGHHKVGGLGFELEA         | 7  | Q9Y277 | VDAC3_HU  | 274  |
| Phyre     | SCSGVEFSTSGHAYTDTGKASGNLETK | 18 | Q9Y277 | VDAC3_HU  | 53   |
| Structure | LPSGKVGFSK                  | 4  | Q9Y285 | SYFA_HUM  | 101  |
| Structure | DSGNKPPGLLPR                | 4  | Q9Y2Q3 | GSTK1_HU  | 54   |
| Structure | KGLYMANDLK                  | 0  | Q9Y2Q3 | GSTK1_HU  | 62   |
| Phyre     | YSPEFKDPLIDKEYYR            | 5  | Q9Y2R9 | RT07_HUM  | 42   |
| Structure | LAAEVTKL VHGR               | 6  | Q9Y2Z4 | SYYM_HUM  | 355  |
| Phyre     | IAFSSTSLLKMAPSAEER          | 9  | Q9Y305 | ACOT9_HU  | 250  |
|           | LEDILESINSIKSR              | 11 | Q9Y3A6 | TMED5_HL  | 164  |
| Phyre     | NYQDTPKQIR                  | 7  | Q9Y3C1 | NOP16_HU  | 146  |
| Structure | KGIVLLELLPK                 | 0  | Q9Y3D6 | FIS1_HUM  | 53   |
| Modeller  | NVTDVVNTCHDAGISKK           | 15 | Q9Y3I0 | RTCB_HUM  | 492  |
| Structure | AYQHKVGNIIDTMITDAFLK        | 4  | Q9Y3Z3 | SAMH1_HL  | 377  |
|           | TAKAIAVTVQEMVTK             | 2  | Q9Y490 | TLN1_HUM  | 1862 |
|           | DLQEVKAAAR                  | 5  | Q9Y490 | TLN1_HUM  | 1068 |
|           | RLQAAGNAVKR                 | 9  | Q9Y490 | TLN1_HUM  | 2464 |
|           | VGDDPAVWQLKNSAK             | 10 | Q9Y490 | TLN1_HUM  | 2115 |
| Structure | KAASITSEVFNK                | 0  | Q9Y5B9 | SP16H_HU  | 185  |
| Structure | FKSYCSNLVR                  | 1  | Q9Y5B9 | SP16H_HU  | 280  |
| Structure | EGPIDLGACNQDDWISAVRPVIEKR   | 23 | Q9Y5K5 | UCHL5_HU  | 206  |
| Structure | IPENNPVKLSCAYSGFSSPR        | 7  | Q9Y624 | JAM1_HUM  | 47   |
| Structure | LVCYNNKITASYEDR             | 6  | Q9Y624 | JAM1_HUM  | 78   |
| Structure | IPENNPVKLSCAYSGFSSPR        | 7  | Q9Y624 | JAM1_HUM  | 47   |
| Structure | LVCYNNKITASYEDR             | 6  | Q9Y624 | JAM1_HUM  | 78   |
|           | SENKNEGQDATMYCKSVGYPHPDWIWR | 14 | Q9Y639 | NPTN_HUM  | 260  |
|           | QVSGQLLEERKK                | 10 | Q9Y6D9 | MD1L1_HL  | 385  |
| Phyre     | AWMAEKDANSVTSSLR            | 5  | Q9Y6E2 | BZW2_HUM  | 198  |
| Structure | GHPEPTISWKK                 | 9  | Q9Y6N7 | ROBO1_HL  | 205  |
| Structure | KDGSPLDDKDER                | 8  | Q9Y6N7 | ROBO1_HL  | 214  |
| Structure | DGSPLDDKDER                 | 7  | Q9Y6N7 | ROBO1_HL  | 214  |
| Modeller  | IKQLENGVLQIR                | 1  | Q9Y6N7 | ROBO1_HL  | 503  |
|           | LYTLKVEAENTHVDPR            | 4  | Q9Y6N8 | CAD10_HU  | 347  |

| geneB     | pdB      | pdB_type  | distance | NetworkDi | NumberIDs | Confidence | NumProtA | MS2ScanN |
|-----------|----------|-----------|----------|-----------|-----------|------------|----------|----------|
| LOC102724 | ####     |           | ####     | Intra     | 1,0       | 0.94       | 2        | 14592    |
| LOC102724 | ####     |           | ####     | Intra     | 3,1       | 1          | 2        | 21277    |
| PGP       | A6NDG6   | Phyre     | 3.8      | Intra     | 1,0       | 1          | 1        | 6420     |
| SMCHD1    | ####     |           | ####     | N/A       | 1,0       | 0.97       | 1        | 22288    |
| HIST1H4A  | 5B0Z     | Structure | ####     |           | 2 3,0     | 0.79       | 1        | 11916    |
| DDX39A    | O00148   | Phyre     | 10.78    | Intra     | 1,0       | 1          | 1        | 13021    |
| ALYREF    | ####     |           | ####     |           | 1 0,1     | 0.85       | 1        | 8437     |
| ACOT7     | 2QQ2     | Structure | 17.28    |           | 1 1,2     | 1          | 1        | 18721    |
| MYO1C     | 4BYF     | Structure | 13.4     | Intra     | 1,0       | 1          | 4        | 23088    |
| MYO1C     | 4BYF     | Structure | 20.44    | Intra     | 1,0       | 0.99       | 4        | 13525    |
| MYO1C     | 4BYF     | Structure | 23.54    | Intra     | 1,0       | 1          | 4        | 25396    |
| MYO1C     | 4BYF     | Structure | 3.97     | Intra     | 1,0       | 1          | 4        | 19957    |
| CALM1     | 4DJC     | Structure | ####     | N/A       | 1,0       | 0.98       | 1        | 15382    |
| PSMD12    | 5VGZ     | Structure | 14.29    | Intra     | 2,0       | 1          | 1        | 25683    |
| PGRMC1    | 4X8Y     | Structure | 7.97     | Intra     | 2,0       | 1          | 1        | 22532    |
| CLIC1     | 4K0N     | Structure | 25.15    | Intra     | 2,0       | 1          | 1        | 22428    |
| DLAT      | P10515   | Unknown   | ####     |           | 1 3,2     | 1          | 1        | 13676    |
| DNM1L     | 4BEJ     | Structure | 26.93    | Intra     | 2,0       | 1          | 1        | 29094    |
| PLOD2     | ####     |           | ####     | Intra     | 1,0       | 0.93       | 1        | 28952    |
| BTN3A1    | ####     |           | ####     | N/A       | 2,2       | 1          | 1        | 19137    |
| FBL       | 2IPX     | Structure | ####     |           | 1 1,0     | 0.98       | 2        | 19092    |
| NOP56     | O00567   | Phyre     | ####     |           | 1 3,1     | 1          | 2        | 26992    |
| DDX3X     | 5E7I     | Structure | 4.32     | Intra     | 2,0       | 1          | 2        | 27385    |
| DDX3X     | 5E7I     | Structure | 15.22    | Intra     | 1,0       | 1          | 2        | 32466    |
| PODXL     | O00592_O | Docking   | 17.51    | N/A       | 5,3       | 1          | 5        | 17787    |
| PODXL     | O00592   | Modeller  | 26.33    | Intra     | 0,3       | 1          | 5        | 8241     |
| PODXL     | O00592   | Modeller  | 10.96    | Intra     | 3,4       | 1          | 5        | 17462    |
| PODXL     | O00592   | Modeller  | 17.04    | Intra     | 4,2       | 1          | 5        | 17086    |
| PODXL     | O00592   | Modeller  | 21.94    | Intra     | 0,2       | 1          | 5        | 8141     |
| KIF3C     | 3B6V     | Structure | 59.95    |           | 1 1,0     | 0.97       | 1        | 30244    |
| BCKDK     | ####     |           | ####     | N/A       | 1,0       | 0.75       | 1        | 25118    |
| UQCQRQ    | 5XTE     | Structure | ####     |           | 2 1,0     | 0.76       | 1        | 23104    |
| SLC27A2   | O14975   | Phyre     | ####     | Intra     | 2,0       | 1          | 1        | 20143    |
| SPTBN2    | ####     |           | ####     | Intra     | 1,0       | 1          | 1        | 22556    |
| PLXNB2    | O15031   | Modeller  | 58.12    | Intra     | 1,2       | 1          | 3        | 35811    |
| PLXNB2    | O15031   | Modeller  | 58.12    | Intra     | 1,0       | 1          | 3        | 32272    |
| PLXNB2    | O15031   | Modeller  | 63.93    | Intra     | 0,2       | 1          | 3        | 11461    |
| PFAS      | O15067   | Modeller  | 49.26    | Intra     | 1,0       | 0.99       | 1        | 21040    |
| ARPC1B    | O15143   | Phyre     | 7.05     | Intra     | 1,0       | 1          | 1        | 28191    |
| ARPC3     | O15145   | Phyre     | ####     |           | 1 3,0     | 0.86       | 1        | 16661    |
| PGRMC2    | O15173   | Phyre     | 14.44    | Intra     | 2,2       | 1          | 1        | 24166    |
| SURF4     | ####     |           | ####     | Intra     | 3,0       | 1          | 1        | 19414    |
| INPPL1    | ####     |           | ####     | Intra     | 2,0       | 1          | 1        | 21881    |
| EIF3D     | ####     |           | ####     |           | 1 4,1     | 1          | 1        | 12200    |
| EIF3C     | Q99613   | Phyre     | ####     |           | 1 2,0     | 1          | 1        | 19019    |
| EIF3H     | O15372   | Phyre     | 20.06    | Intra     | 0,1       | 1          | 1        | 5195     |

|           |        |           |        |       |       |      |   |       |
|-----------|--------|-----------|--------|-------|-------|------|---|-------|
| BCAT2     | 5MPR   | Structure | 12.4   | Intra | 2,2   | 1    | 2 | 16179 |
| BCAT2     | 5MPR   | Structure | 42.04  | Intra | 1,1   | 1    | 2 | 33372 |
| PDIA3     | 3F8U   | Structure | 131.12 |       | 1 1,0 | 0.99 | 1 | 30748 |
| DHX15     | 5XDR   | Structure | 10.92  | Intra | 1,0   | 0.99 | 2 | 15578 |
| DHX15     | 5XDR   | Structure | 15.99  | Intra | 1,1   | 1    | 2 | 24560 |
| RRP8      | 2ZFU   | Structure | 17.19  | Intra | 1,0   | 0.94 | 1 | 27996 |
| CYB5B     | 3NER   | Structure | 10.74  | Intra | 4,4   | 1    | 1 | 26210 |
| PSMD3     | O43242 | Phyre     | ####   |       | 1 2,2 | 1    | 1 | 20835 |
| DARS      | 4J15   | Structure | ####   |       | 1 1,0 | 0.98 | 1 | 22442 |
| HNRNPR    | ####   |           | ####   | Intra | 1,0   | 0.98 | 1 | 31684 |
| NDUFA2    | 1S3A   | Structure | 12.35  | Intra | 1,0   | 1    | 1 | 23073 |
| NDUFS1    | 5XTB   | Structure | ####   |       | 1 2,0 | 1    | 1 | 38761 |
| ACTN4     | O43707 | Phyre     | 21.38  | Intra | 1,0   | 1    | 7 | 14084 |
| ACTN4     | O43707 | Phyre     | 26.42  | Intra | 1,0   | 1    | 7 | 26248 |
| ACTN4     | O43707 | Phyre     | 53.25  | Intra | 3,0   | 1    | 7 | 18513 |
| ACTN4     | 2R0O   | Structure | 29.11  | Intra | 1,0   | 1    | 7 | 14388 |
| ACTN4     | 2R0O   | Structure | 7.91   | Intra | 1,0   | 1    | 7 | 23302 |
| ACTN4     | 2R0O   | Structure | 19.58  | Intra | 1,0   | 1    | 7 | 19432 |
| ACTN4     | 2R0O   | Structure | 19.58  | Intra | 2,0   | 1    | 7 | 19303 |
| ACTN4     | 2R0O   | Structure | ####   |       | 1 6,1 | 1    | 2 | 13915 |
| ACTC1     | P68032 | Phyre     | ####   |       | 1 1,0 | 0.99 | 2 | 12127 |
| SGTA      | 2VYI   | Structure | 15.58  | Intra | 0,1   | 1    | 1 | 7839  |
| NARS      | O43776 | Modeller  | 25.81  | Intra | 1,0   | 0.86 | 1 | 22056 |
| MYO1B     | O43795 | Phyre     | 13.08  | Intra | 1,0   | 1    | 1 | 35813 |
| RRP9      | ####   |           | ####   | Intra | 1,0   | 1    | 1 | 17217 |
| SNU13     | 2OZB   | Structure | ####   |       | 2 1,0 | 0.97 | 1 | 25340 |
| IDH3B     | O43837 | Modeller  | ####   |       | 1 1,0 | 0.83 | 1 | 21518 |
| CALU      | O43852 | Phyre     | 22.15  | Intra | 1,0   | 0.99 | 2 | 11429 |
| CALU      | O43852 | Phyre     | 8.5    | Intra | 0,1   | 0.63 | 2 | 6421  |
| AHCYL1    | 3MTG   | Structure | 27.8   |       | 1 1,1 | 1    | 2 | 15724 |
| AHCYL1    | 3MTG   | Structure | 11.72  | Intra | 2,0   | 1    | 2 | 20769 |
| SMARCA5   | ####   |           | ####   | Intra | 2,1   | 1    | 1 | 24486 |
| OPA1      | O60313 | Phyre     | 15.99  | Intra | 2,0   | 1    | 1 | 22345 |
| FZD6      | ####   |           | ####   | Intra | 1,0   | 0.99 | 1 | 19883 |
| NME2P1    | O60361 | Phyre     | 17.45  | Intra | 0,1   | 1    | 1 | 9387  |
| ACSL4     | O60488 | Phyre     | 25.51  | Intra | 1,0   | 1    | 2 | 23437 |
| ACSL4     | O60488 | Phyre     | 11.55  | Intra | 2,0   | 1    | 2 | 27081 |
| EIF4EBP3  | ####   |           | ####   | N/A   | 1,0   | 0.86 | 1 | 25916 |
| KPNA6     | 4UAD   | Structure | 8.49   | Intra | 1,0   | 1    | 1 | 23649 |
| CTNND1    | 3L6X   | Structure | 14.12  | Intra | 1,0   | 1    | 1 | 20542 |
| HIST1H2BK | 2CV5   | Structure | 18.13  | Intra | 4,4   | 1    | 5 | 19643 |
| HIST1H2BK | 2CV5   | Structure | 22.3   | Intra | 2,2   | 1    | 5 | 12707 |
| HIST1H2BK | ####   |           | ####   | Intra | 0,1   | 1    | 5 | 3119  |
| HIST1H2BK | 2CV5   | Structure | 47.49  |       | 1 0,1 | 1    | 5 | 8973  |
| HIST1H2BK | ####   |           | ####   | Intra | 0,2   | 1    | 5 | 3170  |
| HIST1H2BK | 2CV5   | Structure | ####   |       | 1 0,1 | 1    | 1 | 3480  |
| HIST1H2BK | 2CV5   | Structure | ####   |       | 2 0,1 | 0.8  | 1 | 8165  |

|           |           |           |        |       |      |      |   |       |
|-----------|-----------|-----------|--------|-------|------|------|---|-------|
| HIST1H4A  | 5B0Z      | Structure | ####   | 1     | 2,0  | 1    | 1 | 11296 |
| HIST1H2BK | 2CV5      | Structure | ####   | 1     | 1,1  | 1    | 1 | 8572  |
| ABCB7     | O75027    | Phyre     | 31.52  | Intra | 1,0  | 1    | 1 | 17543 |
| IGSF3     | O75054    | Phyre     | ####   | Intra | 0,1  | 1    | 1 | 13267 |
| DNAJC13   | ####      | ####      | ####   | Intra | 1,0  | 0.99 | 1 | 16265 |
| H2AFY     | 1ZR5      | Structure | 9.24   | Intra | 4,0  | 1    | 1 | 23053 |
| FLNB      | ####      | ####      | ####   | Intra | 1,2  | 1    | 5 | 20563 |
| FLNB      | ####      | ####      | ####   | Intra | 1,0  | 1    | 5 | 29265 |
| FLNB      | ####      | ####      | ####   | Intra | 1,2  | 1    | 5 | 19630 |
| FLNB      | ####      | ####      | ####   | Intra | 0,2  | 1    | 5 | 8809  |
| FLNB      | ####      | ####      | ####   | Intra | 1,2  | 1    | 5 | 26029 |
| CS        | O75390    | Modeller  | 31.1   | Intra | 0,1  | 1    | 1 | 11474 |
| CS        | O75390    | Modeller  | ####   | 2     | 4,0  | 0.83 | 1 | 19100 |
| SEC22B    | O75396    | Phyre     | 13.95  | Intra | 1,0  | 1    | 2 | 25455 |
| SEC22B    | O75396    | Phyre     | 8.89   | Intra | 11,0 | 1    | 2 | 20813 |
| PRPF40A   | ####      | ####      | ####   | Intra | 2,0  | 1    | 1 | 18404 |
| VPS26A    | 2FAU      | Structure | 15.21  | Intra | 1,0  | 1    | 1 | 24093 |
| NDUFS3    | ####      | ####      | ####   | 1     | 2,0  | 0.85 | 1 | 28408 |
| ECI2      | ####      | ####      | ####   | Intra | 1,0  | 1    | 1 | 29361 |
| SF3B1     | 5IFE      | Structure | 33.89  | Intra | 1,0  | 0.99 | 1 | 17343 |
| CSDE1     | ####      | ####      | ####   | Intra | 1,0  | 1    | 1 | 33080 |
| SNRNP200  | 5URJ      | Structure | 37.46  | Intra | 1,0  | 1    | 4 | 25134 |
| SNRNP200  | 5URJ      | Structure | 100.3  | Intra | 1,0  | 1    | 4 | 27168 |
| SNRNP200  | 5URJ      | Structure | 104.06 | Intra | 1,0  | 1    | 4 | 28749 |
| SNRNP200  | 5URJ      | Structure | 36.37  | Intra | 1,0  | 1    | 4 | 28013 |
| PALM      | ####      | ####      | ####   | Intra | 1,0  | 0.97 | 1 | 13594 |
| DCTN3     | ####      | ####      | ####   | Intra | 1,0  | 0.99 | 1 | 20644 |
| ATP5H     | O75947    | Phyre     | 12.01  | Intra | 1,0  | 1    | 4 | 23684 |
| ATP5H     | O75947    | Phyre     | 12.23  | Intra | 1,1  | 1    | 4 | 19791 |
| ATP5H     | O75947    | Phyre     | 12.23  | Intra | 1,0  | 1    | 4 | 17449 |
| ATP5H     | O75947    | Phyre     | 20.57  | Intra | 2,1  | 1    | 4 | 19132 |
| ATP5J     | P18859    | Phyre     | ####   | 1     | 2,0  | 1    | 1 | 26365 |
| ATP5F1    | P24539    | Phyre     | ####   | 1     | 1,0  | 0.95 | 2 | 21050 |
| ATP5H     | O75947    | Phyre     | ####   | 1     | 1,0  | 0.98 | 2 | 16901 |
| FLOT1     | O75955_O` | Docking   | 18.34  | 1     | 3,0  | 1    | 2 | 17473 |
| FLOT1     | ####      | ####      | ####   | Intra | 1,0  | 0.99 | 2 | 14316 |
| FLOT1     | ####      | ####      | ####   | 1     | 2,0  | 1    | 3 | 15959 |
| FLOT2     | ####      | ####      | ####   | 1     | 2,2  | 1    | 3 | 9105  |
| FLOT1     | ####      | ####      | ####   | 1     | 1,0  | 0.98 | 3 | 25797 |
| ATP5L     | ####      | ####      | ####   | Intra | 0,1  | 1    | 1 | 9689  |
| WFS1      | ####      | ####      | ####   | Intra | 2,0  | 1    | 1 | 25780 |
| SRP72     | O76094    | Phyre     | ####   | Intra | 1,1  | 1    | 2 | 22072 |
| SRP72     | O76094    | Phyre     | 26.86  | Intra | 1,0  | 0.99 | 2 | 17156 |
| MTA2      | ####      | ####      | ####   | 1     | 1,0  | 0.89 | 2 | 17087 |
| HDAC1     | 4BKX      | Structure | ####   | 1     | 1,0  | 0.84 | 2 | 15529 |
| TOMM70    | ####      | ####      | ####   | Intra | 1,0  | 0.97 | 2 | 8794  |
| TOMM70    | O94826    | Phyre     | 15.13  | Intra | 2,1  | 1    | 2 | 17772 |

|        |        |           |       |       |       |      |    |       |
|--------|--------|-----------|-------|-------|-------|------|----|-------|
| PRPF6  | 509Z   | Structure | 23.09 | Intra | 2,2   | 1    | 1  | 18904 |
| PRPF6  | 509Z   | Structure | ####  |       | 2 0,1 | 0.83 | 1  | 10455 |
| GLS    | 3U09   | Structure | 19.36 | Intra | 3,0   | 1    | 1  | 21692 |
| PGM3   | O95394 | Modeller  | 13.06 | Intra | 1,0   | 0.99 | 1  | 21719 |
| BAG2   | O95816 | Phyre     | ####  | Intra | 3,2   | 1    | 3  | 9760  |
| BAG2   | O95816 | Phyre     | ####  | Intra | 1,0   | 0.99 | 3  | 10676 |
| BAG2   | ####   |           | ####  | Intra | 1,0   | 0.93 | 3  | 11211 |
| AIFM1  | 5KVI   | Structure | 23.49 | Intra | 0,1   | 1    | 7  | 5739  |
| AIFM1  | 5KVI   | Structure | 17.55 | Intra | 2,1   | 1    | 7  | 11818 |
| AIFM1  | 5KVI   | Structure | 7.07  | Intra | 1,0   | 1    | 7  | 24470 |
| AIFM1  | ####   |           | ####  | Intra | 1,0   | 1    | 7  | 23456 |
| AIFM1  | 5KVI   | Structure | 17.25 | Intra | 1,0   | 1    | 7  | 11873 |
| AIFM1  | 5KVI   | Structure | 15.59 | Intra | 1,0   | 1    | 7  | 17737 |
| AIFM1  | 5KVI   | Structure | 12.55 | Intra | 1,2   | 1    | 7  | 22724 |
| LDHA   | 5W8J   | Structure | 10.35 | Intra | 11,4  | 1    | 6  | 23011 |
| LDHA   | 5W8J   | Structure | 11.77 | Intra | 5,1   | 1    | 6  | 33251 |
| LDHA   | 5W8J   | Structure | 17.81 | Intra | 5,0   | 1    | 6  | 21979 |
| LDHA   | 5W8J   | Structure | 50.35 | Intra | 2,0   | 1    | 6  | 31338 |
| LDHA   | 5W8J   | Structure | 27.36 | Intra | 2,1   | 1    | 6  | 25421 |
| LDHA   | 5W8J   | Structure | 34.17 | Intra | 0,1   | 1    | 6  | 9469  |
| ENO1   | 2PSN   | Structure | ####  |       | 1 1,0 | 1    | 1  | 30894 |
| LDHB   | 1I0Z   | Structure | ####  |       | 1 1,0 | 1    | 1  | 22665 |
| GLUD1  | 1L1F   | Structure | 30.31 | Intra | 2,1   | 1    | 3  | 28081 |
| GLUD1  | 1L1F   | Structure | 30.31 | Intra | 1,0   | 1    | 3  | 26196 |
| GLUD1  | 1L1F   | Structure | 34.98 | Intra | 1,0   | 1    | 3  | 24125 |
| CYB5R3 | 1UMK   | Structure | 21.1  | Intra | 1,0   | 1    | 2  | 24451 |
| CYB5R3 | 1UMK   | Structure | 11.17 | Intra | 1,0   | 1    | 2  | 19566 |
| PNP    | ####   |           | ####  | Intra | 1,0   | 1    | 1  | 28914 |
| GOT2   | 5AX8   | Structure | 15.54 | Intra | 0,1   | 1    | 7  | 6347  |
| GOT2   | 5AX8   | Structure | 14.05 | Intra | 0,1   | 1    | 7  | 16439 |
| GOT2   | 5AX8   | Structure | 16.63 | Intra | 2,0   | 1    | 7  | 27329 |
| GOT2   | 5AX8   | Structure | 12.84 | Intra | 3,1   | 1    | 7  | 16205 |
| GOT2   | 5AX8   | Structure | 22.56 | Intra | 2,0   | 1    | 7  | 21790 |
| GOT2   | 5AX8   | Structure | 21.91 | Intra | 0,1   | 1    | 7  | 6333  |
| GOT2   | 5AX8   | Structure | 20.47 | Intra | 1,0   | 1    | 7  | 24360 |
| EGFR   | 3QWQ   | Structure | 5.99  | Intra | 1,0   | 1    | 2  | 12158 |
| EGFR   | ####   |           | ####  | Intra | 2,0   | 1    | 2  | 30089 |
| PGK1   | 2WZD   | Structure | 15.47 | Intra | 1,0   | 1    | 20 | 23014 |
| PGK1   | 2WZD   | Structure | 19.75 | Intra | 1,0   | 1    | 20 | 30254 |
| PGK1   | 2WZD   | Structure | 15.64 | Intra | 2,0   | 1    | 20 | 23813 |
| PGK1   | 2WZD   | Structure | 12.73 | Intra | 1,0   | 1    | 20 | 33974 |
| PGK1   | 2WZD   | Structure | 16.29 | Intra | 3,1   | 1    | 20 | 19574 |
| PGK1   | 2WZD   | Structure | 11.11 | Intra | 2,1   | 1    | 20 | 22820 |
| PGK1   | 2WZD   | Structure | 20.23 | Intra | 1,0   | 1    | 20 | 18431 |
| PGK1   | 2WZD   | Structure | 16.29 | Intra | 9,2   | 1    | 20 | 18240 |
| PGK1   | 2WZD   | Structure | 11.11 | Intra | 3,1   | 1    | 20 | 21665 |
| PGK1   | 2WZD   | Structure | 23.04 | Intra | 1,2   | 1    | 20 | 27383 |

|       |           |           |       |       |       |      |    |       |
|-------|-----------|-----------|-------|-------|-------|------|----|-------|
| PGK1  | 2WZD      | Structure | 9.39  | Intra | 2,1   | 1    | 20 | 31660 |
| PGK1  | P00558    | Phyre     | 7.53  | Intra | 3,2   | 1    | 20 | 9782  |
| PGK1  | 2WZD      | Structure | 17.22 | Intra | 0,1   | 1    | 20 | 7929  |
| PGK1  | 2WZD      | Structure | 15.39 | Intra | 1,2   | 1    | 20 | 18345 |
| PGK1  | 2WZD      | Structure | 14    | Intra | 2,0   | 1    | 20 | 27792 |
| PGK1  | 2WZD      | Structure | 18.83 | Intra | 2,1   | 1    | 20 | 21065 |
| PGK1  | 2WZD      | Structure | 21.93 | Intra | 2,0   | 1    | 20 | 15588 |
| PGK1  | 2WZD      | Structure | 14.33 | Intra | 3,0   | 1    | 20 | 22758 |
| PGK1  | 2WZD      | Structure | 18.66 | Intra | 0,1   | 1    | 20 | 8944  |
| PGK1  | P00558    | Phyre     | 4.58  | Intra | 6,2   | 1    | 20 | 9472  |
| ASS1  | P00966_PC | Docking   | 59.29 |       | 1 1,0 | 0.97 | 2  | 11834 |
| ASS1  | P00966    | Phyre     | ####  | Intra | 2,1   | 1    | 2  | 9374  |
| HLA-C | 5VGE      | Structure | ####  |       | 1 0,2 | 1    | 1  | 11076 |
| LMNA  | ####      |           | ####  | Intra | 1,0   | 1    | 19 | 31951 |
| LMNA  | ####      |           | ####  | Intra | 2,1   | 1    | 19 | 25025 |
| LMNA  | P02545    | Phyre     | 6.84  | Intra | 5,0   | 1    | 19 | 6815  |
| LMNA  | ####      |           | ####  | Intra | 1,0   | 1    | 19 | 18816 |
| LMNA  | P02545    | Phyre     | 37.41 | Intra | 1,0   | 1    | 19 | 15564 |
| LMNA  | ####      |           | ####  | Intra | 2,1   | 1    | 19 | 17544 |
| LMNA  | ####      |           | ####  | Intra | 1,0   | 1    | 19 | 36433 |
| LMNA  | ####      |           | ####  | Intra | 1,2   | 1    | 19 | 21247 |
| LMNA  | ####      |           | ####  | Intra | 2,0   | 1    | 19 | 19984 |
| LMNA  | ####      |           | ####  | Intra | 1,0   | 1    | 19 | 18274 |
| LMNA  | ####      |           | ####  | Intra | 1,1   | 1    | 19 | 21924 |
| LMNA  | ####      |           | ####  | Intra | 1,0   | 1    | 19 | 20107 |
| LMNA  | ####      |           | ####  |       | 1 1,0 | 1    | 19 | 17461 |
| LMNA  | ####      |           | ####  | Intra | 2,0   | 1    | 19 | 21403 |
| LMNA  | ####      |           | ####  | Intra | 1,0   | 1    | 19 | 23401 |
| LMNA  | ####      |           | ####  |       | 1 1,0 | 1    | 19 | 15649 |
| LMNA  | ####      |           | ####  | Intra | 1,0   | 1    | 19 | 18513 |
| LMNA  | ####      |           | ####  | Intra | 5,3   | 1    | 19 | 11809 |
| LMNA  | ####      |           | ####  | Intra | 2,0   | 1    | 19 | 16842 |
| LMNA  | ####      |           | ####  |       | 1 0,1 | 1    | 3  | 12231 |
| LMNA  | ####      |           | ####  |       | 1 3,0 | 1    | 3  | 16135 |
| LMNA  | ####      |           | ####  |       | 1 2,1 | 1    | 3  | 14350 |
| TFRC  | 3S9L      | Structure | 40.28 |       | 1 1,0 | 1    | 57 | 18889 |
| TFRC  | 3S9L      | Structure | 71.67 |       | 1 1,0 | 1    | 57 | 32596 |
| TFRC  | 3S9L      | Structure | 36.58 | Intra | 1,0   | 1    | 57 | 29672 |
| TFRC  | 3S9L      | Structure | 16.6  | Intra | 1,1   | 1    | 57 | 33004 |
| TFRC  | 3S9L      | Structure | 17.4  | Intra | 5,4   | 1    | 57 | 20484 |
| TFRC  | 3S9L      | Structure | 29.75 | Intra | 3,0   | 1    | 57 | 19234 |
| TFRC  | 3S9L      | Structure | 11.72 | Intra | 2,3   | 1    | 57 | 21806 |
| TFRC  | 3S9L      | Structure | 11.72 | Intra | 5,1   | 1    | 57 | 20432 |
| TFRC  | 3S9L      | Structure | 10.5  | Intra | 5,1   | 1    | 57 | 14460 |
| TFRC  | 3S9L      | Structure | 14.39 | Intra | 0,3   | 1    | 57 | 9217  |
| TFRC  | 3S9L      | Structure | 17.62 | Intra | 3,4   | 1    | 57 | 21885 |
| TFRC  | 3S9L      | Structure | 24.21 | Intra | 1,0   | 1    | 57 | 27472 |

|      |      |           |             |       |      |    |       |
|------|------|-----------|-------------|-------|------|----|-------|
| TFRC | 3S9L | Structure | 15.63 Intra | 11,13 | 1    | 57 | 33862 |
| TFRC | 3S9L | Structure | 80.58       | 1 1,0 | 1    | 57 | 17209 |
| TFRC | 3S9L | Structure | 26.63 Intra | 1,1   | 1    | 57 | 32487 |
| TFRC | 3S9L | Structure | 12.02 Intra | 0,1   | 1    | 57 | 15741 |
| TFRC | 3S9L | Structure | 11.47 Intra | 4,4   | 1    | 57 | 27300 |
| TFRC | 3S9L | Structure | 11.47 Intra | 2,1   | 1    | 57 | 25330 |
| TFRC | 3S9L | Structure | 11.47 Intra | 1,4   | 1    | 57 | 23312 |
| TFRC | 3S9L | Structure | 11.47 Intra | 0,3   | 1    | 57 | 8383  |
| TFRC | 3S9L | Structure | 23.6 Intra  | 1,1   | 1    | 57 | 28634 |
| TFRC | 3S9L | Structure | 10.08 Intra | 3,0   | 1    | 57 | 16331 |
| TFRC | 3S9L | Structure | 24.47 Intra | 1,1   | 1    | 57 | 26344 |
| TFRC | 3S9L | Structure | 14.81 Intra | 15,12 | 1    | 57 | 28724 |
| TFRC | 3S9L | Structure | 17.35 Intra | 2,1   | 1    | 57 | 21872 |
| TFRC | 3S9L | Structure | 10.79 Intra | 4,0   | 1    | 57 | 20600 |
| TFRC | 3S9L | Structure | 10.79 Intra | 6,3   | 1    | 57 | 19955 |
| TFRC | 3S9L | Structure | 23.17 Intra | 1,0   | 1    | 57 | 24734 |
| TFRC | 3S9L | Structure | 18.19 Intra | 2,4   | 1    | 57 | 28906 |
| TFRC | 3S9L | Structure | 33.02 Intra | 2,2   | 1    | 57 | 13198 |
| TFRC | 3S9L | Structure | 21.08 Intra | 2,2   | 1    | 57 | 36494 |
| TFRC | 3S9L | Structure | 28.01 Intra | 2,0   | 1    | 57 | 13540 |
| TFRC | 3S9L | Structure | 11.75 Intra | 2,2   | 1    | 57 | 13713 |
| TFRC | 3S9L | Structure | 10.71 Intra | 7,0   | 1    | 57 | 25114 |
| TFRC | 3S9L | Structure | 10.71 Intra | 1,0   | 1    | 57 | 22711 |
| TFRC | 3S9L | Structure | 5.6 Intra   | 2,0   | 1    | 57 | 17414 |
| TFRC | 3S9L | Structure | 27.58 Intra | 0,1   | 1    | 57 | 12732 |
| TFRC | 3S9L | Structure | 24.91 Intra | 1,0   | 1    | 57 | 28256 |
| TFRC | 3S9L | Structure | 22.41 Intra | 1,0   | 1    | 57 | 22799 |
| TFRC | 3S9L | Structure | 15.78 Intra | 4,4   | 1    | 57 | 36764 |
| TFRC | 3S9L | Structure | 40.59 Intra | 1,0   | 1    | 57 | 21809 |
| TFRC | 3S9L | Structure | 20.8 Intra  | 1,2   | 1    | 57 | 35929 |
| TFRC | 3S9L | Structure | 37.63       | 1 1,0 | 0.96 | 57 | 6715  |
| TFRC | 3S9L | Structure | 25.46 Intra | 10,7  | 1    | 57 | 20882 |
| TFRC | 3S9L | Structure | 27.79 Intra | 1,0   | 1    | 57 | 31239 |
| TFRC | 3S9L | Structure | 21.49 Intra | 2,0   | 1    | 57 | 21728 |
| TFRC | 3S9L | Structure | 12.9 Intra  | 3,1   | 1    | 57 | 23000 |
| TFRC | 3S9L | Structure | 12.64 Intra | 2,2   | 1    | 57 | 39694 |
| TFRC | 3S9L | Structure | 13.1 Intra  | 5,2   | 1    | 57 | 21772 |
| TFRC | 3S9L | Structure | 13.1 Intra  | 1,1   | 1    | 57 | 20537 |
| TFRC | 3S9L | Structure | 13.8 Intra  | 1,1   | 1    | 57 | 26829 |
| TFRC | 3S9L | Structure | 13.8 Intra  | 1,2   | 1    | 57 | 24037 |
| TFRC | 3S9L | Structure | 10.97 Intra | 1,0   | 1    | 57 | 22051 |
| TFRC | 3S9L | Structure | 14.86 Intra | 1,3   | 1    | 57 | 28142 |
| TFRC | 3S9L | Structure | 12.9 Intra  | 1,0   | 1    | 57 | 21393 |
| TFRC | 3S9L | Structure | 21.94 Intra | 3,9   | 1    | 57 | 27650 |
| TFRC | 3S9L | Structure | 80.77       | 1 4,7 | 1    | 57 | 26934 |
| CD59 | 2J8B | Structure | ####        | 2 1,0 | 0.98 | 1  | 20684 |
| TFRC | 3S9L | Structure | ####        | 2 3,2 | 1    | 2  | 7480  |

|           |        |           |             |     |      |      |    |       |
|-----------|--------|-----------|-------------|-----|------|------|----|-------|
| TFRC      | 3S9L   | Structure | ####        | 2   | 3,1  | 1    | 2  | 8104  |
| CAT       | P04040 | Phyre     | 60.73 Intra | 2,0 |      | 1    | 2  | 18773 |
| CAT       | P04040 | Phyre     | 10.79 Intra | 2,0 |      | 1    | 2  | 17780 |
| ALDOA     | P04075 | Phyre     | 12.95 Intra | 6,3 |      | 1    | 4  | 21925 |
| ALDOA     | P04075 | Phyre     | 17.05 Intra | 1,0 |      | 1    | 4  | 15191 |
| ALDOA     | P04075 | Phyre     | 17.46 Intra | 1,0 |      | 1    | 4  | 21921 |
| ALDOA     | P04075 | Phyre     | 31.16 Intra | 1,0 | 0.99 |      | 4  | 16737 |
| ALDOC     | 1XFB   | Structure | ####        | 1   | 2,2  | 1    | 1  | 23436 |
| ANXA1     | 1AIN   | Structure | 12.77 Intra | 2,2 |      | 1    | 4  | 34064 |
| ANXA1     | 1AIN   | Structure | 12.31 Intra | 2,0 |      | 1    | 4  | 34179 |
| ANXA1     | 1AIN   | Structure | 11.83 Intra | 3,1 |      | 1    | 4  | 24909 |
| ANXA1     | 1AIN   | Structure | 30.62 Intra | 1,0 |      | 1    | 4  | 28132 |
| SOD2      | 5T30   | Structure | 8.6 Intra   | 1,0 | 0.99 |      | 1  | 25375 |
| GAPDH     | 1U8F   | Structure | 7.2 Intra   | 2,0 |      | 1    | 21 | 20774 |
| GAPDH     | 1U8F   | Structure | 20.69 Intra | 1,3 |      | 1    | 21 | 28901 |
| GAPDH     | 1U8F   | Structure | 34.73       | 1   | 3,0  | 1    | 21 | 11688 |
| GAPDH     | 1U8F   | Structure | 29.68 Intra | 4,3 |      | 1    | 21 | 17032 |
| GAPDH     | 1U8F   | Structure | 12.09 Intra | 1,3 |      | 1    | 21 | 27661 |
| GAPDH     | 1U8F   | Structure | 18.27 Intra | 0,1 |      | 1    | 21 | 12114 |
| GAPDH     | 1U8F   | Structure | 22.69 Intra | 1,2 |      | 1    | 21 | 29719 |
| GAPDH     | 1U8F   | Structure | 15.87 Intra | 1,0 |      | 1    | 21 | 11240 |
| GAPDH     | 1U8F   | Structure | 25.04 Intra | 1,4 |      | 1    | 21 | 21987 |
| GAPDH     | 1U8F   | Structure | 20.08 Intra | 3,4 |      | 1    | 21 | 23735 |
| GAPDH     | 1U8F   | Structure | 42.03 Intra | 1,0 |      | 1    | 21 | 16144 |
| GAPDH     | 1U8F   | Structure | 42.03 Intra | 1,0 |      | 1    | 21 | 13640 |
| GAPDH     | 1U8F   | Structure | 28.19       | 1   | 1,1  | 1    | 21 | 21366 |
| GAPDH     | 1U8F   | Structure | 21.62 Intra | 1,0 |      | 1    | 21 | 29250 |
| GAPDH     | 1U8F   | Structure | 12.32 Intra | 1,0 |      | 1    | 21 | 27482 |
| GAPDH     | 1U8F   | Structure | 42.15 Intra | 1,0 |      | 1    | 21 | 11448 |
| GAPDH     | 1U8F   | Structure | 40.26 Intra | 1,1 |      | 1    | 21 | 16574 |
| GAPDH     | 1U8F   | Structure | 25.39 Intra | 2,1 |      | 1    | 21 | 18124 |
| GAPDH     | 1U8F   | Structure | 24.43 Intra | 1,1 |      | 1    | 21 | 19203 |
| GAPDH     | 1U8F   | Structure | 39.7 Intra  | 3,2 |      | 1    | 21 | 17233 |
| GAPDH     | 1U8F   | Structure | 6.35 Intra  | 1,2 |      | 1    | 21 | 13132 |
| DSG2      | 5ERD   | Structure | ####        | 2   | 1,0  | 0.98 | 1  | 24436 |
| RPN1      | P04843 | Unknown   | 16.24 Intra | 2,0 |      | 1    | 9  | 21950 |
| RPN1      | P04843 | Unknown   | 14.11 Intra | 0,1 |      | 1    | 9  | 7077  |
| RPN1      | P04843 | Unknown   | 25.95 Intra | 0,1 |      | 1    | 9  | 8110  |
| RPN1      | P04843 | Unknown   | 20.96 Intra | 1,1 |      | 1    | 9  | 16035 |
| RPN1      | P04843 | Unknown   | 20.96 Intra | 0,1 |      | 1    | 9  | 7968  |
| RPN1      | P04843 | Unknown   | 18.88 Intra | 1,2 |      | 1    | 9  | 19143 |
| RPN1      | P04843 | Unknown   | 8.69 Intra  | 1,0 |      | 1    | 9  | 13671 |
| RPN1      | ####   | ####      | Intra       | 1,0 |      | 1    | 9  | 25604 |
| RPN1      | P04843 | Unknown   | 19.09 Intra | 1,0 |      | 1    | 9  | 34581 |
| HIST1H2AB | ####   | ####      |             | 1   | 0,1  | 1    | 2  | 2300  |
| HIST1H2AB | 5B0Z   | Structure | 26.49       | 1   | 8,2  | 1    | 2  | 28394 |
| HIST1H4A  | 5B0Z   | Structure | 47.76       | 1   | 10,5 | 1    | 6  | 9454  |



|           |        |           |       |           |      |    |       |
|-----------|--------|-----------|-------|-----------|------|----|-------|
| HIST1H4A  | 5B0Z   | Structure | 39.16 | 1 1,0     | 0.99 | 6  | 23904 |
| HIST1H4A  | 5B0Z   | Structure | 36.98 | 1 1,0     | 1    | 6  | 34724 |
| HIST1H4A  | 5B0Z   | Structure | 32.15 | 1 1,0     | 1    | 6  | 27479 |
| HIST1H4A  | 5B0Z   | Structure | 32.15 | 1 9,9     | 1    | 6  | 31230 |
| HIST1H4A  | 5B0Z   | Structure | 32.15 | 1 15,3    | 1    | 6  | 28153 |
| HIST1H2BC | 5GT0   | Structure | ####  | 1 0,2     | 1    | 1  | 3382  |
| HIST1H3A  | P68431 | Phyre     | ####  | 1 0,1     | 1    | 2  | 2469  |
| HIST1H2AB | 5B0Z   | Structure | ####  | 1 0,3     | 1    | 2  | 11986 |
| HIST3H3   | 3A6N   | Structure | ####  | 1 1,0     | 1    | 8  | 14094 |
| HIST3H3   | 3A6N   | Structure | ####  | 1 4,0     | 1    | 8  | 12010 |
| HIST3H3   | 3A6N   | Structure | ####  | 1 1,0     | 1    | 8  | 24601 |
| HIST3H3   | 3A6N   | Structure | ####  | 1 1,0     | 1    | 8  | 23399 |
| HIST3H3   | 3A6N   | Structure | ####  | 1 3,2     | 1    | 8  | 26678 |
| HIST3H3   | 3A6N   | Structure | ####  | 1 1,1     | 1    | 8  | 23324 |
| HIST3H3   | Q16695 | Phyre     | ####  | 1 1,0     | 1    | 8  | 5373  |
| HIST1H2AB | 5B0Z   | Structure | ####  | 1 1,1     | 1    | 8  | 30968 |
| HIST1H2BH | Q93079 | Phyre     | ####  | 1 1,2     | 1    | 3  | 5409  |
| HIST1H2BH | Q93079 | Phyre     | ####  | 1 4,3     | 1    | 3  | 3139  |
| HIST1H2BH | Q93079 | Phyre     | ####  | 1 2,0     | 1    | 3  | 25235 |
| HIST1H2AH | Q96KK5 | Phyre     | ####  | 1 0,1     | 1    | 3  | 2920  |
| HIST1H2AB | 5B0Z   | Structure | ####  | 1 4,2     | 1    | 3  | 26035 |
| HIST1H2AH | Q96KK5 | Phyre     | ####  | 1 3,1     | 1    | 3  | 35623 |
| SLC4A2    | ####   | ####      | N/A   | 2,0       | 1    | 1  | 10261 |
| ATP1A1    | P05023 | Phyre     | 9.35  | Intra 1,2 | 1    | 3  | 27251 |
| ATP1A1    | P05023 | Phyre     | 18.88 | Intra 0,1 | 1    | 3  | 13060 |
| ATP1A1    | P05023 | Phyre     | 27.17 | Intra 1,0 | 1    | 3  | 21356 |
| ATP4A     | ####   | ####      |       | 1 1,0     | 0.94 | 1  | 22655 |
| ATP1B1    | P05026 | Phyre     | 24.94 | Intra 4,6 | 1    | 4  | 27780 |
| ATP1B1    | P05026 | Phyre     | 8.83  | Intra 1,0 | 1    | 4  | 29469 |
| ATP1B1    | P05026 | Phyre     | 11.45 | Intra 3,2 | 1    | 4  | 18315 |
| ATP1B1    | P05026 | Phyre     | 11.45 | Intra 2,0 | 1    | 4  | 16718 |
| SLC25A5   | P05141 | Phyre     | 27.96 | Intra 1,1 | 1    | 22 | 33127 |
| SLC25A5   | P05141 | Phyre     | 20.62 | Intra 1,0 | 1    | 22 | 33835 |
| SLC25A5   | P05141 | Phyre     | 29.68 | Intra 1,0 | 1    | 22 | 27692 |
| SLC25A5   | P05141 | Phyre     | 13.95 | Intra 1,0 | 1    | 22 | 26088 |
| SLC25A5   | P05141 | Phyre     | 12.93 | Intra 0,1 | 1    | 22 | 11392 |
| SLC25A5   | P05141 | Phyre     | 24.27 | Intra 1,0 | 1    | 22 | 13219 |
| SLC25A5   | P05141 | Phyre     | 18.94 | Intra 2,0 | 1    | 22 | 17431 |
| SLC25A5   | P05141 | Phyre     | 32.99 | Intra 1,0 | 1    | 22 | 31894 |
| SLC25A5   | P05141 | Phyre     | 23.6  | Intra 1,1 | 1    | 22 | 23336 |
| SLC25A5   | P05141 | Phyre     | 23.53 | Intra 1,0 | 1    | 22 | 27119 |
| SLC25A5   | P05141 | Phyre     | 9.22  | Intra 2,2 | 1    | 22 | 24222 |
| SLC25A5   | P05141 | Phyre     | 24.4  | Intra 5,0 | 1    | 22 | 21847 |
| SLC25A5   | P05141 | Phyre     | 24.4  | Intra 7,0 | 1    | 22 | 20093 |
| SLC25A5   | P05141 | Phyre     | 14.2  | Intra 4,3 | 1    | 22 | 17261 |
| SLC25A5   | P05141 | Phyre     | 19.12 | Intra 1,0 | 1    | 22 | 17452 |
| SLC25A5   | P05141 | Phyre     | 33.98 | Intra 1,0 | 1    | 22 | 31481 |

|         |           |           |       |       |       |      |    |       |
|---------|-----------|-----------|-------|-------|-------|------|----|-------|
| SLC25A5 | P05141    | Phyre     | 18.61 | Intra | 1,0   | 1    | 22 | 27814 |
| SLC25A5 | P05141    | Phyre     | 22.6  | Intra | 7,5   | 1    | 22 | 35053 |
| SLC25A5 | P05141    | Phyre     | 28.13 | Intra | 1,0   | 1    | 22 | 32256 |
| SLC25A5 | P05141    | Phyre     | 27.32 | Intra | 3,1   | 1    | 22 | 31868 |
| SLC25A5 | P05141    | Phyre     | 6.51  | Intra | 0,1   | 1    | 22 | 15689 |
| SLC25A5 | P05141    | Phyre     | 6.51  | Intra | 2,0   | 1    | 22 | 26394 |
| SLC25A6 | P12236    | Phyre     | ####  |       | 1 1,0 | 1    | 1  | 12631 |
| ALPP    | 1EW2      | Structure | 19.65 | Intra | 1,0   | 1    | 3  | 25721 |
| ALPP    | 1EW2      | Structure | 37    | Intra | 5,3   | 1    | 3  | 22664 |
| ALPP    | 1EW2      | Structure | 31.34 | Intra | 0,1   | 1    | 3  | 7559  |
| EIF2S1  | P05198    | Unknown   | 11.23 | Intra | 1,0   | 1    | 3  | 26785 |
| EIF2S1  | P05198    | Unknown   | 4.18  | Intra | 1,0   | 1    | 3  | 23161 |
| EIF2S1  | P05198    | Unknown   | 27.69 | Intra | 2,0   | 1    | 3  | 21493 |
| ICAM1   | 1MQ8      | Structure | 20.61 | Intra | 1,2   | 1    | 2  | 26081 |
| ICAM1   | ####      |           | ####  | Intra | 2,0   | 1    | 2  | 22298 |
| SLC3A2  | 2DH2      | Structure | ####  |       | 1 1,0 | 0.95 | 1  | 21362 |
| RPLP2   | 4BEH      | Structure | 5.94  | Intra | 2,3   | 1    | 1  | 28729 |
| RPLP0   | P05388    | Phyre     | 21.43 | Intra | 1,0   | 1    | 3  | 29522 |
| RPLP0   | P05388    | Phyre     | 7.88  | Intra | 1,0   | 1    | 3  | 25860 |
| RPLP0   | P05388    | Phyre     | 19.03 | Intra | 1,0   | 1    | 3  | 28346 |
| ITGB1   | 4WK0      | Structure | 19.95 | Intra | 0,2   | 1    | 3  | 12326 |
| ITGB1   | ####      |           | ####  | Intra | 1,0   | 1    | 3  | 23246 |
| ITGB1   | P05556    | Phyre     | 20.17 | Intra | 6,2   | 1    | 3  | 18136 |
| ITGB1   | 4WK0      | Structure | ####  |       | 1 1,0 | 0.98 | 1  | 24494 |
| ITGB1   | 4WK0      | Structure | ####  |       | 1 1,1 | 1    | 1  | 25375 |
| KRT18   | P05783    | Phyre     | 16.29 | Intra | 2,0   | 1    | 23 | 26696 |
| KRT18   | P05783    | Phyre     | 10.83 | Intra | 0,2   | 1    | 23 | 3821  |
| KRT18   | ####      |           | ####  | Intra | 1,0   | 1    | 23 | 10858 |
| KRT18   | P05783    | Phyre     | ####  | Intra | 5,1   | 1    | 23 | 28309 |
| KRT18   | P05783    | Phyre     | ####  | Intra | 3,3   | 1    | 23 | 11376 |
| KRT18   | P05783    | Phyre     | ####  | Intra | 1,1   | 1    | 23 | 9531  |
| KRT18   | P05783    | Phyre     | ####  | Intra | 1,0   | 1    | 23 | 26439 |
| KRT18   | ####      |           | ####  | Intra | 2,0   | 1    | 23 | 10916 |
| KRT18   | ####      |           | ####  | Intra | 2,3   | 1    | 23 | 37179 |
| KRT18   | ####      |           | ####  | Intra | 3,0   | 1    | 23 | 35528 |
| KRT18   | ####      |           | ####  |       | 1 2,1 | 1    | 23 | 16466 |
| KRT18   | ####      |           | ####  | Intra | 6,4   | 1    | 23 | 21603 |
| KRT18   | ####      |           | ####  | Intra | 1,0   | 1    | 23 | 23558 |
| KRT18   | ####      |           | ####  | Intra | 1,0   | 1    | 23 | 20236 |
| KRT18   | P05783    | Phyre     | 10.83 | Intra | 1,0   | 1    | 23 | 9415  |
| KRT18   | P05783_PC | Docking   | 15.31 |       | 1 2,1 | 1    | 23 | 13320 |
| KRT18   | P05783    | Phyre     | ####  | Intra | 4,0   | 1    | 23 | 11484 |
| KRT18   | P05783    | Phyre     | ####  | Intra | 2,0   | 1    | 23 | 29786 |
| KRT18   | ####      |           | ####  |       | 1 7,1 | 1    | 23 | 25778 |
| KRT18   | ####      |           | ####  | Intra | 2,0   | 1    | 23 | 24478 |
| KRT18   | ####      |           | ####  |       | 1 3,0 | 1    | 23 | 28405 |
| KRT18   | P05783    | Phyre     | ####  | Intra | 1,1   | 1    | 23 | 27538 |

|       |        |       |      |       |      |    |       |
|-------|--------|-------|------|-------|------|----|-------|
| KRT18 | ####   |       | #### | 1 2,0 | 1    | 23 | 16260 |
| KRT18 | ####   |       | #### | 1 1,1 | 1    | 54 | 13634 |
| KRT18 | P05783 | Phyre | #### | 1 2,0 | 1    | 54 | 12779 |
| KRT8  | P05787 | Phyre | #### | 1 1,0 | 1    | 54 | 14965 |
| KRT18 | ####   |       | #### | 1 2,2 | 1    | 54 | 16788 |
| KRT18 | P05783 | Phyre | #### | 1 1,0 | 1    | 54 | 16365 |
| KRT8  | P05787 | Phyre | #### | 1 3,1 | 1    | 54 | 12336 |
| KRT8  | P05787 | Phyre | #### | 1 1,2 | 1    | 54 | 7881  |
| KRT8  | P05787 | Phyre | #### | 1 2,2 | 1    | 54 | 18818 |
| KRT8  | P05787 | Phyre | #### | 1 1,0 | 0.99 | 54 | 12056 |
| KRT8  | P05787 | Phyre | #### | 1 1,0 | 1    | 54 | 16547 |
| KRT18 | P05783 | Phyre | #### | 1 4,0 | 1    | 54 | 29509 |
| KRT18 | ####   |       | #### | 1 4,3 | 1    | 54 | 16059 |
| KRT18 | ####   |       | #### | 1 4,4 | 1    | 54 | 21342 |
| KRT18 | ####   |       | #### | 1 2,0 | 1    | 54 | 22823 |
| KRT18 | ####   |       | #### | 1 1,1 | 1    | 54 | 18617 |
| KRT18 | ####   |       | #### | 1 1,1 | 1    | 54 | 15067 |
| KRT8  | P05787 | Phyre | #### | 1 0,1 | 1    | 54 | 3404  |
| KRT8  | P05787 | Phyre | #### | 1 0,5 | 1    | 54 | 12957 |
| KRT8  | P05787 | Phyre | #### | 1 3,1 | 1    | 54 | 28057 |
| KRT8  | P05787 | Phyre | #### | 1 1,0 | 1    | 54 | 29617 |
| KRT8  | P05787 | Phyre | #### | 1 8,1 | 1    | 54 | 18496 |
| KRT8  | P05787 | Phyre | #### | 1 3,2 | 1    | 54 | 13566 |
| KRT8  | P05787 | Phyre | #### | 1 5,1 | 1    | 54 | 13260 |
| KRT8  | P05787 | Phyre | #### | 1 3,2 | 1    | 54 | 37080 |
| KRT8  | P05787 | Phyre | #### | 1 2,1 | 1    | 54 | 15387 |
| KRT8  | P05787 | Phyre | #### | 1 0,1 | 1    | 54 | 7519  |
| KRT8  | P05787 | Phyre | #### | 1 1,0 | 1    | 54 | 16506 |
| KRT8  | P05787 | Phyre | #### | 1 0,1 | 1    | 54 | 8879  |
| KRT8  | P05787 | Phyre | #### | 1 2,2 | 1    | 54 | 19006 |
| KRT18 | ####   |       | #### | 1 1,1 | 1    | 54 | 26184 |
| KRT18 | ####   |       | #### | 1 1,0 | 1    | 54 | 28794 |
| KRT18 | ####   |       | #### | 1 1,0 | 1    | 54 | 27994 |
| KRT8  | P05787 | Phyre | #### | 1 1,0 | 1    | 54 | 31198 |
| KRT8  | P05787 | Phyre | #### | 1 1,0 | 1    | 54 | 23761 |
| KRT8  | P05787 | Phyre | #### | 1 1,2 | 1    | 54 | 21620 |
| KRT8  | P05787 | Phyre | #### | 1 1,1 | 1    | 54 | 37399 |
| KRT8  | P05787 | Phyre | #### | 1 0,1 | 1    | 54 | 5729  |
| KRT8  | P05787 | Phyre | #### | 1 0,1 | 1    | 54 | 7205  |
| KRT8  | P05787 | Phyre | #### | 1 0,1 | 1    | 54 | 14792 |
| KRT8  | P05787 | Phyre | #### | 1 3,0 | 1    | 54 | 29728 |
| KRT18 | ####   |       | #### | 1 4,2 | 1    | 54 | 14459 |
| KRT18 | ####   |       | #### | 1 4,1 | 1    | 54 | 19996 |
| KRT18 | ####   |       | #### | 1 1,0 | 1    | 54 | 23202 |
| KRT18 | ####   |       | #### | 1 1,0 | 1    | 54 | 14342 |
| KRT18 | ####   |       | #### | 1 0,1 | 1    | 54 | 10051 |
| KRT18 | ####   |       | #### | 1 2,1 | 1    | 54 | 22529 |

|       |        |           |             |       |   |    |       |
|-------|--------|-----------|-------------|-------|---|----|-------|
| KRT18 | ####   |           | ####        | 1 2,1 | 1 | 54 | 17861 |
| KRT8  | P05787 | Phyre     | ####        | 1 1,1 | 1 | 54 | 24720 |
| KRT18 | ####   |           | ####        | 1 0,2 | 1 | 54 | 4987  |
| KRT18 | ####   |           | ####        | 1 0,1 | 1 | 54 | 9231  |
| KRT8  | P05787 | Phyre     | ####        | 1 3,0 | 1 | 54 | 23447 |
| KRT8  | P05787 | Phyre     | ####        | 1 1,0 | 1 | 54 | 36125 |
| KRT8  | P05787 | Phyre     | ####        | 1 0,1 | 1 | 54 | 13438 |
| KRT18 | ####   |           | ####        | 1 1,0 | 1 | 54 | 14780 |
| KRT18 | ####   |           | ####        | 2 1,0 | 1 | 6  | 19077 |
| VIM   | ####   |           | ####        | 2 1,0 | 1 | 6  | 30284 |
| VIM   | ####   |           | ####        | 2 1,0 | 1 | 6  | 13011 |
| VIM   | ####   |           | ####        | 2 1,0 | 1 | 6  | 17302 |
| VIM   | 3UF1   | Structure | ####        | 2 2,0 | 1 | 6  | 28664 |
| KRT18 | ####   |           | ####        | 2 1,0 | 1 | 6  | 17478 |
| KRT18 | ####   |           | ####        | 1 1,0 | 1 | 11 | 17223 |
| KRT7  | ####   |           | ####        | 1 1,0 | 1 | 11 | 23538 |
| KRT7  | ####   |           | ####        | 1 3,2 | 1 | 11 | 22117 |
| KRT7  | ####   |           | ####        | 1 1,0 | 1 | 11 | 17194 |
| KRT7  | P08729 | Phyre     | ####        | 1 2,1 | 1 | 11 | 20499 |
| KRT7  | P08729 | Phyre     | ####        | 1 2,1 | 1 | 11 | 19048 |
| KRT7  | P08729 | Phyre     | ####        | 1 3,0 | 1 | 11 | 17560 |
| KRT18 | ####   |           | ####        | 1 0,1 | 1 | 11 | 10199 |
| KRT7  | P08729 | Phyre     | ####        | 1 5,5 | 1 | 11 | 24877 |
| KRT7  | P08729 | Phyre     | ####        | 1 1,0 | 1 | 11 | 20841 |
| KRT18 | ####   |           | ####        | 1 0,1 | 1 | 11 | 3234  |
| EPPK1 | ####   |           | ####        | 2 3,2 | 1 | 1  | 23687 |
| KRT8  | P05787 | Phyre     | 27.97 Intra | 1,4   | 1 | 85 | 25551 |
| KRT8  | P05787 | Phyre     | 57.9 Intra  | 2,1   | 1 | 85 | 15873 |
| KRT8  | P05787 | Phyre     | 27.97 Intra | 2,3   | 1 | 85 | 24349 |
| KRT8  | P05787 | Phyre     | 52.36 Intra | 1,1   | 1 | 85 | 10371 |
| KRT8  | P05787 | Phyre     | 43.39 Intra | 0,1   | 1 | 85 | 6468  |
| KRT8  | P05787 | Phyre     | 57.9 Intra  | 0,3   | 1 | 85 | 5663  |
| KRT8  | ####   |           | #### Intra  | 0,1   | 1 | 85 | 5618  |
| KRT8  | P05787 | Phyre     | 52.36 Intra | 3,1   | 1 | 85 | 11000 |
| KRT8  | P05787 | Phyre     | 52.36 Intra | 0,2   | 1 | 85 | 5082  |
| KRT8  | ####   |           | #### N/A    | 2,0   | 1 | 85 | 11900 |
| KRT8  | ####   |           | #### Intra  | 2,1   | 1 | 85 | 17732 |
| KRT8  | P05787 | Phyre     | #### Intra  | 1,0   | 1 | 85 | 13791 |
| KRT8  | P05787 | Phyre     | #### Intra  | 2,0   | 1 | 85 | 22017 |
| KRT8  | ####   |           | #### Intra  | 1,0   | 1 | 85 | 11098 |
| KRT8  | P05787 | Phyre     | #### Intra  | 1,0   | 1 | 85 | 13223 |
| KRT8  | P05787 | Phyre     | #### Intra  | 1,0   | 1 | 85 | 20547 |
| KRT8  | ####   |           | #### Intra  | 3,0   | 1 | 85 | 10265 |
| KRT8  | P05787 | Phyre     | #### Intra  | 1,0   | 1 | 85 | 16780 |
| KRT8  | P05787 | Phyre     | #### Intra  | 1,0   | 1 | 85 | 24180 |
| KRT8  | P05787 | Phyre     | #### Intra  | 2,1   | 1 | 85 | 37058 |
| KRT8  | P05787 | Phyre     | #### Intra  | 1,0   | 1 | 85 | 18410 |

|      |                   |       |        |       |     |   |    |       |
|------|-------------------|-------|--------|-------|-----|---|----|-------|
| KRT8 | P05787            | Phyre | 19.01  | Intra | 2,1 | 1 | 85 | 20534 |
| KRT8 | P05787            | Phyre | 21.16  | Intra | 2,3 | 1 | 85 | 26221 |
| KRT8 | P05787            | Phyre | 21.16  | Intra | 1,1 | 1 | 85 | 25520 |
| KRT8 | P05787            | Phyre | 19.01  | Intra | 2,0 | 1 | 85 | 18409 |
| KRT8 | P05787_PC Docking |       | 46.39  | N/A   | 1,0 | 1 | 85 | 17066 |
| KRT8 | P05787            | Phyre | 32.39  | Intra | 4,2 | 1 | 85 | 18766 |
| KRT8 | P05787            | Phyre | 29.76  | Intra | 1,0 | 1 | 85 | 36987 |
| KRT8 | P05787            | Phyre | 27.91  | Intra | 3,1 | 1 | 85 | 15654 |
| KRT8 | P05787            | Phyre | 27.91  | Intra | 3,2 | 1 | 85 | 14389 |
| KRT8 | P05787            | Phyre | 13.19  | Intra | 1,0 | 1 | 85 | 18091 |
| KRT8 | ####              |       | ####   | Intra | 1,1 | 1 | 85 | 15951 |
| KRT8 | P05787            | Phyre | 69.93  | Intra | 3,1 | 1 | 85 | 28851 |
| KRT8 | ####              |       | ####   | Intra | 2,0 | 1 | 85 | 19078 |
| KRT8 | P05787            | Phyre | 39.99  | Intra | 2,1 | 1 | 85 | 21334 |
| KRT8 | P05787            | Phyre | 32.48  | Intra | 1,0 | 1 | 85 | 16872 |
| KRT8 | P05787            | Phyre | 69.08  | Intra | 1,0 | 1 | 85 | 16407 |
| KRT8 | P05787_PC Docking |       | 15.1   | N/A   | 1,1 | 1 | 85 | 14514 |
| KRT8 | P05787            | Phyre | 57.8   | Intra | 2,0 | 1 | 85 | 30786 |
| KRT8 | P05787            | Phyre | 101.04 | Intra | 3,1 | 1 | 85 | 18295 |
| KRT8 | P05787            | Phyre | 41     | Intra | 4,6 | 1 | 85 | 37285 |
| KRT8 | P05787            | Phyre | 69.93  | Intra | 3,0 | 1 | 85 | 25656 |
| KRT8 | ####              |       | ####   | Intra | 3,2 | 1 | 85 | 13793 |
| KRT8 | P05787            | Phyre | 95.03  | Intra | 1,1 | 1 | 85 | 14159 |
| KRT8 | P05787            | Phyre | 95.03  | Intra | 2,2 | 1 | 85 | 12710 |
| KRT8 | P05787            | Phyre | 49.53  | Intra | 0,1 | 1 | 85 | 13406 |
| KRT8 | P05787            | Phyre | 17.23  | Intra | 3,1 | 1 | 85 | 19847 |
| KRT8 | P05787            | Phyre | 81.27  | Intra | 3,0 | 1 | 85 | 17544 |
| KRT8 | ####              |       | ####   | Intra | 1,1 | 1 | 85 | 21003 |
| KRT8 | P05787            | Phyre | 143.05 | Intra | 1,1 | 1 | 85 | 22350 |
| KRT8 | P05787_PC Docking |       | 80.11  | N/A   | 7,4 | 1 | 85 | 20291 |
| KRT8 | P05787            | Phyre | 61.83  | Intra | 1,0 | 1 | 85 | 36038 |
| KRT8 | P05787            | Phyre | ####   | Intra | 2,0 | 1 | 85 | 14769 |
| KRT8 | P05787            | Phyre | ####   | Intra | 1,1 | 1 | 85 | 16666 |
| KRT8 | P05787            | Phyre | ####   | Intra | 2,1 | 1 | 85 | 21974 |
| KRT8 | P05787            | Phyre | ####   | Intra | 1,0 | 1 | 85 | 20985 |
| KRT8 | ####              |       | ####   | N/A   | 3,2 | 1 | 85 | 12243 |
| KRT8 | P05787            | Phyre | ####   | Intra | 2,0 | 1 | 85 | 13295 |
| KRT8 | P05787            | Phyre | ####   | Intra | 4,1 | 1 | 85 | 11911 |
| KRT8 | P05787            | Phyre | ####   | Intra | 3,0 | 1 | 85 | 18208 |
| KRT8 | P05787            | Phyre | ####   | Intra | 2,0 | 1 | 85 | 16097 |
| KRT8 | P05787            | Phyre | 29.9   | Intra | 1,0 | 1 | 85 | 26723 |
| KRT8 | P05787            | Phyre | 10.78  | Intra | 3,3 | 1 | 85 | 17577 |
| KRT8 | P05787            | Phyre | 57.39  | Intra | 1,2 | 1 | 85 | 36838 |
| KRT8 | P05787            | Phyre | 105.02 | Intra | 1,0 | 1 | 85 | 19239 |
| KRT8 | P05787            | Phyre | 14.73  | Intra | 5,0 | 1 | 85 | 16789 |
| KRT8 | P05787            | Phyre | 10.78  | Intra | 1,2 | 1 | 85 | 16520 |
| KRT8 | P05787            | Phyre | 57.39  | Intra | 3,1 | 1 | 85 | 36413 |

|      |           |           |      |              |       |      |    |       |
|------|-----------|-----------|------|--------------|-------|------|----|-------|
| KRT8 | P05787    | Phyre     | #### | Intra        | 1,0   | 1    | 85 | 12895 |
| KRT8 | P05787    | Phyre     |      | 14.73 Intra  | 3,0   | 1    | 85 | 15757 |
| KRT8 | P05787    | Phyre     |      | 90.35 Intra  | 2,2   | 1    | 85 | 38060 |
| KRT8 | P05787    | Phyre     |      | 132.37 Intra | 1,4   | 1    | 85 | 27243 |
| KRT8 | P05787    | Phyre     |      | 64.08 Intra  | 3,2   | 1    | 85 | 12788 |
| KRT8 | P05787    | Phyre     |      | 104.93 Intra | 2,1   | 1    | 85 | 35381 |
| KRT8 | P05787    | Phyre     |      | 132.37 Intra | 2,2   | 1    | 85 | 24379 |
| KRT8 | P05787    | Phyre     |      | 14.63 Intra  | 3,1   | 1    | 85 | 21397 |
| KRT8 | P05787    | Phyre     | #### | Intra        | 0,1   | 1    | 85 | 5769  |
| KRT8 | P05787    | Phyre     | #### | Intra        | 0,1   | 1    | 85 | 6712  |
| KRT8 | P05787    | Phyre     | #### | Intra        | 0,1   | 1    | 85 | 11613 |
| KRT8 | ####      |           | #### | Intra        | 1,1   | 1    | 85 | 10576 |
| KRT8 | ####      |           | #### | N/A          | 2,2   | 1    | 85 | 8538  |
| KRT8 | P05787    | Phyre     | #### | Intra        | 0,1   | 1    | 85 | 6519  |
| KRT8 | P05787    | Phyre     |      | 20.62 Intra  | 1,0   | 1    | 85 | 21726 |
| KRT8 | P05787    | Phyre     |      | 20.62 Intra  | 1,1   | 1    | 85 | 20339 |
| KRT8 | P05787_PC | Docking   |      | 20.76 N/A    | 1,0   | 1    | 85 | 18665 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 17 | 20080 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 17 | 25422 |
| VIM  | 3UF1      | Structure | #### |              | 2 1,0 | 1    | 17 | 25369 |
| VIM  | ####      |           | #### |              | 2 3,0 | 1    | 17 | 18994 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 17 | 32160 |
| VIM  | 3UF1      | Structure | #### |              | 2 1,0 | 1    | 17 | 26480 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 17 | 14649 |
| KRT8 | P05787    | Phyre     | #### |              | 2 3,1 | 1    | 17 | 28838 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 17 | 20531 |
| KRT8 | P05787    | Phyre     | #### |              | 2 0,1 | 1    | 17 | 13000 |
| KRT8 | P05787    | Phyre     | #### |              | 2 0,1 | 1    | 17 | 20595 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 17 | 27116 |
| VIM  | ####      |           | #### |              | 2 3,0 | 1    | 17 | 16864 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 17 | 18443 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 17 | 26948 |
| VIM  | P08670    |           | #### |              | 2 1,0 | 1    | 17 | 34286 |
| VIM  | ####      |           | #### |              | 2 1,0 | 1    | 17 | 32581 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 11 | 38105 |
| KRT7 | ####      |           | #### |              | 2 1,3 | 1    | 11 | 23501 |
| KRT7 | ####      |           | #### |              | 2 0,2 | 1    | 11 | 11869 |
| KRT7 | ####      |           | #### |              | 2 2,0 | 1    | 11 | 26318 |
| KRT7 | P08729    | Phyre     | #### |              | 2 1,2 | 1    | 11 | 17873 |
| KRT8 | P05787    | Phyre     | #### |              | 2 2,2 | 1    | 11 | 19348 |
| KRT8 | P05787    | Phyre     | #### |              | 2 1,0 | 1    | 11 | 14928 |
| KRT7 | P08729    | Phyre     | #### |              | 2 6,3 | 1    | 11 | 19384 |
| KRT7 | ####      |           | #### |              | 2 3,0 | 1    | 11 | 23569 |
| KRT7 | ####      |           | #### |              | 2 1,0 | 1    | 11 | 22922 |
| KRT7 | ####      |           | #### |              | 2 0,2 | 1    | 11 | 11971 |
| KRT8 | P05787    | Phyre     | #### |              | 2 4,0 | 0.83 | 1  | 26254 |
| SHD  | ####      |           | #### |              | 2 1,0 | 0.81 | 1  | 35926 |

|          |        |           |       |       |       |      |    |       |
|----------|--------|-----------|-------|-------|-------|------|----|-------|
| INSR     | 4ZXB   | Structure | 27.79 | Intra | 3,0   | 1    | 1  | 21469 |
| ATP5B    | P06576 | Phyre     | 13.84 | Intra | 0,1   | 1    | 2  | 14395 |
| ATP5B    | P06576 | Phyre     | 18.38 | Intra | 3,1   | 1    | 2  | 25501 |
| ATP5F1   | P24539 | Phyre     | ####  |       | 1 2,2 | 1    | 2  | 5713  |
| ATP5B    | P06576 | Phyre     | ####  |       | 1 1,0 | 0.98 | 2  | 18259 |
| ATP5A1   | P25705 | Phyre     | ####  |       | 1 1,0 | 0.98 | 7  | 16883 |
| ATP5B    | P06576 | Phyre     | ####  |       | 1 2,0 | 1    | 7  | 13196 |
| ATP5B    | P06576 | Phyre     | ####  |       | 1 3,1 | 1    | 7  | 11765 |
| ATP5B    | P06576 | Phyre     | ####  |       | 1 2,0 | 1    | 7  | 11233 |
| ATP5B    | P06576 | Phyre     | ####  |       | 1 2,5 | 1    | 7  | 11280 |
| ATP5A1   | P25705 | Phyre     | ####  |       | 1 1,0 | 0.98 | 7  | 14293 |
| ATP5A1   | P25705 | Phyre     | ####  |       | 1 1,2 | 1    | 7  | 9503  |
| ATP5O    | P48047 | Phyre     | ####  |       | 1 1,1 | 1    | 3  | 19113 |
| ATP5O    | P48047 | Phyre     | ####  |       | 1 0,1 | 0.94 | 3  | 6267  |
| ATP5B    | P06576 | Phyre     | ####  |       | 1 1,1 | 0.98 | 3  | 9097  |
| S100A6   | 1K8U   | Structure | 29.49 | Intra | 1,0   | 1    | 1  | 19276 |
| ENO1     | 2PSN   | Structure | 14.02 | Intra | 1,0   | 1    | 28 | 23730 |
| ENO1     | 2PSN   | Structure | 18.41 | Intra | 8,4   | 1    | 28 | 34120 |
| ENO1     | 2PSN   | Structure | 14.06 | Intra | 3,1   | 1    | 28 | 9566  |
| ENO1     | 2PSN   | Structure | 48.48 | Intra | 2,4   | 1    | 28 | 10868 |
| ENO1     | 2PSN   | Structure | 7.95  | Intra | 3,1   | 1    | 28 | 8166  |
| ENO1     | 2PSN   | Structure | 16.74 | Intra | 0,2   | 1    | 28 | 14010 |
| ENO1     | 2PSN   | Structure | 6.63  | Intra | 4,6   | 1    | 28 | 21423 |
| ENO1     | 2PSN   | Structure | 22.6  | Intra | 4,2   | 1    | 28 | 16812 |
| ENO1     | 2PSN   | Structure | 24.6  | Intra | 1,1   | 1    | 28 | 30741 |
| ENO1     | 2PSN   | Structure | 43.72 | Intra | 2,2   | 1    | 28 | 17937 |
| ENO1     | 2PSN   | Structure | 27.33 | Intra | 2,1   | 1    | 28 | 27561 |
| ENO1     | 2PSN   | Structure | 39.52 | Intra | 4,2   | 1    | 28 | 8876  |
| ENO1     | 2PSN   | Structure | 14.4  | Intra | 4,2   | 1    | 28 | 12442 |
| ENO1     | 2PSN   | Structure | 4.54  | Intra | 0,1   | 1    | 28 | 7329  |
| ENO1     | 2PSN   | Structure | 35.26 | Intra | 0,2   | 1    | 28 | 4107  |
| ENO1     | 2PSN   | Structure | 18.29 | Intra | 7,5   | 1    | 28 | 34387 |
| ENO1     | 2PSN   | Structure | 11.71 | Intra | 2,0   | 1    | 28 | 20087 |
| ENO1     | 2PSN   | Structure | 18.79 | Intra | 1,1   | 1    | 28 | 21672 |
| ENO1     | 2PSN   | Structure | 29.19 | Intra | 0,1   | 1    | 28 | 12550 |
| ENO1     | 2PSN   | Structure | 23.15 | Intra | 7,0   | 1    | 28 | 15121 |
| ENO1     | 2PSN   | Structure | 11.65 | Intra | 1,0   | 1    | 28 | 23305 |
| ENO1     | 2PSN   | Structure | 9.64  | Intra | 3,1   | 1    | 28 | 17824 |
| ENO1     | 2PSN   | Structure | 9.64  | Intra | 5,3   | 1    | 28 | 27212 |
| ENO1     | 2PSN   | Structure | 20.25 | Intra | 3,0   | 1    | 28 | 27800 |
| ENO1     | 2PSN   | Structure | 11.88 | Intra | 2,1   | 1    | 28 | 40685 |
| ENO1     | 2PSN   | Structure | 42.58 | Intra | 1,0   | 1    | 28 | 12317 |
| ENO1     | 2PSN   | Structure | 42.58 | Intra | 0,2   | 1    | 28 | 4551  |
| ENO1     | 2PSN   | Structure | 33.5  | Intra | 0,1   | 1    | 28 | 10207 |
| HSP90AB1 | 3PRY   | Structure | ####  |       | 1 1,0 | 0.98 | 1  | 20132 |
| ENO1     | 2PSN   | Structure | ####  |       | 2 1,0 | 0.99 | 1  | 34278 |
| GPI      | 1JIQ   | Structure | 76.85 | Intra | 1,0   | 1    | 4  | 36160 |

|        |        |           |       |       |       |      |    |       |
|--------|--------|-----------|-------|-------|-------|------|----|-------|
| GPI    | 1JIQ   | Structure | 73.75 | Intra | 1,0   | 1    | 4  | 16558 |
| GPI    | 1JIQ   | Structure | 23.08 | Intra | 0,2   | 1    | 4  | 7843  |
| GPI    | 1JIQ   | Structure | 18.17 | Intra | 0,1   | 1    | 4  | 8757  |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 19198 |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 13694 |
| NPM1   | ####   | ####      |       | Intra | 4,1   | 1    | 29 | 19227 |
| NPM1   | ####   | ####      |       | Intra | 1,2   | 1    | 29 | 13214 |
| NPM1   | ####   | ####      |       | Intra | 5,3   | 1    | 29 | 18137 |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 6622  |
| NPM1   | ####   | ####      |       | Intra | 4,1   | 1    | 29 | 6044  |
| NPM1   | ####   | ####      |       | Intra | 2,0   | 1    | 29 | 20725 |
| NPM1   | ####   | ####      |       | Intra | 0,1   | 1    | 29 | 11540 |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 17558 |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 9712  |
| NPM1   | ####   | ####      |       | Intra | 0,1   | 1    | 29 | 4143  |
| NPM1   | ####   | ####      |       | Intra | 0,2   | 1    | 29 | 4269  |
| NPM1   | ####   | ####      |       | Intra | 2,0   | 1    | 29 | 14583 |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 21859 |
| NPM1   | ####   | ####      |       | Intra | 0,1   | 1    | 29 | 5750  |
| NPM1   | ####   | ####      |       | Intra | 1,2   | 1    | 29 | 9192  |
| NPM1   | ####   | ####      |       | Intra | 1,2   | 1    | 29 | 8668  |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 18712 |
| NPM1   | ####   | ####      |       | Intra | 2,0   | 1    | 29 | 7943  |
| NPM1   | ####   | ####      |       | Intra | 0,2   | 1    | 29 | 5187  |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 16014 |
| NPM1   | ####   | ####      |       | Intra | 2,0   | 1    | 29 | 18682 |
| NPM1   | ####   | ####      |       | Intra | 1,0   | 1    | 29 | 15402 |
| NPM1   | ####   | ####      |       | Intra | 2,0   | 1    | 29 | 15691 |
| NPM1   | 5EHD   | Structure | 9.86  |       | 1 1,0 | 1    | 29 | 33547 |
| NPM1   | ####   | ####      |       | Intra | 3,2   | 1    | 29 | 20749 |
| NPM1   | ####   | ####      |       | Intra | 5,1   | 1    | 29 | 19930 |
| NPM1   | ####   | ####      |       | Intra | 1,2   | 1    | 29 | 18922 |
| TPM3   | P06753 | Phyre     | 24.46 | Intra | 1,0   | 1    | 4  | 22648 |
| TPM3   | P06753 | Phyre     | 15.39 | Intra | 2,0   | 1    | 4  | 13736 |
| TPM3   | P06753 | Phyre     | 10.67 | Intra | 3,1   | 1    | 4  | 20377 |
| TPM3   | P06753 | Phyre     | 22.54 | Intra | 3,0   | 1    | 4  | 11367 |
| ACTC1  | P68032 | Phyre     | ####  |       | 1 2,0 | 1    | 1  | 15608 |
| ACTBL2 | Q562R1 | Phyre     | ####  |       | 2 0,1 | 0.98 | 1  | 9229  |
| ITGAV  | 3IJE   | Structure | 10    | Intra | 1,0   | 1    | 3  | 21941 |
| ITGAV  | 3IJE   | Structure | 30.41 | Intra | 1,0   | 1    | 3  | 32724 |
| ITGAV  | 3IJE   | Structure | 19.99 | Intra | 2,0   | 1    | 3  | 24378 |
| ITGAV  | 3IJE   | Structure | ####  |       | 1 1,0 | 0.98 | 1  | 28724 |
| EPHX1  | P07099 | Phyre     | 35.91 | Intra | 3,0   | 1    | 1  | 21874 |
| LDHB   | 1IOZ   | Structure | 12.58 | Intra | 1,2   | 1    | 5  | 31963 |
| LDHB   | 1IOZ   | Structure | 11.53 | Intra | 2,0   | 1    | 5  | 36138 |
| LDHB   | 1IOZ   | Structure | 17.62 | Intra | 1,0   | 1    | 5  | 23754 |
| LDHB   | 1IOZ   | Structure | 27.41 | Intra | 1,2   | 1    | 5  | 27154 |



|          |        |           |       |       |       |      |    |       |
|----------|--------|-----------|-------|-------|-------|------|----|-------|
| LDHB     | 1IOZ   | Structure | 14.16 | Intra | 1,0   | 1    | 5  | 21087 |
| P4HB     | 4EKZ   | Structure | 15.92 | Intra | 5,2   | 1    | 7  | 22714 |
| P4HB     | 4EKZ   | Structure | 5.43  | Intra | 5,1   | 1    | 7  | 23297 |
| P4HB     | 4EKZ   | Structure | 22.63 | Intra | 2,2   | 1    | 7  | 32174 |
| P4HB     | 4EKZ   | Structure | 16.92 | Intra | 4,0   | 1    | 7  | 17052 |
| P4HB     | 4EKZ   | Structure | 16.13 | Intra | 1,0   | 1    | 7  | 19246 |
| P4HB     | 4EKZ   | Structure | 17.72 | Intra | 1,0   | 1    | 7  | 38200 |
| P4HB     | 4EKZ   | Structure | 17.88 | Intra | 1,0   | 1    | 7  | 29344 |
| ANXA2    | 5LPU   | Structure | 14.57 | Intra | 1,0   | 1    | 20 | 30530 |
| ANXA2    | 5LPU   | Structure | 11.44 | Intra | 1,0   | 1    | 20 | 35789 |
| ANXA2    | 5LPU   | Structure | 12.72 | Intra | 2,1   | 1    | 20 | 27015 |
| ANXA2    | 5LPU   | Structure | 18.73 | Intra | 1,0   | 1    | 20 | 26567 |
| ANXA2    | 5LPU   | Structure | 7.31  | Intra | 4,2   | 1    | 20 | 14163 |
| ANXA2    | 5LPU   | Structure | 15.11 | Intra | 0,2   | 1    | 20 | 15403 |
| ANXA2    | 5LPU   | Structure | 21.57 | Intra | 3,0   | 1    | 20 | 17018 |
| ANXA2    | 5LPU   | Structure | 21.57 | Intra | 8,1   | 1    | 20 | 15264 |
| ANXA2    | 5LPU   | Structure | 22.92 | Intra | 2,0   | 1    | 20 | 20814 |
| ANXA2    | 5LPU   | Structure | 12.02 | Intra | 2,1   | 1    | 20 | 26111 |
| ANXA2    | 5LPU   | Structure | 12.02 | Intra | 3,1   | 1    | 20 | 24773 |
| ANXA2    | 5LPU   | Structure | 12.67 | Intra | 0,1   | 1    | 20 | 8285  |
| ANXA2    | 5LPU   | Structure | 14.69 | Intra | 1,0   | 1    | 20 | 22655 |
| ANXA2    | 5LPU   | Structure | 20.59 | Intra | 7,1   | 1    | 20 | 20972 |
| ANXA2    | 5LPU   | Structure | 26.02 | Intra | 1,0   | 1    | 20 | 29097 |
| ANXA2    | 5LPU   | Structure | 20.59 | Intra | 3,3   | 1    | 20 | 19273 |
| ANXA2    | 5LPU   | Structure | 10.25 | Intra | 2,2   | 1    | 20 | 25001 |
| ANXA2    | 5LPU   | Structure | 10.25 | Intra | 0,2   | 1    | 20 | 12235 |
| ANXA2    | 5LPU   | Structure | 10.42 | Intra | 1,2   | 1    | 20 | 21451 |
| ANXA2    | 5LPU   | Structure | 10.42 | Intra | 0,1   | 1    | 20 | 11131 |
| ANXA2    | 5LPU   | Structure | ####  |       | 1 3,0 | 0.73 | 1  | 17486 |
| TUBB     | 5N5N   | Structure | 31.03 | Intra | 1,0   | 1    | 2  | 23982 |
| TUBB     | 5N5N   | Structure | 20.65 | Intra | 1,0   | 1    | 2  | 25977 |
| PFN1     | 4X1L   | Structure | 18.92 | Intra | 2,0   | 1    | 4  | 28869 |
| PFN1     | 4X1L   | Structure | 19.24 | Intra | 1,0   | 1    | 4  | 31795 |
| PFN1     | 4X1L   | Structure | 16.83 | Intra | 1,0   | 1    | 4  | 30426 |
| PFN1     | 4X1L   | Structure | 8.86  | Intra | 4,2   | 1    | 4  | 25025 |
| ACTB     | 6ANU   | Structure | ####  |       | 1 1,0 | 0.98 | 1  | 27615 |
| EPRS     | P07814 | Phyre     | 29.48 | Intra | 4,1   | 1    | 6  | 29338 |
| EPRS     | P07814 | Phyre     | 29.48 | Intra | 2,0   | 1    | 6  | 28518 |
| EPRS     | ####   | ####      |       |       | 1 1,0 | 1    | 6  | 25415 |
| EPRS     | P07814 | Phyre     | 30.55 | Intra | 2,0   | 1    | 6  | 16203 |
| EPRS     | ####   | ####      |       | Intra | 0,1   | 1    | 6  | 11307 |
| EPRS     | P07814 | Phyre     | 10.85 | Intra | 1,0   | 1    | 6  | 29528 |
| HSP90AA1 | 3Q6M   | Structure | 11.34 | Intra | 1,0   | 1    | 12 | 16347 |
| HSP90AA1 | 3Q6M   | Structure | 11.34 | Intra | 0,1   | 1    | 12 | 7638  |
| HSP90AA1 | 3Q6M   | Structure | 9.76  | Intra | 2,0   | 1    | 12 | 15969 |
| HSP90AA1 | P07900 | Phyre     | 16.82 | Intra | 2,3   | 1    | 12 | 25405 |
| HSP90AA1 | 3Q6M   | Structure | 18.47 | Intra | 1,0   | 1    | 12 | 28420 |

|          |                   |           |       |           |      |    |       |
|----------|-------------------|-----------|-------|-----------|------|----|-------|
| HSP90AA1 | 3Q6M              | Structure | 36.47 | 1 2,2     | 1    | 12 | 20835 |
| HSP90AA1 | P07900            | Phyre     | 16.9  | Intra 1,0 | 1    | 12 | 17296 |
| HSP90AA1 | 3Q6M              | Structure | 20.38 | Intra 2,1 | 1    | 12 | 18898 |
| HSP90AA1 | 3Q6M              | Structure | 20.38 | Intra 9,3 | 1    | 12 | 17788 |
| HSP90AA1 | 3Q6M              | Structure | 23.75 | Intra 0,1 | 1    | 12 | 8337  |
| HSP90AA1 | P07900            | Phyre     | 17.81 | Intra 1,0 | 1    | 12 | 14327 |
| HSP90AA1 | P07900            | Phyre     | 20.93 | Intra 2,0 | 1    | 12 | 21507 |
| HSP90AA1 | 3Q6M              | Structure | ####  | 1 1,1     | 1    | 7  | 24480 |
| HSP90AB1 | 3PRY              | Structure | ####  | 1 1,0     | 1    | 7  | 20680 |
| HSP90AA1 | 3Q6M              | Structure | ####  | 1 1,0     | 1    | 7  | 17187 |
| HSP90AA1 | 3Q6M              | Structure | ####  | 1 10,4    | 1    | 7  | 21718 |
| HSP90AA1 | 3Q6M              | Structure | ####  | 1 1,0     | 1    | 7  | 21741 |
| HSP90AB1 | P08238            | Phyre     | ####  | 1 3,1     | 1    | 7  | 19723 |
| HSP90AB1 | P08238            | Phyre     | ####  | 1 2,0     | 1    | 7  | 20909 |
| STIP1    | P31948            | Phyre     | ####  | 1 2,0     | 1    | 1  | 20971 |
| HNRNPC   | ####              | ####      |       | 1 3,2     | 1    | 12 | 12056 |
| HNRNPC   | ####              | ####      | Intra | 0,2       | 1    | 12 | 5437  |
| HNRNPC   | ####              | ####      | Intra | 1,1       | 1    | 12 | 10509 |
| HNRNPC   | ####              | ####      | Intra | 0,1       | 1    | 12 | 4359  |
| HNRNPC   | ####              | ####      | Intra | 0,2       | 1    | 12 | 5039  |
| HNRNPC   | P07910_PC Docking |           | 13.9  | 1 2,1     | 1    | 12 | 15683 |
| HNRNPC   | ####              | ####      | Intra | 2,0       | 1    | 12 | 17354 |
| HNRNPC   | ####              | ####      | Intra | 4,1       | 1    | 12 | 23245 |
| HNRNPC   | ####              | ####      | Intra | 1,0       | 1    | 12 | 12189 |
| HNRNPC   | 2MZ1              | Structure | 11.05 | Intra 1,0 | 1    | 12 | 22406 |
| HNRNPC   | 2MZ1              | Structure | 13.16 | Intra 4,1 | 1    | 12 | 17898 |
| HNRNPC   | ####              | ####      |       | 1 4,0     | 1    | 12 | 14092 |
| HNRNPA1  | ####              | ####      |       | 1 1,0     | 1    | 1  | 15001 |
| FH       | 3.00E+04          | Structure | 14.46 | 1 2,0     | 1    | 9  | 13712 |
| FH       | 3.00E+04          | Structure | 26.09 | Intra 2,0 | 1    | 9  | 18948 |
| FH       | 3.00E+04          | Structure | 10.83 | Intra 1,2 | 1    | 9  | 33237 |
| FH       | 3.00E+04          | Structure | 14.46 | Intra 0,1 | 1    | 9  | 4956  |
| FH       | 3.00E+04          | Structure | 14.46 | 1 0,1     | 1    | 9  | 3913  |
| FH       | 3.00E+04          | Structure | 25.88 | Intra 1,0 | 1    | 9  | 31009 |
| FH       | 3.00E+04          | Structure | 22.36 | Intra 1,1 | 1    | 9  | 29821 |
| FH       | 3.00E+04          | Structure | 17.19 | Intra 0,1 | 1    | 9  | 9043  |
| FH       | 3.00E+04          | Structure | 17.19 | Intra 2,0 | 1    | 9  | 24711 |
| IGF1R    | ####              | ####      | Intra | 1,0       | 1    | 4  | 20490 |
| IGF1R    | 1IGR              | Structure | 11.68 | Intra 0,1 | 1    | 4  | 4255  |
| IGF1R    | 1IGR              | Structure | 11.68 | Intra 7,2 | 1    | 4  | 9579  |
| IGF1R    | 1IGR              | Structure | 33.93 | Intra 2,0 | 1    | 4  | 14692 |
| ANXA6    | P08133_PC Docking |           | 14.33 | N/A 1,0   | 1    | 1  | 33834 |
| CD55     | 1OK3              | Structure | 11.05 | Intra 4,7 | 1    | 2  | 26123 |
| CD55     | 1OK3              | Structure | 19.64 | Intra 1,0 | 0.94 | 2  | 25015 |
| CD55     | 1OK3              | Structure | ####  | 2 1,0     | 0.98 | 1  | 24498 |
| SLC3A2   | 2DH2              | Structure | 14.94 | Intra 2,1 | 1    | 14 | 26275 |
| SLC3A2   | 2DH2              | Structure | 11.55 | Intra 5,3 | 1    | 14 | 24266 |

|          |           |           |       |       |       |      |    |       |
|----------|-----------|-----------|-------|-------|-------|------|----|-------|
| SLC3A2   | 2DH2      | Structure | 15.38 | Intra | 1,0   | 1    | 14 | 34597 |
| SLC3A2   | 2DH2      | Structure | 16.32 | Intra | 1,0   | 1    | 14 | 29586 |
| SLC3A2   | 2DH2      | Structure | 18.67 | Intra | 1,3   | 1    | 14 | 31455 |
| SLC3A2   | 2DH2      | Structure | 12.7  | Intra | 0,1   | 1    | 14 | 11677 |
| SLC3A2   | 2DH2      | Structure | 12.54 | Intra | 2,1   | 1    | 14 | 23510 |
| SLC3A2   | 2DH2      | Structure | 21.19 | Intra | 4,0   | 1    | 14 | 20745 |
| SLC3A2   | P08195_PC | Docking   | 20.07 | N/A   | 3,0   | 1    | 14 | 22424 |
| SLC3A2   | 2DH2      | Structure | 13.97 | Intra | 3,2   | 1    | 14 | 27403 |
| SLC3A2   | 2DH2      | Structure | 16.01 | Intra | 3,2   | 1    | 14 | 25785 |
| SLC3A2   | 2DH2      | Structure | 15.94 | Intra | 6,3   | 1    | 14 | 23723 |
| SLC3A2   | 2DH2      | Structure | 10.4  | Intra | 9,2   | 1    | 14 | 23780 |
| SLC3A2   | 2DH2      | Structure | 15.15 | Intra | 4,0   | 1    | 14 | 21848 |
| SLC3A2   | 2DH2      | Structure | ####  |       | 2 1,0 | 0.81 | 3  | 21551 |
| SLC3A2   | 2DH2      | Structure | ####  |       | 2 4,1 | 1    | 3  | 22122 |
| CD59     | 2J8B      | Structure | ####  |       | 2 1,0 | 0.89 | 3  | 18466 |
| SLC3A2   | 2DH2      | Structure | ####  |       | 1 1,0 | 0.94 | 1  | 24623 |
| SLC3A2   | 2DH2      | Structure | ####  |       | 1 2,0 | 1    | 1  | 20923 |
| SLC3A2   | 2DH2      | Structure | ####  |       | 2 3,0 | 1    | 3  | 21206 |
| SLC3A2   | 2DH2      | Structure | ####  |       | 2 2,0 | 1    | 3  | 22077 |
| ATP1B3   | P54709    | Phyre     | ####  |       | 2 1,0 | 0.82 | 3  | 17929 |
| SLC3A2   | 2DH2      | Structure | ####  |       | 3 4,2 | 1    | 1  | 21399 |
| PFKM     | 4OMT      | Structure | 20.53 | Intra | 1,0   | 1    | 1  | 26707 |
| HSP90AB1 | P08238    | Phyre     | 44.73 | Intra | 1,0   | 1    | 37 | 27418 |
| HSP90AB1 | P08238    | Phyre     | 17.89 | Intra | 7,2   | 1    | 37 | 25699 |
| HSP90AB1 | P08238    | Phyre     | 9.76  | Intra | 1,0   | 1    | 37 | 15209 |
| HSP90AB1 | P08238    | Phyre     | 16.82 | Intra | 3,5   | 1    | 37 | 26475 |
| HSP90AB1 | 3PRY      | Structure | 17.03 | Intra | 1,0   | 1    | 37 | 22376 |
| HSP90AB1 | 3PRY      | Structure | 18.47 | Intra | 4,1   | 1    | 37 | 28678 |
| HSP90AB1 | 3PRY      | Structure | 28.74 |       | 1 3,2 | 1    | 37 | 22936 |
| HSP90AB1 | 3PRY      | Structure | 18.6  | Intra | 0,1   | 1    | 37 | 11343 |
| HSP90AB1 | P08238    | Phyre     | 29.1  | Intra | 2,2   | 1    | 37 | 20589 |
| HSP90AB1 | P08238    | Phyre     | 17.89 | Intra | 7,3   | 1    | 37 | 22947 |
| HSP90AB1 | 3PRY      | Structure | 17.17 | Intra | 0,1   | 1    | 37 | 12693 |
| HSP90AB1 | P08238    | Phyre     | 23.03 | Intra | 3,1   | 1    | 37 | 17983 |
| HSP90AB1 | P08238    | Phyre     | 23.03 | Intra | 2,0   | 1    | 37 | 16162 |
| HSP90AB1 | P08238    | Phyre     | 17.13 | Intra | 1,0   | 1    | 37 | 18294 |
| HSP90AB1 | P08238    | Phyre     | 14.32 | Intra | 1,0   | 1    | 37 | 17549 |
| HSP90AB1 | P08238    | Phyre     | 20.38 | Intra | 5,2   | 1    | 37 | 20016 |
| HSP90AB1 | P08238    | Phyre     | 16.24 | Intra | 3,0   | 1    | 37 | 18346 |
| HSP90AB1 | P08238    | Phyre     | 20.38 | Intra | 11,1  | 1    | 37 | 18798 |
| HSP90AB1 | P08238    | Phyre     | 16.24 | Intra | 2,0   | 1    | 37 | 16511 |
| HSP90AB1 | P08238    | Phyre     | 23.75 | Intra | 0,1   | 1    | 37 | 5577  |
| HSP90AB1 | P08238    | Phyre     | 13.74 | Intra | 1,0   | 1    | 37 | 9014  |
| HSP90AB1 | 3PRY      | Structure | 6.47  | Intra | 0,1   | 1    | 37 | 9042  |
| HSP90AB1 | 3PRY      | Structure | 17.81 | Intra | 5,0   | 1    | 37 | 16789 |
| HSP90AB1 | P08238    | Phyre     | 27.72 | Intra | 1,0   | 1    | 37 | 16851 |
| HSP90AB1 | P08238    | Phyre     | 17.13 | Intra | 2,0   | 1    | 37 | 15145 |

|          |           |           |        |       |       |      |    |       |
|----------|-----------|-----------|--------|-------|-------|------|----|-------|
| HSP90AB1 | P08238    | Phyre     | 20.93  | Intra | 1,2   | 1    | 37 | 16270 |
| HSP90AB1 | P08238    | Phyre     | 10.95  | Intra | 1,0   | 1    | 37 | 17178 |
| HSP90AB1 | P08238    | Phyre     | 13.74  | Intra | 1,0   | 1    | 37 | 10058 |
| HSP90AB1 | 3PRY      | Structure | 23.83  | Intra | 0,1   | 1    | 37 | 10361 |
| HSP90AB1 | P08238    | Phyre     | 18.61  | Intra | 2,0   | 1    | 37 | 24754 |
| HSP90AB1 | 3PRY      | Structure | 18.43  | Intra | 1,0   | 1    | 37 | 20669 |
| HSP90AB1 | P08238_PC | Docking   | 11.88  |       | 1 3,0 | 1    | 37 | 4092  |
| HSP90AB1 | P08238    | Phyre     | 17.89  | Intra | 1,0   | 1    | 37 | 21233 |
| HSP90AB1 | P08238    | Phyre     | 28.45  | Intra | 2,1   | 1    | 37 | 17967 |
| HSP90AB1 | P08238    | Phyre     | 20.93  | Intra | 6,2   | 1    | 37 | 18961 |
| HSP90AB1 | P08238    | Phyre     | 9.07   | Intra | 1,0   | 1    | 37 | 19222 |
| HSP90AB1 | P08238    | Phyre     | 16.02  | Intra | 1,1   | 1    | 37 | 24535 |
| STIP1    | P31948    | Phyre     | ####   |       | 1 1,0 | 0.98 | 5  | 19949 |
| STIP1    | P31948    | Phyre     | ####   |       | 1 1,0 | 0.99 | 5  | 23009 |
| HSP90AB1 | 3PRY      | Structure | ####   |       | 1 2,0 | 1    | 5  | 14661 |
| HSP90AB1 | 3PRY      | Structure | ####   |       | 1 0,1 | 0.93 | 5  | 7667  |
| HSP90AB1 | 3PRY      | Structure | ####   |       | 1 0,1 | 0.98 | 5  | 10536 |
| CHORDC1  | ####      | ####      |        |       | 1 3,0 | 1    | 1  | 25119 |
| SNRPB2   | 1A9N      | Structure | 12.96  | Intra | 1,0   | 0.99 | 1  | 30283 |
| VIM      | ####      | ####      |        | Intra | 0,1   | 1    | 69 | 11722 |
| VIM      | ####      | ####      |        | Intra | 6,4   | 1    | 69 | 22670 |
| VIM      | ####      | ####      |        | Intra | 4,0   | 1    | 69 | 20506 |
| VIM      | ####      | ####      |        | Intra | 3,1   | 1    | 69 | 21163 |
| VIM      | ####      | ####      |        | Intra | 1,0   | 1    | 69 | 20326 |
| VIM      | P08670    |           | 125.77 | Intra | 2,1   | 1    | 69 | 19971 |
| VIM      | ####      | ####      |        | Intra | 6,2   | 1    | 69 | 21163 |
| VIM      | ####      | ####      |        |       | 1 1,0 | 1    | 69 | 21032 |
| VIM      | P08670    | ####      |        | Intra | 3,4   | 1    | 69 | 30550 |
| VIM      | ####      | ####      |        | Intra | 0,1   | 1    | 69 | 11651 |
| VIM      | ####      | ####      |        |       | 1 2,1 | 1    | 69 | 21467 |
| VIM      | P08670    |           | 14.21  | Intra | 2,5   | 1    | 69 | 30631 |
| VIM      | P08670    |           | 28.14  | Intra | 10,4  | 1    | 69 | 27187 |
| VIM      | ####      | ####      |        | Intra | 4,2   | 1    | 69 | 31736 |
| VIM      | ####      | ####      |        | Intra | 3,1   | 1    | 69 | 20952 |
| VIM      | ####      | ####      |        | Intra | 7,2   | 1    | 69 | 22993 |
| VIM      | P08670    |           | 24.66  | Intra | 2,1   | 1    | 69 | 20821 |
| VIM      | ####      | ####      |        | Intra | 1,0   | 1    | 69 | 15572 |
| VIM      | P08670    |           | 34.15  | Intra | 2,2   | 1    | 69 | 14938 |
| VIM      | ####      | ####      |        |       | 1 3,0 | 1    | 69 | 4675  |
| VIM      | ####      | ####      |        | Intra | 1,0   | 1    | 69 | 26276 |
| VIM      | P08670    |           | 15.4   | Intra | 3,3   | 1    | 69 | 35317 |
| VIM      | 3UF1      | Structure | 16.88  |       | 1 2,0 | 1    | 69 | 31758 |
| VIM      | ####      | ####      |        | Intra | 3,2   | 1    | 69 | 19882 |
| VIM      | P08670    | ####      |        | Intra | 6,2   | 1    | 69 | 18594 |
| VIM      | P08670    | ####      |        | Intra | 11,5  | 1    | 69 | 30654 |
| VIM      | P08670    | ####      |        | Intra | 1,0   | 1    | 69 | 25779 |
| VIM      | ####      | ####      |        | Intra | 5,4   | 1    | 69 | 30163 |

|       |        |           |       |       |      |      |    |       |
|-------|--------|-----------|-------|-------|------|------|----|-------|
| VIM   | ####   |           | ####  | Intra | 3,0  | 1    | 69 | 22785 |
| VIM   | ####   |           | ####  | Intra | 3,0  | 1    | 69 | 18465 |
| VIM   | ####   |           | ####  | Intra | 5,2  | 1    | 69 | 20613 |
| VIM   | P08670 |           | ####  | Intra | 7,4  | 1    | 69 | 18158 |
| VIM   | 3UF1   | Structure | 9.87  | 1     | 1,0  | 1    | 69 | 30160 |
| VIM   | ####   |           | ####  | Intra | 1,0  | 1    | 69 | 33908 |
| VIM   | ####   |           | ####  | Intra | 1,0  | 1    | 69 | 27897 |
| VIM   | ####   |           | ####  | Intra | 1,0  | 1    | 69 | 23815 |
| VIM   | ####   |           | ####  | Intra | 0,4  | 1    | 69 | 11603 |
| VIM   | P08670 |           | ####  | Intra | 1,0  | 1    | 69 | 19360 |
| VIM   | ####   |           | ####  | Intra | 6,2  | 1    | 69 | 18959 |
| VIM   | ####   |           | ####  | Intra | 5,0  | 1    | 69 | 16318 |
| VIM   | ####   |           | ####  | Intra | 5,2  | 1    | 69 | 15807 |
| VIM   | ####   |           | ####  | Intra | 0,1  | 1    | 69 | 6583  |
| VIM   | ####   |           | ####  | Intra | 1,1  | 1    | 69 | 31673 |
| VIM   | 3UF1   | Structure | 81.57 | Intra | 1,0  | 1    | 69 | 24321 |
| VIM   | ####   |           | ####  | Intra | 3,1  | 1    | 69 | 21788 |
| VIM   | P08670 |           | ####  | Intra | 3,2  | 1    | 69 | 31594 |
| VIM   | ####   |           | ####  | Intra | 2,0  | 1    | 69 | 26788 |
| VIM   | ####   |           | ####  | Intra | 3,4  | 1    | 69 | 31290 |
| VIM   | ####   |           | ####  | Intra | 4,4  | 1    | 69 | 23144 |
| VIM   | ####   |           | ####  | Intra | 2,1  | 1    | 69 | 20759 |
| VIM   | ####   |           | ####  | Intra | 0,1  | 1    | 69 | 10973 |
| VIM   | ####   |           | ####  | Intra | 2,1  | 1    | 69 | 21135 |
| VIM   | ####   |           | ####  | Intra | 0,3  | 1    | 69 | 5427  |
| VIM   | ####   |           | ####  | Intra | 4,2  | 1    | 69 | 24485 |
| VIM   | ####   |           | ####  | 1     | 2,1  | 1    | 69 | 20811 |
| VIM   | P08670 |           | ####  | Intra | 4,0  | 1    | 69 | 20374 |
| VIM   | ####   |           | ####  | Intra | 16,6 | 1    | 69 | 23689 |
| VIM   | P08670 |           | ####  | Intra | 4,2  | 1    | 69 | 33106 |
| VIM   | P08670 |           | ####  | Intra | 3,1  | 1    | 69 | 28692 |
| VIM   | ####   |           | ####  | Intra | 2,0  | 1    | 69 | 28730 |
| VIM   | ####   |           | ####  | Intra | 1,0  | 1    | 69 | 31383 |
| VIM   | ####   |           | ####  | Intra | 2,1  | 1    | 69 | 25148 |
| VIM   | ####   |           | ####  | Intra | 4,2  | 1    | 69 | 22566 |
| VIM   | ####   |           | ####  | 1     | 3,2  | 1    | 69 | 24726 |
| VIM   | P08670 |           | ####  | Intra | 1,1  | 1    | 69 | 22335 |
| VIM   | ####   |           | ####  | Intra | 1,0  | 1    | 69 | 20122 |
| VIM   | P08670 |           | 37.91 | Intra | 0,1  | 1    | 69 | 17646 |
| VIM   | ####   |           | ####  | Intra | 6,4  | 1    | 69 | 30849 |
| VIM   | ####   |           | ####  | Intra | 0,2  | 1    | 69 | 9180  |
| VIM   | 3UF1   | Structure | ####  | 2     | 1,0  | 1    | 4  | 26059 |
| KRT7  | ####   |           | ####  | 2     | 3,0  | 1    | 4  | 26193 |
| KRT7  | ####   |           | ####  | 2     | 2,0  | 1    | 4  | 25585 |
| KRT7  | P08729 | Phyre     | ####  | 2     | 2,0  | 1    | 4  | 19667 |
| VIM   | P08670 |           | ####  | 2     | 1,0  | 0.89 | 1  | 37272 |
| RPS17 | 5FLX   | Structure | 9.26  | Intra | 1,0  | 1    | 2  | 19478 |

|           |           |           |       |       |       |      |    |       |
|-----------|-----------|-----------|-------|-------|-------|------|----|-------|
| RPS17     | 5FLX      | Structure | 15.87 | Intra | 2,0   | 1    | 2  | 15328 |
| RPSA      | 3BCH      | Structure | ####  |       | 1 2,0 | 1    | 1  | 22319 |
| KRT7      | P08729    | Phyre     | 9     | Intra | 10,2  | 1    | 14 | 21219 |
| KRT7      | P08729    | Phyre     | 33.05 | Intra | 2,0   | 1    | 14 | 22693 |
| KRT7      | ####      | ####      |       | Intra | 0,1   | 1    | 14 | 15108 |
| KRT7      | P08729    | Phyre     | 8.85  | Intra | 5,1   | 1    | 14 | 19978 |
| KRT7      | P08729    | Phyre     | 33.19 | Intra | 1,0   | 1    | 14 | 17039 |
| KRT7      | ####      | ####      |       | Intra | 2,1   | 1    | 14 | 30441 |
| KRT7      | ####      | ####      |       | Intra | 4,0   | 1    | 14 | 29823 |
| KRT7      | ####      | ####      |       | Intra | 3,0   | 1    | 14 | 24792 |
| KRT7      | P08729    | Phyre     | 94.08 | Intra | 2,0   | 1    | 14 | 20338 |
| KRT7      | ####      | ####      |       | Intra | 2,0   | 1    | 14 | 14329 |
| KRT7      | ####      | ####      |       | Intra | 1,0   | 1    | 14 | 19395 |
| KRT7      | P08729    | Phyre     | 101.9 | Intra | 2,0   | 1    | 14 | 17283 |
| KRT7      | P08729    | Phyre     | 9     | Intra | 1,0   | 1    | 14 | 24089 |
| KRT7      | P08729_PC | Docking   | 15.86 | N/A   | 3,1   | 1    | 14 | 18562 |
| ANXA5     | 2XO3      | Structure | ####  |       | 2 2,0 | 0.8  | 1  | 35147 |
| LGALS1    | 4Q27      | Structure | 22.15 | Intra | 2,0   | 1    | 2  | 24416 |
| LGALS1    | 4Q27      | Structure | 22.15 | Intra | 1,0   | 1    | 2  | 21968 |
| HMGB1     | 2YRQ      | Structure | 25.86 | Intra | 1,0   | 0.94 | 4  | 14140 |
| HMGB1     | 2YRQ      | Structure | 49.64 | Intra | 1,0   | 1    | 4  | 20669 |
| HMGB1     | 2YRQ      | Structure | 17.01 | Intra | 0,1   | 1    | 4  | 5765  |
| HMGB1     | 2YRQ      | Structure | 23.2  | Intra | 1,0   | 1    | 4  | 13784 |
| CLTA      | P09496    | Phyre     | 16.38 | Intra | 2,2   | 1    | 2  | 21345 |
| CLTA      | ####      | ####      |       | Intra | 4,1   | 1    | 2  | 24657 |
| CLTA      | P09496    | Phyre     | ####  |       | 1 1,0 | 0.84 | 6  | 14476 |
| CLTC      | Q00610    | Phyre     | ####  |       | 1 2,2 | 1    | 6  | 19835 |
| CLTC      | Q00610    | Phyre     | ####  |       | 1 1,0 | 1    | 6  | 17303 |
| CLTC      | Q00610    | Phyre     | ####  |       | 1 4,2 | 1    | 6  | 28847 |
| CLTC      | Q00610    | Phyre     | ####  |       | 1 2,0 | 1    | 6  | 24872 |
| CLTC      | Q00610    | Phyre     | ####  |       | 1 2,1 | 1    | 6  | 31234 |
| HIST1H2BH | Q93079    | Phyre     | ####  |       | 2 1,0 | 0.66 | 1  | 24175 |
| CLTB      | ####      | ####      |       | Intra | 0,1   | 1    | 2  | 9125  |
| CLTB      | ####      | ####      |       | Intra | 2,1   | 1    | 2  | 23038 |
| DLD       | 5J5Z      | Structure | 16.04 | Intra | 2,0   | 1    | 4  | 16119 |
| DLD       | 5J5Z      | Structure | 43.32 | Intra | 3,2   | 1    | 4  | 14543 |
| DLD       | 5J5Z      | Structure | 43.32 | Intra | 4,1   | 1    | 4  | 13268 |
| DLD       | 5J5Z      | Structure | 16.74 | Intra | 1,0   | 1    | 4  | 24437 |
| HNRNPA1   | ####      | ####      |       |       | 1 2,0 | 0.97 | 9  | 6974  |
| HNRNPA1   | 1L3K      | Structure | 25.12 | Intra | 2,0   | 1    | 9  | 25912 |
| HNRNPA1   | ####      | ####      |       | Intra | 1,1   | 1    | 9  | 14805 |
| HNRNPA1   | ####      | ####      |       | Intra | 2,0   | 1    | 9  | 20348 |
| HNRNPA1   | 1L3K      | Structure | 18.22 | Intra | 1,0   | 1    | 9  | 24587 |
| HNRNPA1   | P09651    | Phyre     | ####  | Intra | 2,1   | 1    | 9  | 27711 |
| HNRNPA1   | ####      | ####      |       |       | 1 3,2 | 1    | 9  | 18838 |
| HNRNPA1   | 1L3K      | Structure | 8.37  | Intra | 0,1   | 1    | 9  | 9595  |
| HNRNPA1   | ####      | ####      |       | Intra | 2,1   | 1    | 9  | 15316 |

|           |        |           |       |            |      |    |       |
|-----------|--------|-----------|-------|------------|------|----|-------|
| HNRNPA1   | ####   |           | ####  | 1 2,0      | 1    | 2  | 14440 |
| HNRNPA1   | ####   |           | ####  | 1 1,1      | 1    | 2  | 9286  |
| HNRNPA1   | ####   |           | ####  | 1 2,0      | 1    | 2  | 21664 |
| HNRNPM    | ####   |           | ####  | 1 1,0      | 1    | 2  | 17697 |
| HNRNPA1   | ####   |           | ####  | 1 2,0      | 1    | 1  | 21079 |
| HNRNPU    | ####   |           | ####  | 1 1,0      | 0.95 | 1  | 23062 |
| HNRNPA1   | ####   |           | ####  | 2 0,2      | 0.9  | 1  | 8389  |
| SNRPA1    | ####   |           | ####  | Intra 2,0  | 1    | 1  | 31870 |
| PARP1     | ####   |           | ####  | Intra 1,0  | 1    | 3  | 16424 |
| PARP1     | 4DQY   | Structure | 15.02 | Intra 1,0  | 1    | 3  | 16157 |
| PARP1     | 4DQY   | Structure | 15.02 | Intra 4,0  | 1    | 3  | 19886 |
| IFIT1     | 5UDI   | Structure | 20.31 | Intra 0,1  | 1    | 1  | 9535  |
| HIST1H2BH | Q93079 | Phyre     | ####  | 1 2,1      | 0.86 | 1  | 3810  |
| HSPA1A    | P0DMV8 | Phyre     | 36.77 | Intra 2,1  | 1    | 8  | 15422 |
| HSPA1A    | P0DMV8 | Phyre     | 36.77 | Intra 2,0  | 1    | 8  | 14910 |
| HSPA1A    | P0DMV8 | Phyre     | 36.77 | Intra 2,0  | 1    | 8  | 14910 |
| HSPA1A    | P0DMV8 | Phyre     | 36.77 | Intra 0,2  | 1    | 8  | 7728  |
| HSPA1A    | 5BN8   | Structure | 9.52  | Intra 1,2  | 1    | 8  | 17133 |
| HSPA1A    | P0DMV8 | Phyre     | 12.29 | Intra 0,2  | 1    | 8  | 5683  |
| HSPA1A    | P0DMV8 | Phyre     | 18.4  | Intra 1,0  | 1    | 8  | 14263 |
| HSPA1A    | 5BN8   | Structure | 26.87 | Intra 1,0  | 1    | 8  | 21495 |
| CALM1     | 4DJC   | Structure | 51.46 | Intra 2,0  | 1    | 1  | 28247 |
| HLA-C     | 5VGE   | Structure | ####  | 1 2,1      | 1    | 2  | 22649 |
| HLA-C     | 5VGE   | Structure | ####  | 1 3,1      | 1    | 2  | 19892 |
| HIST1H1E  | P10412 | Modeller  | 29    | Intra 1,0  | 1    | 3  | 4239  |
| HIST1H1E  | P10412 | Modeller  | 59.65 | Intra 1,0  | 0.72 | 3  | 4779  |
| HIST1H1E  | P10412 | Modeller  | 15.22 | Intra 1,0  | 1    | 3  | 15935 |
| DLAT      | P10515 | Unknown   | 16.08 | Intra 3,0  | 1    | 1  | 21722 |
| PTPRF     | ####   |           | ####  | Intra 10,6 | 1    | 8  | 22689 |
| PTPRF     | ####   |           | ####  | Intra 1,0  | 1    | 8  | 21265 |
| PTPRF     | ####   |           | ####  | Intra 1,0  | 1    | 8  | 20483 |
| PTPRF     | ####   |           | ####  | Intra 2,0  | 1    | 8  | 22968 |
| PTPRF     | ####   |           | ####  | Intra 0,3  | 1    | 8  | 6701  |
| PTPRF     | 1LAR   | Structure | 9.44  | Intra 1,0  | 1    | 8  | 13426 |
| PTPRF     | ####   |           | ####  | Intra 5,2  | 1    | 8  | 29898 |
| PTPRF     | ####   |           | ####  | Intra 10,2 | 1    | 8  | 27577 |
| PTPRF     | ####   |           | ####  | 2 1,0      | 0.95 | 1  | 21595 |
| TXN       | 4OO4   | Structure | 10.14 | Intra 1,0  | 1    | 1  | 19310 |
| TXN       | 4OO4   | Structure | ####  | 3 0,1      | 0.77 | 1  | 12917 |
| COX7A2    | ####   |           | ####  | 3 2,0      | 1    | 1  | 28458 |
| HSPD1     | 4PJ1   | Structure | 43.41 | Intra 2,0  | 1    | 55 | 19963 |
| HSPD1     | 4PJ1   | Structure | 49.68 | Intra 1,3  | 1    | 55 | 24347 |
| HSPD1     | 4PJ1   | Structure | 12.64 | Intra 2,1  | 1    | 55 | 24537 |
| HSPD1     | 4PJ1   | Structure | 24.17 | 1 1,0      | 1    | 55 | 9547  |
| HSPD1     | 4PJ1   | Structure | 23.5  | Intra 5,3  | 1    | 55 | 13770 |
| HSPD1     | 4PJ1   | Structure | 12.37 | Intra 4,1  | 1    | 55 | 13375 |
| HSPD1     | 4PJ1   | Structure | 17.62 | 1 1,0      | 1    | 55 | 16087 |

|       |      |           |             |       |   |    |       |
|-------|------|-----------|-------------|-------|---|----|-------|
| HSPD1 | 4PJ1 | Structure | 17.07 Intra | 2,0   | 1 | 55 | 17683 |
| HSPD1 | 4PJ1 | Structure | 18.6 Intra  | 2,0   | 1 | 55 | 16635 |
| HSPD1 | 4PJ1 | Structure | 11.16 Intra | 0,1   | 1 | 55 | 10293 |
| HSPD1 | 4PJ1 | Structure | 19.96 Intra | 2,0   | 1 | 55 | 13124 |
| HSPD1 | 4PJ1 | Structure | 13.87 Intra | 1,2   | 1 | 55 | 21124 |
| HSPD1 | 4PJ1 | Structure | 18.09 Intra | 3,1   | 1 | 55 | 23044 |
| HSPD1 | 4PJ1 | Structure | 18.09 Intra | 11,2  | 1 | 55 | 19821 |
| HSPD1 | 4PJ1 | Structure | 15 Intra    | 0,1   | 1 | 55 | 12263 |
| HSPD1 | 4PJ1 | Structure | 24.05 Intra | 1,0   | 1 | 55 | 30489 |
| HSPD1 | 4PJ1 | Structure | 23.13 Intra | 4,1   | 1 | 55 | 21332 |
| HSPD1 | 4PJ1 | Structure | 7.41 Intra  | 4,2   | 1 | 55 | 26665 |
| HSPD1 | 4PJ1 | Structure | 7.41 Intra  | 2,0   | 1 | 55 | 21917 |
| HSPD1 | 4PJ1 | Structure | 12.13       | 1 1,0 | 1 | 55 | 17603 |
| HSPD1 | 4PJ1 | Structure | 28.14 Intra | 6,2   | 1 | 55 | 23239 |
| HSPD1 | 4PJ1 | Structure | 28.14 Intra | 14,3  | 1 | 55 | 19791 |
| HSPD1 | 4PJ1 | Structure | 9.93 Intra  | 2,0   | 1 | 55 | 21891 |
| HSPD1 | 4PJ1 | Structure | 32.32 Intra | 1,0   | 1 | 55 | 22933 |
| HSPD1 | 4PJ1 | Structure | 21.29 Intra | 4,2   | 1 | 55 | 34230 |
| HSPD1 | 4PJ1 | Structure | 21.29 Intra | 6,0   | 1 | 55 | 31130 |
| HSPD1 | 4PJ1 | Structure | 35.95 Intra | 2,1   | 1 | 55 | 21309 |
| HSPD1 | 4PJ1 | Structure | 19.55 Intra | 1,2   | 1 | 55 | 24293 |
| HSPD1 | 4PJ1 | Structure | 19.55 Intra | 4,0   | 1 | 55 | 24276 |
| HSPD1 | 4PJ1 | Structure | 19.56 Intra | 1,0   | 1 | 55 | 27467 |
| HSPD1 | 4PJ1 | Structure | 62.61 Intra | 1,0   | 1 | 55 | 24072 |
| HSPD1 | 4PJ1 | Structure | 21.27 Intra | 2,2   | 1 | 55 | 26012 |
| HSPD1 | 4PJ1 | Structure | 57.58 Intra | 2,1   | 1 | 55 | 25358 |
| HSPD1 | 4PJ1 | Structure | 21.94 Intra | 1,1   | 1 | 55 | 26408 |
| HSPD1 | 4PJ1 | Structure | 13.7 Intra  | 2,1   | 1 | 55 | 12780 |
| HSPD1 | 4PJ1 | Structure | 17.18 Intra | 2,0   | 1 | 55 | 16783 |
| HSPD1 | 4PJ1 | Structure | 14.25 Intra | 2,1   | 1 | 55 | 22495 |
| HSPD1 | 4PJ1 | Structure | 7.87 Intra  | 2,0   | 1 | 55 | 12923 |
| HSPD1 | 4PJ1 | Structure | 16.41 Intra | 3,0   | 1 | 55 | 16785 |
| HSPD1 | 4PJ1 | Structure | 17.55 Intra | 0,1   | 1 | 55 | 12130 |
| HSPD1 | 4PJ1 | Structure | 19.02       | 1 2,0 | 1 | 55 | 21697 |
| HSPD1 | 4PJ1 | Structure | 40.3 Intra  | 2,0   | 1 | 55 | 27001 |
| HSPD1 | 4PJ1 | Structure | 42.24 Intra | 6,2   | 1 | 55 | 24278 |
| HSPD1 | 4PJ1 | Structure | 13.16 Intra | 1,0   | 1 | 55 | 27063 |
| HSPD1 | 4PJ1 | Structure | 35.65 Intra | 3,2   | 1 | 55 | 26345 |
| HSPD1 | 4PJ1 | Structure | 35.65 Intra | 1,1   | 1 | 55 | 24848 |
| HSPD1 | 4PJ1 | Structure | 11.1 Intra  | 0,2   | 1 | 55 | 13954 |
| HSPD1 | 4PJ1 | Structure | 28.13 Intra | 1,0   | 1 | 55 | 32136 |
| HSPD1 | 4PJ1 | Structure | 45.11 Intra | 2,0   | 1 | 55 | 20169 |
| HSPD1 | 4PJ1 | Structure | 24.17 Intra | 9,4   | 1 | 55 | 10854 |
| HSPD1 | 4PJ1 | Structure | 12.37 Intra | 3,2   | 1 | 55 | 14691 |
| HSPD1 | 4PJ1 | Structure | 23.5 Intra  | 3,1   | 1 | 55 | 14993 |
| HSPD1 | 4PJ1 | Structure | 13.7 Intra  | 0,1   | 1 | 55 | 8071  |
| HSPD1 | 4PJ1 | Structure | 7.87 Intra  | 4,0   | 1 | 55 | 14105 |



|        |        |           |             |       |      |    |       |
|--------|--------|-----------|-------------|-------|------|----|-------|
| HSPD1  | 4PJ1   | Structure | 24.17       | 1 3,2 | 1    | 55 | 11944 |
| HSPD1  | 4PJ1   | Structure | ####        | 2 0,1 | 0.8  | 1  | 12488 |
| HSPE1  | 4PJ1   | Structure | 53.66       | 1 1,0 | 0.99 | 2  | 23912 |
| HSPD1  | P10809 | Phyre     | ####        | 1 1,0 | 0.94 | 2  | 27547 |
| HSPA5  | 6ASY   | Structure | 10.99 Intra | 1,0   | 1    | 11 | 10035 |
| HSPA5  | 6ASY   | Structure | 49.1 Intra  | 1,0   | 1    | 11 | 17638 |
| HSPA5  | 6ASY   | Structure | 19.57 Intra | 1,0   | 1    | 11 | 26175 |
| HSPA5  | 6ASY   | Structure | 67.75 Intra | 2,0   | 1    | 11 | 20088 |
| HSPA5  | 6ASY   | Structure | 19.41 Intra | 1,0   | 1    | 11 | 18905 |
| HSPA5  | 6ASY   | Structure | 89.16 Intra | 2,0   | 1    | 11 | 12695 |
| HSPA5  | 6ASY   | Structure | 20.06 Intra | 3,1   | 1    | 11 | 14091 |
| HSPA5  | 6ASY   | Structure | 31.56 Intra | 6,0   | 1    | 11 | 26830 |
| HSPA5  | 6ASY   | Structure | 16.02 Intra | 1,1   | 1    | 11 | 18034 |
| HSPA5  | 6ASY   | Structure | 15.87 Intra | 1,0   | 1    | 11 | 10430 |
| HSPA5  | 6ASY   | Structure | 9.97 Intra  | 2,0   | 1    | 11 | 11846 |
| HSPA8  | 4H5R   | Structure | 9.52 Intra  | 2,2   | 1    | 11 | 19357 |
| HSPA8  | 4H5R   | Structure | 12.04 Intra | 5,1   | 1    | 11 | 24120 |
| HSPA8  | 4H5R   | Structure | 16.78 Intra | 0,2   | 1    | 11 | 6823  |
| HSPA8  | 4H5R   | Structure | 14.95 Intra | 7,0   | 1    | 11 | 17433 |
| HSPA8  | 4H5R   | Structure | 14.95 Intra | 4,0   | 1    | 11 | 16452 |
| HSPA8  | 4H5R   | Structure | 27.94 Intra | 1,0   | 1    | 11 | 27217 |
| HSPA8  | 4H5R   | Structure | 19.76 Intra | 2,0   | 1    | 11 | 19846 |
| HSPA8  | P11142 | Phyre     | 46.31 Intra | 1,0   | 1    | 11 | 12607 |
| HSPA8  | P11142 | Phyre     | 42.45 Intra | 0,2   | 1    | 11 | 8273  |
| HSPA8  | P11142 | Phyre     | 12.29 Intra | 3,0   | 1    | 11 | 15221 |
| HSPA8  | 4H5R   | Structure | 30.18 Intra | 6,2   | 1    | 11 | 27555 |
| HSPA8  | P11142 | Phyre     | ####        | 1 1,0 | 1    | 1  | 14229 |
| HSPA8  | 4H5R   | Structure | ####        | 1 1,0 | 0.99 | 1  | 20762 |
| RALA   | 2BOV   | Structure | 14.97 Intra | 2,0   | 1    | 1  | 17734 |
| SPTB   | ####   | ####      |             | 1 1,0 | 0.86 | 1  | 38651 |
| ACADM  | 2A1T   | Structure | 27.21 Intra | 1,0   | 1    | 1  | 8919  |
| TOP1   | 1K4T   | Structure | ####        | 1 0,4 | 0.84 | 1  | 13721 |
| TOP2A  | P11388 | Modeller  | 16.54 Intra | 1,0   | 1    | 2  | 22274 |
| TOP2A  | 4FM9   | Structure | 18.16 Intra | 6,1   | 1    | 2  | 11541 |
| G6PD   | 1QKI   | Structure | 13.92 Intra | 1,0   | 0.99 | 1  | 17075 |
| MTHFD1 | P11586 | Phyre     | 17.76 Intra | 1,0   | 1    | 2  | 32180 |
| MTHFD1 | P11586 | Phyre     | 13.53 Intra | 1,0   | 1    | 2  | 23582 |
| IGF2R  | P11717 | Modeller  | 46.87 Intra | 1,0   | 1    | 2  | 26360 |
| IGF2R  | P11717 | Modeller  | 50.24 Intra | 3,1   | 1    | 2  | 12899 |
| PABPC1 | P11940 | Phyre     | 34.34 Intra | 2,0   | 1    | 13 | 24158 |
| PABPC1 | P11940 | Phyre     | 10.45 Intra | 3,2   | 1    | 13 | 29174 |
| PABPC1 | P11940 | Phyre     | 26.99 Intra | 2,0   | 1    | 13 | 18379 |
| PABPC1 | 4F02   | Structure | 12.48 Intra | 1,0   | 1    | 13 | 19394 |
| PABPC1 | 4F02   | Structure | 12.48 Intra | 3,0   | 1    | 13 | 18966 |
| PABPC1 | 4F02   | Structure | 12.48 Intra | 2,0   | 1    | 13 | 17202 |
| PABPC1 | 4F02   | Structure | 12.48 Intra | 0,1   | 1    | 13 | 9271  |
| PABPC1 | P11940 | Phyre     | 26.12 Intra | 1,0   | 1    | 13 | 17772 |

|         |           |           |       |       |       |      |    |       |
|---------|-----------|-----------|-------|-------|-------|------|----|-------|
| PABPC1  | 4F02      | Structure | 9.05  | Intra | 1,0   | 1    | 13 | 19525 |
| PABPC1  | 4F02      | Structure | 12.15 | Intra | 2,0   | 1    | 13 | 14663 |
| PABPC1  | 4F02      | Structure | 9.05  | Intra | 3,2   | 1    | 13 | 23233 |
| PABPC1  | P11940    | Phyre     | 7.95  | Intra | 4,1   | 1    | 13 | 28130 |
| PABPC1  | P11940    | Phyre     | 7.95  | Intra | 1,0   | 1    | 13 | 27498 |
| PCNA    | ####      | ####      |       |       | 1 3,3 | 1    | 3  | 25418 |
| PCNA    | 1U7B      | Structure | 10.08 | Intra | 1,1   | 1    | 3  | 22820 |
| PCNA    | 1U7B      | Structure | 7.25  | Intra | 1,0   | 0.99 | 3  | 22383 |
| HARS    | ####      | ####      |       | Intra | 0,1   | 1    | 1  | 4923  |
| SLC25A6 | P12236    | Phyre     | 27.96 | Intra | 1,0   | 1    | 10 | 33975 |
| SLC25A6 | P12236    | Phyre     | 23.6  | Intra | 1,1   | 1    | 10 | 24142 |
| SLC25A6 | P12236    | Phyre     | 23.53 | Intra | 1,0   | 1    | 10 | 30733 |
| SLC25A6 | P12236    | Phyre     | 9.22  | Intra | 3,2   | 1    | 10 | 23910 |
| SLC25A6 | P12236    | Phyre     | 24.4  | Intra | 2,1   | 1    | 10 | 20188 |
| SLC25A6 | P12236    | Phyre     | 24.4  | Intra | 4,1   | 1    | 10 | 18422 |
| SLC25A6 | P12236_P1 | Docking   | 16.35 |       | 1 2,0 | 1    | 10 | 19978 |
| SLC25A6 | P12236    | Phyre     | 14.2  | Intra | 3,2   | 1    | 10 | 16897 |
| SLC25A6 | P12236    | Phyre     | 22.6  | Intra | 11,1  | 1    | 10 | 34354 |
| SLC25A6 | P12236    | Phyre     | 27.32 | Intra | 1,0   | 1    | 10 | 33884 |
| MTA1    | ####      | ####      |       |       | 2 1,0 | 0.75 | 1  | 24629 |
| SLC25A6 | P12236    | Phyre     | ####  |       | 2 1,0 | 0.98 | 1  | 20313 |
| IMPDH2  | ####      | ####      |       | Intra | 1,0   | 1    | 3  | 23000 |
| IMPDH2  | ####      | ####      |       | Intra | 1,0   | 1    | 3  | 16706 |
| IMPDH2  | 1NF7      | Structure | 23.44 | Intra | 1,0   | 1    | 3  | 27501 |
| ACTN1   | P12814    | Phyre     | 11.89 | Intra | 1,0   | 1    | 2  | 22982 |
| ACTN1   | P12814_P1 | Docking   | 59.31 |       | 1 0,1 | 1    | 2  | 8518  |
| ACTN1   | 2EYI      | Structure | ####  |       | 2 4,0 | 1    | 1  | 14052 |
| XRCC6   | ####      | ####      |       | Intra | 2,1   | 1    | 1  | 23616 |
| XRCC5   | P13010    | Phyre     | ####  |       | 1 2,2 | 1    | 2  | 21244 |
| XRCC6   | ####      | ####      |       |       | 1 1,0 | 0.98 | 2  | 18252 |
| XRCC5   | 1JEY      | Structure | 32.81 | Intra | 1,0   | 1    | 2  | 25453 |
| XRCC5   | 1JEY      | Structure | 19.18 | Intra | 2,0   | 1    | 2  | 18973 |
| COX4I1  | P13073    | Phyre     | 11.42 | Intra | 2,0   | 1    | 1  | 16027 |
| EEF2    | P13639    | Phyre     | 5.28  | Intra | 1,2   | 1    | 34 | 25681 |
| EEF2    | P13639    | Phyre     | 27.86 | Intra | 1,0   | 1    | 34 | 15383 |
| EEF2    | P13639    | Phyre     | 17.27 | Intra | 4,0   | 1    | 34 | 14356 |
| EEF2    | P13639    | Phyre     | 22.08 | Intra | 2,1   | 1    | 34 | 33603 |
| EEF2    | P13639    | Phyre     | 17.44 | Intra | 2,0   | 1    | 34 | 19047 |
| EEF2    | P13639    | Phyre     | 34.11 | Intra | 1,0   | 1    | 34 | 17076 |
| EEF2    | P13639    | Phyre     | 36.28 | Intra | 2,0   | 1    | 34 | 19827 |
| EEF2    | P13639    | Phyre     | 27.86 | Intra | 5,1   | 1    | 34 | 14430 |
| EEF2    | P13639    | Phyre     | 8.88  | Intra | 4,4   | 1    | 34 | 14668 |
| EEF2    | ####      | ####      |       | Intra | 8,1   | 1    | 34 | 14628 |
| EEF2    | ####      | ####      |       | Intra | 2,1   | 1    | 34 | 14932 |
| EEF2    | ####      | ####      |       | Intra | 1,3   | 1    | 34 | 14058 |
| EEF2    | P13639    | Phyre     | 22.31 | Intra | 4,1   | 1    | 34 | 20337 |
| EEF2    | P13639    | Phyre     | 9.84  | Intra | 1,0   | 1    | 34 | 15795 |

|         |        |           |      |             |       |      |    |       |
|---------|--------|-----------|------|-------------|-------|------|----|-------|
| EEF2    | P13639 | Phyre     | #### | Intra       | 3,0   | 1    | 34 | 15798 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 3,0   | 1    | 34 | 20073 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 2,0   | 1    | 34 | 23733 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 1,0   | 1    | 34 | 21899 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 3,0   | 1    | 34 | 14179 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 1,0   | 1    | 34 | 10906 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 3,0   | 1    | 34 | 18303 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 1,0   | 1    | 34 | 22439 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 2,0   | 1    | 34 | 18518 |
| EEF2    | P13639 | Phyre     | #### | Intra       | 0,1   | 1    | 34 | 7341  |
| EEF2    | P13639 | Phyre     | #### | Intra       | 0,1   | 1    | 34 | 9869  |
| EEF2    | P13639 | Phyre     |      | 21.87 Intra | 4,2   | 1    | 34 | 20263 |
| EEF2    | P13639 | Phyre     |      | 12.67 Intra | 3,2   | 1    | 34 | 26778 |
| EEF2    | P13639 | Phyre     |      | 12.67 Intra | 4,1   | 1    | 34 | 24949 |
| EEF2    | P13639 | Phyre     |      | 25.34 Intra | 2,1   | 1    | 34 | 11683 |
| EEF2    | P13639 | Phyre     |      | 28.21 Intra | 5,3   | 1    | 34 | 16838 |
| EEF2    | P13639 | Phyre     |      | 24.62 Intra | 1,0   | 1    | 34 | 19817 |
| EEF2    | P13639 | Phyre     |      | 6.13 Intra  | 1,0   | 1    | 34 | 17016 |
| EEF2    | P13639 | Phyre     |      | 16.97 Intra | 0,1   | 1    | 34 | 9576  |
| EEF2    | P13639 | Phyre     |      | 5.28 Intra  | 4,2   | 1    | 34 | 22252 |
| PDIA4   | 3IDV   | Structure |      | 12.27 Intra | 1,0   | 1    | 4  | 24149 |
| PDIA4   | P13667 | Phyre     |      | 11.32 Intra | 1,0   | 1    | 4  | 21751 |
| PDIA4   | P13667 | Phyre     |      | 43.78 Intra | 1,0   | 1    | 4  | 29948 |
| PDIA4   | P13667 | Phyre     |      | 16.98 Intra | 0,2   | 1    | 4  | 5981  |
| PLS3    | 1AOA   | Structure |      | 17.36 Intra | 1,0   | 1    | 1  | 22970 |
| PLS3    | P13797 | Phyre     | #### |             | 2 4,1 | 1    | 1  | 20849 |
| ETFA    | 2A1U   | Structure |      | 17.95 Intra | 1,0   | 0.99 | 1  | 21327 |
| LRPPRC  | P42704 | Modeller  | #### |             | 2 0,2 | 0.93 | 1  | 20208 |
| GYS1    | P13807 | Phyre     |      | 31.36 Intra | 2,0   | 1    | 1  | 31221 |
| PRKCSH  | P14314 | iTasser   | #### | Intra       | 2,0   | 1    | 4  | 23004 |
| PRKCSH  | P14314 | iTasser   | #### | Intra       | 4,1   | 1    | 4  | 21335 |
| PRKCSH  | ####   |           | #### | Intra       | 2,2   | 1    | 4  | 17857 |
| PRKCSH  | ####   |           | #### | Intra       | 2,0   | 1    | 4  | 16146 |
| PKM     | 3GR4   | Structure |      | 13.48 Intra | 1,0   | 0.94 | 8  | 28926 |
| PKM     | 3GR4   | Structure |      | 14.9 Intra  | 1,0   | 0.86 | 8  | 9479  |
| PKM     | 3GR4   | Structure |      | 29.72 Intra | 2,1   | 1    | 8  | 16026 |
| PKM     | 3GR4   | Structure |      | 12.68 Intra | 1,0   | 1    | 8  | 15473 |
| PKM     | 3GR4   | Structure |      | 65.72       | 1 1,0 | 0.99 | 8  | 12229 |
| PKM     | 3GR4   | Structure |      | 15.92 Intra | 0,1   | 1    | 8  | 8559  |
| PKM     | 3GR4   | Structure |      | 21.21 Intra | 1,1   | 1    | 8  | 32446 |
| PKM     | 3GR4   | Structure |      | 12.83 Intra | 2,0   | 1    | 8  | 17960 |
| HSP90B1 | P14625 | Phyre     |      | 29.6 Intra  | 3,2   | 1    | 27 | 28150 |
| HSP90B1 | 4NH9   | Structure |      | 17.59 Intra | 2,0   | 1    | 27 | 24847 |
| HSP90B1 | P14625 | Phyre     |      | 10 Intra    | 1,0   | 1    | 27 | 18905 |
| HSP90B1 | P14625 | Phyre     | #### | Intra       | 2,0   | 1    | 27 | 12929 |
| HSP90B1 | P14625 | Phyre     |      | 13.25 Intra | 1,0   | 1    | 27 | 17893 |
| HSP90B1 | P14625 | Phyre     |      | 28.51 Intra | 2,2   | 1    | 27 | 19269 |

|         |        |           |       |       |       |      |    |       |
|---------|--------|-----------|-------|-------|-------|------|----|-------|
| HSP90B1 | P14625 | Phyre     | 41.11 | Intra | 1,0   | 1    | 27 | 24841 |
| HSP90B1 | P14625 | Phyre     | 39.71 | Intra | 1,0   | 1    | 27 | 23847 |
| HSP90B1 | P14625 | Phyre     | 9.46  | Intra | 1,1   | 1    | 27 | 31214 |
| HSP90B1 | P14625 | Phyre     | 38.43 | Intra | 0,1   | 1    | 27 | 6907  |
| HSP90B1 | P14625 | Phyre     | 16.95 | Intra | 2,0   | 1    | 27 | 17137 |
| HSP90B1 | P14625 | Phyre     | 13.97 | Intra | 1,0   | 1    | 27 | 30807 |
| HSP90B1 | P14625 | Phyre     | 13.87 | Intra | 1,0   | 1    | 27 | 14541 |
| HSP90B1 | P14625 | Phyre     | 16.73 | Intra | 1,0   | 1    | 27 | 13828 |
| HSP90B1 | P14625 | Phyre     | 20.29 | Intra | 0,1   | 1    | 27 | 9404  |
| HSP90B1 | P14625 | Phyre     | 19.02 | Intra | 1,0   | 1    | 27 | 24216 |
| HSP90B1 | P14625 | Phyre     | 25.84 | Intra | 1,0   | 1    | 27 | 20386 |
| HSP90B1 | P14625 | Phyre     | 42.85 | Intra | 2,0   | 1    | 27 | 19035 |
| HSP90B1 | P14625 | Phyre     | 37.6  | Intra | 1,0   | 1    | 27 | 20917 |
| HSP90B1 | P14625 | Phyre     | 8.67  | Intra | 1,0   | 1    | 27 | 28541 |
| HSP90B1 | P14625 | Phyre     | 24.57 | Intra | 1,0   | 1    | 27 | 18193 |
| HSP90B1 | P14625 | Phyre     | 7.87  | Intra | 1,0   | 1    | 27 | 16589 |
| HSP90B1 | P14625 | Phyre     | 17.22 | Intra | 2,1   | 1    | 27 | 16480 |
| HSP90B1 | P14625 | Phyre     | 17.22 | Intra | 3,0   | 1    | 27 | 15603 |
| HSP90B1 | P14625 | Phyre     | 20.52 | Intra | 1,0   | 1    | 27 | 21196 |
| HSP90B1 | P14625 | Phyre     | 15.81 | Intra | 2,0   | 1    | 27 | 20210 |
| HSP90B1 | 4NH9   | Structure | 16.25 | Intra | 0,1   | 1    | 27 | 17073 |
| IDE     | 2WK3   | Structure | 41.13 | Intra | 1,0   | 1    | 4  | 20373 |
| IDE     | 2WK3   | Structure | 39.79 | Intra | 0,1   | 1    | 4  | 8799  |
| IDE     | 2WK3   | Structure | 62.81 | Intra | 1,0   | 1    | 4  | 15818 |
| IDE     | 2WK3   | Structure | 48.56 | Intra | 1,0   | 0.97 | 4  | 17168 |
| HNRNPL  | 3TO8   | Structure | 13.34 | Intra | 3,3   | 1    | 3  | 23396 |
| HNRNPL  | 3TO8   | Structure | 21.39 | Intra | 1,0   | 1    | 3  | 12842 |
| HNRNPL  | P14866 | Phyre     | 18.49 | Intra | 7,2   | 1    | 3  | 12422 |
| UQCRB   | 5XTE   | Structure | 67.2  |       | 1 1,0 | 0.98 | 1  | 30990 |
| AKR1B1  | 1US0   | Structure | 19.44 | Intra | 1,1   | 1    | 2  | 20679 |
| AKR1B1  | 1US0   | Structure | 8.45  | Intra | 3,0   | 1    | 2  | 29729 |
| GSPT1   | P15170 | Phyre     | 20.68 | Intra | 1,0   | 1    | 3  | 20218 |
| GSPT1   | P15170 | Phyre     | 22.53 | Intra | 2,0   | 1    | 3  | 24201 |
| GSPT1   | P15170 | Phyre     | 27.38 | Intra | 2,0   | 1    | 3  | 20400 |
| CD46    | 5FO8   | Structure | 10.82 | Intra | 3,0   | 1    | 1  | 11938 |
| RPS2    | 5FLX   | Structure | ####  |       | 1 2,0 | 1    | 1  | 25265 |
| DSP     | ####   |           | ####  | Intra | 1,0   | 1    | 11 | 17585 |
| DSP     | ####   |           | ####  | Intra | 2,0   | 1    | 11 | 13847 |
| DSP     | ####   |           | ####  | Intra | 1,0   | 1    | 11 | 24405 |
| DSP     | ####   |           | ####  | Intra | 1,0   | 1    | 11 | 22588 |
| DSP     | ####   |           | ####  | Intra | 0,1   | 1    | 11 | 12137 |
| DSP     | ####   |           | ####  | Intra | 1,1   | 1    | 11 | 17627 |
| DSP     | ####   |           | ####  | Intra | 2,0   | 1    | 11 | 11240 |
| DSP     | ####   |           | ####  | Intra | 3,2   | 1    | 11 | 15158 |
| DSP     | 5DZZ   | Structure | 10.56 | Intra | 2,0   | 1    | 11 | 21199 |
| DSP     | ####   |           | ####  | Intra | 3,2   | 1    | 11 | 17659 |
| DSP     | ####   |           | ####  | Intra | 1,0   | 1    | 11 | 18765 |

|          |        |           |             |       |      |   |       |
|----------|--------|-----------|-------------|-------|------|---|-------|
| CD44     | 1UUH   | Structure | 65.09       | 1 2,1 | 1    | 1 | 11963 |
| CBR1     | 1WMA   | Structure | 25.95 Intra | 1,1   | 1    | 2 | 11995 |
| CBR1     | 1WMA   | Structure | 25.95 Intra | 0,1   | 1    | 2 | 6470  |
| HIST1H1B | P16401 | Modeller  | 5.49 Intra  | 1,0   | 1    | 5 | 16634 |
| HIST1H1B | P16401 | Modeller  | 21.32 Intra | 1,0   | 1    | 5 | 5687  |
| HIST1H1B | P16401 | Modeller  | 10.64 Intra | 0,1   | 1    | 5 | 7009  |
| HIST1H1B | P16401 | Modeller  | 10.02 Intra | 6,1   | 1    | 5 | 9766  |
| HIST1H1B | P16401 | Modeller  | 9.48 Intra  | 1,0   | 1    | 5 | 27265 |
| HIST1H1C | P16403 | Modeller  | 19.11 Intra | 1,0   | 1    | 9 | 10244 |
| HIST1H1C | ####   | ####      | Intra       | 1,0   | 1    | 9 | 15585 |
| HIST1H1C | P16403 | Modeller  | 10.66 Intra | 0,1   | 1    | 9 | 7153  |
| HIST1H1C | P16403 | Modeller  | 7.46 Intra  | 0,3   | 1    | 9 | 8153  |
| HIST1H1C | P16403 | Modeller  | ####        | Intra | 1,0  | 9 | 19675 |
| HIST1H1C | P16403 | Modeller  | 12.18 Intra | 1,0   | 1    | 9 | 21178 |
| HIST1H1C | P16403 | Modeller  | 9.5 Intra   | 6,2   | 1    | 9 | 23852 |
| HIST1H1C | P16403 | Modeller  | 16.81 Intra | 1,0   | 1    | 9 | 19906 |
| HIST1H1C | ####   | ####      | Intra       | 2,0   | 1    | 9 | 21293 |
| HIST1H1C | P16403 | Modeller  | ####        | 2 5,0 | 0.89 | 1 | 20492 |
| POR      | 3QE2   | Structure | 17.51 Intra | 3,0   | 1    | 1 | 18234 |
| ATP2A2   | P16615 | Phyre     | 18.73 Intra | 3,0   | 1    | 4 | 25321 |
| ATP2A2   | ####   | ####      | Intra       | 2,0   | 1    | 4 | 17378 |
| ATP2A2   | P16615 | Phyre     | 17.56 Intra | 3,1   | 1    | 4 | 13821 |
| ATP2A2   | P16615 | Phyre     | ####        | Intra | 2,0  | 4 | 24108 |
| ITGA2    | P17301 | Phyre     | 19.21 Intra | 2,0   | 1    | 3 | 23381 |
| ITGA2    | P17301 | Phyre     | 10.81 Intra | 1,0   | 1    | 3 | 36940 |
| ITGA2    | 1V7P   | Structure | 11.9 Intra  | 2,0   | 1    | 3 | 22185 |
| ITGA2    | 1V7P   | Structure | ####        | 2 0,1 | 0.8  | 1 | 7693  |
| NPR3     | 1YK0   | Structure | 17.82       | 1 1,2 | 1    | 1 | 20295 |
| DDX5     | 4A4D   | Structure | 10.41 Intra | 1,0   | 1    | 1 | 22947 |
| PFKP     | 4XYJ   | Structure | ####        | 1 1,0 | 0.82 | 2 | 27131 |
| PFKL     | P17858 | Phyre     | ####        | 1 1,0 | 0.98 | 2 | 30894 |
| PSMC3    | 5M32   | Structure | 21.79 Intra | 3,0   | 1    | 1 | 21916 |
| TCP1     | P17987 | Phyre     | 16.55 Intra | 0,1   | 1    | 2 | 12821 |
| TCP1     | P17987 | Phyre     | 8.37 Intra  | 1,0   | 1    | 2 | 27466 |
| TCP1     | P17987 | Phyre     | ####        | 1 0,2 | 1    | 2 | 17391 |
| CCT8     | P50990 | Phyre     | ####        | 1 1,0 | 1    | 2 | 20482 |
| CCT4     | P50991 | Phyre     | ####        | 1 0,1 | 0.87 | 2 | 7069  |
| TCP1     | P17987 | Phyre     | ####        | 1 0,1 | 0.93 | 2 | 10547 |
| CCT2     | P78371 | Phyre     | ####        | 1 2,0 | 1    | 2 | 12673 |
| CCT2     | P78371 | Phyre     | ####        | 1 5,0 | 1    | 2 | 11427 |
| RPL35A   | ####   | ####      |             | 1 4,0 | 1    | 1 | 13758 |
| RPL6     | Q02878 | Phyre     | ####        | 1 4,2 | 1    | 1 | 17092 |
| ITGB5    | P18084 | Phyre     | 10.16 Intra | 1,1   | 1    | 3 | 33382 |
| ITGB5    | P18084 | Phyre     | 14.03 Intra | 0,2   | 1    | 3 | 12550 |
| ITGB5    | P18084 | Phyre     | 12.35 Intra | 2,1   | 1    | 3 | 19857 |
| RPL7     | P18124 | Phyre     | 21.64 Intra | 4,2   | 1    | 3 | 19014 |
| RPL7     | P18124 | Phyre     | 19.24 Intra | 0,2   | 1    | 3 | 13250 |

|        |           |           |        |       |       |      |    |       |
|--------|-----------|-----------|--------|-------|-------|------|----|-------|
| RPL7   | P18124    | Phyre     | 5.48   | Intra | 0,2   | 0.86 | 3  | 11346 |
| RPL7   | P18124    | Phyre     | ####   |       | 1 1,2 | 1    | 1  | 9939  |
| VCL    | 1TR2      | Structure | 7.79   | Intra | 4,0   | 1    | 1  | 18320 |
| RPL17  | ####      |           | ####   | N/A   | 1,0   | 0.96 | 2  | 27424 |
| RPL17  | P18621    | Phyre     | 15.15  | Intra | 1,0   | 1    | 2  | 12525 |
| PGAM1  | 4GPZ      | Structure | 28.68  | Intra | 2,0   | 1    | 4  | 31150 |
| PGAM1  | 4GPZ      | Structure | 21.06  |       | 1 3,1 | 1    | 4  | 21283 |
| PGAM1  | 4GPZ      | Structure | 14.12  | Intra | 5,1   | 1    | 4  | 15985 |
| PGAM1  | 4GPZ      | Structure | 19.51  | Intra | 1,0   | 1    | 4  | 14861 |
| CD58   | 1CCZ      | Structure | 11.11  | Intra | 2,2   | 1    | 1  | 20740 |
| NCL    | ####      |           | ####   | Intra | 1,0   | 1    | 28 | 8149  |
| NCL    | ####      |           | ####   | Intra | 1,0   | 1    | 28 | 11052 |
| NCL    | 2KRR      | Structure | 13.88  | Intra | 0,2   | 1    | 28 | 12020 |
| NCL    | 2KRR      | Structure | 20.88  | Intra | 1,1   | 1    | 28 | 32564 |
| NCL    | P19338    | Phyre     | 21.57  | Intra | 3,0   | 1    | 28 | 10364 |
| NCL    | P19338    | Phyre     | 41.74  | Intra | 1,0   | 1    | 28 | 17773 |
| NCL    | P19338    | Phyre     | 10.27  | Intra | 1,0   | 1    | 28 | 25407 |
| NCL    | ####      |           | ####   | Intra | 1,0   | 1    | 28 | 6574  |
| NCL    | ####      |           | ####   | Intra | 1,0   | 1    | 28 | 7912  |
| NCL    | 2KRR      | Structure | 34.71  | Intra | 0,1   | 1    | 28 | 7823  |
| NCL    | 2KRR      | Structure | 9.19   | Intra | 3,2   | 1    | 28 | 19609 |
| NCL    | 2KRR      | Structure | 18.13  | Intra | 4,2   | 1    | 28 | 18283 |
| NCL    | 2KRR      | Structure | 14.21  | Intra | 1,0   | 1    | 28 | 26945 |
| NCL    | P19338    | Phyre     | 16.62  | Intra | 1,0   | 1    | 28 | 18538 |
| NCL    | 2KRR      | Structure | 32.43  | Intra | 1,0   | 1    | 28 | 25715 |
| NCL    | 2KRR      | Structure | 9.54   | Intra | 6,1   | 1    | 28 | 24649 |
| NCL    | P19338    | Phyre     | 16.39  | Intra | 0,1   | 1    | 28 | 8849  |
| NCL    | P19338    | Phyre     | 34.42  | Intra | 1,0   | 1    | 28 | 20673 |
| NCL    | P19338    | Phyre     | 27.32  | Intra | 1,2   | 1    | 28 | 25303 |
| NCL    | P19338    | Phyre     | 20.76  | Intra | 5,0   | 1    | 28 | 18370 |
| NCL    | 2KRR      | Structure | 28.04  | Intra | 3,2   | 1    | 28 | 25904 |
| NCL    | 2KRR      | Structure | 31.84  | Intra | 1,0   | 1    | 28 | 24259 |
| NCL    | 2KRR      | Structure | 15.86  | Intra | 1,0   | 1    | 28 | 22513 |
| NCL    | P19338    | Phyre     | 38.36  | Intra | 2,0   | 1    | 28 | 29372 |
| NCL    | P19338_P1 | Docking   | 20.96  |       | 1 1,1 | 1    | 28 | 24680 |
| NCL    | 2KRR      | Structure | 11.32  | Intra | 1,0   | 1    | 28 | 22188 |
| NCL    | P19338    | Phyre     | 10.27  | Intra | 2,1   | 1    | 28 | 25520 |
| NCL    | P19338    | Phyre     | 11.63  | Intra | 1,0   | 1    | 28 | 26013 |
| NDUFV2 | 5XTB      | Structure | 15.76  | Intra | 0,1   | 1    | 1  | 15504 |
| ANXA11 | P50995    | Phyre     | ####   |       | 1 1,0 | 0.99 | 1  | 19718 |
| BTF3   | ####      |           | ####   | Intra | 1,0   | 0.99 | 1  | 14741 |
| PSMB1  | 5LE5      | Structure | 7.77   | Intra | 1,0   | 0.94 | 2  | 21146 |
| PSMB1  | 5LE5      | Structure | 22.49  | Intra | 1,0   | 1    | 2  | 22745 |
| PSMB4  | 5LE5      | Structure | 101.63 |       | 1 1,0 | 0.98 | 1  | 22172 |
| PSMB1  | P20618    | Phyre     | ####   |       | 1 4,5 | 1    | 3  | 29433 |
| PSMB1  | P20618    | Phyre     | ####   |       | 1 1,0 | 1    | 3  | 27752 |
| PSMB1  | P20618    | Phyre     | ####   |       | 1 2,1 | 1    | 3  | 27012 |

|       |           |           |       |           |      |    |       |
|-------|-----------|-----------|-------|-----------|------|----|-------|
| PSMB7 | 5LE5      | Structure | 97.65 | 1 1,1     | 0.99 | 1  | 10636 |
| M6PR  | P20645    | Phyre     | 15.42 | Intra 1,0 | 0.99 | 2  | 16123 |
| M6PR  | P20645    | Phyre     | 31.29 | Intra 1,0 | 0.99 | 2  | 5332  |
| LMNB1 | P20700_P2 | Docking   | 23.52 | 1 0,1     | 1    | 6  | 12814 |
| LMNB1 | ####      | ####      | Intra | 2,0       | 1    | 6  | 20245 |
| LMNB1 | 3JT0      | Structure | 12.73 | Intra 2,2 | 1    | 6  | 15117 |
| LMNB1 | ####      | ####      | Intra | 2,2       | 1    | 6  | 16323 |
| LMNB1 | ####      | ####      | Intra | 4,1       | 1    | 6  | 20436 |
| LMNB1 | ####      | ####      | Intra | 1,0       | 1    | 6  | 13925 |
| FLNA  | ####      | ####      | Intra | 1,0       | 1    | 5  | 21263 |
| FLNA  | ####      | ####      | Intra | 1,0       | 1    | 5  | 21943 |
| FLNA  | ####      | ####      | Intra | 5,1       | 1    | 5  | 15702 |
| FLNA  | ####      | ####      | Intra | 1,0       | 1    | 5  | 10238 |
| FLNA  | ####      | ####      | Intra | 1,0       | 1    | 5  | 18527 |
| NT5E  | 4H1S      | Structure | 13.98 | 1 1,1     | 1    | 1  | 23226 |
| VDAC1 | 5XDO      | Structure | 20.02 | Intra 2,0 | 1    | 10 | 29690 |
| VDAC1 | 5XDO      | Structure | 25.79 | Intra 2,2 | 1    | 10 | 24640 |
| VDAC1 | 5XDO      | Structure | 18.02 | Intra 3,3 | 1    | 10 | 17419 |
| VDAC1 | 5XDO      | Structure | 37.37 | Intra 2,0 | 1    | 10 | 21719 |
| VDAC1 | 5XDO      | Structure | 34.49 | Intra 4,6 | 1    | 10 | 25582 |
| VDAC1 | 5XDO      | Structure | 30.48 | Intra 2,2 | 1    | 10 | 24385 |
| VDAC1 | 5XDO      | Structure | 20.67 | Intra 0,1 | 1    | 10 | 8700  |
| VDAC1 | 5XDO      | Structure | 20.67 | Intra 2,0 | 1    | 10 | 20859 |
| VDAC1 | 5XDO      | Structure | 12.18 | Intra 0,1 | 1    | 10 | 6505  |
| VDAC1 | 5XDO      | Structure | 22.02 | Intra 1,0 | 1    | 10 | 25982 |
| CD9   | P21926    | Phyre     | 9.67  | Intra 2,0 | 1    | 5  | 35152 |
| CD9   | P21926    | Phyre     | 9.01  | Intra 5,3 | 1    | 5  | 10979 |
| CD9   | P21926    | Phyre     | 14.43 | Intra 1,0 | 1    | 5  | 32395 |
| CD9   | P21926    | Phyre     | 17.32 | Intra 3,2 | 1    | 5  | 13638 |
| CD9   | P21926    | Phyre     | 21.3  | Intra 3,4 | 1    | 5  | 18955 |
| AHNAK | ####      | ####      | 2 1,0 | 0.89      | 1    | 1  | 16763 |
| COMT  | 4PYI      | Structure | 4.84  | Intra 0,1 | 1    | 1  | 15522 |
| FBL   | ####      | ####      | Intra | 1,0       | 1    | 3  | 16351 |
| FBL   | 2IPX      | Structure | 15.81 | Intra 1,0 | 1    | 3  | 19075 |
| FBL   | ####      | ####      | Intra | 1,0       | 1    | 3  | 15295 |
| GART  | P22102    | Phyre     | 23.7  | Intra 1,0 | 1    | 2  | 23420 |
| GART  | 2QK4      | Structure | 6.09  | Intra 0,1 | 1    | 2  | 8131  |
| PAICS | P22234    | Unknown   | ####  | Intra 3,1 | 1    | 9  | 17547 |
| PAICS | P22234_P2 | Docking   | 56.35 | 1 1,0     | 1    | 9  | 19635 |
| PAICS | 2H31      | Structure | 22.17 | Intra 1,0 | 1    | 9  | 20285 |
| PAICS | 2H31      | Structure | 29.81 | Intra 0,1 | 1    | 9  | 10848 |
| PAICS | 2H31      | Structure | 29.81 | Intra 1,0 | 1    | 9  | 26827 |
| PAICS | 2H31      | Structure | 27.59 | Intra 1,0 | 1    | 9  | 15607 |
| PAICS | 2H31      | Structure | 5.17  | Intra 3,0 | 1    | 9  | 22681 |
| PAICS | ####      | ####      | Intra | 1,0       | 1    | 9  | 25092 |
| PAICS | 2H31      | Structure | 20.53 | Intra 1,2 | 1    | 9  | 21918 |
| UBA1  | 4P22      | Structure | 14.63 | Intra 1,0 | 0.99 | 1  | 19146 |

|          |           |           |       |       |       |      |    |       |
|----------|-----------|-----------|-------|-------|-------|------|----|-------|
| NME2     | 1NSK      | Structure | 16.3  | Intra | 3,0   | 1    | 6  | 23898 |
| NME2     | 1NSK      | Structure | 25.95 | Intra | 2,0   | 1    | 6  | 15836 |
| NME2     | 1NSK      | Structure | 25.95 | Intra | 1,1   | 1    | 6  | 13947 |
| NME2     | 1NSK      | Structure | 19.47 | Intra | 2,0   | 1    | 6  | 22401 |
| NME2     | 1NSK      | Structure | 9.46  |       | 1 2,0 | 1    | 6  | 20663 |
| NME2     | 1NSK      | Structure | 9.46  | Intra | 4,1   | 1    | 6  | 19712 |
| FDXR     | P22570    | Phyre     | 23.26 | Intra | 2,0   | 1    | 1  | 18035 |
| HNRNPA2B | 5WWG      | Structure | 43.53 | Intra | 1,0   | 1    | 18 | 9123  |
| HNRNPA2B | 5WWG      | Structure | 25.12 | Intra | 4,0   | 1    | 18 | 26254 |
| HNRNPA2B | 5WWG      | Structure | 29.84 | Intra | 1,2   | 1    | 18 | 23599 |
| HNRNPA2B | 5WWG      | Structure | 29.84 | Intra | 1,1   | 1    | 18 | 20379 |
| HNRNPA2B | 5WWG      | Structure | 31.11 | Intra | 3,1   | 1    | 18 | 8717  |
| HNRNPA2B | 5WWG      | Structure | 29.52 | Intra | 1,1   | 1    | 18 | 23219 |
| HNRNPA2B | 5WWG      | Structure | 25.45 | Intra | 4,3   | 1    | 18 | 10864 |
| HNRNPA2B | 5WWG      | Structure | 31.19 | Intra | 0,3   | 1    | 18 | 6061  |
| HNRNPA2B | 5WWG      | Structure | 14.75 | Intra | 4,1   | 1    | 18 | 26614 |
| HNRNPA2B | 5WWG      | Structure | 22.1  | Intra | 1,2   | 1    | 18 | 24167 |
| HNRNPA2B | 5WWG      | Structure | 22.1  | Intra | 4,2   | 1    | 18 | 22264 |
| HNRNPA2B | 5WWG      | Structure | 14.51 | Intra | 0,1   | 1    | 18 | 4029  |
| HNRNPA2B | P22626_P2 | Docking   | 56.98 |       | 1 4,0 | 1    | 18 | 26573 |
| HNRNPA2B | 5WWG      | Structure | 16.61 | Intra | 1,0   | 1    | 18 | 14832 |
| HNRNPA2B | 5WWG      | Structure | 24.06 | Intra | 4,4   | 1    | 18 | 9955  |
| HNRNPA2B | 5WWG      | Structure | 7.52  | Intra | 0,1   | 1    | 18 | 4399  |
| HNRNPA2B | 5WWG      | Structure | 8.37  | Intra | 0,3   | 1    | 18 | 9765  |
| HNRNPA2B | P22626_P2 | Docking   | 20.18 |       | 1 2,0 | 1    | 18 | 9805  |
| UQCRC2   | 5XTE      | Structure | 29.55 | Intra | 0,1   | 1    | 3  | 10500 |
| UQCRC2   | 5XTE      | Structure | 13.72 | Intra | 2,1   | 1    | 3  | 21687 |
| UQCRC2   | 5XTE      | Structure | 20.44 | Intra | 3,0   | 1    | 3  | 15406 |
| SFPQ     | 4WIJ      | Structure | 23.64 | Intra | 2,0   | 1    | 11 | 27955 |
| SFPQ     | 4WIJ      | Structure | 23.38 | Intra | 2,1   | 1    | 11 | 21901 |
| SFPQ     | 4WIJ      | Structure | 23.07 | Intra | 10,4  | 1    | 11 | 22879 |
| SFPQ     | 4WIJ      | Structure | 22.13 | Intra | 2,1   | 1    | 11 | 19206 |
| SFPQ     | 4WIJ      | Structure | 22.13 | Intra | 3,2   | 1    | 11 | 17944 |
| SFPQ     | 4WIJ      | Structure | 23.58 | Intra | 1,0   | 1    | 11 | 20996 |
| SFPQ     | 4WIJ      | Structure | 8.85  | Intra | 3,0   | 1    | 11 | 17374 |
| SFPQ     | ####      | ####      |       | Intra | 2,0   | 1    | 11 | 8796  |
| SFPQ     | 4WIJ      | Structure | 35.58 | Intra | 4,1   | 1    | 11 | 18225 |
| SFPQ     | 4WIJ      | Structure | 35.58 | Intra | 3,0   | 1    | 11 | 16917 |
| SFPQ     | 4WIJ      | Structure | 9.94  | Intra | 1,0   | 1    | 11 | 28895 |
| NONO     | 3SDE      | Structure | ####  |       | 1 2,0 | 1    | 3  | 20957 |
| NONO     | 3SDE      | Structure | ####  |       | 1 1,0 | 0.98 | 3  | 18502 |
| SFPQ     | ####      | ####      |       |       | 1 3,2 | 1    | 3  | 16309 |
| PPIB     | 3ICH      | Structure | 11.29 | Intra | 2,1   | 1    | 13 | 27744 |
| PPIB     | 3ICH      | Structure | 21.08 | Intra | 3,0   | 1    | 13 | 18748 |
| PPIB     | ####      | ####      |       |       | 1 2,0 | 1    | 13 | 14177 |
| PPIB     | 3ICH      | Structure | 9.39  | Intra | 4,2   | 1    | 13 | 24829 |
| PPIB     | 3ICH      | Structure | 14.39 | Intra | 4,0   | 1    | 13 | 25616 |



|          |           |           |       |       |       |      |    |       |
|----------|-----------|-----------|-------|-------|-------|------|----|-------|
| PPIB     | 3ICH      | Structure | 26.09 | Intra | 0,1   | 1    | 13 | 11838 |
| PPIB     | 3ICH      | Structure | 20.74 | Intra | 4,2   | 1    | 13 | 29946 |
| PPIB     | 3ICH      | Structure | 28.6  | Intra | 3,0   | 1    | 13 | 35049 |
| PPIB     | 3ICH      | Structure | 12.33 | Intra | 4,1   | 1    | 13 | 16319 |
| PPIB     | 3ICH      | Structure | 15.18 | Intra | 0,1   | 1    | 13 | 6560  |
| PPIB     | 3ICH      | Structure | 31.02 | Intra | 2,1   | 1    | 13 | 28293 |
| PPIB     | 3ICH      | Structure | 20.74 | Intra | 2,2   | 1    | 13 | 30059 |
| PPIB     | 3ICH      | Structure | 29.31 | Intra | 1,1   | 1    | 13 | 32803 |
| PPIB     | 3ICH      | Structure | ####  |       | 2 1,0 | 0.98 | 1  | 19507 |
| PPIB     | 3ICH      | Structure | ####  |       | 2 1,0 | 0.98 | 1  | 18928 |
| WARS     | 5UJJ      | Structure | 23.82 | Intra | 1,0   | 0.97 | 3  | 20818 |
| WARS     | 5UJJ      | Structure | 18.85 | Intra | 0,1   | 1    | 3  | 7539  |
| WARS     | 5UJJ      | Structure | 25.75 | Intra | 1,0   | 0.99 | 3  | 17775 |
| RPS3     | 1WH9      | Structure | 26.33 | Intra | 2,1   | 1    | 6  | 27865 |
| RPS3     | 1WH9      | Structure | 20.94 | Intra | 1,0   | 1    | 6  | 16157 |
| RPS3     | P23396    | Phyre     | 34.69 | Intra | 1,0   | 1    | 6  | 23312 |
| RPS3     | 1WH9      | Structure | 18.87 | Intra | 7,2   | 1    | 6  | 27033 |
| RPS3     | P23396    | Phyre     | 38.97 | Intra | 1,0   | 1    | 6  | 18875 |
| RPS3     | P23396    | Phyre     | 22.44 | Intra | 3,4   | 1    | 6  | 30508 |
| RPS3     | P23396    | Phyre     | ####  |       | 2 0,1 | 0.98 | 2  | 10597 |
| FAU      | 5FLX      | Structure | ####  |       | 2 0,2 | 1    | 2  | 14728 |
| RPS3     | P23396    | Phyre     | ####  |       | 1 1,0 | 0.89 | 2  | 19476 |
| RPS3     | P23396    | Phyre     | ####  |       | 1 4,1 | 1    | 2  | 18722 |
| CFL1     | 5L6W      | Structure | 19.28 | Intra | 1,0   | 0.93 | 3  | 11897 |
| CFL1     | 5L6W      | Structure | 12.36 | Intra | 2,0   | 1    | 3  | 16489 |
| CFL1     | 5L6W      | Structure | 8.44  | Intra | 3,0   | 1    | 3  | 14141 |
| VAMP1    | P23763    | Phyre     | 16.44 | Intra | 3,1   | 1    | 1  | 19821 |
| EEF1B2   | P24534    | Phyre     | 7.28  | Intra | 4,0   | 1    | 2  | 10547 |
| EEF1B2   | P24534    | Phyre     | 10.68 | Intra | 1,0   | 0.97 | 2  | 11912 |
| EEF1B2   | P24534    | Phyre     | ####  |       | 1 0,1 | 0.8  | 1  | 10121 |
| ATP5A1   | P25705    | Phyre     | ####  |       | 1 2,1 | 1    | 2  | 15639 |
| ATP5A1   | P25705    | Phyre     | ####  |       | 1 2,1 | 0.94 | 2  | 6945  |
| ACAT1    | 2IB8      | Structure | 16.94 | Intra | 1,1   | 1    | 5  | 38472 |
| ACAT1    | 2IB8      | Structure | 4.21  |       | 1 3,2 | 1    | 5  | 33010 |
| ACAT1    | 2IB8      | Structure | 27.53 | Intra | 2,0   | 1    | 5  | 26330 |
| ACAT1    | 2IB8      | Structure | 9.99  | Intra | 2,0   | 1    | 5  | 18630 |
| ACAT1    | 2IB8      | Structure | 34.59 | Intra | 0,1   | 1    | 5  | 13375 |
| MCM3     | P25205    | Phyre     | 22.47 | Intra | 1,1   | 1    | 1  | 25454 |
| HIST1H4A | P62805    | Phyre     | ####  |       | 2 0,1 | 0.83 | 1  | 4602  |
| ATP5A1   | P25705    | Phyre     | 8.95  | Intra | 1,1   | 1    | 5  | 12025 |
| ATP5A1   | P25705    | Phyre     | 17.47 | Intra | 2,0   | 1    | 5  | 7968  |
| ATP5A1   | P25705_P2 | Docking   | 12.39 |       | 1 1,1 | 1    | 5  | 4697  |
| ATP5A1   | P25705    | Phyre     | 20.23 | Intra | 1,0   | 1    | 5  | 18432 |
| ATP5A1   | P25705    | Phyre     | 14.77 | Intra | 2,1   | 1    | 5  | 28067 |
| PSMA1    | ####      | ####      |       |       | 1 2,1 | 0.91 | 1  | 8087  |
| PSMA2    | 5LE5      | Structure | 91.8  |       | 1 0,4 | 1    | 1  | 11018 |
| PSMA2    | 5LE5      | Structure | 86.32 |       | 1 2,1 | 1    | 2  | 31081 |

|        |           |           |             |       |      |   |       |
|--------|-----------|-----------|-------------|-------|------|---|-------|
| PSMA2  | 5LE5      | Structure | 86.32       | 1 1,2 | 1    | 2 | 29455 |
| MSN    | P26038    | Phyre     | 12.4 Intra  | 0,1   | 1    | 4 | 6874  |
| MSN    | 1E5W      | Structure | 22.25 Intra | 1,0   | 1    | 4 | 30776 |
| MSN    | 1E5W      | Structure | 21.4 Intra  | 1,0   | 1    | 4 | 31483 |
| MSN    | 1E5W      | Structure | 18.18 Intra | 1,0   | 1    | 4 | 37746 |
| RPL13  | P26373    | Phyre     | 26.09 Intra | 0,2   | 1    | 8 | 3951  |
| RPL13  | P26373    | Phyre     | 20.61 Intra | 4,2   | 1    | 8 | 19228 |
| RPL13  | P26373    | Phyre     | 20.45 Intra | 0,2   | 1    | 8 | 4917  |
| RPL13  | P26373    | Phyre     | 8.61 Intra  | 3,2   | 1    | 8 | 20732 |
| RPL13  | P26373    | Phyre     | 62.83 Intra | 1,0   | 1    | 8 | 19263 |
| RPL13  | P26373    | Phyre     | 14.29 Intra | 2,0   | 1    | 8 | 21679 |
| RPL13  | P26373    | Phyre     | 28.17 Intra | 2,1   | 1    | 8 | 21556 |
| RPL13  | P26373    | Phyre     | 26.71 Intra | 1,1   | 1    | 8 | 18132 |
| RPL13  | P26373    | Phyre     | ####        | 2 5,0 | 0.93 | 1 | 17290 |
| IVD    | 1IVH      | Structure | 15.98 Intra | 1,0   | 0.97 | 1 | 16042 |
| S100A4 | 3C1V      | Structure | 12.75 Intra | 1,0   | 1    | 4 | 25374 |
| S100A4 | 3C1V      | Structure | 14.33 Intra | 3,1   | 1    | 4 | 30108 |
| S100A4 | 3C1V      | Structure | 10.79 Intra | 0,1   | 0.84 | 4 | 9697  |
| S100A4 | 3C1V      | Structure | 11.93 Intra | 2,0   | 1    | 4 | 30660 |
| PTBP1  | P26599    | Unknown   | 13.09 Intra | 1,0   | 1    | 8 | 31546 |
| PTBP1  | 3ZZY      | Structure | 17.77 Intra | 3,1   | 1    | 8 | 32377 |
| PTBP1  | ####      | ####      | Intra       | 1,0   | 1    | 8 | 16763 |
| PTBP1  | 3ZZY      | Structure | 19.31 Intra | 3,3   | 1    | 8 | 29279 |
| PTBP1  | ####      | ####      | Intra       | 5,4   | 1    | 8 | 18885 |
| PTBP1  | ####      | ####      | Intra       | 3,1   | 1    | 8 | 16870 |
| PTBP1  | 3ZZY      | Structure | 20.91 Intra | 2,1   | 1    | 8 | 22657 |
| PTBP1  | 3ZZY      | Structure | 13.32 Intra | 0,3   | 1    | 8 | 10553 |
| PTBP1  | 3ZZY      | Structure | ####        | 2 2,0 | 0.89 | 1 | 28216 |
| TARS   | P26639    | Phyre     | 39.45 Intra | 1,0   | 1    | 2 | 14560 |
| TARS   | P26639    | Phyre     | 28.44 Intra | 5,4   | 1    | 2 | 15344 |
| EEF1G  | ####      | ####      | Intra       | 2,1   | 1    | 4 | 2804  |
| EEF1G  | ####      | ####      | Intra       | 1,0   | 0.97 | 4 | 8991  |
| EEF1G  | ####      | ####      | Intra       | 1,0   | 1    | 4 | 17620 |
| EEF1G  | 5JPO      | Structure | 43.61 Intra | 1,0   | 1    | 4 | 26585 |
| FKBP2  | ####      | ####      | Intra       | 1,0   | 0.99 | 1 | 22662 |
| RPL10  | 2PA2      | Structure | 19.23 Intra | 2,0   | 1    | 8 | 15744 |
| RPL10  | P27635    | Phyre     | 8.37 Intra  | 2,1   | 1    | 8 | 16348 |
| RPL10  | P27635    | Phyre     | 8.37 Intra  | 5,3   | 1    | 8 | 14956 |
| RPL10  | P27635    | Phyre     | 44.62 Intra | 1,0   | 1    | 8 | 17488 |
| RPL10  | P27635_P2 | Docking   | 65.64 N/A   | 1,0   | 1    | 8 | 40493 |
| RPL10  | P27635    | Phyre     | 12.44 Intra | 1,1   | 1    | 8 | 21059 |
| RPL10  | P27635    | Phyre     | 17.7 Intra  | 1,0   | 1    | 8 | 14031 |
| RPL10  | P27635    | Phyre     | 11.89 Intra | 3,0   | 1    | 8 | 25711 |
| CALR   | 3POW      | Structure | 19.91 Intra | 1,0   | 1    | 4 | 10707 |
| CALR   | P27797    | Phyre     | 21.66 Intra | 4,2   | 1    | 4 | 15066 |
| CALR   | 3POW      | Structure | 29.32 Intra | 2,0   | 1    | 4 | 16936 |
| CALR   | 3POW      | Structure | 26.82 Intra | 3,0   | 1    | 4 | 13811 |

|        |        |           |       |       |       |      |    |       |
|--------|--------|-----------|-------|-------|-------|------|----|-------|
| CANX   | P27824 | Phyre     | 13.84 | Intra | 0,1   | 1    | 3  | 7251  |
| CANX   | P27824 | Phyre     | ####  | Intra | 1,0   | 1    | 3  | 23169 |
| CANX   | P27824 | Phyre     | 17.35 | Intra | 1,0   | 1    | 3  | 31029 |
| PSMB5  | ####   |           | ####  |       | 1 0,1 | 0.98 | 1  | 6721  |
| NDUFS1 | P28331 | Modeller  | ####  |       | 1 1,0 | 0.88 | 1  | 28358 |
| TKT    | 4KXW   | Structure | 52.99 | Intra | 5,0   | 1    | 13 | 13352 |
| TKT    | 4KXW   | Structure | 52.99 | Intra | 1,0   | 1    | 13 | 14237 |
| TKT    | 4KXW   | Structure | 56.9  | Intra | 2,0   | 1    | 13 | 13942 |
| TKT    | 4KXW   | Structure | 15.07 | Intra | 3,0   | 1    | 13 | 18213 |
| TKT    | 4KXW   | Structure | 15.07 | Intra | 0,1   | 1    | 13 | 9410  |
| TKT    | 4KXW   | Structure | 13.72 | Intra | 1,0   | 1    | 13 | 18466 |
| TKT    | 4KXW   | Structure | 14.03 | Intra | 1,0   | 1    | 13 | 8216  |
| TKT    | 4KXW   | Structure | 23.2  | Intra | 3,2   | 1    | 13 | 24774 |
| TKT    | 4KXW   | Structure | 19.75 | Intra | 4,2   | 1    | 13 | 16187 |
| TKT    | 4KXW   | Structure | 10.57 | Intra | 2,1   | 1    | 13 | 13107 |
| TKT    | 4KXW   | Structure | 18.35 | Intra | 2,1   | 1    | 13 | 15999 |
| TKT    | 4KXW   | Structure | 16.68 | Intra | 2,1   | 1    | 13 | 16649 |
| TKT    | 4KXW   | Structure | 27.1  | Intra | 4,1   | 1    | 13 | 20955 |
| EEF1D  | ####   |           | ####  | Intra | 1,1   | 1    | 1  | 32701 |
| ERP29  | 2QC7   | Structure | 7.11  | Intra | 1,0   | 1    | 2  | 20865 |
| ERP29  | 2QC7   | Structure | 22.33 | Intra | 0,1   | 1    | 2  | 13333 |
| PRDX6  | 5B6M   | Structure | 39.89 | Intra | 2,0   | 1    | 3  | 20685 |
| PRDX6  | 5B6M   | Structure | 19.21 | Intra | 1,0   | 1    | 3  | 28419 |
| PRDX6  | 5B6M   | Structure | 35.55 | Intra | 1,0   | 0.99 | 3  | 19560 |
| PRDX5  | ####   |           | ####  | N/A   | 0,1   | 0.99 | 1  | 1867  |
| RPL12  | 5A8L   | Structure | 9.55  | Intra | 3,0   | 1    | 2  | 15918 |
| RPL12  | 5A8L   | Structure | 13.7  | Intra | 2,0   | 1    | 2  | 21545 |
| ECHS1  | P30084 | Phyre     | 46.01 | Intra | 0,1   | 1    | 2  | 10741 |
| ECHS1  | P30084 | Phyre     | 40.49 | Intra | 0,1   | 1    | 2  | 9905  |
| PEBP1  | 1BEH   | Structure | 9.93  | Intra | 1,0   | 1    | 1  | 31021 |
| PDIA3  | 3F8U   | Structure | 21.46 | Intra | 2,1   | 1    | 7  | 14073 |
| PDIA3  | 3F8U   | Structure | 23.29 | Intra | 1,0   | 1    | 7  | 13772 |
| PDIA3  | 3F8U   | Structure | 12.66 | Intra | 1,2   | 1    | 7  | 20915 |
| PDIA3  | 3F8U   | Structure | 45.59 | Intra | 2,0   | 1    | 7  | 23224 |
| PDIA3  | 3F8U   | Structure | 14.32 | Intra | 3,0   | 1    | 7  | 17755 |
| PDIA3  | 3F8U   | Structure | 24.78 | Intra | 1,3   | 1    | 7  | 20319 |
| PDIA3  | 3F8U   | Structure | 23.79 | Intra | 2,0   | 1    | 7  | 13770 |
| PPIF   | 4O8H   | Structure | 21.39 | Intra | 2,2   | 1    | 1  | 18677 |
| PPIF   | 4O8H   | Structure | ####  |       | 1 4,0 | 1    | 1  | 15843 |
| SRI    | 1JUO   | Structure | 15.31 | Intra | 3,0   | 1    | 1  | 30265 |
| SDHA   | P31040 | Modeller  | 10.92 | Intra | 1,0   | 1    | 1  | 16959 |
| SDHA   | P31040 | Modeller  | ####  |       | 2 0,2 | 1    | 1  | 7386  |
| MAT2A  | 5A1I   | Structure | 10.41 | Intra | 3,1   | 1    | 5  | 15005 |
| MAT2A  | 5A1I   | Structure | 20.53 | Intra | 1,1   | 1    | 5  | 13943 |
| MAT2A  | 5A1I   | Structure | 22.82 | Intra | 3,1   | 1    | 5  | 12354 |
| MAT2A  | 5A1I   | Structure | 18.87 | Intra | 2,0   | 1    | 5  | 17022 |
| MAT2A  | 5A1I   | Structure | 26.03 | Intra | 1,0   | 0.94 | 5  | 22362 |

|       |        |           |        |       |       |      |    |       |
|-------|--------|-----------|--------|-------|-------|------|----|-------|
| CPS1  | 5DOT   | Structure | 19.24  | Intra | 1,0   | 1    | 30 | 18570 |
| CPS1  | 5DOT   | Structure | 18.39  | Intra | 2,1   | 1    | 30 | 25039 |
| CPS1  | 5DOT   | Structure | 18.39  | Intra | 4,1   | 1    | 30 | 23503 |
| CPS1  | 5DOT   | Structure | 18.07  | Intra | 2,3   | 1    | 30 | 36259 |
| CPS1  | 5DOT   | Structure | 159.09 |       | 1 1,0 | 0.99 | 30 | 31762 |
| CPS1  | 5DOT   | Structure | 9.81   | Intra | 0,2   | 1    | 30 | 11616 |
| CPS1  | 5DOT   | Structure | 20.31  | Intra | 0,1   | 1    | 30 | 14111 |
| CPS1  | 5DOT   | Structure | 20.31  | Intra | 0,1   | 1    | 30 | 13929 |
| CPS1  | 5DOT   | Structure | 31.28  | Intra | 0,1   | 1    | 30 | 14432 |
| CPS1  | 5DOT   | Structure | 20.78  | Intra | 3,2   | 1    | 30 | 27868 |
| CPS1  | 5DOT   | Structure | 20.78  | Intra | 0,1   | 1    | 30 | 14203 |
| CPS1  | 5DOT   | Structure | 25.4   | Intra | 0,1   | 1    | 30 | 13917 |
| CPS1  | 5DOT   | Structure | 12.21  | Intra | 1,0   | 1    | 30 | 33389 |
| CPS1  | P31327 | Phyre     | 26.82  | Intra | 2,0   | 1    | 30 | 34652 |
| CPS1  | 5DOT   | Structure | 20.11  | Intra | 1,2   | 1    | 30 | 20659 |
| CPS1  | 5DOT   | Structure | 20.11  | Intra | 4,1   | 1    | 30 | 18681 |
| CPS1  | 5DOT   | Structure | 18.63  | Intra | 3,2   | 1    | 30 | 22120 |
| CPS1  | 5DOT   | Structure | 18.63  | Intra | 9,1   | 1    | 30 | 20362 |
| CPS1  | 5DOT   | Structure | 18.76  | Intra | 1,1   | 1    | 30 | 27374 |
| CPS1  | 5DOT   | Structure | 25.44  | Intra | 1,0   | 1    | 30 | 13944 |
| CPS1  | 5DOT   | Structure | 15.19  | Intra | 4,2   | 1    | 30 | 24439 |
| CPS1  | 5DOT   | Structure | 15.19  | Intra | 2,1   | 1    | 30 | 23118 |
| CPS1  | 5DOT   | Structure | 47.58  | Intra | 1,0   | 1    | 30 | 31244 |
| CPS1  | 5DOT   | Structure | 21.76  | Intra | 2,0   | 1    | 30 | 22755 |
| CPS1  | 5DOT   | Structure | 26.75  | Intra | 2,2   | 1    | 30 | 32771 |
| CPS1  | 5DOT   | Structure | 26.75  | Intra | 1,0   | 1    | 30 | 31432 |
| CPS1  | 5DOT   | Structure | 17.65  | Intra | 1,2   | 1    | 30 | 23373 |
| CPS1  | 5DOT   | Structure | 7.91   | Intra | 1,0   | 1    | 30 | 19548 |
| CPS1  | 5DOT   | Structure | 26.64  | Intra | 0,2   | 1    | 30 | 13579 |
| CPS1  | 5DOT   | Structure | 9.19   | Intra | 1,0   | 1    | 30 | 30487 |
| YWHAB | 5N10   | Structure | 9.64   | Intra | 2,0   | 1    | 3  | 12599 |
| YWHAB | 5N10   | Structure | 9.64   | Intra | 2,1   | 1    | 3  | 6482  |
| YWHAB | 5N10   | Structure | 28.14  | Intra | 7,0   | 1    | 3  | 24955 |
| STIP1 | P31948 | Phyre     | 10.61  | Intra | 1,3   | 1    | 7  | 24161 |
| STIP1 | P31948 | Phyre     | 13.79  | Intra | 3,0   | 1    | 7  | 21331 |
| STIP1 | P31948 | Phyre     | 23.13  | Intra | 1,4   | 1    | 7  | 27254 |
| STIP1 | P31948 | Phyre     | 10.35  | Intra | 1,0   | 1    | 7  | 21479 |
| STIP1 | P31948 | Phyre     | 15.71  | Intra | 1,0   | 1    | 7  | 19654 |
| STIP1 | 1ELR   | Structure | 27.58  | Intra | 1,0   | 1    | 7  | 12966 |
| STIP1 | P31948 | Phyre     | 16.18  | Intra | 5,3   | 1    | 7  | 15396 |
| STIP1 | P31948 | Phyre     | ####   |       | 2 2,1 | 0.89 | 1  | 11301 |
| L1CAM | ####   |           | ####   | N/A   | 2,0   | 1    | 7  | 21536 |
| L1CAM | P32004 | Phyre     | ####   | Intra | 4,1   | 1    | 7  | 20460 |
| L1CAM | ####   |           | ####   | N/A   | 0,1   | 1    | 7  | 10453 |
| L1CAM | P32004 | Phyre     | 16.1   | Intra | 1,1   | 1    | 7  | 20675 |
| L1CAM | P32004 | Phyre     | 9.18   | Intra | 1,1   | 1    | 7  | 17569 |
| L1CAM | P32004 | Phyre     | 32.49  | Intra | 3,1   | 1    | 7  | 23962 |

|        |           |           |       |       |       |      |    |       |
|--------|-----------|-----------|-------|-------|-------|------|----|-------|
| L1CAM  | P32004    | Phyre     | 61.98 | Intra | 7,4   | 1    | 7  | 28708 |
| PRDX2  | 5IJT      | Structure | 17.63 | Intra | 1,0   | 1    | 6  | 17289 |
| PRDX2  | 5IJT      | Structure | 9.85  | Intra | 1,0   | 1    | 6  | 25343 |
| PRDX2  | 5IJT      | Structure | 18.45 | Intra | 2,0   | 1    | 6  | 21099 |
| PRDX2  | 5IJT      | Structure | 17.62 |       | 1 1,0 | 1    | 6  | 40047 |
| PRDX2  | 5IJT      | Structure | 6.35  | Intra | 2,0   | 1    | 6  | 24582 |
| PRDX2  | 5IJT      | Structure | 14.54 | Intra | 2,1   | 1    | 6  | 14991 |
| PRDX1  | 4XCS      | Structure | ####  |       | 1 2,0 | 0.98 | 3  | 18636 |
| PRDX1  | 4XCS      | Structure | ####  |       | 1 1,0 | 0.98 | 3  | 24692 |
| PRDX2  | 5IJT      | Structure | ####  |       | 1 2,0 | 1    | 3  | 34558 |
| CDA    | 1MQ0      | Structure | 40.9  |       | 1 1,0 | 1    | 1  | 27217 |
| RPL9   | P32969    | Phyre     | 48.51 | Intra | 2,0   | 1    | 5  | 19696 |
| RPL9   | 2CQL      | Structure | 26.14 | Intra | 2,0   | 1    | 5  | 23614 |
| RPL9   | 2CQL      | Structure | 11.93 | Intra | 2,2   | 1    | 5  | 18138 |
| RPL9   | P32969    | Phyre     | 20.76 | Intra | 1,0   | 1    | 5  | 24940 |
| RPL9   | 2CQL      | Structure | 14.15 | Intra | 1,0   | 1    | 5  | 23731 |
| RPL13A | P40429    | Phyre     | ####  |       | 1 1,0 | 0.98 | 1  | 17508 |
| RPL9   | P32969    | Phyre     | ####  |       | 2 4,0 | 0.81 | 1  | 18089 |
| KIF5B  | ####      | ####      |       |       | 1 1,0 | 0.69 | 3  | 17259 |
| KIF5B  | ####      | ####      |       | Intra | 1,0   | 1    | 3  | 18887 |
| KIF5B  | ####      | ####      |       | Intra | 0,2   | 1    | 3  | 3561  |
| DUT    | 3ARA      | Structure | 22.27 | Intra | 2,1   | 1    | 2  | 28072 |
| DUT    | ####      | ####      |       | Intra | 1,2   | 1    | 2  | 9395  |
| MCM4   | P33991    | Phyre     | ####  | Intra | 2,1   | 1    | 4  | 32781 |
| MCM4   | P33991    | Phyre     | 8.22  | Intra | 2,0   | 1    | 4  | 21505 |
| MCM4   | P33991    | Phyre     | 17.38 | Intra | 1,0   | 1    | 4  | 14940 |
| MCM4   | P33991_P3 | Docking   | 22.77 |       | 1 1,1 | 1    | 4  | 29598 |
| MCM4   | P33991    | Phyre     | ####  |       | 1 1,0 | 0.83 | 2  | 23534 |
| MCM4   | P33991    | Phyre     | ####  |       | 1 1,0 | 0.98 | 2  | 21296 |
| SHMT2  | P34897    | Modeller  | 19.36 | Intra | 0,1   | 1    | 11 | 6591  |
| SHMT2  | P34897    | Modeller  | 31.07 | Intra | 6,3   | 1    | 11 | 21213 |
| SHMT2  | P34897_P3 | Docking   | 20.47 |       | 1 3,5 | 1    | 11 | 30732 |
| SHMT2  | P34897    | Modeller  | 20.62 | Intra | 2,0   | 1    | 11 | 29876 |
| SHMT2  | P34897    | Modeller  | 20.76 | Intra | 1,0   | 1    | 11 | 23585 |
| SHMT2  | P34897    | Modeller  | 15.4  | Intra | 1,0   | 1    | 11 | 20119 |
| SHMT2  | P34897    | Modeller  | 51.05 | Intra | 1,2   | 1    | 11 | 15034 |
| SHMT2  | P34897    | Modeller  | 53.72 | Intra | 2,0   | 1    | 11 | 31207 |
| SHMT2  | P34897    | Modeller  | 44.69 | Intra | 1,0   | 1    | 11 | 24078 |
| SHMT2  | P34897    | Modeller  | 38.1  | Intra | 3,2   | 1    | 11 | 17612 |
| SHMT2  | P34897    | Modeller  | 32.43 | Intra | 4,0   | 1    | 11 | 20920 |
| HSPA4  | P34932    | Phyre     | 16.33 | Intra | 1,1   | 1    | 1  | 19317 |
| GPC1   | 4AD7      | Structure | 15.75 | Intra | 2,1   | 1    | 2  | 22649 |
| GPC1   | 4AD7      | Structure | 16.35 | Intra | 0,1   | 1    | 2  | 12805 |
| PHB    | P35232_P3 | Docking   | 77.51 | N/A   | 4,2   | 1    | 3  | 16290 |
| PHB    | P35232    | Phyre     | ####  | Intra | 1,1   | 1    | 3  | 14572 |
| PHB    | P35232    | Phyre     | 11.49 | Intra | 1,1   | 1    | 3  | 33740 |
| PHB    | P35232    | Phyre     | ####  |       | 1 0,1 | 1    | 8  | 17538 |

|       |        |           |             |       |      |    |       |
|-------|--------|-----------|-------------|-------|------|----|-------|
| PHB   | P35232 | Phyre     | ####        | 1 1,0 | 1    | 8  | 11188 |
| PHB   | P35232 | Phyre     | ####        | 1 1,2 | 1    | 8  | 18256 |
| PHB   | P35232 | Phyre     | ####        | 1 1,0 | 1    | 8  | 16387 |
| PHB2  | ####   |           | ####        | 1 5,4 | 1    | 8  | 15737 |
| PHB2  | ####   |           | ####        | 1 3,2 | 1    | 8  | 14361 |
| PHB   | P35232 | Phyre     | ####        | 1 2,3 | 1    | 8  | 31052 |
| PHB   | P35232 | Phyre     | ####        | 1 2,1 | 1    | 8  | 34935 |
| RFC2  | P35250 | Phyre     | 20.03 Intra | 2,0   | 1    | 2  | 25700 |
| RFC2  | P35250 | Phyre     | 30.91 Intra | 1,0   | 1    | 2  | 23801 |
| AGL   | P35573 | Phyre     | #### Intra  | 1,0   | 0.97 | 1  | 26190 |
| MYH9  | P35579 | Phyre     | 6.4 Intra   | 2,2   | 1    | 15 | 14863 |
| MYH9  | ####   |           | #### Intra  | 1,0   | 1    | 15 | 17925 |
| MYH9  | P35579 | Phyre     | 21.34 Intra | 1,0   | 1    | 15 | 23698 |
| MYH9  | P35579 | Phyre     | 10.13 Intra | 3,0   | 1    | 15 | 18332 |
| MYH9  | ####   |           | #### Intra  | 2,2   | 1    | 15 | 31807 |
| MYH9  | ####   |           | #### Intra  | 2,3   | 1    | 15 | 19388 |
| MYH9  | ####   |           | #### Intra  | 0,1   | 1    | 15 | 9377  |
| MYH9  | ####   |           | #### Intra  | 0,1   | 1    | 15 | 5599  |
| MYH9  | ####   |           | #### Intra  | 1,0   | 1    | 15 | 17558 |
| MYH9  | P35579 | Phyre     | 13.64 Intra | 0,1   | 1    | 15 | 12820 |
| MYH9  | P35579 | Phyre     | 13.64 Intra | 1,0   | 1    | 15 | 31820 |
| MYH9  | P35579 | Phyre     | 18.54 Intra | 2,0   | 1    | 15 | 32483 |
| MYH9  | ####   |           | #### Intra  | 1,0   | 1    | 15 | 10890 |
| MYH9  | ####   |           | #### Intra  | 3,0   | 1    | 15 | 17568 |
| MYH9  | ####   |           | #### Intra  | 2,0   | 1    | 15 | 17782 |
| MYH10 | 4PD3   | Structure | 25.37 Intra | 1,1   | 1    | 1  | 22932 |
| BSG   | 4U0Q   | Structure | 37.95 Intra | 0,1   | 1    | 8  | 10640 |
| BSG   | 4U0Q   | Structure | 32.53 Intra | 5,0   | 1    | 8  | 29374 |
| BSG   | 4U0Q   | Structure | 32.53 Intra | 5,0   | 1    | 8  | 27982 |
| BSG   | 4U0Q   | Structure | 35.34 Intra | 0,4   | 1    | 8  | 6105  |
| BSG   | 4U0Q   | Structure | 5.68 Intra  | 0,3   | 1    | 8  | 9905  |
| BSG   | 4U0Q   | Structure | 5.68 Intra  | 0,3   | 1    | 8  | 9211  |
| BSG   | 4U0Q   | Structure | 23.97 Intra | 0,2   | 1    | 8  | 6919  |
| BSG   | 4U0Q   | Structure | 25.83 Intra | 0,1   | 1    | 8  | 11061 |
| FUS   | ####   |           | #### Intra  | 1,0   | 1    | 4  | 21527 |
| FUS   | ####   |           | #### Intra  | 1,0   | 1    | 4  | 20261 |
| FUS   | ####   |           | #### Intra  | 2,0   | 1    | 4  | 21165 |
| FUS   | ####   |           | #### Intra  | 0,1   | 1    | 4  | 11160 |
| ATP5E | P56381 | Phyre     | ####        | 1 1,0 | 0.89 | 1  | 8773  |
| RPL4  | P36578 | Phyre     | 9.97 Intra  | 7,4   | 1    | 9  | 20850 |
| RPL4  | P36578 | Phyre     | 14.8 Intra  | 1,0   | 1    | 9  | 21880 |
| RPL4  | P36578 | Phyre     | 13.82 Intra | 1,0   | 1    | 9  | 19109 |
| RPL4  | P36578 | Phyre     | 14.56 Intra | 2,0   | 1    | 9  | 28214 |
| RPL4  | P36578 | Phyre     | 10.41 Intra | 2,0   | 1    | 9  | 10729 |
| RPL4  | P36578 | Phyre     | 20.34 Intra | 2,1   | 1    | 9  | 16578 |
| RPL4  | P36578 | Phyre     | 13.34 Intra | 4,1   | 1    | 9  | 18616 |
| RPL4  | P36578 | Phyre     | 29.15 Intra | 4,0   | 1    | 9  | 15907 |

|        |           |           |        |       |       |      |    |       |
|--------|-----------|-----------|--------|-------|-------|------|----|-------|
| RPL4   | P36578    | Phyre     | 29.15  | Intra | 6,0   | 1    | 9  | 14435 |
| RPL28  | ####      |           | ####   |       | 1 1,0 | 0.98 | 1  | 15551 |
| RPL18  | Q07020    | Modeller  | ####   |       | 1 1,0 | 0.94 | 4  | 24126 |
| RPL18  | Q07020    | Modeller  | ####   |       | 1 4,0 | 1    | 4  | 22418 |
| RPL18  | Q07020    | Modeller  | ####   |       | 1 1,0 | 0.98 | 4  | 13911 |
| RPL4   | P36578    | Phyre     | ####   |       | 1 4,2 | 1    | 4  | 19380 |
| LONP1  | P36776    | Phyre     | 38.92  | Intra | 1,0   | 1    | 9  | 30861 |
| LONP1  | P36776    | Phyre     | 27.76  | Intra | 1,0   | 1    | 9  | 31465 |
| LONP1  | ####      |           | ####   | Intra | 2,2   | 1    | 9  | 23170 |
| LONP1  | ####      |           | ####   | Intra | 1,1   | 1    | 9  | 35227 |
| LONP1  | ####      |           | ####   |       | 1 1,0 | 1    | 9  | 22241 |
| LONP1  | ####      |           | ####   | Intra | 1,0   | 1    | 9  | 20435 |
| LONP1  | ####      |           | ####   | Intra | 1,0   | 1    | 9  | 22270 |
| LONP1  | ####      |           | ####   | Intra | 0,1   | 1    | 9  | 18777 |
| LONP1  | P36776    | Phyre     | 12.82  | Intra | 1,0   | 1    | 9  | 30712 |
| PGM1   | 5JN5      | Structure | 13.9   | Intra | 0,1   | 0.85 | 1  | 15437 |
| TGFBR1 | 1B6C      | Structure | 11.95  | Intra | 1,0   | 0.99 | 1  | 18357 |
| LTBR   | ####      |           | ####   | Intra | 1,0   | 0.86 | 1  | 8863  |
| SRP14  | P37108    | Unknown   | 14.34  | Intra | 4,2   | 1    | 2  | 17951 |
| SRP14  | P37108    | Unknown   | 4.73   | Intra | 1,0   | 0.99 | 2  | 17408 |
| TALDO1 | 1F05      | Structure | 35.84  | Intra | 0,1   | 1    | 2  | 11518 |
| TALDO1 | 1F05      | Structure | 17.91  | Intra | 1,0   | 0.99 | 2  | 18910 |
| ETFB   | 1EFV      | Structure | 10.31  | Intra | 1,0   | 1    | 2  | 25420 |
| ETFB   | 1EFV      | Structure | 9.77   | Intra | 1,0   | 0.97 | 2  | 22587 |
| RBMX   | ####      |           | ####   | Intra | 1,0   | 1    | 2  | 10205 |
| RBMX   | 2MB0      | Structure | 15.96  | Intra | 4,1   | 1    | 2  | 24348 |
| HSPA9  | P38646_P3 | Docking   | 109.37 |       | 1 1,1 | 1    | 14 | 5879  |
| HSPA9  | P38646    | Phyre     | 16.62  | Intra | 1,1   | 1    | 14 | 15729 |
| HSPA9  | P38646    | Phyre     | 18.32  | Intra | 1,2   | 1    | 14 | 9557  |
| HSPA9  | 4KBO      | Structure | 13     | Intra | 1,0   | 1    | 14 | 16898 |
| HSPA9  | 4KBO      | Structure | 20.01  | Intra | 2,0   | 1    | 14 | 23702 |
| HSPA9  | P38646    | Phyre     | 22.07  | Intra | 1,0   | 1    | 14 | 10262 |
| HSPA9  | P38646    | Phyre     | 22.07  | Intra | 1,2   | 1    | 14 | 8421  |
| HSPA9  | P38646    | Phyre     | 22.2   | Intra | 0,2   | 1    | 14 | 4401  |
| HSPA9  | 4KBO      | Structure | 17.02  | Intra | 2,0   | 1    | 14 | 17179 |
| HSPA9  | 4KBO      | Structure | 18.93  | Intra | 2,2   | 1    | 14 | 33294 |
| HSPA9  | 4KBO      | Structure | 18.93  | Intra | 0,2   | 1    | 14 | 12242 |
| HSPA9  | 4KBO      | Structure | 21.02  | Intra | 2,0   | 1    | 14 | 25723 |
| HSPA9  | 4KBO      | Structure | 13.33  | Intra | 1,0   | 1    | 14 | 26577 |
| HSPA9  | 4KBO      | Structure | 27.83  | Intra | 7,5   | 1    | 14 | 27837 |
| EIF4A3 | 4C9B      | Structure | 10.68  | Intra | 1,0   | 1    | 2  | 18350 |
| EIF4A3 | 4C9B      | Structure | 30.24  | Intra | 1,0   | 1    | 2  | 24261 |
| PNN    | ####      |           | ####   |       | 1 1,0 | 0.81 | 1  | 16458 |
| RPS19  | 5FLX      | Structure | 9.68   | Intra | 0,1   | 1    | 1  | 5769  |
| RPS16  | P62249    | Phyre     | ####   |       | 1 1,0 | 1    | 1  | 23938 |
| RPS19  | P39019    | Phyre     | ####   |       | 1 2,0 | 0.99 | 1  | 16382 |
| RPL3   | P39023    | Phyre     | 12.89  | Intra | 1,0   | 1    | 5  | 18694 |

|        |           |           |       |       |       |      |    |       |
|--------|-----------|-----------|-------|-------|-------|------|----|-------|
| RPL3   | P39023    | Phyre     | 20.33 | Intra | 3,0   | 1    | 5  | 20583 |
| RPL3   | P39023    | Phyre     | 15.12 | Intra | 2,2   | 1    | 5  | 21951 |
| RPL3   | P39023    | Phyre     | 10.46 | Intra | 1,0   | 1    | 5  | 17008 |
| RPL3   | P39023    | Phyre     | 19.76 | Intra | 2,0   | 1    | 5  | 22721 |
| RPL3   | P39023    | Phyre     | ####  |       | 2 2,0 | 0.98 | 1  | 22108 |
| CAPG   | 1J72      | Structure | 53.68 | Intra | 1,0   | 0.97 | 1  | 14292 |
| IL6ST  | 3L5H      | Structure | 6.88  | Intra | 1,0   | 1    | 2  | 18282 |
| IL6ST  | 3L5H      | Structure | 6.88  | Intra | 1,0   | 1    | 2  | 18878 |
| TXLNA  | ####      |           | ####  | Intra | 1,1   | 1    | 1  | 8730  |
| CCT6A  | P40227    | Phyre     | 18.88 | Intra | 1,0   | 0.99 | 3  | 30729 |
| CCT6A  | P40227    | Phyre     | 22.57 | Intra | 0,1   | 1    | 3  | 8725  |
| CCT6A  | P40227    | Phyre     | 33.4  | Intra | 1,0   | 1    | 3  | 30141 |
| CCT8   | P50990    | Phyre     | ####  |       | 1 4,0 | 1    | 2  | 20838 |
| CCT8   | P50990    | Phyre     | ####  |       | 1 2,2 | 1    | 2  | 24384 |
| RPL13A | P40429    | Phyre     | 27.69 | Intra | 1,0   | 1    | 5  | 26343 |
| RPL13A | P40429    | Phyre     | 10.94 | Intra | 2,0   | 1    | 5  | 24208 |
| RPL13A | P40429    | Phyre     | 10.56 | Intra | 2,0   | 1    | 5  | 24429 |
| RPL13A | P40429    | Phyre     | 8.33  | Intra | 2,1   | 1    | 5  | 22624 |
| RPL13A | P40429    | Phyre     | 19.34 | Intra | 1,0   | 1    | 5  | 29573 |
| MDH1   | P40925    | Phyre     | 5.2   | Intra | 3,0   | 1    | 2  | 13417 |
| MDH1   | P40925    | Phyre     | 5.2   | Intra | 2,0   | 1    | 2  | 11564 |
| MDH2   | 2DFD      | Structure | 28.26 | Intra | 2,0   | 1    | 13 | 29247 |
| MDH2   | 2DFD      | Structure | 38.35 | Intra | 1,0   | 1    | 13 | 31101 |
| MDH2   | 2DFD      | Structure | 11.63 | Intra | 2,1   | 1    | 13 | 34029 |
| MDH2   | 2DFD      | Structure | 25.23 |       | 1 1,0 | 0.97 | 13 | 16172 |
| MDH2   | 2DFD      | Structure | 14.18 | Intra | 2,2   | 1    | 13 | 21930 |
| MDH2   | 2DFD      | Structure | 25.68 | Intra | 1,0   | 1    | 13 | 26810 |
| MDH2   | 2DFD      | Structure | 31.64 | Intra | 3,4   | 1    | 13 | 24481 |
| MDH2   | 2DFD      | Structure | 26.53 | Intra | 4,2   | 1    | 13 | 14305 |
| MDH2   | 2DFD      | Structure | 8.58  | Intra | 2,0   | 1    | 13 | 24599 |
| MDH2   | 2DFD      | Structure | 8.58  | Intra | 1,0   | 1    | 13 | 22247 |
| MDH2   | 2DFD      | Structure | 25.78 | Intra | 1,0   | 1    | 13 | 12314 |
| MDH2   | 2DFD      | Structure | 25.78 | Intra | 1,0   | 1    | 13 | 10221 |
| MDH2   | 2DFD      | Structure | 11.73 | Intra | 3,0   | 1    | 13 | 8170  |
| HADHA  | P40939    | Phyre     | 16.93 | Intra | 2,1   | 1    | 4  | 25507 |
| HADHA  | P40939    | Phyre     | 14.65 | Intra | 1,0   | 1    | 4  | 30485 |
| HADHA  | P40939    | Phyre     | 31    | Intra | 2,1   | 1    | 4  | 33246 |
| HADHA  | P40939_P4 | Docking   | 57.61 |       | 1 1,0 | 1    | 4  | 32079 |
| WNT5A  | P41221    | Phyre     | 28.92 | Intra | 2,0   | 1    | 1  | 16362 |
| IARS   | P41252    | Phyre     | 24.18 | Intra | 0,1   | 1    | 5  | 11534 |
| IARS   | ####      |           | ####  | Intra | 0,1   | 1    | 5  | 17107 |
| IARS   | ####      |           | ####  | Intra | 1,0   | 1    | 5  | 24140 |
| IARS   | P41252    | Phyre     | 10.74 | Intra | 2,1   | 1    | 5  | 13715 |
| IARS   | P41252    | Phyre     | 20.64 | Intra | 2,2   | 1    | 5  | 26740 |
| IARS   | ####      |           | ####  |       | 1 0,1 | 0.98 | 1  | 15147 |
| EIF1   | 4KZY      | Structure | 11.71 | Intra | 2,0   | 1    | 1  | 35033 |
| ECI1   | 1SG4      | Structure | 32.35 | Intra | 2,0   | 1    | 2  | 25649 |



|         |        |           |             |       |      |   |       |
|---------|--------|-----------|-------------|-------|------|---|-------|
| ECI1    | 1SG4   | Structure | 22.14       | 1 0,2 | 1    | 2 | 2603  |
| TMPO    | ####   |           | #### Intra  | 2,0   | 1    | 1 | 25152 |
| LRPPRC  | P42704 | Modeller  | 61.6 Intra  | 0,2   | 1    | 1 | 14719 |
| ACAA2   | 4C2K   | Structure | 16.22 Intra | 1,1   | 1    | 1 | 32026 |
| RPL35   | P42766 | Phyre     | 16.5 Intra  | 3,0   | 1    | 3 | 26317 |
| RPL35   | P42766 | Phyre     | 20.92 Intra | 0,1   | 1    | 3 | 6321  |
| RPL35   | P42766 | Phyre     | 15.47 Intra | 1,0   | 1    | 3 | 24170 |
| ECE1    | ####   |           | #### Intra  | 2,0   | 1    | 1 | 14922 |
| SLC1A3  | P43003 | Phyre     | 34.71 Intra | 0,2   | 1    | 4 | 10835 |
| SLC1A3  | P43003 | Phyre     | 30.35 Intra | 0,1   | 1    | 4 | 13601 |
| SLC1A3  | ####   |           | #### Intra  | 3,1   | 1    | 4 | 9535  |
| SLC1A3  | ####   |           | #### N/A    | 1,0   | 0.75 | 4 | 7650  |
| MCAM    | P43121 | Phyre     | 13.08 Intra | 0,1   | 1    | 5 | 12771 |
| MCAM    | P43121 | Phyre     | 13.08 Intra | 1,1   | 1    | 5 | 36444 |
| MCAM    | P43121 | Phyre     | 13.08 Intra | 1,3   | 1    | 5 | 34945 |
| MCAM    | P43121 | Phyre     | 13.28 Intra | 1,0   | 1    | 5 | 39697 |
| MCAM    | P43121 | Phyre     | 13.28 Intra | 1,0   | 1    | 5 | 38252 |
| MATR3   | ####   |           | #### Intra  | 1,0   | 1    | 2 | 30397 |
| MATR3   | ####   |           | #### Intra  | 0,1   | 1    | 2 | 13256 |
| VDAC2   | P45880 | Phyre     | 19.07 Intra | 2,1   | 1    | 8 | 30670 |
| VDAC2   | P45880 | Phyre     | 12.71 Intra | 2,2   | 1    | 8 | 28264 |
| VDAC2   | P45880 | Phyre     | 35.74 Intra | 1,0   | 1    | 8 | 32665 |
| VDAC2   | P45880 | Phyre     | 28.16 Intra | 2,1   | 1    | 8 | 27418 |
| VDAC2   | P45880 | Phyre     | 23.89 Intra | 2,3   | 1    | 8 | 22508 |
| VDAC2   | P45880 | Phyre     | 31.83 Intra | 1,0   | 1    | 8 | 25346 |
| VDAC2   | P45880 | Phyre     | 28.78 Intra | 0,1   | 0.99 | 8 | 9455  |
| VDAC2   | P45880 | Phyre     | 39.45 Intra | 1,0   | 1    | 8 | 25100 |
| RANGAP1 | P46060 | Modeller  | 10.23 Intra | 1,0   | 1    | 2 | 25277 |
| RANGAP1 | P46060 | Modeller  | 9.14 Intra  | 2,1   | 1    | 2 | 29462 |
| NOP2    | ####   |           | ####        | 1 1,0 | 0.64 | 1 | 29777 |
| RPL5    | P46777 | Phyre     | 23.75 Intra | 1,0   | 1    | 6 | 20457 |
| RPL5    | P46777 | Phyre     | 13.65 Intra | 2,1   | 1    | 6 | 19227 |
| RPL5    | P46777 | Phyre     | 13.65 Intra | 1,0   | 1    | 6 | 16924 |
| RPL5    | P46777 | Phyre     | 13.65 Intra | 0,1   | 1    | 6 | 9304  |
| RPL5    | P46777 | Phyre     | 11.68 Intra | 1,1   | 1    | 6 | 12423 |
| RPL5    | P46777 | Phyre     | 12.18 Intra | 2,1   | 1    | 6 | 15633 |
| RPL21   | P46778 | Phyre     | 5.4 Intra   | 1,0   | 0.99 | 1 | 12645 |
| RPL28   | ####   |           | #### Intra  | 3,0   | 1    | 6 | 16752 |
| RPL28   | ####   |           | #### Intra  | 2,0   | 1    | 6 | 17475 |
| RPL28   | ####   |           | #### Intra  | 1,0   | 0.97 | 6 | 19586 |
| RPL28   | ####   |           | #### N/A    | 1,0   | 0.75 | 6 | 11204 |
| RPL28   | ####   |           | #### Intra  | 1,0   | 1    | 6 | 17006 |
| RPL28   | ####   |           | #### Intra  | 4,1   | 1    | 6 | 11173 |
| RPS9    | 5FLX   | Structure | 12.69 Intra | 1,0   | 1    | 7 | 17183 |
| RPS9    | 5FLX   | Structure | 11.5 Intra  | 3,2   | 1    | 7 | 25330 |
| RPS9    | 5FLX   | Structure | 29.28 Intra | 1,0   | 1    | 7 | 22155 |
| RPS9    | 5FLX   | Structure | 24.64 Intra | 1,1   | 1    | 7 | 22837 |

|         |           |           |       |       |       |      |   |       |
|---------|-----------|-----------|-------|-------|-------|------|---|-------|
| RPS9    | 5FLX      | Structure | 25.88 | Intra | 1,0   | 0.94 | 7 | 10245 |
| RPS9    | 5FLX      | Structure | 13.28 | Intra | 1,0   | 1    | 7 | 29921 |
| RPS9    | 5FLX      | Structure | 12.72 | Intra | 1,0   | 1    | 7 | 15855 |
| RPS24   | P62847    | Phyre     | ####  |       | 1 2,0 | 1    | 1 | 28920 |
| RPS5    | 5FLX      | Structure | 5.76  | Intra | 1,1   | 1    | 2 | 11057 |
| RPS5    | 5FLX      | Structure | 26.93 | Intra | 1,0   | 0.87 | 2 | 10785 |
| RPS5    | P46782    | Phyre     | ####  |       | 1 0,1 | 0.63 | 2 | 16044 |
| RPS5    | P46782    | Phyre     | ####  |       | 1 2,1 | 1    | 2 | 35360 |
| IQGAP1  | ####      | ####      |       | Intra | 1,1   | 1    | 4 | 16618 |
| IQGAP1  | ####      | ####      |       | Intra | 1,1   | 1    | 4 | 22940 |
| IQGAP1  | ####      | ####      |       |       | 1 2,0 | 0.95 | 4 | 12798 |
| IQGAP1  | P46940    | Phyre     | ####  | Intra | 1,1   | 1    | 4 | 22710 |
| MYL6    | P60660    | Phyre     | ####  |       | 1 2,0 | 1    | 1 | 19871 |
| IQGAP1  | ####      | ####      |       |       | 2 1,0 | 1    | 1 | 18274 |
| IQGAP1  | 3FAY      | Structure | ####  |       | 2 2,0 | 1    | 2 | 30861 |
| IQGAP1  | 3FAY      | Structure | ####  |       | 2 2,0 | 1    | 2 | 19642 |
| CAPZB   | P47756    | Phyre     | 10.45 | Intra | 0,1   | 1    | 3 | 10614 |
| CAPZB   | P47756    | Phyre     | 14.43 | Intra | 4,1   | 1    | 3 | 23730 |
| CAPZB   | P47756    | Phyre     | 14.43 | Intra | 2,0   | 1    | 3 | 22607 |
| CAPZB   | P47756    | Phyre     | ####  |       | 1 0,1 | 0.93 | 3 | 7959  |
| CAPZB   | P47756    | Phyre     | ####  |       | 1 2,1 | 1    | 3 | 22704 |
| CAPZB   | P47756    | Phyre     | ####  |       | 1 0,1 | 0.73 | 3 | 11522 |
| EIF1AX  | 4KZY      | Structure | 8.35  | Intra | 1,0   | 0.97 | 1 | 22826 |
| QARS    | ####      | ####      |       | Intra | 3,1   | 1    | 5 | 21459 |
| QARS    | 4YE6      | Structure | 29.01 | Intra | 2,1   | 1    | 5 | 25674 |
| QARS    | 4YE6      | Structure | 29.01 | Intra | 2,0   | 1    | 5 | 24204 |
| QARS    | 4YE6      | Structure | 20.76 | Intra | 2,0   | 1    | 5 | 16736 |
| QARS    | 4YE6      | Structure | 24.72 | Intra | 2,0   | 1    | 5 | 16306 |
| UQCRFS1 | 5XTE      | Structure | 13.29 | Intra | 1,0   | 1    | 2 | 26387 |
| UQCRFS1 | 5XTE      | Structure | 13.29 | Intra | 1,0   | 1    | 2 | 25455 |
| ATP5O   | P48047    | Phyre     | ####  | Intra | 0,1   | 1    | 2 | 13137 |
| ATP5O   | ####      | ####      |       | Intra | 2,0   | 1    | 2 | 23840 |
| ARCN1   | P48444    | Phyre     | 20.48 | Intra | 0,1   | 1    | 1 | 6625  |
| CCT5    | 5UYX      | Structure | 21.34 | Intra | 1,0   | 0.99 | 1 | 13885 |
| CD97    | ####      | ####      |       | Intra | 4,1   | 1    | 1 | 25597 |
| RPL34   | P49207    | Phyre     | 24.75 | Intra | 1,0   | 1    | 3 | 11534 |
| RPL34   | P49207    | Phyre     | 15.3  | Intra | 2,0   | 1    | 3 | 14673 |
| RPL34   | P49207    | Phyre     | 7.32  | Intra | 0,1   | 1    | 3 | 6253  |
| RPL27   | P61353    | Phyre     | ####  |       | 1 2,0 | 1    | 1 | 21655 |
| LMAN1   | P49257_P4 | Docking   | 24.21 | N/A   | 1,0   | 0.97 | 2 | 13602 |
| LMAN1   | P49257_P4 | Docking   | 19.75 | N/A   | 0,1   | 0.99 | 2 | 11002 |
| NASP    | ####      | ####      |       | N/A   | 1,0   | 0.97 | 1 | 30130 |
| FASN    | P49327    | Phyre     | 21.22 | Intra | 1,0   | 1    | 9 | 20368 |
| FASN    | 4PIV      | Structure | 17.37 | Intra | 0,1   | 1    | 9 | 6377  |
| FASN    | P49327    | Phyre     | 12.34 | Intra | 2,0   | 1    | 9 | 21336 |
| FASN    | P49327    | Phyre     | 25.27 | Intra | 3,0   | 1    | 9 | 23810 |
| FASN    | P49327    | Phyre     | 25.27 | Intra | 3,2   | 1    | 9 | 22477 |

|          |        |           |       |       |       |      |   |       |
|----------|--------|-----------|-------|-------|-------|------|---|-------|
| FASN     | P49327 | Phyre     | 19.26 | Intra | 1,0   | 1    | 9 | 27024 |
| FASN     | P49327 | Phyre     | 12.89 | Intra | 2,1   | 1    | 9 | 19237 |
| FASN     | P49327 | Phyre     | 18.39 | Intra | 1,0   | 1    | 9 | 19943 |
| FASN     | P49327 | Phyre     | 9.94  | Intra | 0,1   | 1    | 9 | 5019  |
| TUFM     | ####   | ####      |       | Intra | 1,0   | 1    | 1 | 16146 |
| AARS     | P49588 | Phyre     | 6.13  | Intra | 1,0   | 1    | 4 | 16301 |
| AARS     | P49588 | Phyre     | 9.61  | Intra | 1,0   | 1    | 4 | 14555 |
| AARS     | P49588 | Phyre     | 9.61  | Intra | 2,0   | 1    | 4 | 12771 |
| AARS     | P49588 | Phyre     | 20.51 | Intra | 1,0   | 1    | 4 | 24940 |
| PSMA6    | 5LE5   | Structure | 80.09 |       | 1 2,1 | 1    | 1 | 28801 |
| PSMB3    | 5LE5   | Structure | ####  |       | 2 0,3 | 1    | 1 | 12058 |
| MCM2     | P49736 | Phyre     | 16.44 | Intra | 1,0   | 0.99 | 1 | 14652 |
| ACADVL   | 3B96   | Structure | 24.68 | Intra | 1,1   | 1    | 5 | 26065 |
| ACADVL   | 3B96   | Structure | 26.6  | Intra | 2,1   | 1    | 5 | 23935 |
| ACADVL   | ####   | ####      |       |       | 1 1,0 | 0.97 | 5 | 23199 |
| ACADVL   | 3B96   | Structure | 50.66 | Intra | 3,0   | 1    | 5 | 21217 |
| ACADVL   | 3B96   | Structure | 25.88 | Intra | 2,0   | 1    | 5 | 21343 |
| NUP153   | ####   | ####      |       | Intra | 1,0   | 0.99 | 1 | 25004 |
| RANBP2   | ####   | ####      |       | Intra | 0,2   | 1    | 3 | 8573  |
| RANBP2   | ####   | ####      |       | Intra | 1,0   | 0.99 | 3 | 19967 |
| RANBP2   | ####   | ####      |       | Intra | 1,0   | 1    | 3 | 28355 |
| NDUFV1   | 5XTB   | Structure | 16.45 | Intra | 2,0   | 1    | 1 | 16860 |
| GMPS     | 2VXO   | Structure | 15.48 | Intra | 0,1   | 1    | 2 | 18920 |
| GMPS     | 2VXO   | Structure | 16.05 | Intra | 2,1   | 1    | 2 | 22836 |
| GDI2     | P50395 | Phyre     | 9.01  | Intra | 1,1   | 1    | 1 | 25596 |
| SERPINH1 | P50454 | Phyre     | 21.02 | Intra | 2,0   | 1    | 2 | 20220 |
| SERPINH1 | P50454 | Phyre     | 8.42  | Intra | 1,0   | 1    | 2 | 29767 |
| DNM2     | 2YS1   | Structure | 20.86 | Intra | 0,1   | 1    | 1 | 11724 |
| CDK9     | 4EC9   | Structure | 7.24  | Intra | 1,0   | 0.94 | 1 | 18864 |
| RPL14    | ####   | ####      |       | Intra | 1,1   | 1    | 9 | 7793  |
| RPL14    | ####   | ####      |       |       | 1 0,1 | 1    | 9 | 2969  |
| RPL14    | ####   | ####      |       | Intra | 2,1   | 1    | 9 | 8646  |
| RPL14    | ####   | ####      |       | Intra | 1,0   | 1    | 9 | 7806  |
| RPL14    | ####   | ####      |       | Intra | 1,0   | 1    | 9 | 6913  |
| RPL14    | ####   | ####      |       | Intra | 1,0   | 1    | 9 | 8776  |
| RPL14    | ####   | ####      |       | Intra | 1,0   | 1    | 9 | 6644  |
| RPL14    | ####   | ####      |       | Intra | 1,0   | 1    | 9 | 8081  |
| RPL14    | ####   | ####      |       | Intra | 1,0   | 1    | 9 | 7944  |
| CCT8     | P50990 | Phyre     | 18.8  | Intra | 3,2   | 1    | 4 | 23474 |
| CCT8     | P50990 | Phyre     | 25.13 | Intra | 1,0   | 1    | 4 | 23224 |
| CCT8     | P50990 | Phyre     | 11.86 | Intra | 6,2   | 1    | 4 | 20470 |
| CCT8     | P50990 | Phyre     | 11.86 | Intra | 2,0   | 1    | 4 | 17913 |
| CCT8     | P50990 | Phyre     | ####  |       | 1 1,0 | 0.83 | 1 | 24650 |
| CCT4     | P50991 | Phyre     | 11.38 | Intra | 2,1   | 1    | 7 | 39420 |
| CCT4     | P50991 | Phyre     | 11.38 | Intra | 2,1   | 1    | 7 | 35262 |
| CCT4     | P50991 | Phyre     | 19.25 | Intra | 1,0   | 1    | 7 | 21323 |
| CCT4     | ####   | ####      |       | Intra | 0,1   | 1    | 7 | 4251  |

|         |           |           |       |       |       |      |    |       |
|---------|-----------|-----------|-------|-------|-------|------|----|-------|
| CCT4    | P50991    | Phyre     | 8.99  | Intra | 2,2   | 1    | 7  | 28252 |
| CCT4    | P50991    | Phyre     | 5.93  | Intra | 3,1   | 1    | 7  | 28154 |
| CCT4    | P50991    | Phyre     | 13.51 | Intra | 1,4   | 1    | 7  | 35386 |
| CCT2    | P78371    | Phyre     | ####  |       | 1 0,2 | 1    | 4  | 9316  |
| CCT2    | P78371    | Phyre     | ####  |       | 1 2,2 | 1    | 4  | 14273 |
| CCT2    | P78371    | Phyre     | ####  |       | 1 1,2 | 1    | 4  | 15409 |
| CCT4    | P50991    | Phyre     | ####  |       | 1 1,0 | 0.99 | 4  | 21525 |
| ANXA11  | ####      |           | ####  |       | 1 2,1 | 1    | 1  | 14051 |
| DAP3    | P51398    | Phyre     | 7.43  | Intra | 1,0   | 1    | 2  | 22255 |
| DAP3    | P51398    | Phyre     | 7.6   | Intra | 2,0   | 1    | 2  | 24313 |
| SMARCA4 | ####      |           | ####  |       | 1 1,0 | 0.75 | 1  | 11391 |
| HSD17B4 | ####      |           | ####  | Intra | 1,0   | 0.94 | 2  | 19460 |
| HSD17B4 | 1ZBQ      | Structure | 17.08 | Intra | 1,0   | 1    | 2  | 18294 |
| HNRNPA3 | P51991    | Phyre     | 14.7  | Intra | 0,1   | 1    | 1  | 13765 |
| HNRNPM  | P52272    | Phyre     | 11.33 | Intra | 1,0   | 1    | 4  | 19813 |
| HNRNPM  | ####      |           | ####  | Intra | 2,2   | 1    | 4  | 21591 |
| HNRNPM  | P52272    | Phyre     | 8.65  | Intra | 2,2   | 1    | 4  | 20409 |
| HNRNPM  | P52272    | Phyre     | 13.92 | Intra | 1,0   | 1    | 4  | 31750 |
| ARHGDI  | 1HH4      | Structure | 13.45 | Intra | 1,0   | 0.99 | 1  | 15027 |
| HNRNPF  | P52597    | Phyre     | 42.11 | Intra | 1,0   | 1    | 1  | 32374 |
| MSH6    | ####      |           | ####  | Intra | 2,0   | 1    | 1  | 15161 |
| PPP5C   | 1WAO      | Structure | 17.41 | Intra | 1,1   | 1    | 1  | 14817 |
| ACLY    | 5TE1      | Structure | 22.08 | Intra | 2,1   | 1    | 3  | 26765 |
| ACLY    | 5TE1      | Structure | 30.76 | Intra | 0,2   | 1    | 3  | 6269  |
| ACLY    | 5TE1      | Structure | 21.45 | Intra | 2,0   | 1    | 3  | 23647 |
| COPA    | P53621    | Phyre     | 27.19 | Intra | 3,0   | 1    | 2  | 22838 |
| COPA    | P53621    | Phyre     | 20.4  | Intra | 1,0   | 1    | 2  | 25699 |
| SUB1    | P53999    | Phyre     | ####  | Intra | 1,0   | 1    | 8  | 17617 |
| SUB1    | P53999    | Phyre     | ####  | Intra | 1,0   | 1    | 8  | 21727 |
| SUB1    | 1PCF      | Structure | 14.24 | Intra | 4,2   | 1    | 8  | 28442 |
| SUB1    | 1PCF      | Structure | 14.24 | Intra | 4,2   | 1    | 8  | 27360 |
| SUB1    | 1PCF      | Structure | 14.24 | Intra | 3,0   | 1    | 8  | 26860 |
| SUB1    | 1PCF      | Structure | 11.53 | Intra | 1,1   | 1    | 8  | 27519 |
| SUB1    | 1PCF      | Structure | 5.99  |       | 1 1,0 | 1    | 8  | 27965 |
| SUB1    | ####      |           | ####  | Intra | 1,0   | 1    | 8  | 6865  |
| YARS    | P54577_P5 | Docking   | 22.51 |       | 1 1,0 | 1    | 2  | 10844 |
| YARS    | 1N3L      | Structure | 7.62  | Intra | 1,0   | 1    | 2  | 16879 |
| USP14   | 2AYN      | Structure | 17.61 | Intra | 3,0   | 1    | 1  | 15588 |
| ATP1B3  | P54709    | Phyre     | 13.65 | Intra | 0,1   | 1    | 12 | 13353 |
| ATP1B3  | P54709    | Phyre     | 12.77 | Intra | 1,0   | 1    | 12 | 20838 |
| ATP1B3  | P54709    | Phyre     | 11.45 | Intra | 0,1   | 1    | 12 | 12024 |
| ATP1B3  | P54709    | Phyre     | 15.59 | Intra | 1,0   | 1    | 12 | 19460 |
| ATP1B3  | P54709    | Phyre     | 15.59 | Intra | 1,1   | 1    | 12 | 19862 |
| ATP1B3  | P54709    | Phyre     | 17.25 | Intra | 4,2   | 1    | 12 | 18975 |
| ATP1B3  | P54709    | Phyre     | 17.25 | Intra | 4,2   | 1    | 12 | 16334 |
| ATP1B3  | P54709    | Phyre     | 10.92 | Intra | 0,1   | 1    | 12 | 9985  |
| ATP1B3  | P54709    | Phyre     | 11.51 | Intra | 0,2   | 1    | 12 | 9875  |

|          |        |           |       |       |       |      |    |       |
|----------|--------|-----------|-------|-------|-------|------|----|-------|
| ATP1B3   | P54709 | Phyre     | 12.77 | Intra | 4,0   | 1    | 12 | 19021 |
| ATP1B3   | P54709 | Phyre     | 12.77 | Intra | 1,0   | 1    | 12 | 17648 |
| ATP1B3   | P54709 | Phyre     | 22.23 | Intra | 1,1   | 1    | 12 | 24721 |
| EMP2     | ####   | ####      |       | N/A   | 2,0   | 1    | 1  | 17864 |
| PROCR    | 1LQV   | Structure | ####  |       | 3 6,4 | 1    | 1  | 21880 |
| ALDH18A1 | ####   | ####      |       | Intra | 1,0   | 1    | 3  | 31516 |
| ALDH18A1 | 2H5G   | Structure | 13.44 | Intra | 0,1   | 1    | 3  | 12226 |
| ALDH18A1 | 2H5G   | Structure | 13.38 | Intra | 1,0   | 1    | 3  | 22304 |
| VCP      | 5C1B   | Structure | 13.48 | Intra | 1,0   | 1    | 7  | 22223 |
| VCP      | 5C1B   | Structure | 17.34 | Intra | 3,0   | 1    | 7  | 30519 |
| VCP      | 5C1B   | Structure | 20.51 | Intra | 1,0   | 1    | 7  | 29893 |
| VCP      | 5C1B   | Structure | 23.93 |       | 1 2,2 | 1    | 7  | 24234 |
| VCP      | 5C1B   | Structure | 23.93 | Intra | 7,2   | 1    | 7  | 21981 |
| VCP      | 5C1B   | Structure | 23.93 |       | 1 1,2 | 1    | 7  | 20183 |
| VCP      | 5C1B   | Structure | 11.03 | Intra | 1,2   | 1    | 7  | 29314 |
| ELL      | ####   | ####      |       | N/A   | 1,0   | 0.75 | 1  | 32414 |
| NAP1L1   | P55209 | Phyre     | 27.76 | Intra | 1,0   | 1    | 2  | 22760 |
| NAP1L1   | P55209 | Phyre     | 44.94 | Intra | 2,0   | 1    | 2  | 24483 |
| ADAR     | ####   | ####      |       | Intra | 0,1   | 1    | 2  | 6647  |
| ADAR     | P55265 | Phyre     | ####  | Intra | 2,0   | 1    | 2  | 23706 |
| OXCT1    | 3DLX   | Structure | 25.48 |       | 1 2,1 | 1    | 3  | 11663 |
| OXCT1    | P55809 | Modeller  | 17.11 | Intra | 2,2   | 1    | 3  | 7805  |
| OXCT1    | P55809 | Modeller  | 28.76 | Intra | 1,0   | 1    | 3  | 25098 |
| EIF3B    | P55884 | Phyre     | 15.79 | Intra | 1,0   | 0.97 | 1  | 14027 |
| EIF3A    | ####   | ####      |       |       | 1 1,0 | 0.98 | 1  | 22469 |
| MARS     | 5GL7   | Structure | 12.55 | Intra | 0,2   | 1    | 1  | 12268 |
| ITGA1    | ####   | ####      |       | Intra | 1,0   | 0.98 | 2  | 9267  |
| ITGA1    | ####   | ####      |       | Intra | 2,0   | 1    | 2  | 13794 |
| EPPK1    | ####   | ####      |       | Intra | 1,0   | 1    | 4  | 37421 |
| EPPK1    | ####   | ####      |       | Intra | 1,0   | 1    | 4  | 28655 |
| EPPK1    | ####   | ####      |       | Intra | 1,0   | 1    | 4  | 19501 |
| EPPK1    | ####   | ####      |       | Intra | 3,0   | 1    | 4  | 19869 |
| ARPC4    | P59998 | Phyre     | ####  |       | 1 2,1 | 1    | 1  | 24309 |
| TPI1     | 4POC   | Structure | 16.37 | Intra | 0,2   | 1    | 3  | 8473  |
| TPI1     | 4POC   | Structure | 18.07 | Intra | 0,1   | 1    | 3  | 13432 |
| TPI1     | 4POC   | Structure | 9.7   | Intra | 3,1   | 1    | 3  | 18217 |
| EIF3E    | P60228 | Phyre     | 36.2  | Intra | 2,0   | 1    | 2  | 20459 |
| EIF3E    | ####   | ####      |       | Intra | 0,1   | 1    | 2  | 10785 |
| PAN2     | ####   | ####      |       |       | 1 0,1 | 0.8  | 1  | 9525  |
| EIF3L    | Q9Y262 | Phyre     | ####  |       | 1 0,1 | 0.63 | 2  | 14851 |
| EIF3L    | Q9Y262 | Phyre     | ####  |       | 1 1,0 | 1    | 2  | 27237 |
| SEC61B   | ####   | ####      |       | Intra | 5,1   | 1    | 1  | 7696  |
| MYL6     | P60660 | Phyre     | 15.31 | Intra | 1,1   | 1    | 2  | 35847 |
| MYL6     | P60660 | Phyre     | 14.78 | Intra | 1,0   | 1    | 2  | 25832 |
| ACTB     | 6ANU   | Structure | 33.97 | Intra | 1,1   | 1    | 13 | 36879 |
| ACTB     | 6ANU   | Structure | 35.01 | Intra | 2,0   | 1    | 13 | 18302 |
| ACTB     | 6ANU   | Structure | 8.28  | Intra | 1,0   | 1    | 13 | 27099 |

|         |           |           |       |       |       |      |    |       |
|---------|-----------|-----------|-------|-------|-------|------|----|-------|
| ACTB    | 6ANU      | Structure | 8.28  | Intra | 0,1   | 1    | 13 | 12995 |
| ACTB    | 6ANU      | Structure | 8.28  | Intra | 2,0   | 1    | 13 | 25587 |
| ACTB    | 6ANU      | Structure | 8.28  | Intra | 1,0   | 1    | 13 | 24582 |
| ACTB    | 6ANU      | Structure | 10.89 | Intra | 3,0   | 1    | 13 | 25658 |
| ACTB    | 6ANU      | Structure | 10.89 | Intra | 1,3   | 1    | 13 | 24635 |
| ACTB    | 6ANU      | Structure | 16.67 | Intra | 1,0   | 1    | 13 | 26295 |
| ACTB    | 6ANU      | Structure | 16.67 | Intra | 1,0   | 1    | 13 | 25307 |
| ACTB    | 6ANU      | Structure | 22.9  | Intra | 1,0   | 1    | 13 | 28642 |
| ACTB    | 6ANU      | Structure | 33.33 | Intra | 2,0   | 1    | 13 | 19626 |
| ACTB    | 6ANU      | Structure | 33.33 | Intra | 0,1   | 1    | 13 | 8083  |
| ACTC1   | P68032    | Phyre     | ####  |       | 1 3,2 | 1    | 2  | 28726 |
| ACTC1   | P68032    | Phyre     | ####  |       | 1 4,3 | 1    | 2  | 27536 |
| ACTBL2  | Q562R1    | Phyre     | ####  |       | 1 0,2 | 1    | 1  | 14040 |
| EIF4A1  | 3EIQ      | Structure | 61.44 |       | 1 1,0 | 1    | 4  | 33858 |
| EIF4A1  | 3EIQ      | Structure | 18.58 | Intra | 1,0   | 1    | 4  | 22891 |
| EIF4A1  | 3EIQ      | Structure | 19.23 | Intra | 1,0   | 1    | 4  | 19592 |
| EIF4A1  | 3EIQ      | Structure | 22.59 | Intra | 1,0   | 1    | 4  | 27889 |
| EIF4A2  | 3BOR      | Structure | ####  |       | 1 1,0 | 0.97 | 1  | 33174 |
| S100A10 | 1A4P      | Structure | 9.21  | Intra | 1,1   | 1    | 1  | 9707  |
| DSTN    | P60981    | Phyre     | 8.44  | Intra | 2,0   | 1    | 1  | 18231 |
| RAB8A   | 5SZI      | Structure | 19.81 | Intra | 1,0   | 1    | 1  | 18883 |
| RAB14   | P61106    | Phyre     | 20.37 | Intra | 1,2   | 1    | 1  | 22024 |
| ACTR2   | P61160    | Phyre     | 21.02 | Intra | 1,0   | 1    | 2  | 17208 |
| ACTR2   | P61160    | Phyre     | ####  | Intra | 1,0   | 1    | 2  | 21383 |
| ACTR1A  | P61163    | Phyre     | 21.3  | Intra | 1,0   | 1    | 2  | 22331 |
| ACTR1A  | P61163    | Phyre     | 18.8  | Intra | 0,1   | 1    | 2  | 10381 |
| COPS2   | 4D10      | Structure | 10.53 | Intra | 1,0   | 0.99 | 1  | 22107 |
| ABCE1   | P61221    | Modeller  | 24.08 | Intra | 2,0   | 1    | 3  | 15522 |
| ABCE1   | P61221    | Modeller  | 20.53 | Intra | 1,0   | 0.94 | 3  | 9597  |
| ABCE1   | P61221    | Modeller  | 18.95 | Intra | 3,0   | 1    | 3  | 17358 |
| RPS3A   | 5FLX      | Structure | 11.06 | Intra | 2,0   | 1    | 2  | 15370 |
| RPS3A   | 5FLX      | Structure | 20.65 | Intra | 2,0   | 1    | 2  | 16697 |
| PSME3   | P61289_P6 | Docking   | 19.88 |       | 1 2,1 | 1    | 3  | 11629 |
| PSME3   | P61289    | Phyre     | 23.21 | Intra | 1,2   | 1    | 3  | 18260 |
| PSME3   | P61289    | Phyre     | 13.89 | Intra | 3,2   | 1    | 3  | 28864 |
| RPL27   | P61353    | Phyre     | 12.26 | Intra | 1,0   | 0.99 | 2  | 18088 |
| RPL27   | P61353    | Phyre     | 7.68  | Intra | 1,2   | 1    | 2  | 22564 |
| HSPE1   | 4PJ1      | Structure | 9.31  | Intra | 1,0   | 1    | 17 | 21358 |
| HSPE1   | 4PJ1      | Structure | 7.56  |       | 1 3,2 | 1    | 17 | 15857 |
| HSPE1   | 4PJ1      | Structure | 7.1   | Intra | 1,1   | 1    | 17 | 16730 |
| HSPE1   | 4PJ1      | Structure | 24.76 | Intra | 0,2   | 1    | 17 | 11441 |
| HSPE1   | 4PJ1      | Structure | 17.67 | Intra | 1,2   | 1    | 17 | 25488 |
| HSPE1   | 4PJ1      | Structure | 17.67 | Intra | 1,0   | 1    | 17 | 22314 |
| HSPE1   | 4PJ1      | Structure | 38.54 | Intra | 0,1   | 1    | 17 | 14168 |
| HSPE1   | 4PJ1      | Structure | 21.25 | Intra | 3,2   | 1    | 17 | 28148 |
| HSPE1   | 4PJ1      | Structure | 13.61 | Intra | 0,2   | 1    | 17 | 13750 |
| HSPE1   | 4PJ1      | Structure | 29.72 | Intra | 0,2   | 1    | 17 | 11321 |

|        |        |           |       |       |       |      |    |       |
|--------|--------|-----------|-------|-------|-------|------|----|-------|
| HSPE1  | 4PJ1   | Structure | 29.72 | Intra | 1,0   | 1    | 17 | 28173 |
| HSPE1  | 4PJ1   | Structure | 22.58 | Intra | 2,1   | 1    | 17 | 24399 |
| HSPE1  | 4PJ1   | Structure | 22.58 | Intra | 1,0   | 1    | 17 | 23353 |
| HSPE1  | 4PJ1   | Structure | 18.38 | Intra | 1,0   | 1    | 17 | 29611 |
| HSPE1  | 4PJ1   | Structure | 18.87 | Intra | 1,2   | 1    | 17 | 29265 |
| HSPE1  | 4PJ1   | Structure | 28.06 | Intra | 0,2   | 1    | 17 | 10279 |
| HSPE1  | 4PJ1   | Structure | 28.06 | Intra | 1,1   | 1    | 17 | 26170 |
| B2M    | 5J1A   | Structure | 17.39 | Intra | 3,2   | 1    | 1  | 15757 |
| B2M    | 5J1A   | Structure | ####  |       | 1 3,1 | 1    | 1  | 18457 |
| HNRNPK | 1ZZK   | Structure | 15.78 | Intra | 1,0   | 1    | 5  | 20693 |
| HNRNPK | P61978 | Phyre     | 13.98 | Intra | 1,0   | 1    | 5  | 25053 |
| HNRNPK | ####   |           | ####  | Intra | 2,1   | 1    | 5  | 28132 |
| HNRNPK | P61978 | Phyre     | 8.33  | Intra | 2,0   | 1    | 5  | 14392 |
| HNRNPK | P61978 | Phyre     | 15.42 | Intra | 7,1   | 1    | 5  | 20868 |
| YWHAG  | 3UZD   | Structure | 11.4  | Intra | 1,0   | 1    | 2  | 15257 |
| YWHAG  | 3UZD   | Structure | 28.89 | Intra | 1,0   | 1    | 2  | 24983 |
| RPS7   | 5FLX   | Structure | 28.27 | Intra | 1,0   | 1    | 3  | 19965 |
| RPS7   | 5FLX   | Structure | 16.88 | Intra | 0,1   | 1    | 3  | 6527  |
| RPS7   | 5FLX   | Structure | 12.33 | Intra | 4,1   | 1    | 3  | 14641 |
| PPP1CA | 4G9J   | Structure | 10.77 | Intra | 0,2   | 1    | 1  | 12909 |
| RPS15A | 5FLX   | Structure | 21.56 | Intra | 1,0   | 1    | 4  | 18448 |
| RPS15A | 5FLX   | Structure | 20.18 | Intra | 1,1   | 1    | 4  | 22811 |
| RPS15A | 5FLX   | Structure | 9.12  | Intra | 2,0   | 1    | 4  | 27827 |
| RPS15A | 5FLX   | Structure | 8.92  | Intra | 1,1   | 1    | 4  | 13231 |
| RPL18A | Q02543 | Phyre     | ####  |       | 1 1,0 | 0.98 | 1  | 13992 |
| RPS16  | 5FLX   | Structure | 21.01 | Intra | 1,0   | 1    | 3  | 11700 |
| RPS16  | 5FLX   | Structure | 6.07  | Intra | 5,3   | 1    | 3  | 21291 |
| RPS16  | 5FLX   | Structure | 10.33 | Intra | 3,1   | 1    | 3  | 19077 |
| RPS16  | P62249 | Phyre     | ####  |       | 1 3,1 | 1    | 1  | 29513 |
| YWHAE  | 3UBW   | Structure | 12.99 | Intra | 0,1   | 1    | 1  | 11698 |
| YWHAE  | 3UBW   | Structure | ####  |       | 1 1,0 | 0.98 | 1  | 23943 |
| RPS23  | P62266 | Phyre     | 13.33 | Intra | 0,1   | 1    | 3  | 6151  |
| RPS23  | P62266 | Phyre     | 17.83 | Intra | 0,1   | 1    | 3  | 9105  |
| RPS23  | ####   |           | ####  | N/A   | 1,0   | 0.98 | 3  | 10372 |
| RPS18  | 5FLX   | Structure | 7.7   | Intra | 2,0   | 1    | 1  | 25220 |
| RPS13  | 5FLX   | Structure | 6.59  | Intra | 7,3   | 1    | 10 | 24784 |
| RPS13  | 5FLX   | Structure | 10.63 | Intra | 1,0   | 1    | 10 | 27444 |
| RPS13  | 5FLX   | Structure | 10.66 | Intra | 3,0   | 1    | 10 | 20632 |
| RPS13  | 5FLX   | Structure | 28.44 | Intra | 2,0   | 1    | 10 | 17445 |
| RPS13  | 5FLX   | Structure | 12.71 | Intra | 1,0   | 1    | 10 | 28565 |
| RPS13  | 5FLX   | Structure | 19.44 | Intra | 0,1   | 0.87 | 10 | 14209 |
| RPS13  | 5FLX   | Structure | 25.55 | Intra | 1,0   | 1    | 10 | 15369 |
| RPS13  | 5FLX   | Structure | 22.3  | Intra | 3,0   | 1    | 10 | 22589 |
| RPS13  | 5FLX   | Structure | 34.82 | Intra | 1,1   | 1    | 10 | 13448 |
| RPS13  | 5FLX   | Structure | 40.03 | Intra | 1,0   | 1    | 10 | 23034 |
| RPS11  | 5FLX   | Structure | 20.84 | Intra | 1,0   | 1    | 2  | 21826 |
| RPS11  | 5FLX   | Structure | 12.48 | Intra | 2,0   | 1    | 2  | 21603 |

|          |        |           |             |        |      |    |       |
|----------|--------|-----------|-------------|--------|------|----|-------|
| RPL7A    | P62424 | Phyre     | 23.63 Intra | 3,1    | 1    | 6  | 18780 |
| RPL7A    | P62424 | Phyre     | 16.31 Intra | 3,1    | 1    | 6  | 17108 |
| RPL7A    | P62424 | Phyre     | 7.09 Intra  | 0,1    | 1    | 6  | 11846 |
| RPL7A    | P62424 | Phyre     | 18.67 Intra | 0,1    | 1    | 6  | 10246 |
| RPL7A    | P62424 | Phyre     | 19.78 Intra | 0,1    | 1    | 6  | 11588 |
| RPL7A    | P62424 | Phyre     | 10.68 Intra | 1,0    | 1    | 6  | 15591 |
| RPL36    | Q9Y3U8 | Phyre     | ####        | 1 1,0  | 0.98 | 7  | 16922 |
| RPL7A    | P62424 | Phyre     | ####        | 1 3,0  | 1    | 7  | 18880 |
| RPL7A    | P62424 | Phyre     | ####        | 1 1,0  | 1    | 7  | 24446 |
| RPL7A    | P62424 | Phyre     | ####        | 1 6,3  | 1    | 7  | 30197 |
| RPL7A    | P62424 | Phyre     | ####        | 1 0,2  | 1    | 7  | 10322 |
| RPL7A    | P62424 | Phyre     | ####        | 1 7,0  | 1    | 7  | 28714 |
| RPL7A    | P62424 | Phyre     | ####        | 1 0,1  | 0.83 | 7  | 8711  |
| RAB11A   | 5C46   | Structure | 19.47 Intra | 3,0    | 1    | 1  | 18887 |
| RAB11A   | 5C46   | Structure | ####        | 1 1,0  | 1    | 1  | 17824 |
| RPS4X    | 5A2Q   | Structure | 26.47 Intra | 1,1    | 1    | 5  | 16713 |
| RPS4X    | 5A2Q   | Structure | 24.24 Intra | 2,0    | 1    | 5  | 14372 |
| RPS4X    | 5A2Q   | Structure | 16.66 Intra | 1,0    | 1    | 5  | 29278 |
| RPS4X    | 5A2Q   | Structure | 28.63 Intra | 1,0    | 1    | 5  | 15820 |
| RPS4X    | 5A2Q   | Structure | 22.8 Intra  | 1,0    | 0.99 | 5  | 21937 |
| ACTA2    | P62736 | Phyre     | 24.17 Intra | 0,1    | 1    | 1  | 12510 |
| RPL23A   | P62750 | Phyre     | 13.27 Intra | 3,3    | 1    | 2  | 25175 |
| RPL23A   | P62750 | Phyre     | 13.47 Intra | 1,0    | 0.94 | 2  | 22136 |
| HIST1H4A | 5B0Z   | Structure | 46.88       | 1 1,0  | 1    | 15 | 15207 |
| HIST1H4A | 5B0Z   | Structure | 38.34 Intra | 3,0    | 1    | 15 | 16230 |
| HIST1H4A | 5B0Z   | Structure | 6.9 Intra   | 15,8   | 1    | 15 | 22568 |
| HIST1H4A | 5B0Z   | Structure | 20.88 Intra | 1,0    | 1    | 15 | 21762 |
| HIST1H4A | 5B0Z   | Structure | 6.9 Intra   | 30,8   | 1    | 15 | 19302 |
| HIST1H4A | 5B0Z   | Structure | 20.88 Intra | 2,4    | 1    | 15 | 25294 |
| HIST1H4A | 5B0Z   | Structure | 20.88 Intra | 2,0    | 1    | 15 | 22580 |
| HIST1H4A | 5B0Z   | Structure | 14.98 Intra | 3,1    | 1    | 15 | 32408 |
| HIST1H4A | P62805 | Phyre     | 15.61 Intra | 0,1    | 1    | 15 | 4591  |
| HIST1H4A | P62805 | Phyre     | 5.78 Intra  | 0,2    | 1    | 15 | 3362  |
| HIST1H4A | 5B0Z   | Structure | 39.33       | 1 1,0  | 1    | 15 | 34094 |
| HIST1H4A | 5B0Z   | Structure | 17.45 Intra | 1,0    | 1    | 15 | 31525 |
| HIST1H4A | 5B0Z   | Structure | 17.45       | 1 3,2  | 1    | 15 | 35235 |
| HIST1H4A | 5B0Z   | Structure | 17.45 Intra | 3,0    | 1    | 15 | 32807 |
| HIST1H4A | 5B0Z   | Structure | 17.45       | 1 1,0  | 1    | 15 | 30498 |
| HIST1H3A | P68431 | Phyre     | ####        | 1 0,1  | 1    | 3  | 2414  |
| HIST1H3A | 5AV9   | Structure | ####        | 1 0,2  | 1    | 3  | 7375  |
| HIST1H3A | 5AV9   | Structure | ####        | 1 0,3  | 1    | 3  | 6447  |
| HIST3H3  | 3A6N   | Structure | ####        | 1 19,8 | 1    | 16 | 16576 |
| HIST3H3  | 3A6N   | Structure | ####        | 1 2,2  | 1    | 16 | 24243 |
| HIST3H3  | 3A6N   | Structure | ####        | 1 2,1  | 1    | 16 | 22534 |
| HIST1H4A | 5B0Z   | Structure | ####        | 1 1,0  | 1    | 16 | 32972 |
| HIST1H4A | 5B0Z   | Structure | ####        | 1 7,3  | 1    | 16 | 27565 |
| HIST1H4A | 5B0Z   | Structure | ####        | 1 4,0  | 1    | 16 | 25677 |



|           |        |           |             |        |      |    |       |
|-----------|--------|-----------|-------------|--------|------|----|-------|
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 3,0  | 1    | 16 | 29744 |
| HIST3H3   | 3A6N   | Structure | ####        | 1 2,0  | 1    | 16 | 17749 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 1,0  | 1    | 16 | 25448 |
| HIST3H3   | 3A6N   | Structure | ####        | 1 1,3  | 1    | 16 | 5997  |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 7,5  | 1    | 16 | 8675  |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 1,0  | 1    | 16 | 29034 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 1,0  | 1    | 16 | 34094 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 1,0  | 1    | 16 | 32934 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 2,0  | 1    | 16 | 17011 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 6,4  | 1    | 16 | 30120 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 3,2  | 1    | 2  | 16211 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 1,0  | 1    | 2  | 25558 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 5,2  | 1    | 14 | 10964 |
| HIST1H2BH | Q93079 | Phyre     | ####        | 1 5,7  | 1    | 14 | 19267 |
| HIST1H2BH | Q93079 | Phyre     | ####        | 1 1,0  | 1    | 14 | 9962  |
| HIST1H2BH | Q93079 | Phyre     | ####        | 1 1,0  | 1    | 14 | 8693  |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 1,0  | 1    | 14 | 8779  |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 4,2  | 1    | 14 | 15181 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 2,1  | 1    | 14 | 26022 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 2,0  | 1    | 14 | 28409 |
| HIST1H2BH | Q93079 | Phyre     | ####        | 1 1,4  | 1    | 14 | 27538 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 7,3  | 1    | 14 | 8890  |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 3,0  | 1    | 14 | 20483 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 2,0  | 1    | 14 | 20789 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 4,2  | 1    | 14 | 23120 |
| HIST1H2BH | Q93079 | Phyre     | ####        | 1 2,0  | 1    | 14 | 25571 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 12,9 | 1    | 7  | 9705  |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 3,0  | 1    | 7  | 21822 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 8,3  | 1    | 7  | 25633 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 4,1  | 1    | 7  | 34214 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 2,0  | 1    | 7  | 27099 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 8,6  | 1    | 7  | 30918 |
| HIST1H4A  | 5B0Z   | Structure | ####        | 1 20,3 | 1    | 7  | 27908 |
| HIST1H2BC | 5GT0   | Structure | ####        | 1 0,1  | 0.83 | 1  | 3335  |
| RAN       | 5CIQ   | Structure | 16.64 Intra | 2,0    | 1    | 8  | 16862 |
| RAN       | 5CIQ   | Structure | 14.49 Intra | 7,4    | 1    | 8  | 15266 |
| RAN       | 5CIQ   | Structure | 13.21 Intra | 2,2    | 1    | 8  | 25103 |
| RAN       | 5CIQ   | Structure | 17.25 Intra | 4,2    | 1    | 8  | 16900 |
| RAN       | 5CIQ   | Structure | 13.45 Intra | 1,0    | 1    | 8  | 13202 |
| RAN       | 5CIQ   | Structure | 12.82 Intra | 1,0    | 1    | 8  | 22371 |
| RAN       | 5CIQ   | Structure | 15.26 Intra | 4,0    | 1    | 8  | 15327 |
| RAN       | 5CIQ   | Structure | 17.25 Intra | 0,1    | 1    | 8  | 9272  |
| RPS24     | 5FLX   | Structure | 16.11 Intra | 2,1    | 1    | 1  | 10102 |
| RPS26     | P62854 | Phyre     | 16.02 Intra | 0,4    | 1    | 1  | 12389 |
| RPS28     | 5FLX   | Structure | 18.27 Intra | 3,0    | 1    | 1  | 17230 |
| RPS28     | 5FLX   | Structure | #### N/A    | 1,1    | 0.96 | 1  | 7169  |
| FAU       | 5FLX   | Structure | 5.87 Intra  | 3,0    | 1    | 1  | 20463 |

|           |        |           |       |       |       |      |    |       |
|-----------|--------|-----------|-------|-------|-------|------|----|-------|
| GNB2      | P62879 | Phyre     | 19.23 | Intra | 0,1   | 1    | 1  | 15036 |
| RPL30     | 3VI6   | Structure | 17.07 | Intra | 2,0   | 1    | 3  | 22058 |
| RPL30     | 3VI6   | Structure | 24.2  | Intra | 1,0   | 0.94 | 3  | 16920 |
| RPL30     | 3VI6   | Structure | 10.24 | Intra | 2,0   | 1    | 3  | 24061 |
| RPL31     | P62899 | Phyre     | 14.48 | Intra | 1,0   | 0.99 | 2  | 17131 |
| RPL31     | P62899 | Phyre     | 16.67 | Intra | 1,0   | 0.99 | 2  | 15282 |
| RPL10A    | P62906 | Phyre     | 10.97 | Intra | 1,0   | 1    | 5  | 27669 |
| RPL10A    | P62906 | Phyre     | 12.58 | Intra | 2,0   | 1    | 5  | 21090 |
| RPL10A    | P62906 | Phyre     | 18.24 | Intra | 1,0   | 1    | 5  | 25204 |
| RPL10A    | P62906 | Phyre     | 14.96 | Intra | 2,1   | 1    | 5  | 19542 |
| RPL10A    | P62906 | Phyre     | 13.53 | Intra | 1,0   | 1    | 5  | 23600 |
| RPL10A    | P62906 | Phyre     | ####  |       | 2 3,0 | 0.73 | 1  | 12754 |
| RPL32     | P62910 | Phyre     | 19.47 | Intra | 2,0   | 1    | 2  | 12946 |
| RPL32     | P62910 | Phyre     | 5.19  | Intra | 3,0   | 1    | 2  | 12828 |
| RPL11     | 4XXB   | Structure | 21.56 | Intra | 1,0   | 1    | 1  | 23913 |
| RPL8      | P62917 | Phyre     | 11.23 | Intra | 0,1   | 1    | 3  | 10364 |
| RPL8      | P62917 | Phyre     | 34.13 | Intra | 2,2   | 1    | 3  | 21278 |
| RPL8      | P62917 | Phyre     | 26.5  | Intra | 2,0   | 1    | 3  | 17035 |
| PPIA      | 4N1M   | Structure | 11.52 | Intra | 7,4   | 1    | 10 | 13951 |
| PPIA      | 4N1M   | Structure | 23.02 | Intra | 1,0   | 1    | 10 | 24205 |
| PPIA      | 4N1M   | Structure | 15.14 | Intra | 1,0   | 1    | 10 | 22420 |
| PPIA      | 4N1M   | Structure | 14.13 | Intra | 1,0   | 1    | 10 | 13298 |
| PPIA      | 4N1M   | Structure | 12.71 | Intra | 8,2   | 1    | 10 | 23159 |
| PPIA      | 4N1M   | Structure | 21.81 | Intra | 0,4   | 1    | 10 | 6513  |
| PPIA      | 4N1M   | Structure | 21.81 | Intra | 2,4   | 1    | 10 | 24235 |
| PPIA      | P62937 | Unknown   | ####  | Intra | 1,0   | 1    | 10 | 27352 |
| PPIA      | 4N1M   | Structure | 16.77 | Intra | 2,2   | 1    | 10 | 30030 |
| PPIA      | 4N1M   | Structure | 16.77 | Intra | 2,0   | 1    | 10 | 28245 |
| UBA52     | 5HPL   | Structure | 16.78 | Intra | 0,2   | 1    | 6  | 8207  |
| UBA52     | 5HPL   | Structure | 19.77 | Intra | 5,8   | 1    | 6  | 22606 |
| UBA52     | 5HPL   | Structure | 12.61 | Intra | 1,0   | 1    | 6  | 22082 |
| UBA52     | 5HPL   | Structure | 23.26 | Intra | 4,0   | 1    | 6  | 19736 |
| UBA52     | 5HPL   | Structure | 18.18 | Intra | 1,3   | 1    | 6  | 25532 |
| UBA52     | 5HPL   | Structure | 13.19 | Intra | 1,1   | 1    | 6  | 21817 |
| UBA52     | 5HPL   | Structure | ####  |       | 2 0,4 | 1    | 1  | 6603  |
| UBA52     | 5HPL   | Structure | ####  |       | 2 2,0 | 1    | 2  | 22113 |
| UBA52     | 5HPL   | Structure | ####  |       | 2 1,1 | 1    | 2  | 22388 |
| HIST1H2BH | Q93079 | Phyre     | ####  |       | 2 1,0 | 0.99 | 1  | 24491 |
| YWHAZ     | 1QJB   | Structure | 9.64  | Intra | 4,1   | 1    | 6  | 12251 |
| YWHAZ     | 1QJB   | Structure | 41.16 | Intra | 0,1   | 1    | 6  | 5154  |
| YWHAZ     | 1QJB   | Structure | 9.64  | Intra | 8,3   | 1    | 6  | 11494 |
| YWHAZ     | 1QJB   | Structure | 28.14 | Intra | 1,0   | 1    | 6  | 22969 |
| YWHAZ     | 1QJB   | Structure | 33.59 | Intra | 1,0   | 0.94 | 6  | 21431 |
| YWHAZ     | 1QJB   | Structure | 12.98 | Intra | 0,1   | 1    | 6  | 12132 |
| SUMO1     | 1WYW   | Structure | 4.44  | Intra | 1,0   | 1    | 1  | 17934 |
| RACK1     | 4AOW   | Structure | 12.94 | Intra | 0,1   | 1    | 1  | 14540 |
| UBE2I     | 2GRR   | Structure | 16.3  | Intra | 1,0   | 0.97 | 1  | 18743 |

|          |           |           |       |       |       |      |    |       |
|----------|-----------|-----------|-------|-------|-------|------|----|-------|
| YBX1     | ####      |           | ####  | Intra | 2,0   | 1    | 1  | 24465 |
| TPM4     | P67936    | Phyre     | 10.67 | Intra | 3,1   | 1    | 1  | 21453 |
| ACTC1    | P68032    | Phyre     | ####  |       | 2 2,0 | 1    | 1  | 16507 |
| ACTC1    | P68032    | Phyre     | 13.13 | Intra | 1,0   | 1    | 13 | 28242 |
| ACTC1    | P68032    | Phyre     | 16.06 | Intra | 1,2   | 1    | 13 | 26424 |
| ACTC1    | P68032    | Phyre     | 16.06 | Intra | 1,0   | 1    | 13 | 25598 |
| ACTC1    | P68032    | Phyre     | 16.06 | Intra | 1,0   | 1    | 13 | 25694 |
| ACTC1    | P68032    | Phyre     | 16.06 | Intra | 0,1   | 1    | 13 | 14328 |
| ACTC1    | P68032    | Phyre     | 44.76 | Intra | 9,2   | 1    | 13 | 17690 |
| ACTC1    | P68032    | Phyre     | 51.19 | Intra | 1,0   | 1    | 13 | 17246 |
| ACTC1    | P68032    | Phyre     | 51.19 | Intra | 0,2   | 1    | 13 | 6687  |
| ACTC1    | P68032_P6 | Docking   | 15.86 |       | 1 3,0 | 1    | 13 | 20802 |
| ACTC1    | P68032    | Phyre     | 9.96  | Intra | 3,2   | 1    | 13 | 22635 |
| ACTC1    | P68032    | Phyre     | 9.96  | Intra | 11,2  | 1    | 13 | 21241 |
| ACTC1    | P68032    | Phyre     | 9.96  | Intra | 6,2   | 1    | 13 | 21836 |
| ACTC1    | P68032    | Phyre     | 9.96  | Intra | 5,4   | 1    | 13 | 20449 |
| PLEC     | ####      |           | ####  |       | 1 1,1 | 1    | 1  | 11370 |
| LIMA1    | ####      |           | ####  |       | 1 1,0 | 0.98 | 2  | 20390 |
| LIMA1    | ####      |           | ####  |       | 1 2,0 | 1    | 2  | 17974 |
| UBE2L3   | 4Q5E      | Structure | 9.25  | Intra | 1,0   | 0.99 | 1  | 10796 |
| EEF1A1   | P68104    | Phyre     | ####  | Intra | 4,1   | 1    | 13 | 24992 |
| EEF1A1   | P68104    | Phyre     | 12.14 | Intra | 1,1   | 1    | 13 | 28624 |
| EEF1A1   | P68104    | Phyre     | 24.16 | Intra | 1,1   | 1    | 13 | 19846 |
| EEF1A1   | P68104    | Phyre     | 24.16 | Intra | 3,0   | 1    | 13 | 18035 |
| EEF1A1   | ####      |           | ####  | Intra | 0,1   | 1    | 13 | 3613  |
| EEF1A1   | P68104    | Phyre     | 29.74 | Intra | 1,0   | 1    | 13 | 33808 |
| EEF1A1   | P68104_P6 | Docking   | 25.85 |       | 1 1,0 | 1    | 13 | 33113 |
| EEF1A1   | P68104    | Phyre     | 20.32 | Intra | 1,0   | 1    | 13 | 32429 |
| EEF1A1   | P68104    | Phyre     | 17.84 | Intra | 1,0   | 1    | 13 | 34038 |
| EEF1A1   | ####      |           | ####  | Intra | 2,2   | 1    | 13 | 6460  |
| EEF1A1   | P68104    | Phyre     | ####  | Intra | 1,1   | 1    | 13 | 24427 |
| EEF1A1   | P68104    | Phyre     | 44.34 | Intra | 3,0   | 1    | 13 | 26753 |
| EEF1A1   | P68104    | Phyre     | ####  | Intra | 2,1   | 1    | 13 | 24613 |
| EEF1A1   | P68104    | Phyre     | ####  |       | 2 2,0 | 0.8  | 1  | 13244 |
| TUBA1A   | 5JCO      | Structure | ####  |       | 1 1,0 | 1    | 1  | 24361 |
| HIST1H3A | P68431    | Phyre     | 50.47 | Intra | 1,0   | 1    | 8  | 14425 |
| HIST1H3A | P68431    | Phyre     | 43.19 | Intra | 1,0   | 1    | 8  | 15667 |
| HIST1H3A | P68431    | Phyre     | 11.91 | Intra | 5,1   | 1    | 8  | 8106  |
| HIST1H3A | P68431    | Phyre     | 9.69  | Intra | 0,1   | 1    | 8  | 3228  |
| HIST1H3A | P68431    | Phyre     | 10.62 | Intra | 0,2   | 1    | 8  | 2408  |
| HIST1H3A | P68431    | Phyre     | 84.28 | Intra | 0,2   | 1    | 8  | 6229  |
| HIST1H3A | P68431    | Phyre     | 16.73 | Intra | 4,0   | 1    | 8  | 6541  |
| HIST1H3A | P68431    | Phyre     | 26.1  | Intra | 1,0   | 1    | 8  | 6424  |
| HIST1H3A | P68431    | Phyre     | ####  |       | 1 1,0 | 1    | 1  | 8839  |
| GTF2I    | ####      |           | ####  | Intra | 2,1   | 1    | 3  | 21892 |
| GTF2I    | ####      |           | ####  | Intra | 1,0   | 1    | 3  | 23166 |
| GTF2I    | ####      |           | ####  | Intra | 1,0   | 1    | 3  | 21775 |

|         |           |           |        |       |       |      |    |       |
|---------|-----------|-----------|--------|-------|-------|------|----|-------|
| CCT2    | P78371    | Phyre     | 23.81  | Intra | 1,0   | 0.99 | 2  | 10586 |
| CCT2    | P78371_P7 | Docking   | 66.44  | N/A   | 1,0   | 1    | 2  | 35953 |
| GSTO1   | 4YQU      | Structure | 36.16  | Intra | 1,0   | 0.99 | 3  | 19089 |
| GSTO1   | 4YQU      | Structure | 41.07  | Intra | 2,0   | 1    | 3  | 14430 |
| GSTO1   | 4YQU      | Structure | 9.32   | Intra | 1,0   | 1    | 3  | 21822 |
| PRKDC   | P78527    |           | 81.52  | Intra | 1,0   | 1    | 11 | 17587 |
| PRKDC   | 5LUQ      | Structure | 54.48  | Intra | 0,2   | 1    | 11 | 10073 |
| PRKDC   | P78527    |           | 214.58 | Intra | 1,0   | 1    | 11 | 22673 |
| PRKDC   | P78527    |           | 30.05  | Intra | 1,0   | 1    | 11 | 16541 |
| PRKDC   | 5LUQ      | Structure | 162.9  | Intra | 2,1   | 1    | 11 | 30734 |
| PRKDC   | P78527    |           | 19.76  | Intra | 1,0   | 1    | 11 | 16802 |
| PRKDC   | P78527    |           | 53.69  | Intra | 3,0   | 1    | 11 | 26625 |
| PRKDC   | 5LUQ      | Structure | 23.42  | Intra | 1,0   | 1    | 11 | 29271 |
| PRKDC   | 5LUQ      | Structure | 24.5   | Intra | 3,0   | 1    | 11 | 17608 |
| PRKDC   | P78527    |           | 172.7  | Intra | 1,0   | 1    | 11 | 23673 |
| PRKDC   | 5LUQ      | Structure | 23.84  | Intra | 0,1   | 1    | 11 | 10544 |
| ADAM17  | ####      |           | ####   | Intra | 1,0   | 0.99 | 1  | 11980 |
| RPL24   | 5A2Q      | Structure | 24.28  | Intra | 2,1   | 1    | 3  | 11866 |
| RPL24   | 5A2Q      | Structure | 8.9    | Intra | 4,1   | 1    | 3  | 21789 |
| RPL24   | 5A2Q      | Structure | 8.9    | Intra | 2,0   | 1    | 3  | 18751 |
| RPL19   | P84098    | Phyre     | 19.89  | Intra | 3,0   | 1    | 4  | 16279 |
| RPL19   | P84098    | Phyre     | 19.89  | Intra | 0,1   | 1    | 4  | 6832  |
| RPL19   | P84098    | Phyre     | 21.07  | Intra | 2,1   | 1    | 4  | 3453  |
| RPL19   | P84098    | Phyre     | 28.48  | Intra | 1,0   | 0.94 | 4  | 8253  |
| CYCS    | 5TY3      | Structure | 15.12  | Intra | 2,0   | 1    | 1  | 21267 |
| TFAM    | 3TQ6      | Structure | 10.7   | Intra | 3,0   | 1    | 4  | 26359 |
| TFAM    | 3TQ6      | Structure | 5.32   | Intra | 1,0   | 0.99 | 4  | 13127 |
| TFAM    | 3TQ6      | Structure | 20.98  | Intra | 1,0   | 0.94 | 4  | 20447 |
| TFAM    | 3TQ6      | Structure | 8.86   | Intra | 2,0   | 1    | 4  | 21431 |
| SLC25A3 | Q00325    | Phyre     | 11.04  | Intra | 1,0   | 0.97 | 1  | 16005 |
| HDLBP   | 2CTK      | Structure | 12.54  | Intra | 2,1   | 1    | 3  | 15413 |
| HDLBP   | ####      |           | ####   | N/A   | 4,1   | 1    | 3  | 15046 |
| HDLBP   | ####      |           | ####   | Intra | 2,0   | 1    | 3  | 15046 |
| DZIP3   | ####      |           | ####   |       | 2 1,0 | 0.98 | 1  | 14265 |
| CLTC    | Q00610    | Phyre     | 26.66  | Intra | 2,0   | 1    | 14 | 20379 |
| CLTC    | Q00610    | Phyre     | 52.65  | Intra | 1,0   | 1    | 14 | 29639 |
| CLTC    | Q00610    | Phyre     | 65.99  | Intra | 1,3   | 1    | 14 | 14919 |
| CLTC    | Q00610    | Phyre     | 145.63 | Intra | 1,0   | 1    | 14 | 29093 |
| CLTC    | Q00610    | Phyre     | 13.32  | Intra | 1,0   | 1    | 14 | 16085 |
| CLTC    | Q00610    | Phyre     | 29.56  | Intra | 2,0   | 1    | 14 | 22690 |
| CLTC    | Q00610    | Phyre     | 22.28  | Intra | 1,0   | 1    | 14 | 32456 |
| CLTC    | 4G55      | Structure | 9.73   | Intra | 1,0   | 1    | 14 | 23201 |
| CLTC    | Q00610    | Phyre     | 47.04  | Intra | 2,1   | 1    | 14 | 17208 |
| CLTC    | Q00610    | Phyre     | 117.4  | Intra | 2,1   | 1    | 14 | 24563 |
| CLTC    | Q00610    | Phyre     | 18.71  | Intra | 2,2   | 1    | 14 | 21898 |
| CLTC    | Q00610    | Phyre     | 17.24  | Intra | 1,1   | 1    | 14 | 19295 |
| CLTC    | Q00610    | Phyre     | 9.87   | Intra | 0,2   | 1    | 14 | 9807  |

|        |          |           |       |       |       |      |    |       |
|--------|----------|-----------|-------|-------|-------|------|----|-------|
| CLTC   | ####     |           | ####  | 1     | 1,0   | 0.75 | 14 | 17658 |
| HNRNPU | ####     |           | ####  | N/A   | 4,1   | 1    | 23 | 31979 |
| HNRNPU | ####     |           | ####  | Intra | 1,0   | 1    | 23 | 28469 |
| HNRNPU | ####     |           | ####  | Intra | 2,1   | 1    | 23 | 21572 |
| HNRNPU | ####     |           | ####  | Intra | 3,0   | 1    | 23 | 28951 |
| HNRNPU | ####     |           | ####  | Intra | 1,0   | 1    | 23 | 26543 |
| HNRNPU | ####     |           | ####  | Intra | 2,2   | 1    | 23 | 12005 |
| HNRNPU | ####     |           | ####  | Intra | 2,2   | 1    | 23 | 12573 |
| HNRNPU | ####     |           | ####  | Intra | 1,0   | 1    | 23 | 18454 |
| HNRNPU | ####     |           | ####  | Intra | 1,0   | 1    | 23 | 21513 |
| HNRNPU | ####     |           | ####  | Intra | 8,3   | 1    | 23 | 13734 |
| HNRNPU | ####     |           | ####  | Intra | 2,2   | 1    | 23 | 29364 |
| HNRNPU | ####     |           | ####  | Intra | 2,1   | 1    | 23 | 23651 |
| HNRNPU | ####     |           | ####  | Intra | 6,0   | 1    | 23 | 21753 |
| HNRNPU | ####     |           | ####  | Intra | 2,0   | 1    | 23 | 20378 |
| HNRNPU | ####     |           | ####  | N/A   | 1,0   | 0.99 | 23 | 27157 |
| HNRNPU | ####     |           | ####  | Intra | 1,0   | 1    | 23 | 26643 |
| HNRNPU | ####     |           | ####  | Intra | 4,1   | 1    | 23 | 27485 |
| HNRNPU | ####     |           | ####  | Intra | 4,0   | 1    | 23 | 21753 |
| HNRNPU | ####     |           | ####  | Intra | 0,1   | 1    | 23 | 11460 |
| HNRNPU | ####     |           | ####  | Intra | 2,0   | 1    | 23 | 25711 |
| HNRNPU | ####     |           | ####  | Intra | 1,1   | 1    | 23 | 20599 |
| HNRNPU | ####     |           | ####  | Intra | 0,1   | 1    | 23 | 13359 |
| HNRNPU | Q00839   | Phyre     | 12.82 | Intra | 0,1   | 1    | 23 | 11455 |
| SPTBN1 | ####     |           | ####  | Intra | 1,0   | 1    | 7  | 34195 |
| SPTBN1 | ####     |           | ####  | Intra | 2,0   | 1    | 7  | 26271 |
| SPTBN1 | Q01082   | Phyre     | 23.99 | Intra | 0,1   | 1    | 7  | 13813 |
| SPTBN1 | 3EDV     | Structure | 16.83 | Intra | 4,0   | 1    | 7  | 16772 |
| SPTBN1 | 3EDV     | Structure | 8.45  | Intra | 5,0   | 1    | 7  | 24772 |
| SPTBN1 | Q01082   | Phyre     | 10.62 | Intra | 1,0   | 1    | 7  | 15357 |
| SPTBN1 | ####     |           | ####  | Intra | 0,1   | 1    | 7  | 13702 |
| SPTBN1 | ####     |           | ####  |       | 1 1,0 | 0.97 | 3  | 27981 |
| SPTBN1 | ####     |           | ####  |       | 1 2,0 | 1    | 3  | 24599 |
| SPTAN1 | Q13813   | Phyre     | ####  |       | 1 2,0 | 1    | 3  | 35291 |
| SPTBN1 | Q01082   | Phyre     | ####  |       | 2 2,0 | 0.63 | 1  | 17389 |
| SET    | 2.00E+50 | Structure | 17    | Intra | 3,1   | 1    | 7  | 26903 |
| SET    | Q01105   | Unknown   | ####  | Intra | 0,1   | 1    | 7  | 3399  |
| SET    | 2.00E+50 | Structure | 9.94  | Intra | 1,1   | 1    | 7  | 27094 |
| SET    | 2.00E+50 | Structure | 29.96 | Intra | 0,1   | 1    | 7  | 8055  |
| SET    | 2.00E+50 | Structure | 42.25 | Intra | 1,0   | 1    | 7  | 21357 |
| SET    | 2.00E+50 | Structure | 27.13 | Intra | 2,0   | 1    | 7  | 30502 |
| SET    | 2.00E+50 | Structure | 10.25 | Intra | 1,1   | 1    | 7  | 18583 |
| SLC7A5 | ####     |           | ####  | Intra | 1,0   | 1    | 1  | 16478 |
| PFKP   | 4XYJ     | Structure | 21.63 | Intra | 2,0   | 1    | 8  | 13276 |
| PFKP   | 4XYJ     | Structure | 15.7  | Intra | 1,0   | 1    | 8  | 27357 |
| PFKP   | 4XYJ     | Structure | 18.85 | Intra | 3,0   | 1    | 8  | 24042 |
| PFKP   | 4XYJ     | Structure | 16.3  | Intra | 2,1   | 1    | 8  | 23194 |

|         |           |           |        |       |       |      |   |       |
|---------|-----------|-----------|--------|-------|-------|------|---|-------|
| PFKP    | 4XYJ      | Structure | 12.46  | Intra | 3,2   | 1    | 8 | 17824 |
| PFKP    | 4XYJ      | Structure | 32.66  |       | 1 3,0 | 1    | 8 | 28346 |
| PFKP    | 4XYJ      | Structure | 20.53  | Intra | 2,0   | 1    | 8 | 33050 |
| PFKP    | 4XYJ      | Structure | 8.68   | Intra | 1,0   | 1    | 8 | 23304 |
| DSG1    | ####      | ####      | N/A    |       | 1,0   | 0.76 | 1 | 18604 |
| RPL18A  | Q02543    | Phyre     | 26.94  | Intra | 1,0   | 1    | 2 | 13852 |
| RPL18A  | Q02543    | Phyre     | 28.05  | Intra | 1,0   | 1    | 2 | 22055 |
| FKBP4   | 1QZ2      | Structure | 17.31  | Intra | 1,0   | 1    | 3 | 20540 |
| FKBP4   | 1QZ2      | Structure | 12.22  | Intra | 0,1   | 1    | 3 | 5965  |
| FKBP4   | 1QZ2      | Structure | 16.91  | Intra | 1,0   | 1    | 3 | 19648 |
| RPL6    | Q02878    | Phyre     | 14.21  | Intra | 1,0   | 1    | 1 | 22320 |
| TOP2B   | 3QX3      | Structure | 21.68  | Intra | 1,0   | 0.86 | 1 | 11802 |
| EIF4G1  | ####      | ####      |        | Intra | 2,0   | 1    | 1 | 10298 |
| NOTCH2  | ####      | ####      |        | Intra | 3,1   | 1    | 1 | 6989  |
| GLO1    | 3W0T      | Structure | 18.35  | Intra | 4,0   | 1    | 3 | 15937 |
| GLO1    | 3W0T      | Structure | 18.35  | Intra | 1,3   | 1    | 3 | 15342 |
| GLO1    | 3W0T      | Structure | 14.37  | Intra | 2,0   | 1    | 3 | 22894 |
| PSME1   | 1AVO      | Structure | 16.72  | Intra | 1,1   | 1    | 1 | 15221 |
| PRDX1   | 4XCS      | Structure | 6.35   | Intra | 2,0   | 1    | 4 | 28974 |
| PRDX1   | 4XCS      | Structure | 13.81  | Intra | 1,1   | 1    | 4 | 20864 |
| PRDX1   | 4XCS      | Structure | 13.81  | Intra | 0,1   | 1    | 4 | 11175 |
| PRDX1   | 4XCS      | Structure | 16.52  |       | 1 1,0 | 1    | 4 | 29668 |
| RPL18   | Q07020    | Modeller  | 12.37  | Intra | 1,0   | 1    | 5 | 29740 |
| RPL18   | Q07020    | Modeller  | 27.24  | Intra | 2,0   | 1    | 5 | 15003 |
| RPL18   | Q07020    | Modeller  | 12.44  | Intra | 0,1   | 1    | 5 | 8687  |
| RPL18   | Q07020    | Modeller  | 21.03  | Intra | 1,0   | 1    | 5 | 24680 |
| RPL18   | Q07020    | Modeller  | 8.22   | Intra | 4,1   | 1    | 5 | 25718 |
| C1QBP   | 1P32      | Structure | 16.15  | Intra | 1,2   | 1    | 3 | 2772  |
| C1QBP   | 1P32      | Structure | 17.02  | Intra | 0,1   | 0.89 | 3 | 8141  |
| C1QBP   | 1P32      | Structure | 17.02  | Intra | 0,1   | 0.86 | 3 | 10326 |
| CKAP4   | Q07065    | Phyre     | 17.08  | Intra | 1,0   | 1    | 8 | 11312 |
| CKAP4   | Q07065    | Phyre     | 14.48  | Intra | 2,0   | 1    | 8 | 8088  |
| CKAP4   | Q07065    | Phyre     | 8.03   | Intra | 1,0   | 1    | 8 | 28342 |
| CKAP4   | Q07065_Qi | Docking   | 207.79 |       | 1 1,0 | 1    | 8 | 22038 |
| CKAP4   | ####      | ####      |        | Intra | 4,2   | 1    | 8 | 16597 |
| CKAP4   | Q07065_Qi | Docking   | 84.44  |       | 1 1,1 | 1    | 8 | 36898 |
| CKAP4   | Q07065    | Phyre     | 6.37   | Intra | 3,1   | 1    | 8 | 22609 |
| CKAP4   | Q07065    | Phyre     | 6.37   | Intra | 3,0   | 1    | 8 | 21873 |
| COL16A1 | ####      | ####      | N/A    |       | 0,1   | 1    | 1 | 4623  |
| KLC1    | 3NF1      | Structure | 17.11  | Intra | 1,0   | 1    | 1 | 15479 |
| DHX9    | Q08211    | Phyre     | 15.47  | Intra | 0,1   | 1    | 2 | 13154 |
| DHX9    | Q08211    | Phyre     | 11.08  | Intra | 1,0   | 0.99 | 2 | 21078 |
| GOLGA3  | ####      | ####      |        |       | 1 1,0 | 0.69 | 1 | 36049 |
| NSUN2   | ####      | ####      |        | Intra | 1,0   | 0.99 | 2 | 11974 |
| NSUN2   | Q08J23    | Phyre     | ####   | Intra | 0,2   | 1    | 2 | 7367  |
| AHNAK   | ####      | ####      |        |       | 1 1,0 | 1    | 2 | 23448 |
| AHNAK   | ####      | ####      |        |       | 1 1,0 | 0.69 | 2 | 22593 |

|         |        |           |       |       |       |      |    |       |
|---------|--------|-----------|-------|-------|-------|------|----|-------|
| AP1B1   | 4P6Z   | Structure | 17.06 | Intra | 2,0   | 1    | 1  | 24877 |
| PMPCA   | ####   | ####      |       | Intra | 1,0   | 1    | 2  | 20609 |
| PMPCA   | Q10713 | Phyre     | 12.49 | Intra | 1,0   | 1    | 2  | 25454 |
| NUP160  | ####   | ####      |       |       | 1 2,0 | 0.67 | 1  | 16302 |
| TBL3    | Q12788 | Phyre     | 10.6  | Intra | 2,0   | 1    | 1  | 25292 |
| ASPH    | 5JQY   | Structure | 20.36 | Intra | 1,0   | 0.99 | 1  | 27687 |
| ILF2    | Q12905 | Phyre     | 11.2  | Intra | 1,0   | 1    | 1  | 22400 |
| ILF2    | Q12905 | Phyre     | ####  |       | 1 1,0 | 0.9  | 2  | 27018 |
| ILF3    | Q12906 | Phyre     | ####  |       | 1 1,0 | 0.95 | 2  | 30643 |
| ILF3    | Q12906 | Phyre     | ####  |       | 2 2,0 | 1    | 1  | 17013 |
| TRAP1   | Q12931 | Phyre     | 18.14 | Intra | 1,0   | 1    | 5  | 21539 |
| TRAP1   | 5Y3N   | Structure | 12.56 | Intra | 0,1   | 1    | 5  | 8035  |
| TRAP1   | 5Y3N   | Structure | 14.69 | Intra | 1,0   | 1    | 5  | 18367 |
| TRAP1   | ####   | ####      |       | Intra | 1,0   | 1    | 5  | 21960 |
| TRAP1   | Q12931 | Phyre     | ####  | Intra | 1,0   | 1    | 5  | 26102 |
| ECH1    | ####   | ####      |       | Intra | 1,0   | 1    | 4  | 20843 |
| ECH1    | 2VRE   | Structure | 19.17 | Intra | 2,0   | 1    | 4  | 23160 |
| ECH1    | 2VRE   | Structure | 19.17 | Intra | 3,0   | 1    | 4  | 22039 |
| ECH1    | ####   | ####      |       | Intra | 1,0   | 1    | 4  | 19174 |
| COASY   | Q13057 | Phyre     | 12.16 | Intra | 1,0   | 0.94 | 1  | 19440 |
| ACACA   | 4ASI   | Structure | 79.73 | Intra | 1,0   | 0.97 | 1  | 25550 |
| TARDBP  | Q13148 | Phyre     | 16.95 | Intra | 1,0   | 1    | 1  | 13941 |
| HNRNPA0 | Q13151 | Phyre     | 19.29 | Intra | 2,0   | 1    | 2  | 19610 |
| HNRNPA0 | ####   | ####      |       | Intra | 1,1   | 1    | 2  | 19923 |
| SRSF5   | Q13243 | Phyre     | 10.04 | Intra | 1,0   | 0.99 | 1  | 12838 |
| G3BP2   | ####   | ####      |       |       | 1 2,0 | 1    | 1  | 11179 |
| PABPC4  | Q13310 | Phyre     | 24.16 | Intra | 2,0   | 1    | 1  | 14251 |
| TCOF1   | ####   | ####      |       | Intra | 3,0   | 1    | 4  | 9356  |
| TCOF1   | ####   | ####      |       | Intra | 1,0   | 1    | 4  | 11936 |
| TCOF1   | ####   | ####      |       | Intra | 1,0   | 0.94 | 4  | 10692 |
| TCOF1   | ####   | ####      |       | Intra | 1,0   | 1    | 4  | 11249 |
| ADAM9   | Q13443 | Phyre     | 35.31 | Intra | 2,2   | 1    | 1  | 19260 |
| SMAD4   | 1DD1   | Structure | 9.69  | Intra | 1,0   | 0.94 | 1  | 23032 |
| MTM1    | ####   | ####      |       | N/A   | 1,0   | 0.97 | 1  | 33590 |
| SQSTM1  | ####   | ####      |       |       | 1 1,0 | 1    | 1  | 19280 |
| SNW1    | 5MQF   | Structure | 23.75 | Intra | 2,0   | 1    | 1  | 19055 |
| CUL4A   | 2HYE   | Structure | 22.67 | Intra | 1,0   | 1    | 1  | 16524 |
| ALCAM   | 5A2F   | Structure | 12.06 | Intra | 2,2   | 1    | 2  | 31271 |
| ALCAM   | 5A2F   | Structure | 17.93 | Intra | 0,1   | 1    | 2  | 12542 |
| SPTAN1  | 3FB2   | Structure | 23.27 | Intra | 1,0   | 1    | 11 | 33228 |
| SPTAN1  | ####   | ####      |       | Intra | 3,0   | 1    | 11 | 29635 |
| SPTAN1  | ####   | ####      |       | Intra | 2,1   | 1    | 11 | 21411 |
| SPTAN1  | ####   | ####      |       | Intra | 0,1   | 1    | 11 | 10442 |
| SPTAN1  | ####   | ####      |       | Intra | 1,0   | 1    | 11 | 22202 |
| SPTAN1  | ####   | ####      |       | Intra | 1,0   | 1    | 11 | 10874 |
| SPTAN1  | ####   | ####      |       | Intra | 1,0   | 1    | 11 | 19748 |
| SPTAN1  | ####   | ####      |       | Intra | 0,2   | 1    | 11 | 13042 |

|         |          |           |       |       |       |      |    |       |
|---------|----------|-----------|-------|-------|-------|------|----|-------|
| SPTAN1  | ####     |           | ####  | 1     | 1,0   | 0.75 | 11 | 17343 |
| SPTAN1  | ####     |           | ####  | Intra | 1,0   | 1    | 11 | 17698 |
| SPTAN1  | ####     |           | ####  | Intra | 1,0   | 1    | 11 | 27291 |
| DDX39B  | 1XTK     | Structure | 10.64 | Intra | 2,0   | 1    | 4  | 22725 |
| DDX39B  | 1XTK     | Structure | 18.4  | Intra | 1,0   | 1    | 4  | 19588 |
| DDX39B  | 1XTK     | Structure | 24.92 | Intra | 2,0   | 1    | 4  | 22221 |
| DDX39B  | 1XTK     | Structure | 18.54 | Intra | 1,1   | 1    | 4  | 25087 |
| HNRNPD  | 5IM0     | Structure | 6.41  | Intra | 2,0   | 1    | 5  | 28026 |
| HNRNPD  | Q14103   | Phyre     | 24.5  | Intra | 1,0   | 1    | 5  | 28056 |
| HNRNPD  | 5IM0     | Structure | 10.33 | Intra | 1,1   | 1    | 5  | 30772 |
| HNRNPD  | Q14103   | Phyre     | 29.09 | Intra | 1,0   | 1    | 5  | 19760 |
| HNRNPD  | 5IM0     | Structure | 25.4  | Intra | 0,1   | 1    | 5  | 8873  |
| DSG2    | 5ERD     | Structure | 7.89  | Intra | 3,1   | 1    | 5  | 29984 |
| DSG2    | 5ERD     | Structure | 15.4  | Intra | 4,1   | 1    | 5  | 16590 |
| DSG2    | 5ERD     | Structure | 12.66 | Intra | 1,2   | 1    | 5  | 16828 |
| DSG2    | 5ERD     | Structure | 5.05  | Intra | 2,1   | 1    | 5  | 24785 |
| DSG2    | 5ERD     | Structure | 14.99 | Intra | 2,0   | 1    | 5  | 20364 |
| EIF3A   | ####     |           | ####  | Intra | 0,1   | 1    | 3  | 4853  |
| EIF3A   | Q14152   | Phyre     | ####  | Intra | 1,0   | 1    | 3  | 10129 |
| EIF3A   | ####     |           | ####  | Intra | 1,0   | 1    | 3  | 25737 |
| EIF3A   | Q14152   | Phyre     | ####  |       | 1 3,0 | 1    | 2  | 22355 |
| EIF3C   | Q99613   | Phyre     | ####  |       | 1 2,0 | 1    | 2  | 22187 |
| POLA2   | 4Y97     | Structure | 21.82 | Intra | 1,0   | 1    | 1  | 24619 |
| DYNC1H1 | Q14204   | Modeller  | 53.9  | Intra | 1,0   | 1    | 7  | 40782 |
| DYNC1H1 | Q14204   | Modeller  | 30.73 | Intra | 1,2   | 1    | 7  | 27053 |
| DYNC1H1 | 5NUG     | Structure | 39.94 | Intra | 1,0   | 1    | 7  | 19850 |
| DYNC1H1 | Q14204   | Modeller  | 21.46 | Intra | 1,0   | 1    | 7  | 21129 |
| DYNC1H1 | Q14204   | Modeller  | 38.34 | Intra | 1,1   | 1    | 7  | 13859 |
| DYNC1H1 | 5NUG     | Structure | 27.22 | Intra | 2,0   | 1    | 7  | 33388 |
| DYNC1H1 | 5NUG     | Structure | 54.78 | Intra | 1,0   | 1    | 7  | 16223 |
| CTTN    | ####     |           | ####  | Intra | 0,1   | 1    | 1  | 4787  |
| MCM6    | Q14566   | Phyre     | 20.98 | Intra | 2,0   | 1    | 5  | 20832 |
| MCM6    | Q14566   | Phyre     | 16.64 | Intra | 1,0   | 1    | 5  | 19907 |
| MCM6    | Q14566   | Phyre     | 11.46 | Intra | 1,0   | 1    | 5  | 22348 |
| MCM6    | Q14566   | Phyre     | 24.49 | Intra | 1,0   | 1    | 5  | 19958 |
| MCM6    | Q14566   | Phyre     | 13.03 | Intra | 1,0   | 1    | 5  | 17802 |
| SMC3    | ####     |           | ####  |       | 1 1,0 | 0.98 | 2  | 20932 |
| SMC1A   | ####     |           | ####  |       | 1 1,0 | 0.98 | 2  | 17998 |
| PDCD11  | ####     |           | ####  | Intra | 1,0   | 0.99 | 2  | 19031 |
| PDCD11  | Q14690   | Phyre     | 10.51 | Intra | 1,0   | 0.99 | 2  | 19929 |
| LBR     | ####     |           | ####  | Intra | 1,0   | 0.99 | 1  | 11567 |
| MVP     | Q14764_Q | Docking   | 21.65 |       | 1 1,1 | 1    | 1  | 23060 |
| GOLGB1  | Q14789   | Phyre     | 16.15 | Intra | 1,0   | 1    | 4  | 26351 |
| GOLGB1  | ####     |           | ####  | Intra | 3,1   | 1    | 4  | 17586 |
| GOLGB1  | ####     |           | ####  | N/A   | 1,0   | 0.76 | 4  | 25275 |
| GOLGB1  | ####     |           | ####  | Intra | 2,0   | 1    | 4  | 22363 |
| ENY2    | 4DHX     | Structure | ####  |       | 2 1,0 | 0.99 | 1  | 17508 |



|         |        |           |       |       |       |      |    |       |
|---------|--------|-----------|-------|-------|-------|------|----|-------|
| NUMA1   | ####   |           | ####  | Intra | 1,1   | 1    | 1  | 10546 |
| NUMA1   | ####   |           | ####  |       | 2 0,1 | 0.63 | 1  | 4147  |
| PSME4   | Q14997 | Phyre     | ####  | Intra | 2,0   | 1    | 1  | 20495 |
| PCLAF   | ####   |           | ####  | Intra | 1,0   | 0.97 | 1  | 12100 |
| PSMD6   | 5M32   | Structure | 15.14 | Intra | 0,1   | 1    | 2  | 2845  |
| PSMD6   | 5M32   | Structure | 15.78 | Intra | 1,1   | 1    | 2  | 14918 |
| EFTUD2  | 5O9Z   | Structure | 16.07 | Intra | 3,1   | 1    | 2  | 21052 |
| EFTUD2  | 5O9Z   | Structure | 16.46 | Intra | 1,0   | 1    | 2  | 25080 |
| ARL6IP1 | Q15041 | Phyre     | 15.44 | Intra | 2,1   | 1    | 1  | 17854 |
| ACOX1   | Q15067 | Phyre     | 30.79 | Intra | 2,0   | 1    | 4  | 22415 |
| ACOX1   | Q15067 | Phyre     | 25.3  | Intra | 5,0   | 1    | 4  | 16105 |
| ACOX1   | Q15067 | Phyre     | 17.78 | Intra | 1,0   | 1    | 4  | 23619 |
| ACOX1   | Q15067 | Phyre     | 25.3  | Intra | 1,1   | 1    | 4  | 14011 |
| EEA1    | 1JOC   | Structure | 10.67 | Intra | 1,0   | 1    | 1  | 19857 |
| PDIA6   | ####   |           | ####  | Intra | 1,0   | 0.93 | 3  | 8861  |
| PDIA6   | ####   |           | ####  | Intra | 3,0   | 1    | 3  | 13149 |
| PDIA6   | ####   |           | ####  | Intra | 1,0   | 0.97 | 3  | 9397  |
| PLEC    | ####   |           | ####  | Intra | 0,2   | 1    | 51 | 4879  |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 16137 |
| PLEC    | 5J1I   | Structure | 17.13 | Intra | 1,0   | 1    | 51 | 25236 |
| PLEC    | ####   |           | ####  | Intra | 3,0   | 1    | 51 | 11650 |
| PLEC    | ####   |           | ####  | Intra | 2,1   | 1    | 51 | 20043 |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 16598 |
| PLEC    | ####   |           | ####  | Intra | 2,0   | 1    | 51 | 27362 |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 17010 |
| PLEC    | ####   |           | ####  | Intra | 1,1   | 1    | 51 | 16903 |
| PLEC    | ####   |           | ####  | Intra | 5,1   | 1    | 51 | 9586  |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 16961 |
| PLEC    | ####   |           | ####  | Intra | 0,1   | 1    | 51 | 12093 |
| PLEC    | ####   |           | ####  | Intra | 4,0   | 1    | 51 | 12544 |
| PLEC    | ####   |           | ####  | Intra | 3,0   | 1    | 51 | 13442 |
| PLEC    | ####   |           | ####  | Intra | 2,1   | 1    | 51 | 29215 |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 19602 |
| PLEC    | ####   |           | ####  | Intra | 1,1   | 1    | 51 | 28635 |
| PLEC    | ####   |           | ####  | Intra | 3,2   | 1    | 51 | 15723 |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 10643 |
| PLEC    | ####   |           | ####  | Intra | 5,1   | 1    | 51 | 15785 |
| PLEC    | ####   |           | ####  | Intra | 5,4   | 1    | 51 | 10702 |
| PLEC    | ####   |           | ####  | Intra | 3,0   | 1    | 51 | 19615 |
| PLEC    | Q15149 | Unknown   | 64.6  | Intra | 0,1   | 1    | 51 | 9017  |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 11971 |
| PLEC    | ####   |           | ####  | Intra | 2,0   | 1    | 51 | 19797 |
| PLEC    | ####   |           | ####  | Intra | 0,1   | 1    | 51 | 10243 |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 33004 |
| PLEC    | ####   |           | ####  | Intra | 2,0   | 1    | 51 | 20490 |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 23017 |
| PLEC    | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 19287 |

|        |        |           |       |       |       |      |    |       |
|--------|--------|-----------|-------|-------|-------|------|----|-------|
| PLEC   | ####   |           | ####  | Intra | 2,0   | 1    | 51 | 27390 |
| PLEC   | ####   |           | ####  | Intra | 1,1   | 1    | 51 | 19929 |
| PLEC   | ####   |           | ####  | Intra | 0,1   | 1    | 51 | 10101 |
| PLEC   | ####   |           | ####  | Intra | 1,0   | 1    | 51 | 13537 |
| PLEC   | ####   |           | ####  | Intra | 2,1   | 1    | 51 | 13774 |
| PLEC   | ####   |           | ####  | Intra | 3,0   | 1    | 51 | 25073 |
| PLEC   | ####   |           | ####  | Intra | 8,1   | 1    | 51 | 19416 |
| PLEC   | ####   |           | ####  | Intra | 0,1   | 1    | 51 | 7233  |
| PLEC   | ####   |           | ####  | Intra | 2,2   | 1    | 51 | 25610 |
| PLEC   | 5J1I   | Structure | 25.64 | Intra | 3,2   | 1    | 51 | 23677 |
| PLEC   | ####   |           | ####  | Intra | 0,1   | 1    | 51 | 15245 |
| PLEC   | ####   |           | ####  | Intra | 3,1   | 1    | 51 | 19359 |
| PLEC   | ####   |           | ####  | Intra | 2,0   | 1    | 51 | 23978 |
| PLEC   | ####   |           | ####  | Intra | 2,1   | 1    | 51 | 18024 |
| PLEC   | ####   |           | ####  | Intra | 3,3   | 1    | 51 | 16656 |
| PLEC   | ####   |           | ####  | Intra | 6,2   | 1    | 51 | 16982 |
| PLEC   | ####   |           | ####  | Intra | 2,1   | 1    | 51 | 26311 |
| PLEC   | ####   |           | ####  | N/A   | 2,0   | 1    | 51 | 11875 |
| PLEC   | ####   |           | ####  | Intra | 1,1   | 1    | 51 | 34316 |
| PLEC   | ####   |           | ####  | Intra | 2,0   | 1    | 51 | 20637 |
| PLEC   | ####   |           | ####  | Intra | 0,1   | 1    | 51 | 7157  |
| PLEC   | ####   |           | ####  |       | 2 0,1 | 0.85 | 1  | 7729  |
| NONO   | ####   |           | ####  | Intra | 1,0   | 1    | 8  | 18117 |
| NONO   | 3SDE   | Structure | 18.83 | Intra | 2,2   | 1    | 8  | 22646 |
| NONO   | 3SDE   | Structure | 24.27 | Intra | 1,0   | 1    | 8  | 17894 |
| NONO   | 3SDE   | Structure | 8.69  | Intra | 0,2   | 1    | 8  | 6165  |
| NONO   | 3SDE   | Structure | 10.83 | Intra | 1,0   | 1    | 8  | 16198 |
| NONO   | ####   |           | ####  | Intra | 2,0   | 1    | 8  | 16336 |
| NONO   | Q15233 | Phyre     | ####  | Intra | 2,1   | 1    | 8  | 19497 |
| NONO   | Q15233 | Phyre     | ####  | Intra | 1,0   | 1    | 8  | 16564 |
| PTPRK  | ####   |           | ####  | Intra | 1,0   | 0.94 | 2  | 17289 |
| PTPRK  | ####   |           | ####  | Intra | 1,0   | 1    | 2  | 22588 |
| PWP2   | ####   |           | ####  | Intra | 1,0   | 0.93 | 1  | 29865 |
| RNPS1  | 4A8X   | Structure | 13.69 | Intra | 1,0   | 0.94 | 1  | 27168 |
| RCN1   | Q15293 | Phyre     | 8.5   | Intra | 3,2   | 1    | 1  | 16038 |
| ELOC   | 1VCB   | Structure | ####  | 1 2,0 |       | 1    | 1  | 26964 |
| DHCR24 | Q15392 | Modeller  | 27.91 | Intra | 2,0   | 1    | 2  | 17525 |
| DHCR24 | Q15392 | Modeller  | 30.79 | Intra | 3,0   | 1    | 2  | 29614 |
| SF3B5  | Q9BWJ5 | Phyre     | ####  | 1 1,1 |       | 0.99 | 1  | 8209  |
| SAFB   | ####   |           | ####  | Intra | 0,1   | 1    | 1  | 4735  |
| SF3A1  | ####   |           | ####  | Intra | 0,1   | 0.99 | 1  | 14499 |
| RHOH   | ####   |           | ####  | N/A   | 1,0   | 0.86 | 1  | 11848 |
| MAPRE1 | 2R8U   | Structure | 9.2   | Intra | 1,0   | 0.99 | 1  | 21952 |
| NSDHL  | Q15738 | Modeller  | 29.48 | Intra | 1,0   | 1    | 2  | 35527 |
| NSDHL  | Q15738 | Modeller  | 21.32 | Intra | 1,0   | 1    | 2  | 21300 |
| 7-Sep  | ####   |           | ####  | 1 3,0 |       | 0.96 | 1  | 12876 |
| DDB1   | 3EI3   | Structure | 11.2  | Intra | 1,0   | 1    | 1  | 36387 |

|           |          |           |       |       |        |      |    |       |
|-----------|----------|-----------|-------|-------|--------|------|----|-------|
| FSCN1     | 3LLP     | Structure | 10    | Intra | 0,1    | 1    | 1  | 11382 |
| HIST3H3   | 3A6N     | Structure | 54.91 |       | 1 3,0  | 1    | 13 | 17953 |
| HIST3H3   | 3A6N     | Structure | 20.41 | Intra | 1,1    | 1    | 13 | 20675 |
| HIST3H3   | Q16695   | Phyre     | 16.83 | Intra | 2,0    | 1    | 13 | 9420  |
| HIST3H3   | Q16695   | Phyre     | 16.73 | Intra | 3,2    | 1    | 13 | 7417  |
| HIST3H3   | Q16695   | Phyre     | 50.47 | Intra | 2,0    | 1    | 13 | 17230 |
| HIST3H3   | Q16695   | Phyre     | 21.86 | Intra | 1,1    | 1    | 13 | 7376  |
| HIST3H3   | Q16695   | Phyre     | 10.62 | Intra | 1,0    | 1    | 13 | 4529  |
| HIST3H3   | Q16695   | Phyre     | 19.69 | Intra | 1,2    | 1    | 13 | 5606  |
| HIST3H3   | Q16695_Q | Docking   | 17.61 |       | 1 4,1  | 1    | 13 | 5368  |
| HIST3H3   | Q16695   | Phyre     | 53.2  | Intra | 7,4    | 1    | 13 | 15910 |
| HIST3H3   | 3A6N     | Structure | 38.65 | Intra | 1,0    | 1    | 13 | 21448 |
| HIST3H3   | 3A6N     | Structure | 28.26 | Intra | 2,1    | 1    | 13 | 25291 |
| HIST3H3   | 3A6N     | Structure | 28.26 | Intra | 2,1    | 1    | 13 | 23426 |
| HIST3H3   | 3A6N     | Structure | ####  |       | 1 4,0  | 1    | 1  | 14066 |
| TTN       | ####     | ####      |       |       | 2 5,0  | 0.79 | 1  | 18139 |
| HIST3H3   | 3A6N     | Structure | ####  |       | 1 2,2  | 1    | 13 | 17636 |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 10,4 | 1    | 13 | 23536 |
| HIST3H3   | 3A6N     | Structure | ####  |       | 1 6,7  | 1    | 13 | 15484 |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 2,1  | 1    | 13 | 19522 |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 1,0  | 1    | 13 | 8544  |
| HIST3H3   | 3A6N     | Structure | ####  |       | 1 5,0  | 1    | 13 | 14692 |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 3,1  | 1    | 13 | 8121  |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 1,2  | 1    | 13 | 6750  |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 4,2  | 1    | 13 | 18618 |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 1,0  | 1    | 13 | 9914  |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 1,0  | 1    | 13 | 12950 |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 1,1  | 1    | 13 | 36242 |
| HIST1H2BH | Q93079   | Phyre     | ####  |       | 1 1,0  | 1    | 13 | 16491 |
| HIST3H3   | 3A6N     | Structure | ####  |       | 1 2,2  | 1    | 5  | 22816 |
| HIST3H3   | 3A6N     | Structure | ####  |       | 1 1,0  | 1    | 5  | 21922 |
| HIST3H3   | 3A6N     | Structure | ####  |       | 1 3,2  | 1    | 5  | 26215 |
| HIST3H3   | 3A6N     | Structure | ####  |       | 1 5,2  | 1    | 5  | 24481 |
| HIST1H2AH | Q96KK5   | Phyre     | ####  |       | 1 1,0  | 0.98 | 5  | 16774 |
| CLPP      | 1TG6     | Structure | 5.15  | Intra | 1,0    | 1    | 1  | 28437 |
| ATXN10    | ####     | ####      |       |       | 2 0,1  | 0.92 | 1  | 10375 |
| TST       | Q16762   | Phyre     | 13.77 | Intra | 2,0    | 1    | 1  | 24666 |
| NDUFA9    | 5XTB     | Structure | 13.42 | Intra | 1,0    | 0.94 | 1  | 14066 |
| UGP2      | ####     | ####      |       | Intra | 1,0    | 1    | 6  | 18707 |
| UGP2      | 3R3I     | Structure | 24.8  | Intra | 0,1    | 1    | 6  | 11642 |
| UGP2      | 3R3I     | Structure | 14.55 | Intra | 2,0    | 1    | 6  | 20410 |
| UGP2      | 3R3I     | Structure | 31.32 | Intra | 1,0    | 1    | 6  | 24717 |
| UGP2      | 3R3I     | Structure | 22.14 | Intra | 1,0    | 1    | 6  | 23714 |
| UGP2      | 3R3I     | Structure | 31.58 |       | 1 3,1  | 1    | 6  | 27290 |
| TXNRD1    | 3QFA     | Structure | 26.35 | Intra | 2,0    | 1    | 4  | 15791 |
| TXNRD1    | 3QFA     | Structure | 16.24 | Intra | 1,0    | 1    | 4  | 14987 |
| TXNRD1    | 3QFA     | Structure | 32.68 | Intra | 1,2    | 1    | 4  | 29955 |

|          |           |           |       |       |       |      |    |       |
|----------|-----------|-----------|-------|-------|-------|------|----|-------|
| TXNRD1   | 3QFA      | Structure | 9     | Intra | 1,0   | 1    | 4  | 16134 |
| IMMT     | ####      | ####      |       | Intra | 0,1   | 1    | 4  | 6571  |
| IMMT     | ####      | ####      |       |       | 1 1,0 | 1    | 4  | 11139 |
| IMMT     | ####      | ####      |       | Intra | 2,0   | 1    | 4  | 13367 |
| IMMT     | ####      | ####      |       | Intra | 4,2   | 1    | 4  | 19839 |
| HNRNPUL2 | ####      | ####      |       | Intra | 3,2   | 1    | 2  | 19950 |
| HNRNPUL2 | ####      | ####      |       | Intra | 1,1   | 1    | 2  | 40475 |
| WASHC4   | Q2M389    | Phyre     | 11.99 | Intra | 2,1   | 1    | 1  | 31140 |
| PDCD4    | Q53EL6_Q5 | Docking   | 18.6  |       | 1 0,1 | 0.99 | 1  | 3024  |
| ACTBL2   | Q562R1    | Phyre     | 10.29 | Intra | 0,1   | 1    | 1  | 9627  |
| LIMA1    | ####      | ####      |       |       | 2 0,1 | 0.98 | 1  | 9860  |
| CCDC178  | Q5BJE1_Q5 | Docking   | 81.74 | N/A   | 1,0   | 0.86 | 1  | 13713 |
| ZNF326   | ####      | ####      |       | Intra | 1,0   | 0.94 | 1  | 20931 |
| UBR4     | ####      | ####      |       | Intra | 1,0   | 1    | 1  | 22481 |
| OBSCN    | ####      | ####      |       | N/A   | 1,0   | 0.75 | 1  | 33321 |
| STEAP4   | ####      | ####      |       | N/A   | 1,0   | 1    | 1  | 14851 |
| VASN     | Q6EMK4    | Modeller  | 9.39  | Intra | 1,0   | 0.93 | 1  | 21634 |
| SLC25A24 | Q6NUK1    | Phyre     | 23.97 | Intra | 3,2   | 1    | 2  | 22967 |
| SLC25A24 | Q6NUK1    | Phyre     | 21.28 | Intra | 1,0   | 0.99 | 2  | 18184 |
| CC2D1A   | ####      | ####      |       | Intra | 1,0   | 1    | 1  | 18329 |
| ALKBH5   | 4O7X      | Structure | 21.35 | Intra | 1,0   | 1    | 1  | 14710 |
| TTC37    | ####      | ####      |       | Intra | 2,0   | 1    | 1  | 25554 |
| C1orf228 | ####      | ####      |       | N/A   | 1,0   | 0.97 | 1  | 11965 |
| RHBDF2   | ####      | ####      |       | Intra | 1,0   | 1    | 1  | 24768 |
| CSPG4    | ####      | ####      |       | Intra | 1,3   | 1    | 4  | 30886 |
| CSPG4    | ####      | ####      |       | Intra | 0,1   | 1    | 4  | 15545 |
| CSPG4    | ####      | ####      |       | Intra | 1,1   | 1    | 4  | 23348 |
| CSPG4    | ####      | ####      |       | Intra | 1,4   | 1    | 4  | 27165 |
| IL27RA   | ####      | ####      |       | Intra | 0,1   | 0.87 | 1  | 20203 |
| CD109    | Q6YHK3    | Phyre     | 20.22 | Intra | 2,5   | 1    | 15 | 33326 |
| CD109    | Q6YHK3    | Phyre     | 18.52 | Intra | 2,0   | 1    | 15 | 16142 |
| CD109    | Q6YHK3    | Phyre     | 19.72 | Intra | 0,1   | 1    | 15 | 11112 |
| CD109    | Q6YHK3    | Phyre     | 12.45 | Intra | 3,2   | 1    | 15 | 24672 |
| CD109    | Q6YHK3    | Phyre     | 19.72 | Intra | 0,2   | 1    | 15 | 11040 |
| CD109    | Q6YHK3    | Phyre     | 28.22 | Intra | 1,0   | 1    | 15 | 33291 |
| CD109    | Q6YHK3    | Phyre     | 10.77 | Intra | 1,0   | 1    | 15 | 29470 |
| CD109    | Q6YHK3    | Phyre     | 22.93 | Intra | 3,5   | 1    | 15 | 31458 |
| CD109    | Q6YHK3    | Phyre     | 14.76 | Intra | 1,1   | 1    | 15 | 30293 |
| CD109    | ####      | ####      |       | N/A   | 0,1   | 1    | 15 | 13131 |
| CD109    | Q6YHK3    | Phyre     | 27.73 | Intra | 1,0   | 1    | 15 | 20673 |
| CD109    | Q6YHK3    | Phyre     | 25.42 | Intra | 2,1   | 1    | 15 | 22941 |
| CD109    | Q6YHK3    | Phyre     | 22.31 | Intra | 1,0   | 1    | 15 | 22791 |
| CD109    | Q6YHK3    | Phyre     | 20.13 | Intra | 3,2   | 1    | 15 | 17299 |
| CD109    | Q6YHK3    | Phyre     | 33.37 | Intra | 3,0   | 1    | 15 | 12415 |
| ARHGEF18 | ####      | ####      |       |       | 1 1,0 | 0.97 | 1  | 35945 |
| IKBIP    | Q70UQ0_C  | Docking   | 51.74 | N/A   | 0,1   | 1    | 1  | 4091  |
| TUBA1A   | 5JCO      | Structure | 25.44 | Intra | 1,0   | 0.86 | 1  | 23128 |

|           |                   |           |       |       |       |      |   |       |
|-----------|-------------------|-----------|-------|-------|-------|------|---|-------|
| BTN2A1    | Q7KYR7_Q Docking  |           | 22.74 | N/A   | 1,0   | 1    | 1 | 18334 |
| SND1      | 3BDL              | Structure | 38.12 | Intra | 0,2   | 1    | 6 | 12798 |
| SND1      | 3BDL              | Structure | 34.01 | Intra | 3,0   | 1    | 6 | 18795 |
| SND1      | 3BDL              | Structure | 37.09 | Intra | 1,1   | 1    | 6 | 16670 |
| SND1      | 3BDL              | Structure | 34.01 | Intra | 6,1   | 1    | 6 | 16708 |
| SND1      | 3BDL              | Structure | 30.34 | Intra | 0,3   | 1    | 6 | 13787 |
| SND1      | 3BDL              | Structure | 20.6  | Intra | 1,0   | 1    | 6 | 18614 |
| BZW1      | Q7L1Q6            | Phyre     | 15.79 | Intra | 0,1   | 1    | 1 | 9411  |
| ARC       | ####              |           | ####  | N/A   | 1,0   | 0.75 | 1 | 21642 |
| KTN1      | Q86UP2            | Phyre     | 13.94 | Intra | 1,0   | 1    | 1 | 24229 |
| CAND1     | 1U6G              | Structure | 8.1   | Intra | 2,0   | 1    | 1 | 21673 |
| NLRP3     | ####              |           | ####  |       | 2 1,0 | 0.8  | 1 | 26942 |
| WDR75     | Q8IWA0            | Phyre     | ####  | Intra | 1,0   | 1    | 1 | 26658 |
| PEX5L     | Q8IYB4_Q& Docking |           | 17.12 |       | 1 0,2 | 0.64 | 1 | 3278  |
| ST13P4    | ####              |           | ####  | Intra | 1,0   | 0.99 | 3 | 13440 |
| ST13P4    | Q8IZP2            | Phyre     | 10.92 | Intra | 2,0   | 1    | 3 | 20578 |
| ST13P4    | Q8IZP2            | Phyre     | 9.58  | Intra | 4,1   | 1    | 3 | 23913 |
| HIST3H2BB | Q8N257            | Phyre     | 20.39 | Intra | 1,0   | 1    | 3 | 23180 |
| HIST3H2BB | Q8N257            | Phyre     | 23.46 | Intra | 4,3   | 1    | 3 | 16766 |
| HIST3H2BB | Q8N257            | Phyre     | 34.51 | Intra | 3,0   | 1    | 3 | 13753 |
| HIST3H2BB | Q8N257            | Phyre     | ####  |       | 1 3,1 | 1    | 1 | 8345  |
| STAG2     | 4PJW              | Structure | 13.82 | Intra | 4,0   | 1    | 1 | 25541 |
| EMC1      | Q8N766            | Phyre     | 38.02 | Intra | 2,0   | 1    | 1 | 18441 |
| DCBLD1    | Q8N8Z6            | Phyre     | 23.66 | Intra | 4,0   | 1    | 2 | 11470 |
| DCBLD1    | Q8N8Z6            | Phyre     | 31.18 | Intra | 1,0   | 1    | 2 | 15141 |
| SERBP1    | ####              |           | ####  | Intra | 2,0   | 1    | 2 | 16197 |
| SERBP1    | ####              |           | ####  | Intra | 1,0   | 1    | 2 | 13409 |
| CCDC168   | ####              |           | ####  | N/A   | 1,0   | 0.69 | 1 | 40877 |
| PPHLN1    | ####              |           | ####  | Intra | 1,0   | 1    | 1 | 13615 |
| SYNE1     | ####              |           | ####  |       | 1 1,0 | 0.97 | 1 | 22564 |
| BOD1L1    | ####              |           | ####  | N/A   | 1,0   | 0.75 | 1 | 32306 |
| C9orf43   | ####              |           | ####  | N/A   | 1,0   | 1    | 1 | 21633 |
| UTP15     | Q8TED0            | Modeller  | 18.64 | Intra | 1,0   | 0.97 | 1 | 18351 |
| DOT1L     | ####              |           | ####  | N/A   | 1,0   | 0.69 | 1 | 29708 |
| NUP210    | ####              |           | ####  | Intra | 0,1   | 1    | 2 | 9133  |
| NUP210    | ####              |           | ####  | N/A   | 1,0   | 1    | 2 | 24378 |
| GEMIN5    | 5H3U              | Structure | 25.84 | Intra | 1,0   | 0.99 | 1 | 16852 |
| PNISR     | ####              |           | ####  | N/A   | 1,0   | 0.75 | 1 | 45262 |
| LIPH      | ####              |           | ####  | Intra | 1,0   | 1    | 1 | 16020 |
| PSPC1     | ####              |           | ####  | Intra | 1,0   | 0.99 | 1 | 11998 |
| SYNE2     | ####              |           | ####  | N/A   | 1,0   | 1    | 1 | 13650 |
| TTN       | ####              |           | ####  |       | 1 1,0 | 0.86 | 1 | 22559 |
| DDB2      | 4.00E+54          | Structure | 12.49 | Intra | 1,0   | 0.94 | 1 | 21269 |
| DDX1      | Q92499            | Phyre     | 14.05 | Intra | 1,0   | 1    | 1 | 22394 |
| HSPH1     | Q92598            | Phyre     | ####  | Intra | 2,0   | 1    | 1 | 12809 |
| NUP205    | Q92621            | Phyre     | 25.74 | Intra | 3,0   | 1    | 4 | 16614 |
| NUP205    | Q92621            | Phyre     | 23.49 | Intra | 1,0   | 1    | 4 | 16778 |

|           |          |           |       |       |       |      |   |       |
|-----------|----------|-----------|-------|-------|-------|------|---|-------|
| NUP205    | Q92621   | Phyre     | 14.06 | Intra | 4,0   | 1    | 4 | 16487 |
| NUP205    | Q92621   | Phyre     | 10.11 | Intra | 0,1   | 1    | 4 | 18961 |
| AKAP1     | Q92667   | Phyre     | 10    | Intra | 2,0   | 1    | 1 | 16336 |
| NECTIN2   | ####     | ####      |       |       | 1 1,0 | 0.99 | 1 | 20937 |
| DDX17     | ####     | ####      |       | Intra | 1,2   | 1    | 2 | 24490 |
| DDX17     | Q92841   | Phyre     | 17.26 | Intra | 3,0   | 1    | 2 | 32408 |
| ARHGEF1   | 3ODW     | Structure | 40.17 | Intra | 1,0   | 0.99 | 1 | 22516 |
| UPF1      | ####     | ####      |       | Intra | 2,0   | 1    | 1 | 20532 |
| KHSRP     | 2JVZ     | Structure | 8.8   | Intra | 2,0   | 1    | 2 | 21126 |
| KHSRP     | Q92945   | Phyre     | 13.33 | Intra | 2,0   | 1    | 2 | 18908 |
| USP7      | 5FWI     | Structure | 15.34 | Intra | 1,0   | 1    | 1 | 37477 |
| ATP6VOA1  | Q93050   | Phyre     | 12.05 | Intra | 1,1   | 1    | 1 | 20962 |
| HIST1H2BF | Q93079   | Phyre     | 20.39 | Intra | 2,0   | 1    | 8 | 23347 |
| HIST1H2BF | Q93079   | Phyre     | 20.39 | Intra | 2,0   | 1    | 8 | 19845 |
| HIST1H2BF | Q93079   | Phyre     | 18.44 | Intra | 9,10  | 1    | 8 | 19416 |
| HIST1H2BF | Q93079   | Phyre     | 23.18 | Intra | 4,4   | 1    | 8 | 12449 |
| HIST1H2BF | Q93079   | Phyre     | 19.74 | Intra | 1,0   | 1    | 8 | 20615 |
| HIST1H2BF | Q93079   | Phyre     | 23.46 | Intra | 7,3   | 1    | 8 | 16083 |
| HIST1H2BF | Q93079   | Phyre     | 34.51 | Intra | 3,1   | 1    | 8 | 12686 |
| HIST1H2BF | Q93079   | Phyre     | 14.86 | Intra | 3,0   | 1    | 8 | 5669  |
| HIST1H2AF | Q96KK5   | Phyre     | ####  |       | 1 1,0 | 1    | 8 | 22423 |
| HIST1H2BF | Q93079   | Phyre     | ####  |       | 1 1,1 | 1    | 8 | 22087 |
| HIST1H2BF | Q93079   | Phyre     | ####  |       | 1 2,2 | 1    | 8 | 13753 |
| HIST1H2BF | Q93079   | Phyre     | ####  |       | 1 2,0 | 1    | 8 | 19231 |
| HIST1H2BF | Q93079   | Phyre     | ####  |       | 1 8,5 | 1    | 8 | 7361  |
| HIST1H2BF | Q93079   | Phyre     | ####  |       | 1 2,3 | 1    | 8 | 14613 |
| HIST1H2BF | Q93079   | Phyre     | ####  |       | 1 3,0 | 1    | 8 | 12654 |
| HIST1H2BF | Q93079   | Phyre     | ####  |       | 1 3,5 | 1    | 8 | 24862 |
| IGSF8     | ####     | ####      |       | Intra | 1,0   | 0.99 | 2 | 14112 |
| IGSF8     | Q969P0   | Phyre     | 13.44 | Intra | 9,3   | 1    | 2 | 16894 |
| FUBP1     | 1J4W     | Structure | 18.46 | Intra | 1,0   | 1    | 1 | 20956 |
| LRRC59    | Q96AG4_Q | Docking   | 124.3 | N/A   | 1,0   | 0.97 | 2 | 36621 |
| LRRC59    | Q96AG4   | Phyre     | 5.69  | Intra | 1,0   | 1    | 2 | 34378 |
| COA7      | ####     | ####      |       | Intra | 1,0   | 1    | 2 | 8866  |
| COA7      | Q96BR5   | Phyre     | 10.01 | Intra | 0,1   | 1    | 2 | 7226  |
| AP2M1     | Q96CW1   | Phyre     | 10.09 | Intra | 0,1   | 0.85 | 2 | 7889  |
| AP2M1     | Q96CW1   | Phyre     | 14.66 | Intra | 1,0   | 1    | 2 | 19992 |
| SEH1L     | Q96EE3   | Phyre     | 13.38 | Intra | 1,0   | 0.99 | 1 | 17386 |
| ERO1A     | 3AHQ     | Structure | 15.26 | Intra | 1,0   | 0.99 | 1 | 25825 |
| PGAM5     | 5MUF     | Structure | 24.24 | Intra | 2,0   | 1    | 2 | 11960 |
| PGAM5     | 5MUF     | Structure | 31.25 | Intra | 1,0   | 0.94 | 2 | 16736 |
| FUBP3     | Q96I24   | Phyre     | 14.79 | Intra | 1,0   | 1    | 1 | 17247 |
| KIRREL1   | Q96J84   | Phyre     | 47.66 | Intra | 2,0   | 1    | 1 | 25338 |
| CLPTM1L   | Q96KA5   | Phyre     | 13.93 | Intra | 1,0   | 0.99 | 1 | 21111 |
| HIST1H2AF | ####     | ####      |       |       | 1 1,1 | 1    | 3 | 7946  |
| HIST1H2AF | Q96KK5   | Phyre     | 8.33  | Intra | 2,1   | 1    | 3 | 35169 |
| HIST1H2AF | ####     | ####      |       |       | 1 4,2 | 1    | 3 | 25752 |

|          |          |           |       |       |       |      |   |       |
|----------|----------|-----------|-------|-------|-------|------|---|-------|
| GFM1     | Q96RP9   | Phyre     | 18.39 | Intra | 1,0   | 1    | 1 | 37363 |
| RANBP9   | ####     |           | ####  | Intra | 2,0   | 1    | 1 | 29546 |
| UHRF1    | 2PB7     | Structure | 23.17 | Intra | 1,0   | 1    | 1 | 14888 |
| FAM129B  | ####     |           | ####  | Intra | 2,0   | 1    | 2 | 20020 |
| FAM129B  | ####     |           | ####  | Intra | 1,0   | 1    | 2 | 12700 |
| SDF2     | Q99470   | Phyre     | 13.45 | Intra | 3,1   | 1    | 1 | 12354 |
| SORT1    | 6EHO     | Structure | 15.11 | Intra | 2,0   | 1    | 1 | 16927 |
| DNAJC7   | Q99615   | Phyre     | 12.07 | Intra | 1,0   | 0.99 | 1 | 22414 |
| C12orf57 | ####     |           | ####  | Intra | 2,0   | 1    | 1 | 25695 |
| PHB2     | Q99623_Q | Docking   | 19.74 |       | 1 2,0 | 1    | 9 | 15274 |
| PHB2     | Q99623   | Phyre     | 35.57 | Intra | 0,1   | 1    | 9 | 7571  |
| PHB2     | ####     |           | ####  | Intra | 2,1   | 1    | 9 | 17528 |
| PHB2     | Q99623_Q | Docking   | 14.59 |       | 1 1,0 | 1    | 9 | 15288 |
| PHB2     | ####     |           | ####  | Intra | 1,0   | 1    | 9 | 18505 |
| PHB2     | ####     |           | ####  | Intra | 2,0   | 1    | 9 | 17441 |
| PHB2     | Q99623   | Phyre     | ####  | Intra | 0,2   | 1    | 9 | 10571 |
| PHB2     | Q99623   | Phyre     | 26.16 | Intra | 1,2   | 1    | 9 | 23604 |
| PHB2     | Q99623   | Phyre     | 5.23  | Intra | 1,0   | 1    | 9 | 26095 |
| HSD17B10 | 2O23     | Structure | 18.43 | Intra | 0,1   | 0.85 | 1 | 14595 |
| HNRNPAB  | Q99729   | Phyre     | 29.09 | Intra | 1,0   | 0.99 | 2 | 16037 |
| HNRNPAB  | Q99729   | Phyre     | 24.95 | Intra | 1,0   | 1    | 2 | 19057 |
| CCT7     | Q99832   | Phyre     | 32.64 | Intra | 0,1   | 1    | 5 | 10797 |
| CCT7     | Q99832   | Phyre     | 31.82 | Intra | 0,1   | 1    | 5 | 16757 |
| CCT7     | Q99832   | Phyre     | 10.2  | Intra | 3,2   | 1    | 5 | 28528 |
| CCT7     | Q99832   | Phyre     | 14.05 | Intra | 3,1   | 1    | 5 | 18963 |
| CCT7     | Q99832   | Phyre     | 15.42 | Intra | 1,0   | 1    | 5 | 32331 |
| PRMT1    | Q99873   | Phyre     | 11.98 | Intra | 0,1   | 1    | 1 | 12943 |
| NIPSNAP1 | ####     |           | ####  | Intra | 2,0   | 1    | 1 | 15120 |
| MICU1    | 4NSC     | Structure | 18.47 | Intra | 1,0   | 0.99 | 1 | 18058 |
| C17orf62 | Q9BQA9   | Unknown   | 25.21 | Intra | 1,0   | 1    | 1 | 23568 |
| ESYT1    | Q9BSJ8   | Phyre     | 19.16 | Intra | 0,1   | 1    | 1 | 11950 |
| HNRNPUL1 | ####     |           | ####  | Intra | 1,0   | 0.86 | 1 | 16500 |
| TMEM109  | ####     |           | ####  | N/A   | 1,0   | 0.86 | 1 | 14914 |
| NUP85    | Q9BW27   | Phyre     | 10.47 | Intra | 1,0   | 0.93 | 1 | 12319 |
| ACAT2    | ####     |           | ####  |       | 1 1,0 | 0.97 | 1 | 19719 |
| SRRT     | Q9BXP5   | Phyre     | 10.04 | Intra | 1,0   | 1    | 2 | 30326 |
| SRRT     | Q9BXP5   | Phyre     | ####  | Intra | 2,0   | 1    | 2 | 20096 |
| NIFK     | ####     |           | ####  | Intra | 1,1   | 1    | 1 | 5337  |
| GTPBP4   | Q9BZE4   | Phyre     | 5.07  | Intra | 1,0   | 1    | 1 | 18117 |
| ULBP3    | 1KCG     | Structure | 16.19 | Intra | 3,0   | 1    | 1 | 21339 |
| API5     | 3U0R     | Structure | 12.01 | Intra | 2,0   | 1    | 1 | 23927 |
| WDR12    | Q9GZL7   | Modeller  | 20.71 | Intra | 1,0   | 1    | 1 | 23250 |
| PNN      | ####     |           | ####  | Intra | 1,0   | 1    | 2 | 21072 |
| PNN      | ####     |           | ####  | Intra | 0,1   | 1    | 2 | 8987  |
| CHMP4B   | 4ABM     | Structure | 10.37 | Intra | 1,0   | 0.99 | 1 | 16140 |
| HEATR1   | ####     |           | ####  | Intra | 1,0   | 1    | 1 | 37521 |
| NOL6     | Q9H6R4   | Phyre     | 12.14 | Intra | 1,0   | 0.94 | 2 | 18974 |

|         |          |           |        |       |       |      |   |       |
|---------|----------|-----------|--------|-------|-------|------|---|-------|
| NOL6    | Q9H6R4   | Phyre     | 14.25  | Intra | 1,0   | 0.93 | 2 | 17201 |
| GNB4    | ####     |           | ####   | Intra | 1,0   | 1    | 1 | 26965 |
| CBX8    | 5EQ0     | Structure | 13.06  | Intra | 1,0   | 0.99 | 1 | 29297 |
| MOV10   | Q9HCE1   | Phyre     | 25.08  | Intra | 2,0   | 1    | 2 | 23450 |
| MOV10   | Q9HCE1   | Phyre     | 10.63  | Intra | 2,0   | 1    | 2 | 19682 |
| CELSR2  | Q9HCU4   | Modeller  | 391.73 | Intra | 1,2   | 1    | 3 | 21076 |
| CELSR2  | Q9HCU4   | Modeller  | 394.29 | Intra | 0,1   | 1    | 3 | 12646 |
| CELSR2  | Q9HCU4   | Modeller  | 55.6   | Intra | 3,0   | 1    | 3 | 20147 |
| APMAP   | Q9HDC9   | Phyre     | 10.47  | Intra | 1,0   | 1    | 1 | 27752 |
| ACOT13  | 3F5O     | Structure | 19.35  | Intra | 0,1   | 1    | 2 | 11864 |
| ACOT13  | 3F5O     | Structure | 24.37  |       | 1 1,0 | 1    | 2 | 26851 |
| DDX21   | ####     |           | ####   | N/A   | 1,0   | 0.95 | 3 | 26529 |
| DDX21   | ####     |           | ####   | Intra | 0,1   | 1    | 3 | 2995  |
| DDX21   | Q9NR30   | Phyre     | 13.05  | Intra | 1,0   | 0.94 | 3 | 25515 |
| IARS2   | Q9NSE4   | Phyre     | 6.4    | Intra | 1,0   | 1    | 1 | 29966 |
| TMEM30A | Q9NV96   | Phyre     | 17.17  | Intra | 1,0   | 1    | 2 | 18831 |
| TMEM30A | ####     |           | ####   | N/A   | 1,0   | 1    | 2 | 16329 |
| DNAJC11 | ####     |           | ####   | Intra | 1,0   | 0.99 | 1 | 18909 |
| ATAD3A  | ####     |           | ####   | N/A   | 0,1   | 1    | 6 | 2795  |
| ATAD3A  | ####     |           | ####   | N/A   | 0,1   | 0.99 | 6 | 2649  |
| ATAD3A  | ####     |           | ####   | N/A   | 3,4   | 1    | 6 | 14690 |
| ATAD3A  | ####     |           | ####   | Intra | 0,1   | 1    | 6 | 10156 |
| ATAD3A  | ####     |           | ####   | Intra | 0,1   | 1    | 6 | 7163  |
| ATAD3A  | ####     |           | ####   | N/A   | 3,1   | 1    | 6 | 6213  |
| HEATR5B | ####     |           | ####   |       | 2 0,1 | 0.83 | 1 | 3770  |
| NLE1    | Q9NVX2   | Modeller  | 25.74  | Intra | 2,0   | 1    | 1 | 18123 |
| RBM28   | ####     |           | ####   |       | 1 1,0 | 0.97 | 1 | 47361 |
| TECR    | 2DZJ     | Structure | 16.75  | Intra | 1,0   | 1    | 1 | 22491 |
| RCC2    | 5GWN     | Structure | 19.85  | Intra | 1,0   | 1    | 1 | 26948 |
| TENM3   | Q9P273   | Phyre     | 16.93  | Intra | 2,0   | 1    | 1 | 21294 |
| PTGFRN  | Q9P2B2   | Phyre     | 10.35  | Intra | 2,0   | 1    | 3 | 24093 |
| PTGFRN  | Q9P2B2   | Phyre     | ####   | Intra | 4,0   | 1    | 3 | 21204 |
| PTGFRN  | Q9P2B2   | Phyre     | ####   | Intra | 1,0   | 0.99 | 3 | 20015 |
| RRBP1   | Q9P2E9_Q | Docking   | 17.35  | N/A   | 1,0   | 0.86 | 8 | 12091 |
| RRBP1   | ####     |           | ####   | Intra | 2,2   | 1    | 8 | 4350  |
| RRBP1   | ####     |           | ####   | Intra | 1,0   | 1    | 8 | 4637  |
| RRBP1   | Q9P2E9   | Phyre     | 15.14  | Intra | 1,1   | 1    | 8 | 18280 |
| RRBP1   | ####     |           | ####   | Intra | 3,2   | 1    | 8 | 4239  |
| RRBP1   | ####     |           | ####   | Intra | 1,0   | 1    | 8 | 5080  |
| RRBP1   | ####     |           | ####   | Intra | 1,0   | 1    | 8 | 10186 |
| RRBP1   | ####     |           | ####   | Intra | 1,0   | 1    | 8 | 4637  |
| SRP68   | Q9UHB9   | Modeller  | 38.69  | Intra | 1,0   | 1    | 1 | 34247 |
| 9-Sep   | ####     |           | ####   | Intra | 1,2   | 1    | 1 | 32966 |
| TMEM2   | ####     |           | ####   | Intra | 0,2   | 1    | 3 | 10526 |
| TMEM2   | Q9UHN6   | Phyre     | 23.57  | Intra | 1,0   | 1    | 3 | 27201 |
| TMEM2   | Q9UHN6   | Phyre     | ####   | Intra | 2,0   | 1    | 3 | 23435 |
| PUF60   | Q9UHX1   | Phyre     | 10.12  | Intra | 1,0   | 1    | 1 | 19199 |



|          |                   |           |       |            |      |   |       |
|----------|-------------------|-----------|-------|------------|------|---|-------|
| ATPIF1   | Q9UII2_Q9 Docking |           | 15.66 | 1 1,0      | 1    | 2 | 13528 |
| ATPIF1   | Q9UII2            | Phyre     | 61.4  | Intra 1,0  | 0.97 | 2 | 12380 |
| LNPEP    | ####              | ####      | N/A   | 1,0        | 1    | 1 | 31939 |
| SLC25A13 | 4P5W              | Structure | 13    | Intra 1,0  | 0.94 | 1 | 20149 |
| STOML2   | Q9UJZ1_Q9 Docking |           | 15.08 | N/A 1,2    | 1    | 1 | 27440 |
| RALY     | 1WF1              | Structure | 15.9  | Intra 2,0  | 1    | 1 | 27838 |
| PRPF19   | 4LG8              | Structure | 35.22 | Intra 2,0  | 1    | 1 | 26728 |
| RPL26L1  | Q9UNX3            | Phyre     | 16.58 | Intra 1,0  | 0.99 | 1 | 19574 |
| BAIAP2   | ####              | ####      |       | 1 1,0      | 0.96 | 1 | 30053 |
| SMC3     | ####              | ####      |       | Intra 0,1  | 1    | 1 | 7051  |
| VDAC3    | Q9Y277            | Phyre     | 21.02 | Intra 1,0  | 1    | 2 | 24155 |
| VDAC3    | Q9Y277            | Phyre     | 23.89 | Intra 1,2  | 1    | 2 | 23160 |
| FARSA    | 3L4G              | Structure | 10.19 | Intra 4,0  | 1    | 1 | 14262 |
| GSTK1    | 3RPP              | Structure | 10.94 | Intra 1,0  | 1    | 2 | 20207 |
| GSTK1    | 3RPP              | Structure | 17.09 | Intra 2,0  | 1    | 2 | 19957 |
| MRPS7    | Q9Y2R9            | Phyre     | 36.56 | Intra 1,0  | 1    | 1 | 22572 |
| YARS2    | 2PID              | Structure | 23.41 | Intra 1,0  | 0.97 | 1 | 15318 |
| ACOT9    | ####              | ####      |       | Intra 0,1  | 1    | 1 | 8771  |
| TMED5    | ####              | ####      |       | N/A 1,0    | 0.86 | 1 | 50418 |
| NOP16    | Q9Y3C1            | Phyre     | 15.16 | Intra 1,0  | 0.99 | 1 | 13981 |
| FIS1     | 1PC2              | Structure | 17.41 | Intra 1,0  | 1    | 1 | 28738 |
| RTCB     | Q9Y3I0            | Modeller  | 17.26 | Intra 1,1  | 1    | 1 | 5797  |
| SAMHD1   | 5A00              | Structure | 43.2  | 1 0,1      | 0.99 | 1 | 13269 |
| TLN1     | ####              | ####      |       | Intra 1,0  | 1    | 4 | 28283 |
| TLN1     | ####              | ####      |       | 1 1,0      | 1    | 4 | 14589 |
| TLN1     | ####              | ####      |       | 1 2,0      | 0.95 | 4 | 31028 |
| TLN1     | ####              | ####      |       | Intra 2,0  | 1    | 4 | 19204 |
| SUPT16H  | 5E5B              | Structure | 9.56  | Intra 1,2  | 1    | 2 | 20053 |
| SUPT16H  | 5E5B              | Structure | 21.49 | Intra 1,0  | 1    | 2 | 16508 |
| UCHL5    | 4UEL              | Structure | 6.85  | Intra 2,0  | 1    | 1 | 26008 |
| F11R     | 1NBQ              | Structure | 15.61 | Intra 1,2  | 1    | 4 | 22537 |
| F11R     | 1NBQ              | Structure | 11.94 | Intra 14,6 | 1    | 4 | 21161 |
| F11R     | 1NBQ              | Structure | 8.81  | Intra 8,5  | 1    | 4 | 29155 |
| F11R     | 1NBQ              | Structure | 16.54 | Intra 6,5  | 1    | 4 | 27728 |
| NPTN     | ####              | ####      |       | Intra 1,0  | 0.94 | 1 | 18040 |
| MAD1L1   | ####              | ####      |       | 1 1,0      | 0.75 | 1 | 25126 |
| BZW2     | Q9Y6E2            | Phyre     | 26.57 | Intra 1,0  | 0.99 | 1 | 26008 |
| ROBO1    | 5OPE              | Structure | 36.78 | Intra 2,0  | 1    | 4 | 16115 |
| ROBO1    | 5OPE              | Structure | 44.66 | Intra 1,0  | 1    | 4 | 15768 |
| ROBO1    | 5OPE              | Structure | 44.66 | Intra 0,1  | 1    | 4 | 9295  |
| ROBO1    | Q9Y6N7            | Modeller  | 20.33 | Intra 6,4  | 1    | 4 | 20444 |
| CDH10    | ####              | ####      |       | Intra 1,0  | 1    | 1 | 17704 |

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| iprobability | probability peptide                         |
|--------------|---------------------------------------------|
| 0.999999     | 1 K.SK[325.13]HSNSEHKDSEK.K                 |
| 0.999999     | 1 R.HSDENDGGQPHK[325.13]R.R                 |
| 0.999999     | 1 K.KKPQK[325.13]VAGGAAPSKPASAK.K           |
| 0.999999     | 1 K.KKPQK[325.13]VAGGAAPSKPASAK.K           |
| 0.999999     | 1 K.KPVGAAK[325.13]KPK.K                    |
| 0.999999     | 1 R.IVQK[325.13]HPHTGDTKEEK.D               |
| 0.999999     | 1 K.KKPQK[325.13]VAGGAAPSKPASAK.K           |
| 0.999999     | 1 K.KKPQK[325.13]VAGGAAPSKPASAK.K           |
| 0.999999     | 1 K.KKPQK[325.13]VAGGAAPSKPASAK.K           |
| 0.999999     | 1 R.HSDENDGGQPHK[325.13]R.R                 |
| 0.999999     | 1 K.KPVGAAK[325.13]KPK.K                    |
| 0.999999     | 1 K.SPAKPK[325.13]AVKPK.A                   |
| 0.999999     | 0.9999 K.SPAKPK[325.13]AVKPK.A              |
| 0.999999     | 1 K.K[325.13]C[160.03]GHTNNLRPK.K           |
| 0.999999     | 1 R.IEHIK[325.13]HSK.S                      |
| 0.999999     | 1 K.SAPATGGVK[325.13]KPHR.Y                 |
| 0.999999     | 1 K.RLK[325.13]TDNAGDQHGGGGGGGGGAGAAGGGGGGE |
| 0.999999     | 1 K.SAPATGGVK[325.13]KPHR.Y                 |
| 0.999999     | 1 K.K[325.13]QHIC[160.03]HIQGC[160.03]GK.V  |
| 0.999999     | 1 K.K[325.13]QHIC[160.03]HIQGC[160.03]GK.V  |
| 0.999999     | 1 K.RLK[325.13]TDNAGDQHGGGGGGGGGAGAAGGGGGGE |
| 0.999999     | 1 K.RLK[325.13]TDNAGDQHGGGGGGGGGAGAAGGGGGGE |
| 0.999999     | 1 K.K[325.13]QHIC[160.03]HIQGC[160.03]GK.V  |
| 0.999999     | 1 R.GREEYEGPNK[325.13]KPR.F                 |
| 0.999999     | 1 K.YHTINGHNC[160.03]EVK[325.13]K.A         |
| 0.999999     | 1 R.GREEYEGPNK[325.13]KPR.F                 |
| 0.999999     | 1 K.LAHK[325.13]YRPETK.Q                    |
| 0.999999     | 1 R.GREEYEGPNK[325.13]KPR.F                 |
| 0.999999     | 1 K.YHTINGHNC[160.03]EVK[325.13]K.A         |
| 0.999999     | 1 K.KK[325.13]EVAGAKPHITAAEGK.L             |
| 0.999999     | 1 K.KK[325.13]EVAGAKPHITAAEGK.L             |
| 0.999999     | 1 K.KK[325.13]EVAGAKPHITAAEGK.L             |
| 0.999999     | 1 K.SVHELEKSK[325.13]R.A                    |
| 0.999999     | 1 K.TYHYHC[160.03]GVQDK[325.13]AK.Y         |
| 0.999999     | 1 R.LK[325.13]DAVAHC[160.03]HEAER.N         |
| 0.999999     | 1 K.TYHYHC[160.03]GVQDK[325.13]AK.Y         |
| 0.999999     | 1 K.TYHYHC[160.03]GVQDK[325.13]AK.Y         |
| 0.999999     | 1 R.LK[325.13]DAVAHC[160.03]HEAER.N         |
| 0.999999     | 1 K.TYHYHC[160.03]GVQDK[325.13]AK.Y         |
| 0.999999     | 1 R.ISRPHPSTAESK[325.13]APTPK.F             |
| 0.999999     | 1 R.K[325.13]VAHSDKPGSTSTASFR.D             |
| 0.999999     | 1 R.HGVSHK[325.13]VDDSSGSIGR.R              |
| 0.999999     | 1 R.LK[325.13]DAVAHC[160.03]HEAER.N         |
| 0.999999     | 1 R.LK[325.13]DAVAHC[160.03]HEAER.N         |
| 0.999999     | 1 R.ISRPHPSTAESK[325.13]APTPK.F             |
| 0.999999     | 1 R.ISRPHPSTAESK[325.13]APTPK.F             |

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| 0.999999 | 1 R.K[325.13]HEAFESDLAAHQDR.V                   |
| 0.999999 | 1 R.VLEQHK[325.13]LTKEQWEER.I                   |
| 0.999999 | 1 R.VLEQHK[325.13]LNKDQWEER.I                   |
| 0.999999 | 1 R.HGESGSMVAFHQTQGPSYSESK[325.13]R.L           |
| 0.999999 | 1 R.HGESGSMVAFHQTQGPSYSESK[325.13]R.L           |
| 0.999999 | 1 R.HGESGSMVAFHQTQGPSYSESK[325.13]R.L           |
| 0.999999 | 1 R.KSHLAK[325.13]EGLYQYK.N                     |
| 0.999999 | 1 R.KSHLAK[325.13]EGLYQYK.N                     |
| 0.999999 | 1 K.K[325.13]TGKPMINLYTDKDTGKPK.G               |
| 0.999999 | 1 K.K[325.13]TGKPMINLYTDKDTGKPK.G               |
| 0.999999 | 1 R.IYDLNKPEAEPK[325.13]EISGHTSGIKK.A           |
| 0.999999 | 1 K.NSSYVHGGLDSNGKPADAVYGQK[325.13]EIHR.K       |
| 0.999999 | 1 K.HGEVC[160.03]PAGWKPGSDTIKPDVQK[325.13]SK.E  |
| 0.999999 | 1 K.HGEVC[160.03]PAGWKPGSDTIKPDVQK[325.13]SK.E  |
| 0.999999 | 1 K.HGEVC[160.03]PAGWKPGSDTIKPDVQK[325.13]SK.E  |
| 0.999999 | 1 R.TSTQK[325.13]HTHLAVSFGR.S                   |
| 0.999999 | 1 K.NSSYVHGGLDSNGKPADAVYGQK[325.13]EIHR.K       |
| 0.999999 | 1 R.VSVADHSLHLSK[325.13]AK.I                    |
| 0.999999 | 1 K.HGEVC[160.03]PAGWKPGSDTIKPDVQK[325.13]SK.E  |
| 0.999999 | 1 K.HGEVC[160.03]PAGWKPGSDTIKPDVQK[325.13]SK.E  |
| 0.999999 | 1 R.VHGPGIQSGTTNKPKNK[325.13]FTVETR.G           |
| 0.999999 | 1 R.VSVADHSLHLSK[325.13]AK.I                    |
| 0.999999 | 1 K.NSSYVHGGLDSNGKPADAVYGQK[325.13]EIHR.K       |
| 0.999999 | 1 K.NSSYVHGGLDSNGKPADAVYGQK[325.13]EIHR.K       |
| 0.999999 | 1 R.VHGPGIQSGTTNKPKNK[325.13]FTVETR.G           |
| 0.999999 | 1 R.VHGPGIQSGTTNKPKNK[325.13]FTVETR.G           |
| 0.999999 | 1 R.VHGPGIQSGTTNKPKNK[325.13]FTVETR.G           |
| 0.999999 | 1 R.VHGPGIQSGTTNKPKNK[325.13]FTVETR.G           |
| 0.999999 | 0.9733 R.HQGVMMVGMGQK[325.13]DSYVGDEAQSKR.G     |
| 0.999999 | 1 K.KIEISQHAK[325.13]YTC[160.03]SFC[160.03]GK.T |
| 0.999999 | 1 K.KIEISQHAK[325.13]YTC[160.03]SFC[160.03]GK.T |
| 0.999999 | 1 R.GYWGNK[325.13]IGKPHTVPC[160.03]K.V          |
| 0.999999 | 1 K.KIEISQHAK[325.13]YTC[160.03]SFC[160.03]GK.T |
| 0.999999 | 1 R.TSTQK[325.13]HTHLAVSFGR.S                   |
| 0.999999 | 1 R.IKDHIQNGK[325.13]LDLTK.L                    |
| 0.999999 | 1 R.TSTQK[325.13]HTHLAVSFGR.S                   |
| 0.999999 | 1 K.ATPMPSRPSTTPFIDK[325.13]KPTSAKPSSTTPR.L     |
| 0.999999 | 1 R.TSTQK[325.13]HTHLAVSFGR.S                   |
| 0.999999 | 1 K.TLHPDLGTDKDK[325.13]EQWK.E                  |
| 0.999999 | 1 R.RTANDAVELHIK[325.13]NVQPSDQGHYK.C           |
| 0.999999 | 1 K.ATPMPSRPSTTPFIDK[325.13]KPTSAKPSSTTPR.L     |
| 0.999999 | 1 K.TLHPDLGTDKDK[325.13]EQWK.E                  |
| 0.999999 | 1 R.RTANDAVELHIK[325.13]NVQPSDQGHYK.C           |
| 0.999999 | 1 K.TLHPDLGTDKDK[325.13]EQWK.E                  |
| 0.999999 | 1 R.RTANDAVELHIK[325.13]NVQPSDQGHYK.C           |
| 0.999999 | 1 R.LPPGFSASSTVEKPSK[325.13]VHR.A               |
| 0.999999 | 1 K.K[325.13]KPRPPPALGPEETSASAGLPK.K            |

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| 0.999999 | 0.9961 | R.HQGVMMVGMGQK[325.13]DSYVGDEAQSKR.G                |
| 0.999999 | 1      | K.TLHPDLGTDKDK[325.13]EQWK.E                        |
| 0.999999 | 1      | K.TLHPDLGTDKDK[325.13]EQWK.E                        |
| 0.999999 | 1      | R.LPPGFSASSTVEKPSK[325.13]VHR.A                     |
| 0.999999 | 1      | K.IVLQK[325.13]YHTINGHNAEVR.K                       |
| 0.999999 | 1      | K.K[325.13]KPRPPPALGPEETSASAGLPK.K                  |
| 0.999999 | 1      | K.IVLQK[325.13]YHTINGHNAEVR.K                       |
| 0.999999 | 0.9696 | R.HQGVMMVGMGQK[325.13]DSYVGDEAQSKR.G                |
| 0.999999 | 1      | K.TGVHHYSGNNIELGTAC[160.03]GK[325.13]YYR.V          |
| 0.999999 | 1      | K.TGVHHYSGNNIELGTAC[160.03]GK[325.13]YYR.V          |
| 0.999999 | 1      | K.TGVHHYSGNNIELGTAC[160.03]GK[325.13]YYR.V          |
| 0.999999 | 1      | K.K[325.13]KPRPPPALGPEETSASAGLPK.K                  |
| 0.999999 | 1      | K.IKGEHPGLSIGDVAK[325.13]K.L                        |
| 0.999999 | 1      | K.IVLQK[325.13]YHTINGHNAEVR.K                       |
| 0.999999 | 1      | K.VQQLVPK[325.13]RDHALLEEQSK.Q                      |
| 0.999999 | 1      | K.TGVHHYSGNNIELGTAC[160.03]GK[325.13]YYR.V          |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.IKGEHPGLSIGDVAK[325.13]K.L                        |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | R.RNPDTQWITK[325.13]PVHK.H                          |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.VQQLVPK[325.13]RDHALLEEQSK.Q                      |
| 0.999999 | 1      | K.VQQLVPK[325.13]RDHALLEEQSK.Q                      |
| 0.999999 | 1      | R.RNPDTQWITK[325.13]PVHK.H                          |
| 0.999999 | 1      | K.TYEHFNAMGK[325.13]YVDKR.L                         |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.YEELQSLAGK[325.13]HGDDLRR.T                       |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.ADK[325.13]DYHFKVDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | R.HYC[160.03]GK[325.13]C[160.03]C[160.03]LTYC[160.0 |
| 0.999999 | 1      | K.K[325.13]KHPDASVNFSEFSK.K                         |
| 0.999999 | 1      | R.KLERPPETPTVDPTVK[325.13]YER.Q                     |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.KK[325.13]HPDASVNFSEFSK.K                         |
| 0.999999 | 1      | R.GLVMVKPGSIK[325.13]PHQK.V                         |
| 0.999999 | 1      | K.LK[325.13]NKHEAMITDLEER.L                         |
| 0.999999 | 1      | K.YEELQSLAGK[325.13]HGDDLRR.T                       |
| 0.999999 | 1      | K.YEELQSLAGK[325.13]HGDDLRR.T                       |
| 0.999999 | 1      | K.KHPDASVNFSEFSK[325.13]K.C                         |
| 0.999999 | 1      | K.YEELQSLAGK[325.13]HGDDLRR.T                       |
| 0.999999 | 1      | K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.999999 | 1      | K.YEELQSLAGK[325.13]HGDDLRR.T                       |

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| 0.999999 | 1 K.LHYC[160.03]VSC[160.03]AIHSK[325.13]VVR.N        |
| 0.999999 | 1 K.YEELQSLAGK[325.13]HGDDLRR.T                      |
| 0.999999 | 1 K.KHPDASVNFSEFSK[325.13]K.C                        |
| 0.999999 | 1 K.KHPDASVNFSEFSK[325.13]K.C                        |
| 0.999999 | 1 K.LMC[160.03]SLC[160.03]HC[160.03]PGATIGC[160.03]C |
| 0.999999 | 1 K.LPEGHVPEGAGLK[325.13]GHLPK.V                     |
| 0.999999 | 1 R.DHAVVVGVYRPPPK[325.13]VK.N                       |
| 0.999999 | 1 R.SHKDEVVK[325.13]IQSLAR.M                         |
| 0.999999 | 1 R.DHAVVVGVYRPPPK[325.13]VK.N                       |
| 0.999999 | 1 R.TLDAHEDK[325.13]VWGLHC[160.03]SR.L               |
| 0.999999 | 1 R.ENTHQLTK[325.13]C[160.03]SALATQYMHC[160.03]VN    |
| 0.999999 | 1 R.HLYTK[325.13]DIDIHEVR.I                          |
| 0.999999 | 1 R.HLYTK[325.13]DIDIHEVR.I                          |
| 0.999999 | 1 R.ENTHQLTK[325.13]C[160.03]SALATQYMHC[160.03]VN    |
| 0.999999 | 1 R.ENTHQLTK[325.13]C[160.03]SALATQYMHC[160.03]VN    |
| 0.999999 | 1 R.HLK[325.13]STHSELLEDYYQSGR.M                     |
| 0.999999 | 1 R.HLYTK[325.13]DIDIHEVR.I                          |
| 0.999999 | 1 R.HLYTK[325.13]DIDIHEVR.I                          |
| 0.999999 | 1 R.HLK[325.13]STHSELLEDYYQSGR.M                     |
| 0.999999 | 1 K.KNPIAK[325.13]IHSDLAER.G                         |
| 0.999999 | 1 R.K[325.13]VAC[160.03]IGAWHPAR.V                   |
| 0.999999 | 1 R.HWGGNVLGPK[325.13]SVAR.I                         |
| 0.999999 | 1 R.HLK[325.13]STHSELLEDYYQSGR.M                     |
| 0.999999 | 1 R.HLK[325.13]STHSELLEDYYQSGR.M                     |
| 0.999999 | 1 K.LK[325.13]NWEEGGYFNTDKPHPR.G                     |
| 0.999999 | 1 K.AHLGTALK[325.13]ANPFGGASHAK.G                    |
| 0.999999 | 1 R.HWGGNVLGPK[325.13]SVAR.I                         |
| 0.999999 | 1 K.SYIYSGSHDGHINYWDSETGENDSFAGK[325.13]GHTNQV       |
| 0.999999 | 1 K.SYIYSGSHDGHINYWDSETGENDSFAGK[325.13]GHTNQV       |
| 0.999999 | 1 K.MK[325.13]GYPHWPAR.V                             |
| 0.999999 | 1 K.IGPK[325.13]KPLPDHVSIVEPK.D                      |
| 0.999999 | 1 R.HQAQIDHYLGLANK[325.13]NVK.D                      |
| 0.999999 | 1 R.HQAQIDHYLGLANK[325.13]NVK.D                      |
| 0.999999 | 1 K.LK[325.13]NWEEGGYFNTDKPHPR.G                     |
| 0.999999 | 1 K.IGPK[325.13]KPLPDHVSIVEPK.D                      |
| 0.999999 | 1 K.AHLGTALK[325.13]ANPFGGASHAK.G                    |
| 0.999999 | 1 R.HQAQIDHYLGLANK[325.13]NVK.D                      |
| 0.999999 | 1 R.HQAQIDHYLGLANK[325.13]NVK.D                      |
| 0.999999 | 1 R.ASFNHFDK[325.13]DHGGALGPEEFK.A                   |
| 0.999999 | 1 R.QVRPVTEK[325.13]LPANHPLLTGQR.V                   |
| 0.999999 | 1 K.HKLDVTSVEDYK[325.13]ALQK.Y                       |
| 0.999999 | 1 K.HKLDVTSVEDYK[325.13]ALQK.Y                       |
| 0.999999 | 1 R.HWGGNVLGPK[325.13]SVAR.I                         |
| 0.999999 | 1 K.DAIHFYNK[325.13]SLAEHR.T                         |
| 0.999999 | 1 R.HWGGNVLGPK[325.13]SVAR.I                         |
| 0.999999 | 1 R.LYKEELEQTYHAK[325.13]LENAR.L                     |
| 0.999999 | 1 R.HWGGNVLGPK[325.13]SVAR.I                         |

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| 0.999999 | 1 R.HWGGNVLGPK[325.13]SVAR.I            |
| 0.999999 | 1 R.LYKEELEQTYHAK[325.13]LENAR.L        |
| 0.999999 | 1 R.ASFNHFDK[325.13]DHGGALGPEEFK.A      |
| 0.999999 | 1 R.ASFNHFDK[325.13]DHGGALGPEEFK.A      |
| 0.999999 | 1 R.TKLQNK[325.13]EHVIEALR.R            |
| 0.999999 | 1 R.HFC[160.03]NK[325.13]LWNATK.F       |
| 0.999999 | 1 K.YGLIYHASLVGQTSPK[325.13]HK.G        |
| 0.999999 | 1 K.YGLIYHASLVGQTSPK[325.13]HK.G        |
| 0.999999 | 1 R.ASFNHFDK[325.13]DHGGALGPEEFK.A      |
| 0.999999 | 1 R.HFC[160.03]NK[325.13]LWNATK.F       |
| 0.999999 | 1 R.ASFNHFDK[325.13]DHGGALGPEEFK.A      |
| 0.999999 | 1 K.YGLIYHASLVGQTSPK[325.13]HK.G        |
| 0.999999 | 1 K.YGLIYHASLVGQTSPK[325.13]HK.G        |
| 0.999999 | 1 R.HFC[160.03]NK[325.13]LWNATK.F       |
| 0.999999 | 1 R.ADEARPNTIDFGK[325.13]DDQHFTVTGLHK.G |
| 0.999999 | 1 R.GLK[325.13]YELISETGGSHDKR.F         |
| 0.999999 | 1 R.ADEARPNTIDFGK[325.13]DDQHFTVTGLHK.G |
| 0.999999 | 1 R.ADEARPNTIDFGK[325.13]DDQHFTVTGLHK.G |
| 0.999999 | 1 R.GLK[325.13]YELISETGGSHDKR.F         |
| 0.999999 | 1 R.ADEARPNTIDFGK[325.13]DDQHFTVTGLHK.G |
| 0.999999 | 1 K.KIK[325.13]GC[160.03]WDSIHVVEVQEK.S |
| 0.999999 | 1 K.SPYQEFTDHLVK[325.13]THTR.V          |
| 0.999999 | 1 K.SPYQEFTDHLVK[325.13]THTR.V          |
| 0.999999 | 1 R.KADVIK[325.13]AAHLC[160.03]AEAALR.L |
| 0.999999 | 1 R.ILK[325.13]HGINC[160.03]FINR.Q      |
| 0.999999 | 1 K.SPYQEFTDHLVK[325.13]THTR.V          |
| 0.999999 | 1 R.KADVIK[325.13]AAHLC[160.03]AEAALR.L |
| 0.999999 | 1 K.KIK[325.13]GC[160.03]WDSIHVVEVQEK.S |
| 0.999999 | 1 K.SPYQEFTDHLVK[325.13]THTR.V          |
| 0.999999 | 1 R.KADVIK[325.13]AAHLC[160.03]AEAALR.L |
| 0.999999 | 1 R.ILK[325.13]HGINC[160.03]FINR.Q      |
| 0.999999 | 1 K.SPYQEFTDHLVK[325.13]THTR.V          |
| 0.999999 | 1 K.HPK[325.13]NPEVGLKPVWYSPK.V         |
| 0.999999 | 1 R.GPVLQLHDLK[325.13]R.E               |
| 0.999999 | 1 K.SPYQEFTDHLVK[325.13]THTR.V          |
| 0.999999 | 1 K.HPK[325.13]NPEVGLKPVWYSPK.V         |
| 0.999999 | 1 R.GPVLQLHDLK[325.13]R.E               |
| 0.999999 | 1 K.IVADFSASVK[325.13]KPHTLLQR.V        |
| 0.999999 | 1 R.GTK[325.13]VILHLKEDQTEYLEER.R       |
| 0.999999 | 1 K.K[325.13]HLEINPDHPIVETLR.Q          |
| 0.999999 | 1 R.KADVIK[325.13]AAHLC[160.03]AEAALR.L |
| 0.999999 | 1 K.HPK[325.13]NPEVGLKPVWYSPK.V         |
| 0.999999 | 1 R.IMGPNYTPGK[325.13]KEDLYLKPIQR.T     |
| 0.999999 | 1 R.GTK[325.13]VILHLKEDQTEYLEER.R       |
| 0.999999 | 1 R.GTK[325.13]VILHLKEDQTEYLEER.R       |
| 0.999999 | 1 K.K[325.13]HLEINPDHPIVETLR.Q          |
| 0.999999 | 1 K.K[325.13]HLEINPDHPIVETLR.Q          |

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| 0.999999 | 1 R.GTK[325.13]VILHLKEDQTEYLEER.R                 |
| 0.999999 | 1 R.IMGPNYTPGKK[325.13]EDLYLKPIQR.T               |
| 0.999999 | 1 R.GTK[325.13]VILHLKEDQTEYLEER.R                 |
| 0.999999 | 1 K.MLK[325.13]DKFNEC[160.03]GHVLYADIK.M          |
| 0.999999 | 1 K.K[325.13]HLEINPDHPIVETLR.Q                    |
| 0.999999 | 1 K.K[325.13]HLEINPDHPIVETLR.Q                    |
| 0.999999 | 1 R.IMGPNYTPGKK[325.13]EDLYLKPIQR.T               |
| 0.999999 | 1 K.MLK[325.13]DKFNEC[160.03]GHVLYADIK.M          |
| 0.999999 | 1 K.VIPSPFK[325.13]HADIVTTTTHK.T                  |
| 0.999999 | 1 K.K[325.13]AADHLKPFLDDSTLR.F                    |
| 0.999999 | 1 K.K[325.13]HLEINPDHPIVETLR.Q                    |
| 0.999999 | 1 K.MLK[325.13]DKFNEC[160.03]GHVLYADIK.M          |
| 0.999999 | 1 K.TAITVEHLAIK[325.13]C[160.03]HWTQR.A           |
| 0.999999 | 1 K.TAITVEHLAIK[325.13]C[160.03]HWTQR.A           |
| 0.999999 | 1 K.MLK[325.13]DKFNEC[160.03]GHVLYADIK.M          |
| 0.999999 | 1 K.VIPSPFK[325.13]HADIVTTTTHK.T                  |
| 0.999999 | 1 K.VIPSPFK[325.13]HADIVTTTTHK.T                  |
| 0.999999 | 0.9999 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G   |
| 0.999999 | 1 R.M[147.04]VNHFAIEFK[325.13]R.K                 |
| 0.999999 | 1 R.TFK[325.13]TVFAEHISDEC[160.03]KR.R            |
| 0.999999 | 1 K.TAITVEHLAIK[325.13]C[160.03]HWTQR.A           |
| 0.999999 | 1 R.M[147.04]VNHFAIEFK[325.13]R.K                 |
| 0.999999 | 1 R.KPEDWDERPK[325.13]IPDPEAVKPDWDWEDAPAK.I       |
| 0.999999 | 1 K.LDSGK[325.13]ELHINLIPNKQDR.T                  |
| 0.999999 | 1 K.FVIK[325.13]RPELLTHSTTEVTQPR.T                |
| 0.999999 | 1 R.SYDVPPPPMEPDHPFYSNISK[325.13]DRR.Y            |
| 0.999999 | 1 R.LTVNEAVK[325.13]EGVVGPELHHK.L                 |
| 0.999999 | 1 R.SYDVPPPPMEPDHPFYSNISK[325.13]DRR.Y            |
| 0.999999 | 0.9999 K.VK[325.13]GLVLGPIHK.N                    |
| 0.999999 | 1 K.YDYNSGEELESYK[325.13]GHFGPIHC[160.03]VR.F     |
| 0.999999 | 1 K.YDYNSGEELESYK[325.13]GHFGPIHC[160.03]VR.F     |
| 0.999999 | 1 K.YDYNSGEELESYK[325.13]GHFGPIHC[160.03]VR.F     |
| 0.999999 | 1 K.APAHHPAAISTAK[325.13]FC[160.03]IQEIEK.S       |
| 0.999999 | 1 K.APAHHPAAISTAK[325.13]FC[160.03]IQEIEK.S       |
| 0.999999 | 1 R.WPDVARPPFNPHGGAEPGADSAEGDVGDGDGDFGAGVN        |
| 0.999999 | 1 K.LIK[325.13]GVIVDKDFSHPQMPK.K                  |
| 0.999999 | 1 R.MRGETTLWNP GC[160.03]DHAGIATQVVVEK[325.13]K.I |
| 0.999999 | 1 K.AVIVK[325.13]NIDDGTS DRPYSHALVAGIDR.Y         |
| 0.999999 | 1 R.MAQEVLTHLK[325.13]EHPDAWTR.V                  |
| 0.999999 | 1 K.AVIVK[325.13]NIDDGTS DRPYSHALVAGIDR.Y         |
| 0.999999 | 1 R.WPDVARPPFNPHGGAEPGADSAEGDVGDGDGDFGAGVN        |
| 0.999999 | 1 R.MVNHFAIEFK[325.13]R.K                         |
| 0.999999 | 1 R.WPDVARPPFNPHGGAEPGADSAEGDVGDGDGDFGAGVN        |
| 0.999999 | 1 R.MVNHFAIEFK[325.13]R.K                         |
| 0.999999 | 1 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKF  |
| 0.999999 | 1 R.MVNHFAIEFK[325.13]R.K                         |
| 0.999999 | 1 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKF  |



0.999999 1 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKF  
0.999999 1 R.IVSRPEELREDDVGTGAGLLEIK[325.13]K.I  
0.999999 1 K.RLEAELAAHEPAIQGVLDTGK[325.13]K.L  
0.999999 0.9996 R.MVNHFAIEFK[325.13]R.K  
0.999999 1 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKF  
0.999999 1 R.IVSRPEELREDDVGTGAGLLEIK[325.13]K.I  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKF  
0.999999 1 K.RLEAELAAHEPAIQGVLDTGK[325.13]K.L  
0.999999 1 K.K[325.13]HLEINPDHSIIETLR.Q  
0.999999 1 R.ASEAH[160.03]HYVVVK[325.13]LFSEK.L  
0.999999 1 K.K[325.13]HLEINPDHSIIETLR.Q  
0.999999 1 R.SHFEQWGTLTDC[160.03]VVMRDPNTK[325.13]R.S  
0.999999 1 -.MKVELC[160.03]SFSGYK[325.13]IYPGHGR.R  
0.999999 1 R.HDK[325.13]VEDALNLKEEFDR.L  
0.999999 1 R.RVEHNQSYSQAGITETEWTSK[325.13]GGPLQALTR.E  
0.999999 1 K.NLFTK[325.13]THPQWYPAR.Q  
0.999999 1 K.KADQK[325.13]GVTIIGPATVGGIKPGC[160.03]FK.I  
0.999999 0.9995 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
0.999999 1 K.NLFTK[325.13]THPQWYPAR.Q  
0.999999 1 R.LLFNDVQTLK[325.13]DGRHPQGEQMYR.R  
0.999999 1 K.KADQK[325.13]GVTIIGPATVGGIKPGC[160.03]FK.I  
0.999999 0.973 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
0.999999 1 K.NLFTK[325.13]THPQWYPAR.Q  
0.999999 1 R.RVEHNQSYSQAGITETEWTSK[325.13]GGPLQALTR.E  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.RVEHNQSYSQAGITETEWTSK[325.13]GGPLQALTR.E  
0.999999 1 R.HIDC[160.03]AHVYQNEVEGVAIQEK[325.13]LR.E  
0.999999 1 R.RVEHNQSYSQAGITETEWTSK[325.13]GGPLQALTR.E  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.RVEHNQSYSQAGITETEWTSK[325.13]GGPLQALTR.E  
0.999999 1 R.HIDC[160.03]AHVYQNEVEGVAIQEK[325.13]LR.E  
0.999999 1 K.DKTTGQSK[325.13]GFAFISFHR.R  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 K.DKTTGQSK[325.13]GFAFISFHR.R  
0.999999 1 K.DDQHFTVTGLHK[325.13]GTTYIFR.L  
0.999999 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160  
0.999999 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160  
0.999999 0.9952 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F  
0.999999 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160  
0.999999 1 R.LK[325.13]LEPHEGLLLR.F

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|----------|-----------------------------------------------------|
| 0.999999 | 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160 |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160 |
| 0.999999 | 1 R.LYVHEAVK[325.13]AGVVGPHEQLLSAEK.A               |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160 |
| 0.999999 | 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160 |
| 0.999999 | 0.9927 R.LK[325.13]LEPHEGLLLR.F                     |
| 0.999999 | 1 K.AK[325.13]FVGDPALVLNDIHKK.I                     |
| 0.999999 | 1 R.LLIHQSLAGGIIGVK[325.13]GAK.I                    |
| 0.999999 | 1 K.DIHELFPENK[325.13]LDHVR.A                       |
| 0.999999 | 1 R.LLIHQSLAGGIIGVK[325.13]GAK.I                    |
| 0.999999 | 1 K.DIHELFPENK[325.13]LDHVR.A                       |
| 0.999999 | 1 K.DIHELFPENK[325.13]LDHVR.A                       |
| 0.999999 | 1 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y        |
| 0.999999 | 1 K.DIHELFPENK[325.13]LDHVR.A                       |
| 0.999999 | 1 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y        |
| 0.999999 | 1 K.DIHELFPENK[325.13]LDHVR.A                       |
| 0.999999 | 1 R.HGATHVFASK[325.13]ESEITDEDIDGILER.G             |
| 0.999999 | 1 R.HGATHVFASK[325.13]ESEITDEDIDGILER.G             |
| 0.999999 | 1 K.DAK[325.13]DKLESEMEDAYHEHQANLLR.Q               |
| 0.999999 | 1 K.K[325.13]RTELFIAAEGIHTGQFVYC[160.03]GK.K        |
| 0.999999 | 1 K.SGSSFVHQASFK[325.13]FGQGDLPKPINSDFR.S           |
| 0.999999 | 1 K.DAKDK[325.13]LESEMEDAYHEHQANLLR.Q               |
| 0.999999 | 1 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y        |
| 0.999999 | 1 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y        |
| 0.999999 | 1 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y        |
| 0.999999 | 1 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y        |
| 0.999999 | 1 K.FVIHC[160.03]NSPVWGADKC[160.03]EELLEK[325.13]T  |
| 0.999999 | 1 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y        |
| 0.999999 | 1 R.IHIMPSMNPDGFEAVK[325.13]KPDC[160.03]YYSIGR.E    |
| 0.999999 | 1 K.FVIHC[160.03]NSPVWGADKC[160.03]EELLEK[325.13]T  |
| 0.999999 | 1 K.LNILK[325.13]LAPGGHVGR.F                        |
| 0.999999 | 1 K.LNILK[325.13]LAPGGHVGR.F                        |
| 0.999999 | 1 R.VIHLSNLPHSGYSDSAVLK[325.13]LAEPYGK.I            |
| 0.999999 | 1 R.IGK[325.13]VTSEELHYFVQNHFTSAR.M                 |
| 0.999999 | 1 R.KSEIEYYAMLAK[325.13]TGVHHYSGNNIELGTAC[160.03]   |
| 0.999999 | 1 R.KSEIEYYAMLAK[325.13]TGVHHYSGNNIELGTAC[160.03]   |
| 0.999999 | 1 R.KSEIEYYAMLAK[325.13]TGVHHYSGNNIELGTAC[160.03]   |
| 0.999999 | 1 K.LNILK[325.13]LAPGGHVGR.F                        |
| 0.999999 | 1 R.IGK[325.13]VTSEELHYFVQNHFTSAR.M                 |
| 0.999999 | 1 K.LNILK[325.13]LAPGGHVGR.F                        |
| 0.999999 | 1 R.VIHLSNLPHSGYSDSAVLK[325.13]LAEPYGK.I            |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.VIHLSNLPHSGYSDSAVLK[325.13]LAEPYGK.I            |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.GRLPLLAVC[160.03]DYK[325.13]QVEVTVHK.G          |

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| 0.999999 | 1 K.K[325.13]LNC[160.03]QVIGASVDSHFC[160.03]HLAWVI |
| 0.999999 | 1 R.VIHLSNLP HSGYSDSAVLK[325.13]LAEPYGK.I          |
| 0.999999 | 1 R.VIHLSNLP HSGYSDSAVLK[325.13]LAEPYGK.I          |
| 0.999999 | 1 R.HFLLEEDK[325.13]PEEPTAHAFVSTLTR.G              |
| 0.999999 | 1 R.VIHLSNLP HSGYSDSAVLK[325.13]LAEPYGK.I          |
| 0.999999 | 1 R.HFLLEEDK[325.13]PEEPTAHAFVSTLTR.G              |
| 0.999999 | 1 R.LNRPLTLSEK[325.13]IVYGHLD DPASQEIER.G          |
| 0.999999 | 1 K.QIFLGGVDK[325.13]HTQFWR.Y                      |
| 0.999999 | 1 R.HFLLEEDK[325.13]PEEPTAHAFVSTLTR.G              |
| 0.999999 | 1 K.KVEDAK[325.13]IAILTC[160.03]PFEPPKPK.T         |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                      |
| 0.999999 | 1 R.RLVVFPTDDISLK[325.13]C[160.03]EASGKPEVQFR.W    |
| 0.999999 | 1 K.NRPGSALEK[325.13]EVESMGAHLNAYSTR.E             |
| 0.999999 | 1 K.KVEDAK[325.13]IAILTC[160.03]PFEPPKPK.T         |
| 0.999999 | 1 R.SPEAQPK[325.13]TLPLTGSTFHDQIAML SHR.C          |
| 0.999999 | 1 R.RLVVFPTDDISLK[325.13]C[160.03]EASGKPEVQFR.W    |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                      |
| 0.999999 | 1 R.SPEAQPK[325.13]TLPLTGSTFHDQIAML SHR.C          |
| 0.999999 | 1 K.K[325.13]LNC[160.03]QVIGASVDSHFC[160.03]HLAWVI |
| 0.999999 | 1 K.RVIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I         |
| 0.999999 | 1 K.NRPGSALEK[325.13]EVESMGAHLNAYSTR.E             |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L        |
| 0.999999 | 1 K.RVIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I         |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 K.HKDAAIYLVTSLASK[325.13]AQTQK.H                 |
| 0.999999 | 1 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L        |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 0.9998 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S      |
| 0.999999 | 1 R.ATHYHLSSQVQEMAGK[325.13]IDLLR.D                |
| 0.999999 | 1 R.KLAGANPAVITC[160.03]DELLLGHEK[325.13]APAFR.D   |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.FHILFK[325.13]ALGEEK.G                         |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999999 | 1 K.FLSPVVP NYDNVHPNYHK[325.13]EPFLQQLK.V          |
| 0.999999 | 1 R.SIFGEDALANVSIEK[325.13]PIHQGPDAAVTGHIR.I       |
| 0.999999 | 1 R.FHILFK[325.13]ALGEEK.G                         |
| 0.999999 | 1 K.FLSPVVP NYDNVHPNYHK[325.13]EPFLQQLK.V          |
| 0.999999 | 1 R.FHILFK[325.13]ALGEEK.G                         |
| 0.999999 | 1 R.WGEDNHWIC[160.03]K[325.13]PWNLAR.S             |

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| 0.999999 | 1 R.WGEDNHWIC[160.03]K[325.13]PWNLAR.S             |
| 0.999999 | 1 R.RQQEQQVPILEK[325.13]FC[160.03]FTPHTEEGC[160.03 |
| 0.999999 | 1 R.WGEDNHWIC[160.03]K[325.13]PWNLAR.S             |
| 0.999999 | 1 R.GFGFVTYSC[160.03]VEEVDAAMC[160.03]ARPHK[325.1  |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 R.HGDLDPDIQIK[325.13]HSSLITPLQAVAQR.D            |
| 0.999999 | 1 R.HGDLDPDIQIK[325.13]HSSLITPLQAVAQR.D            |
| 0.999999 | 1 R.KFGEAIGMGFPVK[325.13]VPYR.K                    |
| 0.999999 | 1 R.KFGEAIGMGFPVK[325.13]VPYR.K                    |
| 0.999999 | 1 R.HGDLDPDIQIK[325.13]HSSLITPLQAVAQR.D            |
| 0.999999 | 1 R.HGDLDPDIQIK[325.13]HSSLITPLQAVAQR.D            |
| 0.999999 | 1 R.KFGEAIGMGFPVK[325.13]VPYR.K                    |
| 0.999999 | 0.9999 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E  |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.FGDPVVQSDMK[325.13]HWPQVINDGDKPK.V             |
| 0.999999 | 1 K.SVVLM[147.04]SHLGRPDGVMPDK[325.13]YSLEPVAVI    |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.VYGERPLTK[325.13]DNHLLGTFDLTGIPPAPR.G          |
| 0.999999 | 1 R.QDLMNIAGTTLSSK[325.13]LLTHHK.D                 |
| 0.999999 | 1 K.VYGERPLTK[325.13]DNHLLGTFDLTGIPPAPR.G          |
| 0.999999 | 1 K.SLTNDWEDHLAVK[325.13]HFSVEGQLEFR.A             |
| 0.999999 | 1 K.VYGERPLTK[325.13]DNHLLGTFDLTGIPPAPR.G          |
| 0.999999 | 1 K.VYGERPLTK[325.13]DNHLLGTFDLTGIPPAPR.G          |
| 0.999999 | 1 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                  |
| 0.999999 | 1 K.SVVLM[147.04]SHLGRPDGVMPDK[325.13]YSLEPVAVI    |
| 0.999999 | 1 K.VYGERPLTK[325.13]DNHLLGTFDLTGIPPAPR.G          |
| 0.999999 | 1 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                  |
| 0.999999 | 1 K.IPQK[325.13]GILIGIQSFRPR.F                     |
| 0.999999 | 1 K.SVVLM[147.04]SHLGRPDGVMPDK[325.13]YSLEPVAVI    |
| 0.999999 | 1 R.TREGNDLYHEMIESGVINLK[325.13]DATSK.V            |
| 0.999999 | 1 R.TREGNDLYHEMIESGVINLK[325.13]DATSK.V            |
| 0.999999 | 1 K.IPQK[325.13]GILIGIQSFRPR.F                     |
| 0.999999 | 1 R.TREGNDLYHEMIESGVINLK[325.13]DATSK.V            |
| 0.999999 | 1 K.SVVLM[147.04]SHLGRPDGVMPDK[325.13]YSLEPVAVI    |
| 0.999999 | 1 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                  |
| 0.999999 | 1 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S     |
| 0.999999 | 1 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S     |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETDDSLREHF.K                  |
| 0.999999 | 1 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                  |
| 0.999999 | 1 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                  |
| 0.999999 | 1 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S     |
| 0.999999 | 1 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S     |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETDDSLREHF.K                  |
| 0.999999 | 1 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                  |
| 0.999999 | 1 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S     |
| 0.999999 | 1 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                  |

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| 0.999999 | 1 K.FC[160.03]LDNGAK[325.13]SVVLMShLGRPDGVPMPDK   |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETDDSLREHFKEK.W              |
| 0.999999 | 1 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                 |
| 0.999999 | 1 R.C[160.03]SDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDL   |
| 0.999999 | 1 R.FHK[325.13]LQNVQIALDYLR.H                     |
| 0.999999 | 1 R.C[160.03]SDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDL   |
| 0.999999 | 1 R.C[160.03]SDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDL   |
| 0.999999 | 1 R.FDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V           |
| 0.999999 | 1 R.FDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V           |
| 0.999999 | 1 R.FHK[325.13]LQNVQIALDYLR.H                     |
| 0.999999 | 1 K.KVC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M   |
| 0.999999 | 1 R.FHK[325.13]LQNVQIALDYLR.H                     |
| 0.999999 | 1 R.FHK[325.13]LQNVQIALDYLR.H                     |
| 0.999999 | 1 K.KVC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M   |
| 0.999999 | 1 K.GIYQSLEGAVQAGQLK[325.13]VPPGYHPLDVEKEWGK.L    |
| 0.999999 | 1 K.KVC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M   |
| 0.999999 | 1 K.KVC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M   |
| 0.999999 | 1 K.SVVLMShLGRPDGVPMPDK[325.13]YSLEPVAVELK.S      |
| 0.999999 | 1 K.SVVLMShLGRPDGVPMPDK[325.13]YSLEPVAVELK.S      |
| 0.999999 | 1 K.SVVLMShLGRPDGVPMPDK[325.13]YSLEPVAVELK.S      |
| 0.999999 | 1 R.GNVAGDSK[325.13]NDPPMEAAGFTAQVIILNHGPGQISAG   |
| 0.999999 | 1 R.SSFDWLTGSSTDPLVDHTSPSSDSLFAHK[325.13]R.S      |
| 0.999999 | 1 R.GNVAGDSK[325.13]NDPPMEAAGFTAQVIILNHGPGQISAG   |
| 0.999999 | 1 R.DMFC[160.03]K[325.13]ILHGFK.N                 |
| 0.999999 | 1 R.LVEGILHAPDAGWGNLVYVVNYPK[325.13]DNKR.K        |
| 0.999999 | 1 R.LTPK[325.13]LFHEVVQAFR.A                      |
| 0.999999 | 1 R.DMFC[160.03]K[325.13]ILHGFK.N                 |
| 0.999999 | 1 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V         |
| 0.999999 | 1 R.LTPK[325.13]LFHEVVQAFR.A                      |
| 0.999999 | 1 R.LTPK[325.13]LFHEVVQAFR.A                      |
| 0.999999 | 1 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V         |
| 0.999999 | 1 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V           |
| 0.999999 | 1 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V         |
| 0.999999 | 1 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V         |
| 0.999999 | 1 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V         |
| 0.999999 | 1 R.RLAAVALINAAIQK[325.13]GVAEK.T                 |
| 0.999999 | 1 R.RLAAVALINAAIQK[325.13]GVAEK.T                 |
| 0.999999 | 1 K.KLFVGGLK[325.13]GDVAEGDLIEHFSQFGTVEK.A        |
| 0.999999 | 1 R.RLAAVALINAAIQK[325.13]GVAEK.T                 |
| 0.999999 | 1 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V           |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG   |
| 0.999999 | 1 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T           |
| 0.999999 | 1 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T           |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG   |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG   |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII |

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| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSDFNSDTHSSTFDAG      |
| 0.999999 | 1 R.NHAAPFSK[325.13]VLTFLR.R                        |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPMDDQKI  |
| 0.999999 | 1 R.EIVHLQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSDFNSDTHSSTFDAG      |
| 0.999999 | 1 R.EIVHLQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.NHAAPFSK[325.13]VLTFLR.R                        |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T             |
| 0.999999 | 1 R.NHAAPFSK[325.13]VLTFLR.R                        |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.EIVHLQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.EIVHLQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 R.EIVHLQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 K.NISFTVWDVGGQDK[325.13]IRPLWR.H                  |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII   |
| 0.999999 | 1 K.FYWGHK[325.13]EILIPVFK.N                        |
| 0.999999 | 1 R.K[325.13]DALHLLVFTDDVPDIALDGK.L                 |
| 0.999999 | 1 K.LPSFELLHK[325.13]EMLGGEIIPR.S                   |
| 0.999999 | 1 K.LPSFELLHK[325.13]EMLGGEIIPR.S                   |
| 0.999999 | 1 K.FYWGHK[325.13]EILIPVFK.N                        |
| 0.999999 | 1 R.K[325.13]DALHLLVFTDDVPDIALDGK.L                 |
| 0.999999 | 1 K.LPSFELLHK[325.13]EMLGGEIIPR.S                   |
| 0.999999 | 1 K.LPSFELLHK[325.13]EMLGGEIIPR.S                   |
| 0.999999 | 1 K.FYWGHK[325.13]EILIPVFK.N                        |
| 0.999999 | 1 R.FHMYEGYPLWK[325.13]VTFPVR.V                     |
| 0.999999 | 1 R.K[325.13]DALHLLVFTDDVPDIALDGK.L                 |
| 0.999999 | 1 R.K[325.13]DALHLLVFTDDVPDIALDGK.L                 |
| 0.999999 | 1 R.K[325.13]DALHLLVFTDDVPDIALDGK.L                 |
| 0.999999 | 1 R.K[325.13]DALHLLVFTDDVPDIALDGK.L                 |
| 0.999999 | 1 R.K[325.13]DALHLLVFTDDVPDIALDGK.L                 |
| 0.999999 | 1 R.FHMYEGYPLWK[325.13]VTFPVR.V                     |
| 0.999999 | 0.9999 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR |
| 0.999999 | 1 R.FHMYEGYPLWK[325.13]VTFPVR.V                     |
| 0.999999 | 1 R.FHMYEGYPLWK[325.13]VTFPVR.V                     |
| 0.999999 | 1 R.ISLGMPVGPNAHK[325.13]VPPPWLAMQR.Y               |
| 0.999999 | 1 R.FHMYEGYPLWK[325.13]VTFPVR.V                     |
| 0.999999 | 1 R.KHGLEVIYMIPIDEYC[160.03]VQQLK[325.13]EFEGK.T    |
| 0.999999 | 1 R.DTSFEQHVLWHTGGK[325.13]GVDLVLSLAEEK.L           |
| 0.999999 | 1 R.KFLDGNELTLADC[160.03]NLLPK[325.13]LHIVQVVC[160  |
| 0.999999 | 1 K.DGTTHQTSLELFMYLNEVAGK[325.13]HGVGR.I            |
| 0.999999 | 1 R.DTSFEQHVLWHTGGK[325.13]GVDLVLSLAEEK.L           |
| 0.999999 | 1 R.KFLDGNELTLADC[160.03]NLLPK[325.13]LHIVQVVC[160  |

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| 0.999999 | 1 K.LIPDSIGKDIEK[325.13]AC[160.03]QSIYPLHDFVFR.K           |
| 0.999999 | 1 R.KDGNASGTTLLEALDC[160.03]ILPPTTRPTDK[325.13]PLR.        |
| 0.999999 | 1 R.DTSFEQHVLWHTGGK[325.13]GVDLVLNSLAEEK.L                 |
| 0.999999 | 1 R.KFLDGNELTLADC[160.03]NLLPK[325.13]LHIVQVVC[160.03]PLR. |
| 0.999999 | 1 R.DTSFEQHVLWHTGGK[325.13]GVDLVLNSLAEEK.L                 |
| 0.999999 | 1 K.LIPDSIGK[325.13]DIEKAC[160.03]QSIYPLHDFVFR.K           |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.KDGNASGTTLLEALDC[160.03]ILPPTTRPTDK[325.13]PLR.        |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.KLSAEHK[325.13]EFITALIPEVILC[160.03]TK.E               |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.KLSAEHK[325.13]EFITALIPEVILC[160.03]TK.E               |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.GSHVLSC[160.03]MVK[325.13]TEQC[160.03]LVALLHK.I        |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 K.FHEK[325.13]VIAALLQTMEDQGNQR.V                         |
| 0.999999 | 1 K.QHGIPIVTPK[325.13]NPWSMDENLMHISYEAGILENPK.             |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 K.QHGIPIVTPK[325.13]NPWSMDENLMHISYEAGILENPK.             |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.GSHVLSC[160.03]MVK[325.13]TEQC[160.03]LVALLHK.I        |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 K.QHGIPIVTPK[325.13]NPWSMDENLMHISYEAGILENPK.             |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.VDEVPDGAVKPPTNK[325.13]LPIFFFGTHETAFLGPK.D             |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                         |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                         |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                         |
| 0.999999 | 1 R.VDEVPDGAVKPPTNK[325.13]LPIFFFGTHETAFLGPK.D             |
| 0.999999 | 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.        |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                         |
| 0.999999 | 1 R.VDEVPDGAVKPPTNK[325.13]LPIFFFGTHETAFLGPK.D             |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                         |
| 0.999999 | 1 K.FSDSYASVIK[325.13]ALEHSALAINHK.L                       |
| 0.999999 | 1 R.VDEVPDGAVKPPTNK[325.13]LPIFFFGTHETAFLGPK.D             |
| 0.999999 | 1 K.FSDSYASVIK[325.13]ALEHSALAINHK.L                       |
| 0.999999 | 1 K.GQYISPFHDIPIYADK[325.13]DVFHMOVVEVPR.W                 |
| 0.999999 | 1 K.FSDSYASVIK[325.13]ALEHSALAINHK.L                       |
| 0.999999 | 1 R.GLDISNVK[325.13]HVINFDLPDIEEYVHR.I                     |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                                |
| 0.999999 | 1 R.MVLAAAGGVEHQQLDLAQK[325.13]HLGGIPWTYAEDA               |

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| 0.999999 | 1 K.FSDSYASVIK[325.13]ALEHSALAINHK.L             |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.KGDYLGK[325.13]TVQVVPHTDAIQEWVMR.Q           |
| 0.999999 | 1 R.GITGVDLFGTTDAVVK[325.13]HVLEGHDR.G           |
| 0.999999 | 1 K.FSDSYASVIK[325.13]ALEHSALAINHK.L             |
| 0.999999 | 1 R.MVLAAAGGVEHQQLDLAQK[325.13]HLGGIPWTYAEDA     |
| 0.999999 | 1 R.SPLVAAMQHFLPVLK[325.13]DR.F                  |
| 0.999999 | 1 R.SPLVAAMQHFLPVLK[325.13]DR.F                  |
| 0.999999 | 1 R.KGISDLVLK[325.13]EYLDNVQLGHILER.E            |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.GITGVDLFGTTDAVVK[325.13]HVLEGHDR.G           |
| 0.999999 | 1 K.FSDSYASVIK[325.13]ALEHSALAINHK.L             |
| 0.999999 | 1 R.SPLVAAMQHFLPVLK[325.13]DR.F                  |
| 0.999999 | 1 R.SPLVAAMQHFLPVLK[325.13]DR.F                  |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.RGVMLAVDAVIAELK[325.13]K.Q                   |
| 0.999999 | 1 K.C[160.03]QFGLAQEC[160.03]LHHAQDYGGLLLLATASGN |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.VGPAVELALAQVK[325.13]ARPDLLPGWTVR.T          |
| 0.999999 | 1 R.VGPAVELALAQVK[325.13]ARPDLLPGWTVR.T          |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 K.SKDDQVTVIGAGVTLHEALAAELLK[325.13]K.E         |
| 0.999999 | 1 R.GITGVDLFGTTDAVVK[325.13]HVLEGHDR.G           |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.GITGVDLFGTTDAVVK[325.13]HVLEGHDR.G           |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.GITGVDLFGTTDAVVK[325.13]HVLEGHDR.G           |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.GITGVDLFGTTDAVVK[325.13]HVLEGHDR.G           |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.FTAQGLPDLNHSQVYAVK[325.13]TVLQRPLSLIQPPGTC   |
| 0.999999 | 1 R.GAEVHLPWNHDFTK[325.13]MEYDGILIAGGPGNPALAI    |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.GAEVHLPWNHDFTK[325.13]MEYDGILIAGGPGNPALAI    |
| 0.999999 | 1 K.KQDEPIDLFMIEIMEMK[325.13]HK.S                |
| 0.999999 | 1 R.FLSHSLVELLNQISPTFK[325.13]K.N                |
| 0.999999 | 1 K.KQDEPIDLFMIEIMEMK[325.13]HK.S                |
| 0.999999 | 1 K.IVTTTGAVPGRPTMMISTTAMNTALLQWHPPK[325.13]EI   |
| 0.999999 | 1 R.IPLSDLTHQISK[325.13]DYGVYLED SGHTLR.G        |
| 0.999999 | 1 K.VVLK[325.13]SKDDQVTVIGAGVTLHEALAAELLK.K      |
| 0.999999 | 1 K.IVTTTGAVPGRPTMMISTTAMNTALLQWHPPK[325.13]EI   |
| 0.999999 | 1 R.TVDLSSHLAK[325.13]VTAEVVLAHLGGGSTSR.A        |
| 0.999999 | 1 R.TVDLSSHLAK[325.13]VTAEVVLAHLGGGSTSR.A        |
| 0.999999 | 1 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPSGK.L   |



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| 0.999999 | 1 R.TVDLSSHLAK[325.13]VTAEVVLAHLGGGSTSR.A           |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSGK.L     |
| 0.999999 | 1 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSGK.L     |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSGK.L     |
| 0.999999 | 1 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSGK.L     |
| 0.999999 | 1 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSGK.L     |
| 0.999999 | 1 R.DMVGIAQTGSGK[325.13]TLAYLLPAIVHINHQPYLER.G      |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSGK.L     |
| 0.999999 | 1 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSGK.L     |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 K.AIGPHDVLATLLNNLK[325.13]VQER.Q                  |
| 0.999999 | 1 K.GIIRPGTAFELLEQAATGYVIDPIK[325.13]GLK.L          |
| 0.999999 | 1 K.AIGPHDVLATLLNNLK[325.13]VQER.Q                  |
| 0.999999 | 1 K.GIIRPGTAFELLEQAATGYVIDPIK[325.13]GLK.L          |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 R.GHYTIGK[325.13]EIIDLVLDR.I                      |
| 0.999999 | 1 K.GIIRPGTAFELLEQAATGYVIDPIK[325.13]GLK.L          |
| 0.999999 | 1 K.GIIRPGTAFELLEQAATGYVIDPIK[325.13]GLK.L          |
| 0.999999 | 1 K.LPIFFFGTHETAFLGPK[325.13]DIFPYSENK.E            |
| 0.999999 | 1 R.HLGYTLC[160.03]K[325.13]QIGTLAELR.E             |
| 0.999999 | 1 R.HLGYTLC[160.03]K[325.13]QIGTLAELR.E             |
| 0.999999 | 1 R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H              |
| 0.999999 | 1 R.HLGYTLC[160.03]K[325.13]QIGTLAELR.E             |
| 0.999999 | 1 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTSGGFTS    |
| 0.999999 | 1 R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H              |
| 0.999999 | 1 K.NMPLQHLEQIK[325.13]ELEK.E                       |
| 0.999999 | 1 R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H              |
| 0.999999 | 1 K.LPNFGFVVDSEPVQK[325.13]VLSNRPIMFR.G             |
| 0.999999 | 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                |
| 0.999999 | 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                |
| 0.999999 | 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                |
| 0.999999 | 1 R.YVEPIEDVPC[160.03]GNIVGLVGVDQFLVK[325.13]TGTTI' |
| 0.999999 | 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                |
| 0.999999 | 1 R.YVEPIEDVPC[160.03]GNIVGLVGVDQFLVK[325.13]TGTTI' |
| 0.999999 | 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                |
| 0.999999 | 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                |
| 0.999999 | 1 R.FHNLEGFLEEFADIAD[325.13]EDQIK.K                 |
| 0.999999 | 1 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR.   |
| 0.999999 | 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                |

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| 0.999999 | 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W               |
| 0.999999 | 1 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR.  |
| 0.999999 | 1 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR.  |
| 0.999999 | 1 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR.  |
| 0.999999 | 1 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR.  |
| 0.999999 | 1 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR.  |
| 0.999999 | 1 K.ESWHGKPLPK[325.13]NMAEQIIQEISQIQSK.K           |
| 0.999999 | 1 K.ESWHGKPLPK[325.13]NMAEQIIQEISQIQSK.K           |
| 0.999999 | 1 R.ASLSLWQAMEK[325.13]GLVPQNEGLPLLQVQLATGGVV      |
| 0.999999 | 1 R.LPGGHQTVLFSATLPK[325.13]LLVEFAR.A              |
| 0.999999 | 1 R.LPGGHQTVLFSATLPK[325.13]LLVEFAR.A              |
| 0.999999 | 1 K.LVLPMIK[325.13]EHIMQMLQNPDWK.Y                 |
| 0.999999 | 1 R.LGGIGQFLAK[325.13]AIEPPPLDAVIEAEHTLR.E         |
| 0.999999 | 1 R.K[325.13]NAFALLVEMGHAFRL.F                     |
| 0.999999 | 1 R.SELIAK[325.13]IPNFWVTTFVNHPQVSALLGEEDEEALHYL   |
| 0.999999 | 1 R.NQLTAMSSVLAK[325.13]ALEVIKPAHILQEK.E           |
| 0.999999 | 1 R.NQLTAMSSVLAK[325.13]ALEVIKPAHILQEK.E           |
| 0.999999 | 1 R.WLPAGDALLQMITIHLSPVTAQK[325.13]YR.C            |
| 0.999999 | 1 R.WLPAGDALLQMITIHLSPVTAQK[325.13]YR.C            |
| 0.999999 | 1 R.WLPAGDALLQMITIHLSPVTAQK[325.13]YR.C            |
| 0.999999 | 1 R.WLPAGDALLQMITIHLSPVTAQK[325.13]YR.C            |
| 0.999999 | 1 R.WLPAGDALLQMITIHLSPVTAQK[325.13]YR.C            |
| 0.999999 | 1 K.VK[325.13]PIVAKLIAALSTPSQQVQESVASC[160.03]LPPL |
| 0.999999 | 1 K.VK[325.13]PIVAKLIAALSTPSQQVQESVASC[160.03]LPPL |
| 0.999999 | 1 K.VK[325.13]PIVAKLIAALSTPSQQVQESVASC[160.03]LPPL |
| 0.999999 | 1 K.VK[325.13]PIVAKLIAALSTPSQQVQESVASC[160.03]LPPL |
| 0.999999 | 1 K.VKPIVAK[325.13]LIAALSTPSQQVQESVASC[160.03]LPPL |
| 0.999999 | 1 K.KLDSLTTSGFPPVGAATLVDEVGVDAK[325.13]HVAEDLC     |
| 0.999999 | 1 K.KLDSLTTSGFPPVGAATLVDEVGVDAK[325.13]HVAEDLC     |
| 0.999999 | 1 K.KLDSLTTSGFPPVGAATLVDEVGVDAK[325.13]HVAEDLC     |
| 0.999999 | 1 K.KLDSLTTSGFPPVGAATLVDEVGVDAK[325.13]HVAEDLC     |
| 0.999999 | 1 K.EPEKEIRPALELLEPIEQK[325.13]FVSISDLLVPK.D       |
| 0.999999 | 1 K.AQTQK[325.13]HGITQANELVNLTEFFVNHILPDLK.S       |
| 0.999999 | 1 K.SLADELALVDVLEDK[325.13]LKGEMMDLQHGSFLQTPK.     |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII  |
| 0.999999 | 1 K.KTESHHK[325.13]AK.G                            |
| 0.999999 | 1 K.AKKPAGAAKK[325.13]PK.K                         |
| 0.999999 | 1 R.KSAPATGGVK[325.13]KPHR.Y                       |
| 0.999999 | 1 K.FPHSAHQK[325.13]YVR.Q                          |
| 0.999999 | 1 R.SSFHYSGLK[325.13]HEDKR.G                       |
| 0.999999 | 1 R.TYHYHC[160.03]ALHDK[325.13]AQIR.E              |
| 0.999999 | 1 R.RNPDTQWITKPVHK[325.13]HR.E                     |
| 0.999999 | 1 R.RNPDTQWITKPVHK[325.13]HR.E                     |
| 0.999999 | 1 R.RGYHK[325.13]VSLQVHPDR.V                       |
| 0.999999 | 1 R.RGYHK[325.13]VSLQVHPDR.V                       |
| 0.999999 | 1 K.LGLAK[325.13]SIHHAR.V                          |
| 0.999999 | 1 R.MISK[325.13]QFHHQLR.V                          |

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| 0.999999 | 1 R.LNFSHGTHEYHAETIK[325.13]NVR.T                   |
| 0.999999 | 1 R.LNFSHGTHEYHAETIK[325.13]NVR.T                   |
| 0.999999 | 1 R.LNFSHGTHEYHAETIK[325.13]NVR.T                   |
| 0.999999 | 1 R.LNFSHGTHEYHAETIK[325.13]NVR.T                   |
| 0.999999 | 1 K.EKPGPEDK[325.13]LHEQC[160.03]RPWR.K             |
| 0.999999 | 1 K.DWHRPC[160.03]LK[325.13]C[160.03]EK.C           |
| 0.999999 | 1 R.IC[160.03]HGK[325.13]PVTQVTWHGR.G               |
| 0.999999 | 1 R.HPFIVNHPK[325.13]VGR.V                          |
| 0.999999 | 1 R.LNFSHGTHEYHAETIK[325.13]NVR.T                   |
| 0.999999 | 1 R.LNFSHGTHEYHAETIK[325.13]NVR.T                   |
| 0.999999 | 1 R.LNFSHGTHEYHAETIK[325.13]NVR.T                   |
| 0.999999 | 1 K.DWHRPC[160.03]LK[325.13]C[160.03]EK.C           |
| 0.999999 | 1 R.IC[160.03]HGK[325.13]PVTQVTWHGR.G               |
| 0.999999 | 1 R.IC[160.03]HGK[325.13]PVTQVTWHGR.G               |
| 0.999999 | 1 K.LITQTFSHHNQLAQK[325.13]TR.R                     |
| 0.999999 | 1 K.LITQTFSHHNQLAQK[325.13]TR.R                     |
| 0.999999 | 1 K.FWHK[325.13]AC[160.03]FHC[160.03]ETC[160.03]K.M |
| 0.999999 | 1 R.LLLSK[325.13]GHSC[160.03]YRPR.R                 |
| 0.999999 | 1 R.HK[325.13]NM[147.04]SVHLSPC[160.03]FR.D         |
| 0.999999 | 1 K.ALLNNSHYHMAHGK[325.13]DFASR.G                   |
| 0.999999 | 1 R.HK[325.13]NM[147.04]SVHLSPC[160.03]FR.D         |
| 0.999999 | 1 K.ALLNNSHYHMAHGK[325.13]DFASR.G                   |
| 0.999999 | 1 R.HK[325.13]NM[147.04]SVHLSPC[160.03]FR.D         |
| 0.999999 | 1 K.KAHLGTALK[325.13]ANPFGGASHAK.G                  |
| 0.999999 | 1 K.KAHLGTALK[325.13]ANPFGGASHAK.G                  |
| 0.999999 | 1 K.KAHLGTALK[325.13]ANPFGGASHAK.G                  |
| 0.999999 | 1 K.KAHLGTALK[325.13]ANPFGGASHAK.G                  |
| 0.999999 | 1 K.AAVVK[325.13]FHPIQGHR.V                         |
| 0.999999 | 1 K.STHDHWK[325.13]ALVTK.K                          |
| 0.999999 | 1 R.SIQGHHC[160.03]LLVK[325.13]K.G                  |
| 0.999999 | 1 K.STHDHWK[325.13]ALVTK.K                          |
| 0.999999 | 1 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                 |
| 0.999999 | 1 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                 |
| 0.999999 | 1 K.STHDHWK[325.13]ALVTK.K                          |
| 0.999999 | 1 K.K[325.13]LFVGGIKEDTEEHHLR.D                     |
| 0.999999 | 1 K.K[325.13]LFVGGIKEDTEEHHLR.D                     |
| 0.999999 | 1 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                 |
| 0.999999 | 1 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                 |
| 0.999999 | 1 K.YKDAIHFNK[325.13]SLAEHR.T                       |
| 0.999999 | 1 K.K[325.13]LFVGGIKEDTEEHHLR.D                     |
| 0.999999 | 1 K.YKDAIHFNK[325.13]SLAEHR.T                       |
| 0.999999 | 1 K.K[325.13]LFVGGIKEDTEEHHLR.D                     |
| 0.999999 | 1 R.VTSLGK[325.13]DWHRPC[160.03]LK.C                |
| 0.999999 | 1 K.YKDAIHFNK[325.13]SLAEHR.T                       |
| 0.999999 | 1 K.YKDAIHFNK[325.13]SLAEHR.T                       |
| 0.999999 | 1 R.HM[147.04]YHSLYK[325.13]VK.G                    |
| 0.999999 | 1 R.KVDSK[325.13]SLFHYR.Q                           |

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| 0.999999 | 1 K.LHYC[160.03]VSC[160.03]AIHSK[325.13]VVR.N   |
| 0.999999 | 1 K.K[325.13]LFVGGIKEDTEEHHLR.D                 |
| 0.999999 | 1 R.HK[325.13]NMSVHLSPC[160.03]FR.D             |
| 0.999999 | 1 R.KVDSK[325.13]SLFHYR.Q                       |
| 0.999999 | 1 K.LHYC[160.03]VSC[160.03]AIHSK[325.13]VVR.N   |
| 0.999999 | 1 R.HLYTK[325.13]DIDIHEVR.I                     |
| 0.999999 | 1 K.K[325.13]LFVGGIKEDTEEHHLR.D                 |
| 0.999999 | 1 K.K[325.13]LFVGGIKEDTEEHHLR.D                 |
| 0.999999 | 1 K.KFSGK[325.13]HVVFIAQR.R                     |
| 0.999999 | 1 K.KFSGK[325.13]HVVFIAQR.R                     |
| 0.999999 | 1 R.HK[325.13]NMSVHLSPC[160.03]FR.D             |
| 0.999999 | 1 R.ERHPGSFDVVHVK[325.13]DANGNSFATR.L           |
| 0.999999 | 1 R.HK[325.13]NMSVHLSPC[160.03]FR.D             |
| 0.999999 | 1 R.HLYTK[325.13]DIDIHEVR.I                     |
| 0.999999 | 1 R.HMYHSLYLK[325.13]VK.G                       |
| 0.999999 | 1 R.HK[325.13]NMSVHLSPC[160.03]FR.D             |
| 0.999999 | 1 K.NHHC[160.03]K[325.13]LTQVLNTHYVAPR.R        |
| 0.999999 | 1 R.HLYTK[325.13]DIDIHEVR.I                     |
| 0.999999 | 1 K.TFHHVYSGK[325.13]DLIAQAR.T                  |
| 0.999999 | 1 R.HK[325.13]NMSVHLSPC[160.03]FR.D             |
| 0.999999 | 1 K.NHHC[160.03]K[325.13]LTQVLNTHYVAPR.R        |
| 0.999999 | 1 R.HMYHSLYLK[325.13]VK.G                       |
| 0.999999 | 1 K.NHHC[160.03]K[325.13]LTQVLNTHYVAPR.R        |
| 0.999999 | 1 K.AHLGTALK[325.13]ANPFGGASHAK.G               |
| 0.999999 | 1 R.NGMVLKPHFHK[325.13]DWQR.R                   |
| 0.999999 | 1 R.NGMVLKPHFHK[325.13]DWQR.R                   |
| 0.999999 | 1 R.HRPELIDYGK[325.13]LR.K                      |
| 0.999999 | 1 R.IYC[160.03]KPHFNQLFK[325.13]SK.G            |
| 0.999999 | 1 R.NLHK[325.13]LLYNRPGTVSSLK.K                 |
| 0.999999 | 1 K.IHLAQSLHK[325.13]LSTAC[160.03]PGR.V         |
| 0.999999 | 1 R.HK[325.13]NMSVHLSPC[160.03]FR.D             |
| 0.999999 | 1 K.IHLAQSLHK[325.13]LSTAC[160.03]PGR.V         |
| 0.999999 | 1 K.LFVGGIK[325.13]EDTEEHHLR.D                  |
| 0.999999 | 1 K.FLK[325.13]HWDHLTQVK.K                      |
| 0.999999 | 1 K.TLTSGGHAHEGKPYC[160.03]NHPC[160.03]YAAMFGPI |
| 0.999999 | 1 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF  |
| 0.999999 | 1 K.TLTSGGHAHEGKPYC[160.03]NHPC[160.03]YAAMFGPI |
| 0.999999 | 1 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF  |
| 0.999999 | 1 K.LFVGGIK[325.13]EDTEEHHLR.D                  |
| 0.999999 | 1 R.NLHK[325.13]LLYNRPGTVSSLK.K                 |
| 0.999999 | 1 K.TIHK[325.13]YVHLFPK.L                       |
| 0.999999 | 1 K.FLK[325.13]HWDHLTQVK.K                      |
| 0.999999 | 1 K.EGVVGPELHHK[325.13]LLSAER.A                 |
| 0.999999 | 1 K.TIHK[325.13]YVHLFPK.L                       |
| 0.999999 | 1 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF  |
| 0.999999 | 1 R.KIFVGTK[325.13]GIPHLVTHDAR.T                |
| 0.999999 | 1 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF  |

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| 0.999999 | 1 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF |
| 0.999999 | 1 R.YTC[160.03]HVQHEGLPK[325.13]PLTLR.W        |
| 0.999999 | 1 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF |
| 0.999999 | 1 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF |
| 0.999999 | 1 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF |
| 0.999999 | 1 K.HKSDFGK[325.13]FVLSSGK.F                   |
| 0.999999 | 1 R.DHC[160.03]VAHK[325.13]LFNNLK.-            |
| 0.999999 | 1 K.LFVGGIK[325.13]EDTEEHHLR.D                 |
| 0.999999 | 1 K.LFVGGIK[325.13]EDTEEHHLR.D                 |
| 0.999999 | 1 R.DHC[160.03]VAHK[325.13]LFNNLK.-            |
| 0.999999 | 1 R.KAVIVK[325.13]NIDDGTSRDPYSHALVAGIDR.Y      |
| 0.999999 | 1 R.KAVIVK[325.13]NIDDGTSRDPYSHALVAGIDR.Y      |
| 0.999999 | 1 K.HK[325.13]TGPNLHGLFGR.K                    |
| 0.999999 | 1 R.YTC[160.03]HVQHEGLPK[325.13]PLTLR.W        |
| 0.999999 | 1 R.KAVIVK[325.13]NIDDGTSRDPYSHALVAGIDR.Y      |
| 0.999999 | 1 R.KAVIVK[325.13]NIDDGTSRDPYSHALVAGIDR.Y      |
| 0.999999 | 1 R.YTC[160.03]HVQHEGLPK[325.13]PLTLR.W        |
| 0.999999 | 1 K.HK[325.13]TGPNLHGLFGR.K                    |
| 0.999999 | 1 K.HPK[325.13]NPEVGLKPVWYSPK.V                |
| 0.999999 | 1 R.GC[160.03]GPEK[325.13]DHVYLQLHHLPEQLATR.L  |
| 0.999999 | 1 R.KVDWLTEK[325.13]MHAR.D                     |
| 0.999999 | 1 R.GC[160.03]GPEK[325.13]DHVYLQLHHLPEQLATR.L  |
| 0.999999 | 1 K.HPK[325.13]NPEVGLKPVWYSPK.V                |
| 0.999999 | 1 R.GC[160.03]GPEK[325.13]DHVYLQLHHLPEQLATR.L  |
| 0.999999 | 1 R.KVDWLTEK[325.13]MHAR.D                     |
| 0.999999 | 1 K.HPK[325.13]NPEVGLKPVWYSPK.V                |
| 0.999999 | 1 R.GFIYVHK[325.13]PPVHIR.F                    |
| 0.999999 | 1 R.AFDSAVAK[325.13]ALEHHR.S                   |
| 0.999999 | 1 R.GFIYVHK[325.13]PPVHIR.F                    |
| 0.999999 | 1 K.K[325.13]IHLVVLVKPSGAR.C                   |
| 0.999999 | 1 R.HPALFK[325.13]AIGVKPPR.G                   |
| 0.999999 | 1 R.GHLAK[325.13]IYAMHWGTDSR.L                 |
| 0.999999 | 1 R.AFDSAVAK[325.13]ALEHHR.S                   |
| 0.999999 | 1 K.K[325.13]HLEINPDHPIVETLR.Q                 |
| 0.999999 | 1 R.GHLAK[325.13]IYAMHWGTDSR.L                 |
| 0.999999 | 1 K.K[325.13]IHLVVLVKPSGAR.C                   |
| 0.999999 | 1 K.IMEHAGK[325.13]NQVLVHVHRSR.K               |
| 0.999999 | 1 K.K[325.13]IHLVVLVKPSGAR.C                   |
| 0.999999 | 1 R.AISHEHSPSDLEAHFVPLVK[325.13]R.L            |
| 0.999999 | 1 R.AISHEHSPSDLEAHFVPLVK[325.13]R.L            |
| 0.999999 | 1 K.IMEHAGK[325.13]NQVLVHVHRSR.K               |
| 0.999999 | 1 K.K[325.13]IHLVVLVKPSGAR.C                   |
| 0.999999 | 1 R.GKDHVVSDFSEHGSLK[325.13]YLHENLPIPQR.N      |
| 0.999999 | 1 R.GKDHVVSDFSEHGSLK[325.13]YLHENLPIPQR.N      |
| 0.999999 | 1 R.GKDHVVSDFSEHGSLK[325.13]YLHENLPIPQR.N      |
| 0.999999 | 1 K.KFLDAGHK[325.13]LNFAVASR.K                 |
| 0.999999 | 1 K.IFVGTK[325.13]GIPHLVTHDAR.T                |

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| 0.999999 | 1 R.HPDSHQLFIGNLPHEVDK[325.13]SELK.D                    |
| 0.999999 | 1 R.HPDSHQLFIGNLPHEVDK[325.13]SELK.D                    |
| 0.999999 | 1 R.HFQSC[160.03]SQC[160.03]LSAPPVQC[160.03]GWC[160.03] |
| 0.999999 | 1 R.MAQEVLTHLK[325.13]EHPPDAWTR.V                       |
| 0.999999 | 1 R.HFQSC[160.03]SQC[160.03]LSAPPVQC[160.03]GWC[160.03] |
| 0.999999 | 1 R.HFQSC[160.03]SQC[160.03]LSAPPVQC[160.03]GWC[160.03] |
| 0.999999 | 1 K.MK[325.13]VVEVLAGHGHLYSR.I                          |
| 0.999999 | 1 R.MDYVEINIDHK[325.13]FHR.H                            |
| 0.999999 | 1 R.AHMESDKHLEALC[160.03]LFK[325.13]AEHWNR.C            |
| 0.999999 | 1 K.WRPVDLAQVK[325.13]GHRL.G                            |
| 0.999999 | 1 K.WRPVDLAQVK[325.13]GHRL.G                            |
| 0.999999 | 1 R.ADEARPNTIDFGKDDQHFTVTGLHK[325.13]GTITYFR.L          |
| 0.999999 | 1 R.ADEARPNTIDFGKDDQHFTVTGLHK[325.13]GTITYFR.L          |
| 0.999999 | 1 K.WRPVDLAQVK[325.13]GHRL.G                            |
| 0.999999 | 1 K.WRPVDLAQVK[325.13]GHRL.G                            |
| 0.999999 | 1 K.WRPVDLAQVK[325.13]GHRL.G                            |
| 0.999999 | 1 R.ADEARPNTIDFGKDDQHFTVTGLHK[325.13]GTITYFR.L          |
| 0.999999 | 1 R.ADEARPNTIDFGKDDQHFTVTGLHK[325.13]GTITYFR.L          |
| 0.999999 | 1 K.HEYFMHATDK[325.13]GGLSAVDAFEIHVHR.R                 |
| 0.999999 | 1 K.HEYFMHATDK[325.13]GGLSAVDAFEIHVHR.R                 |
| 0.999999 | 1 K.WRPVDLAQVK[325.13]GHRL.G                            |
| 0.999999 | 1 K.WRPVDLAQVK[325.13]GHRL.G                            |
| 0.999999 | 1 K.HEYFMHATDK[325.13]GGLSAVDAFEIHVHR.R                 |
| 0.999999 | 1 R.FLEGK[325.13]IKPHLMSQELPEDWDKQPVK.V                 |
| 0.999999 | 1 R.GQHVTGSPFQFTVGPLGEGGAHK[325.13]VR.A                 |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.GQHVTGSPFQFTVGPLGEGGAHK[325.13]VR.A                 |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.HEC[160.03]MAPLTALVK[325.13]HMHR.S                  |
| 0.999999 | 1 R.DIFYKPFHGDIQC[160.03]GGHAPGSSK[325.13]SFPC[160.03]  |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.DIFYKPFHGDIQC[160.03]GGHAPGSSK[325.13]SFPC[160.03]  |
| 0.999999 | 1 R.HAYYVTVEAAPYWHLK[325.13]PQSHLYGPGETAR.L             |
| 0.999999 | 1 R.GQHVPGPSFPQFTVGPLGEGGAHK[325.13]VR.A                |
| 0.999999 | 1 K.GK[325.13]WKPPMIDNPYSYGWIWKPR.K                     |
| 0.999999 | 1 R.FDASFFGVHPK[325.13]QAHTMDPQLR.L                     |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                       |
| 0.999999 | 1 R.FDASFFGVHPK[325.13]QAHTMDPQLR.L                     |
| 0.999999 | 1 K.GK[325.13]WKPPMIDNPYSYGWIWKPR.K                     |
| 0.999999 | 1 R.FDASFFGVHPK[325.13]QAHTMDPQLR.L                     |
| 0.999999 | 1 R.IMGLDLPDGGHLTHGYMSDVK[325.13]R.I                    |
| 0.999999 | 1 R.IMGLDLPDGGHLTHGYMSDVK[325.13]R.I                    |

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| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 1 R.LHFHNLVK[325.13]GLTDL SAC[160.03]K.A           |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 1 R.ISAK[325.13]AALAH PFFQDVTKPVPHLR.L             |
| 0.999999 | 1 R.ISAK[325.13]AALAH PFFQDVTKPVPHLR.L             |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 0.9999 K.K[325.13]YVATLGVEVHPLVFHTNR.G             |
| 0.999999 | 1 R.ISAK[325.13]AALAH PFFQDVTKPVPHLR.L             |
| 0.999999 | 1 R.LHFHNLVK[325.13]GLTDL SAC[160.03]K.A           |
| 0.999999 | 1 R.LHFHNLVK[325.13]GLTDL SAC[160.03]K.A           |
| 0.999999 | 1 K.K[325.13]YVATLGVEVHPLVFHTNR.G                  |
| 0.999999 | 1 R.LK[325.13]GLGAFVIDSDHLGHR.A                    |
| 0.999999 | 1 K.FKDPNAPK[325.13]RPPSAFFLFC[160.03]SEYRPK.I     |
| 0.999999 | 1 R.RVSEK[325.13]VSHVLAALQAGNR.G                   |
| 0.999999 | 1 R.LK[325.13]GLGAFVIDSDHLGHR.A                    |
| 0.999999 | 1 K.FKDPNAPK[325.13]RPPSAFFLFC[160.03]SEYRPK.I     |
| 0.999999 | 1 K.FHHTFSTEIAK[325.13]FLK.V                       |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFFM[147.04]VVNDAGRP     |
| 0.999999 | 1 R.LK[325.13]GLGAFVIDSDHLGHR.A                    |
| 0.999999 | 1 K.FKDPNAPK[325.13]RPPSAFFLFC[160.03]SEYRPK.I     |
| 0.999999 | 1 K.K[325.13]LNC[160.03]QVIGASVDSHFC[160.03]HLAWVI |
| 0.999999 | 1 K.HLEALC[160.03]LFK[325.13]AEHWNR.C              |
| 0.999999 | 1 R.RVSEK[325.13]VSHVLAALQAGNR.G                   |
| 0.999999 | 1 R.KFGDPVVQSDMK[325.13]HWPFFQVINDGDKPK.V          |
| 0.999999 | 1 K.K[325.13]LNC[160.03]QVIGASVDSHFC[160.03]HLAWVI |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFFM[147.04]VVNDAGRP     |
| 0.999999 | 1 R.KFGDPVVQSDMK[325.13]HWPFFQVINDGDKPK.V          |
| 0.999999 | 1 K.K[325.13]LNC[160.03]QVIGASVDSHFC[160.03]HLAWVI |
| 0.999999 | 1 R.KFGDPVVQSDMK[325.13]HWPFFQVINDGDKPK.V          |
| 0.999999 | 1 K.K[325.13]LNC[160.03]QVIGASVDSHFC[160.03]HLAWVI |
| 0.999999 | 1 K.HLEALC[160.03]LFK[325.13]AEHWNR.C              |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFFM[147.04]VVNDAGRP     |
| 0.999999 | 1 R.GYK[325.13]HPVLLHPLGGWTK.D                     |
| 0.999999 | 1 R.YHEAWQK[325.13]LC[160.03]SAHGVLVPGGFGVR.G      |
| 0.999999 | 1 R.RIPWTAASSQLK[325.13]EHFAQFGHVR.R               |
| 0.999999 | 1 R.GHLENNPALEK[325.13]LLPHIR.G                    |
| 0.999999 | 1 R.RIPWTAASSQLK[325.13]EHFAQFGHVR.R               |
| 0.999999 | 1 R.RIPWTAASSQLK[325.13]EHFAQFGHVR.R               |
| 0.999999 | 1 R.GHLENNPALEK[325.13]LLPHIR.G                    |
| 0.999999 | 1 K.EHYVDLK[325.13]DRPFFAGLVK.Y                    |
| 0.999999 | 1 K.EHYVDLK[325.13]DRPFFAGLVK.Y                    |
| 0.999999 | 1 R.GHLENNPALEK[325.13]LLPHIR.G                    |

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| 0.999999 | 1 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S          |
| 0.999999 | 1 K.DDPSKPVHLTAFLGYK[325.13]AGMTHIVR.E            |
| 0.999999 | 1 K.DDPSKPVHLTAFLGYK[325.13]AGMTHIVR.E            |
| 0.999999 | 1 R.FHILFK[325.13]ALGEEK.G                        |
| 0.999999 | 1 K.HLPPAALHLIAYYK[325.13]ENK.D                   |
| 0.999999 | 1 K.HAHTIK[325.13]PALVGWFGHELSTR.F                |
| 0.999999 | 1 R.LHDLYWQAMK[325.13]TLGVQRPK.L                  |
| 0.999999 | 1 R.FK[325.13]KPGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V  |
| 0.999999 | 1 R.FK[325.13]KPGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V  |
| 0.999999 | 1 R.FHILFK[325.13]ALGEEK.G                        |
| 0.999999 | 1 R.FK[325.13]KPGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V  |
| 0.999999 | 1 K.RPPSAFFLFC[160.03]SEYRPK[325.13]IK.G          |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V          |
| 0.999999 | 1 R.AGKPVIC[160.03]ATQMLESNIK[325.13]KPRPTR.A     |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V          |
| 0.999999 | 1 K.HQGLK[325.13]LATTILQHWK.K                     |
| 0.999999 | 1 R.EHLWK[325.13]LIEGGAHIYVC[160.03]GDAR.N        |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V          |
| 0.999999 | 1 K.HQGLK[325.13]LATTILQHWK.K                     |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V          |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V          |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V          |
| 0.999999 | 1 K.HQGLK[325.13]LATTILQHWK.K                     |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V          |
| 0.999999 | 1 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V          |
| 0.999999 | 1 R.HGDLPIQIK[325.13]HSSLITPLQAVAQR.D             |
| 0.999999 | 1 R.IPWTAASSQLK[325.13]EHFAQFGHVR.R               |
| 0.999999 | 1 K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V |
| 0.999999 | 1 R.IPWTAASSQLK[325.13]EHFAQFGHVR.R               |
| 0.999999 | 1 R.IPWTAASSQLK[325.13]EHFAQFGHVR.R               |
| 0.999999 | 1 R.LLNFLMK[325.13]HVFHPK.R                       |
| 0.999999 | 1 R.IPWTAASSQLK[325.13]EHFAQFGHVR.R               |
| 0.999999 | 1 R.IPWTAASSQLK[325.13]EHFAQFGHVR.R               |
| 0.999999 | 1 R.HSHALVSLFLK[325.13]NLR.L                      |
| 0.999999 | 1 R.HSHALVSLFLK[325.13]NLR.L                      |
| 0.999999 | 1 R.RGNVAGDSK[325.13]NDPPMEAAGFTAQVIILNHPGQISA    |
| 0.999999 | 1 K.DPFAHLPK[325.13]STFVLDEFKR.K                  |
| 0.999999 | 1 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S    |
| 0.999999 | 1 K.DPFAHLPK[325.13]STFVLDEFKR.K                  |
| 0.999999 | 1 R.GHQK[325.13]EGYGLSWNSNLSGHLLSASDDHTVC[160.0   |
| 0.999999 | 1 R.GVTFLFPIQAK[325.13]TFHHVYSGK.D                |
| 0.999999 | 1 R.GVTFLFPIQAK[325.13]TFHHVYSGK.D                |
| 0.999999 | 1 R.GVTFLFPIQAK[325.13]TFHHVYSGK.D                |
| 0.999999 | 1 R.LLQDHPWLLSQNLVVKPDQLIK[325.13]R.R             |
| 0.999999 | 1 R.SK[325.13]ERSLLHGDFHAFSAGPGLFSYIR.H           |
| 0.999999 | 1 K.KSAEFLHMLK[325.13]NAESNAELK.G                 |
| 0.999999 | 1 K.RGILTLK[325.13]YPIEHGIITNWDDMEK.I             |



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| 0.999999 | 1 R.LLQDHPWLLSQNLVVKPDQLIK[325.13]R.R             |
| 0.999999 | 1 R.LLQDHPWLLSQNLVVKPDQLIK[325.13]R.R             |
| 0.999999 | 1 K.RGILTLK[325.13]YPIEHGIITNWDDMEK.I             |
| 0.999999 | 1 R.LLQDHPWLLSQNLVVKPDQLIK[325.13]R.R             |
| 0.999999 | 1 K.KSAEFLHMLK[325.13]NAESNAELK.G                 |
| 0.999999 | 1 K.RGILTLK[325.13]YPIEHGIITNWDDMEK.I             |
| 0.999999 | 1 R.LLQDHPWLLSQNLVVKPDQLIK[325.13]R.R             |
| 0.999999 | 1 R.LLQDHPWLLSQNLVVKPDQLIK[325.13]R.R             |
| 0.999999 | 1 R.AIMKDPDDHTVC[160.03]HLLFANQTEK[325.13]DILLRPE |
| 0.999999 | 1 R.LLQDHPWLLSQNLVVKPDQLIK[325.13]R.R             |
| 0.999999 | 1 R.AIMKDPDDHTVC[160.03]HLLFANQTEK[325.13]DILLRPE |
| 0.999999 | 1 R.TAPDLLPHK[325.13]PLPASAYIEDGRFDLSMPHVQDPSLV   |
| 0.999999 | 1 R.TAPDLLPHK[325.13]PLPASAYIEDGRFDLSMPHVQDPSLV   |
| 0.999999 | 1 R.TAPDLLPHK[325.13]PLPASAYIEDGRFDLSMPHVQDPSLV   |
| 0.999999 | 1 R.TLHTTASNWLHLPQTLSHLK[325.13]R.T               |
| 0.999999 | 1 K.IRPIK[325.13]ASVITQVFHVPLEER.K                |
| 0.999999 | 1 R.TLHTTASNWLHLPQTLSHLK[325.13]R.T               |
| 0.999999 | 1 K.EVAGAKPHITAAEGK[325.13]LHNMIVDLDNVVK.K        |
| 0.999999 | 1 K.ITK[325.13]FENAFLSHVVSQHQALLGTIR.A            |
| 0.999999 | 1 K.ITK[325.13]FENAFLSHVVSQHQALLGTIR.A            |
| 0.999999 | 1 R.VNPC[160.03]IGGVILFHETLYQK[325.13]ADDGRPFQVI  |
| 0.999999 | 1 R.VNPC[160.03]IGGVILFHETLYQK[325.13]ADDGRPFQVI  |
| 0.999999 | 1 K.ITK[325.13]FENAFLSHVVSQHQALLGTIR.A            |
| 0.999999 | 1 R.VNPC[160.03]IGGVILFHETLYQK[325.13]ADDGRPFQVI  |
| 0.999999 | 1 R.VNPC[160.03]IGGVILFHETLYQK[325.13]ADDGRPFQVI  |
| 0.999999 | 1 R.VNPC[160.03]IGGVILFHETLYQK[325.13]ADDGRPFQVI  |
| 0.999999 | 1 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR    |
| 0.999999 | 1 R.HVFWGSGSHTLPALLENLK[325.13]LR.K               |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII |
| 0.999999 | 1 K.TEILPPFFK[325.13]HFWQHR.M                     |
| 0.999999 | 1 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII |
| 0.999999 | 1 R.EIVHLQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII |
| 0.999999 | 0.9998 R.HVFWGSGSHTLPALLENLK[325.13]LR.K          |
| 0.999999 | 1 R.HVFWGSGSHTLPALLENLK[325.13]LR.K               |
| 0.999999 | 1 R.HVFWGSGSHTLPALLENLK[325.13]LR.K               |
| 0.999999 | 1 R.EIVHLQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII |
| 0.999999 | 1 R.HVFWGSGSHTLPALLENLK[325.13]LR.K               |
| 0.999999 | 1 R.HVFWGSGSHTLPALLENLK[325.13]LR.K               |
| 0.999999 | 1 R.HVFWGSGSHTLPALLENLK[325.13]LR.K               |
| 0.999999 | 1 R.ILHLLTQEALSIHG VK[325.13]EAVQLVNTR.E          |
| 0.999999 | 1 R.ILHLLTQEALSIHG VK[325.13]EAVQLVNTR.E          |
| 0.999999 | 1 R.FHMYEGYPLWK[325.13]VTFPVR.V                   |
| 0.999999 | 1 R.HPDSHQLFIGNLPHEVDKSELK[325.13]DFFQSYGNVVELR   |
| 0.999999 | 1 R.HPDSHQLFIGNLPHEVDKSELK[325.13]DFFQSYGNVVELR   |
| 0.999999 | 1 R.HPDSHQLFIGNLPHEVDK[325.13]SELKDFFQSYGNVVELR   |
| 0.999999 | 1 R.HPDSHQLFIGNLPHEVDK[325.13]SELKDFFQSYGNVVELR   |
| 0.999999 | 1 R.HPDSHQLFIGNLPHEVDK[325.13]SELKDFFQSYGNVVELR   |

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| 0.999999 | 1 K.LPQASK[325.13]STSEFIQHIVSLVHHVK.E               |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.LPQASK[325.13]STSEFIQHIVSLVHHVK.E               |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.GDFFPPERPQQLPHGLGGIGMGLPGGGQPIDANHLNK[32        |
| 0.999999 | 1 K.GDFFPPERPQQLPHGLGGIGMGLPGGGQPIDANHLNK[32        |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.NVTLPVAFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V           |
| 0.999999 | 1 R.SPK[325.13]LFYADHPFIFLVR.D                      |
| 0.999999 | 1 K.NVTLPVAFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999999 | 1 R.SPK[325.13]LFYADHPFIFLVR.D                      |
| 0.999999 | 1 K.NVTLPVAFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999999 | 1 K.NVTLPVAFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999999 | 1 R.SPK[325.13]LFYADHPFIFLVR.D                      |
| 0.999999 | 1 K.NVTLPVAFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999999 | 1 K.NVTLPVAFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999999 | 1 K.NVTLPVAFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                  |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                  |
| 0.999999 | 1 R.RPHDYQPLPGMSENPSVYVPGVVSTVVPDSAHK[325.13]L      |
| 0.999999 | 1 R.IHFPLATYAPVISA EK[325.13]AYHEQLSVAEITNAC[160.03 |
| 0.999999 | 1 R.AGLLHNILPSQSTD LHHSVGTELLSLVYK[325.13]GIAPGDE   |
| 0.999999 | 1 R.AGLLHNILPSQSTD LHHSVGTELLSLVYK[325.13]GIAPGDE   |
| 0.999999 | 1 R.AGLLHNILPSQSTD LHHSVGTELLSLVYK[325.13]GIAPGDE   |
| 0.999999 | 1 R.AGLLHNILPSQSTD LHHSVGTELLSLVYK[325.13]GIAPGDE   |
| 0.999999 | 1 R.MVLAAAGGVEHQQLDLAQK[325.13]HLGGIPWTYAEDA        |
| 0.999999 | 1 R.AGLLHNILPSQSTD LHHSVGTELLSLVYK[325.13]GIAPGDE   |
| 0.999999 | 1 R.AGLLHNILPSQSTD LHHSVGTELLSLVYK[325.13]GIAPGDE   |
| 0.999999 | 1 R.IHFPLATYAPVISA EK[325.13]AYHEQLSVAEITNAC[160.03 |
| 0.999999 | 1 R.LGAQALLGAAK[325.13]MLLHSEQHPGQLK.D              |
| 0.999999 | 1 R.IHFPLATYAPVISA EK[325.13]AYHEQLSVAEITNAC[160.03 |
| 0.999999 | 1 R.LGAQALLGAAK[325.13]MLLHSEQHPGQLK.D              |
| 0.999999 | 1 R.IHFPLATYAPVISA EK[325.13]AYHEQLSVAEITNAC[160.03 |
| 0.999999 | 1 R.IHFPLATYAPVISA EK[325.13]AYHEQLSVAEITNAC[160.03 |
| 0.999999 | 1 R.IHFPLATYAPVISA EK[325.13]AYHEQLSVAEITNAC[160.03 |
| 0.999999 | 1 R.LGAQALLGAAK[325.13]MLLHSEQHPGQLK.D              |

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| 0.999999 | 1 R.GAEVHLPWNHDFTK[325.13]MEYDGILIAGGPGNPALAI        |
| 0.999999 | 1 R.LGAQALLGAAK[325.13]MLLHSEQHPGQLK.D               |
| 0.999999 | 1 R.LGAQALLGAAK[325.13]MLLHSEQHPGQLK.D               |
| 0.999999 | 1 R.GAEVHLPWNHDFTK[325.13]MEYDGILIAGGPGNPALAI        |
| 0.999999 | 1 R.LGAQALLGAAK[325.13]MLLHSEQHPGQLK.D               |
| 0.999999 | 1 R.AHMGMFTELAILYSKFK[325.13]PQK.M                   |
| 0.999999 | 1 R.AHMGMFTELAILYSK[325.13]FKPQK.M                   |
| 0.999999 | 1 R.MELLAHLLGEK[325.13]WMGPIPPAVNAR.L                |
| 0.999999 | 1 R.MELLAHLLGEK[325.13]WMGPIPPAVNAR.L                |
| 0.999999 | 1 R.KDGNASGTTLEALDC[160.03]ILPPTRPDTK[325.13]PLRL    |
| 0.999999 | 1 R.IHFPLATYAPVISAEEK[325.13]AYHEQLTVAEITNAC[160.03] |
| 0.999999 | 1 R.INFAVFPSLQGGPHNHAIAAVALK[325.13]QAC[160.03]      |
| 0.999999 | 1 R.INFAVFPSLQGGPHNHAIAAVALK[325.13]QAC[160.03]      |
| 0.999999 | 1 R.K[325.13]KDGAHLMIGSLAEILLK.K                     |
| 0.999999 | 1 R.K[325.13]KDGAHLMIGSLAEILLK.K                     |
| 0.999999 | 1 R.ELDSITPEVLPGWK[325.13]GMSVSDLADKLSTDDLNSLIAI     |
| 0.999999 | 1 R.K[325.13]KDGAHLMIGSLAEILLK.K                     |
| 0.999999 | 1 R.HVLDTLIQLAK[325.13]VFPSHFTQQR.T                  |
| 0.999999 | 1 R.FC[160.03]GLMVQLLHK[325.13]LSVR.A                |
| 0.999999 | 1 R.FC[160.03]GLMVQLLHK[325.13]LSVR.A                |
| 0.999999 | 1 R.HVLDTLIQLAK[325.13]VFPSHFTQQR.T                  |
| 0.999999 | 1 K.DDLRDMFC[160.03]K[325.13]ILHGFK.N                |
| 0.999999 | 1 R.FC[160.03]GLMVQLLHK[325.13]LSVR.A                |
| 0.999999 | 1 R.HVLDTLIQLAK[325.13]VFPSHFTQQR.T                  |
| 0.999999 | 1 R.FC[160.03]GLMVQLLHK[325.13]LSVR.A                |
| 0.999999 | 1 R.HVLDTLIQLAK[325.13]VFPSHFTQQR.T                  |
| 0.999999 | 1 R.HVLDTLIQLAK[325.13]VFPSHFTQQR.T                  |
| 0.999999 | 1 R.SNPK[325.13]IWNVHSVNLVHSLVDK.S                   |
| 0.999999 | 1 R.SNPK[325.13]IWNVHSVNLVHSLVDK.S                   |
| 0.999999 | 1 R.SNPK[325.13]IWNVHSVNLVHSLVDK.S                   |
| 0.999999 | 1 R.SNPK[325.13]IWNVHSVNLVHSLVDK.S                   |
| 0.999999 | 1 K.DGNASGTTLEALDC[160.03]ILPPTRPDTKPLRLPLQDVYK      |
| 0.999999 | 1 K.LSDVDRDGMLDDEEFALASHLIEAK[325.13]LEGHGLPANL      |
| 0.999999 | 1 K.LSDVDRDGMLDDEEFALASHLIEAK[325.13]LEGHGLPANL      |
| 0.999999 | 1 R.GITGVEDKESWHGKPLPK[325.13]NMAEQIIEIYSQIQSK.      |
| 0.999999 | 1 R.HIADLAGNSEVILPVPAFNVINGGSHAGNK[325.13]LAM[1      |
| 0.999999 | 1 R.WHFYDTVK[325.13]GSDWLGDQDAIHYMTEQAPAAVVE         |
| 0.999999 | 1 R.HIADLAGNSEVILPVPAFNVINGGSHAGNK[325.13]LAMQ       |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA        |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA        |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA        |
| 0.999999 | 1 K.HYQFASGAFLHIK[325.13]ETVLSALSR.E                 |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA        |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA        |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA        |
| 0.999999 | 1 K.HYQFASGAFLHIK[325.13]ETVLSALSR.E                 |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA        |

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| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA   |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA   |
| 0.999999 | 1 R.SGPFGQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA   |
| 0.999999 | 1 R.MALIGLGVSHPVLK[325.13]QVAEQFLNMR.G          |
| 0.999999 | 1 R.MALIGLGVSHPVLK[325.13]QVAEQFLNMR.G          |
| 0.999999 | 1 R.MALIGLGVSHPVLK[325.13]QVAEQFLNMR.G          |
| 0.999999 | 1 R.HIADLAGNSEVILPVPAFNVINGGSHAGNK[325.13]LAMQ  |
| 0.999999 | 1 K.K[325.13]SFFQAATEHLLPMGTALPLLEAQAATHLVDPITC |
| 0.999999 | 1 R.GVGAAATAVTQALNELLQHVK[325.13]AHATGAGPAGR.\  |
| 0.999999 | 1 R.GVGAAATAVTQALNELLQHVK[325.13]AHATGAGPAGR.\  |
| 0.999999 | 1 K.K[325.13]SFFQAATEHLLPMGTALPLLEAQAATHLVDPITC |
| 0.999999 | 1 R.GVGAAATAVTQALNELLQHVK[325.13]AHATGAGPAGR.\  |
| 0.999999 | 1 K.HKLDELYPQGYPESVIQHLGYLFLK[325.13]MSPEDIR.K  |
| 0.999999 | 1 K.HKLDELYPQGYPESVIQHLGYLFLK[325.13]MSPEDIR.K  |
| 0.999999 | 1 K.HKLDELYPQGYPESVIQHLGYLFLK[325.13]MSPEDIR.K  |
| 0.999999 | 1 R.FAGLHFFNPVPVMK[325.13]LVEVIK.T              |
| 0.999999 | 1 R.FAGLHFFNPVPVMK[325.13]LVEVIK.T              |
| 0.999999 | 1 R.VTQKSYK[325.13]VSTSGPR.A                    |
| 0.999999 | 1 R.VTQKSYK[325.13]VSTSGPR.A                    |
| 0.999999 | 1 R.K[325.13]YAYSAASGGR.R                       |
| 0.999999 | 1 K.APK[325.13]SAC[160.03]GVC[160.03]PGR.L      |
| 0.999999 | 1 K.APK[325.13]SAC[160.03]GVC[160.03]PGR.L      |
| 0.999999 | 1 K.APK[325.13]SAC[160.03]GVC[160.03]PGR.L      |
| 0.999999 | 1 R.K[325.13]YAYSAASGGR.R                       |
| 0.999999 | 1 R.NK[325.13]STESLQANVQR.L                     |
| 0.999999 | 1 R.NK[325.13]STESLQANVQR.L                     |
| 0.999999 | 1 R.AQLGGPEAAK[325.13]SDETAAK.-                 |
| 0.999999 | 1 R.GDGTGGK[325.13]SIYGER.F                     |
| 0.999999 | 1 K.IVSGK[325.13]DYNVTANSK.L                    |
| 0.999999 | 1 K.IVSGK[325.13]DYNVTANSK.L                    |
| 0.999999 | 1 R.GDGTGGK[325.13]SIYGER.F                     |
| 0.999999 | 1 K.IVSGK[325.13]DYNVTANSK.L                    |
| 0.999999 | 1 K.IVSGK[325.13]DYNVTANSK.L                    |
| 0.999999 | 1 K.IVSGK[325.13]DYNVTANSK.L                    |
| 0.999999 | 1 K.IVSGK[325.13]DYNVTANSK.L                    |
| 0.999999 | 1 R.AAQNISK[325.13]TIATSQNR.I                   |
| 0.999999 | 1 K.IVADK[325.13]DYSVTANSK.I                    |
| 0.999999 | 1 K.IVADK[325.13]DYSVTANSK.I                    |
| 0.999999 | 1 K.IVADK[325.13]DYSVTANSK.I                    |
| 0.999999 | 1 K.TPK[325.13]GPSSVEDIK.A                      |
| 0.999999 | 1 K.ALAAAGYDVEK[325.13]NNSR.I                   |
| 0.999999 | 1 K.FAAK[325.13]GEGQLGPAER.A                    |
| 0.999999 | 1 K.FAAK[325.13]GEGQLGPAER.A                    |
| 0.999999 | 1 R.NVESYTK[325.13]LGNPTR.S                     |
| 0.999999 | 1 R.ALSTGEK[325.13]GFGYK.G                      |
| 0.999999 | 1 R.ALSTGEK[325.13]GFGYK.G                      |
| 0.999999 | 1 R.DAGEYEC[160.03]HTPSTDK[325.13]QYFGSYSK.M    |

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| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 R.DAGEYEC[160.03]HTPSTDK[325.13]QYFGSYS.AK.M |
| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 R.LQAEIDNIK[325.13]NQR.A                     |
| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 R.ILNEK[325.13]VNTPTTTVYR.C                  |
| 0.999999 | 1 R.GEIIAK[325.13]QGGGGGGGSPGIER.M             |
| 0.999999 | 1 K.IQQDSGC[160.03]K[325.13]VQISPDSGGLPER.S    |
| 0.999999 | 1 K.IQQDSGC[160.03]K[325.13]VQISPDSGGLPER.S    |
| 0.999999 | 1 K.VK[325.13]AFGPGLQGSAGSPAR.F                |
| 0.999999 | 1 R.SSGPYGGGGQYFAK[325.13]PR.N                 |
| 0.999999 | 1 K.VK[325.13]AFGPGLQGSAGSPAR.F                |
| 0.999999 | 1 R.TK[325.13]STGGAPTFNVTVT.K.T                |
| 0.999999 | 1 R.ILNEK[325.13]VNTPTTTVYR.C                  |
| 0.999999 | 1 R.YALYDATYETK[325.13]ESK.K                   |
| 0.999999 | 1 R.NDNDTFTVK[325.13]YTPR.G                    |
| 0.999999 | 1 R.NDNDTFTVK[325.13]YTPR.G                    |
| 0.999999 | 1 R.YALYDATYETK[325.13]ESK.K                   |
| 0.999999 | 1 K.GIVEFSGK[325.13]PAAR.K                     |
| 0.999999 | 1 R.NDNDTFTVK[325.13]YTPR.G                    |
| 0.999999 | 1 R.LVC[160.03]YNNK[325.13]ITASYEDR.V          |
| 0.999999 | 1 K.GIVEFSGK[325.13]PAAR.K                     |
| 0.999999 | 1 K.SK[325.13]FADLSEAANR.N                     |
| 0.999999 | 1 K.GLGLSK[325.13]AYVGQK.S                     |
| 0.999999 | 1 K.AGLQVYNK[325.13]C[160.03]WK.F              |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                |
| 0.999999 | 1 K.AGLQVYNK[325.13]C[160.03]WK.F              |
| 0.999999 | 1 R.VIIK[325.13]YYTR.L                         |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                |
| 0.999999 | 1 K.GGVVLK[325.13]EDALPGQK.T                   |
| 0.999999 | 1 K.GGVVLK[325.13]EDALPGQK.T                   |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                 |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                 |
| 0.999999 | 1 K.GGVVLK[325.13]EDALPGQK.T                   |
| 0.999999 | 1 K.GGVVLK[325.13]EDALPGQK.T                   |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                |
| 0.999999 | 1 K.GC[160.03]GVVK[325.13]FESPEVAER.A          |
| 0.999999 | 1 K.GIVEFASK[325.13]PAAR.K                     |
| 0.999999 | 1 R.INVYYNEATGGK[325.13]YVPR.A                 |
| 0.999999 | 1 K.AGLQVYNK[325.13]C[160.03]WK.F              |

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| 0.999999 | 1 K.GIVEFASK[325.13]PAAR.K                              |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 K.AGLQVYNK[325.13]C[160.03]WK.F                       |
| 0.999999 | 1 R.INVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 K.AGLQVYNK[325.13]C[160.03]WK.F                       |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                    |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 K.AGLQVYNK[325.13]C[160.03]WK.F                       |
| 0.999999 | 1 R.INVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                    |
| 0.999999 | 1 K.AGLQVYNK[325.13]C[160.03]WK.F                       |
| 0.999999 | 1 R.VEWK[325.13]FDQGDTR.L                               |
| 0.999999 | 1 R.LLEAAQSTK[325.13]GYSPYSVSGSGTAGSR.T                 |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 K.LTFDSSFSPNTGK[325.13]K.N                            |
| 0.999999 | 1 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                    |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 R.DNTNEIYSGK[325.13]FC[160.03]EC[160.03]DNFNC[160.03] |
| 0.999999 | 1 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                    |
| 0.999999 | 1 R.LLEAAQSTK[325.13]GYSPYSVSGSGTAGSR.T                 |
| 0.999999 | 1 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                    |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 K.LTFDSSFSPNTGK[325.13]K.N                            |
| 0.999999 | 1 R.ISVYYNEATGGK[325.13]YVPR.A                          |
| 0.999999 | 1 R.EIAQDFK[325.13]TDLR.F                               |
| 0.999999 | 1 R.EIAQDFK[325.13]TDLR.F                               |
| 0.999999 | 1 R.TAQSTPSAPPQK[325.13]VMC[160.03]VSMGSTTVR.V          |
| 0.999999 | 1 R.LVVPATQC[160.03]GSLIGK[325.13]GGC[160.03]K.I        |
| 0.999999 | 1 K.IPGEK[325.13]DSVIC[160.03]LK.G                      |
| 0.999999 | 1 K.FSAYIK[325.13]NSNPALNDNLEK.G                        |
| 0.999999 | 1 K.FYEAFSK[325.13]NLK.L                                |
| 0.999999 | 1 K.IPGEK[325.13]DSVIC[160.03]LK.G                      |
| 0.999999 | 1 K.FSAYIK[325.13]NSNPALNDNLEK.G                        |
| 0.999999 | 1 R.LVVPATQC[160.03]GSLIGK[325.13]GGC[160.03]K.I        |
| 0.999999 | 1 K.IPGEK[325.13]DSVIC[160.03]LK.G                      |
| 0.999999 | 1 K.FSAYIK[325.13]NSNPALNDNLEK.G                        |
| 0.999999 | 1 K.IPGEK[325.13]DSVIC[160.03]LK.G                      |
| 0.999999 | 1 K.FSAYIK[325.13]NSNPALNDNLEK.G                        |
| 0.999999 | 1 K.IPGEK[325.13]DSVIC[160.03]LK.G                      |
| 0.999999 | 1 R.FQLQATTK[325.13]EGPGEAIVR.E                         |
| 0.999999 | 1 R.C[160.03]SYC[160.03]NNK[325.13]LSLGTASYLHGR.I       |
| 0.999999 | 1 K.EDLYLK[325.13]PIQR.T                                |
| 0.999999 | 1 K.GIVPLAK[325.13]VDC[160.03]TANTNTC[160.03]NK.Y       |
| 0.999999 | 1 R.TLLAK[325.13]NLPYK.V                                |
| 0.999999 | 1 K.EDK[325.13]DAQFYC[160.03]ELNYR.L                    |
| 0.999999 | 1 R.K[325.13]DGSC[160.03]GVAYVVQEPGDYEVSVK.F            |

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| 0.999999 | 1 R.TLLAK[325.13]NLPYK.V                           |
| 0.999999 | 1 K.EDLYLK[325.13]PIQR.T                           |
| 0.999999 | 1 R.TLLAK[325.13]NLPYK.V                           |
| 0.999999 | 1 R.TVIEQSWGSPK[325.13]VTK.D                       |
| 0.999999 | 1 K.LTFDITTFSPNTGK[325.13]K.S                      |
| 0.999999 | 1 R.TLLAK[325.13]NLPYK.V                           |
| 0.999999 | 1 K.FGEVVDC[160.03]TIK[325.13]MDPNTGR.S            |
| 0.999999 | 1 R.TLLAK[325.13]NLPYK.V                           |
| 0.999999 | 1 R.K[325.13]DGSC[160.03]GVAYVVQEPGDYEVSVK.F       |
| 0.999999 | 1 R.AK[325.13]VTLNGVPAQPLGPR.A                     |
| 0.999999 | 1 R.TLLIK[325.13]TVETR.D                           |
| 0.999999 | 1 K.LTFDITTFSPNTGK[325.13]K.S                      |
| 0.999999 | 1 R.FQLQATTK[325.13]EGPGEAIVR.E                    |
| 0.999999 | 1 K.K[325.13]VWLDPNETNEIANANSR.Q                   |
| 0.999999 | 1 R.ALQASALK[325.13]AWGGK.K                        |
| 0.999999 | 1 R.FQLQATTK[325.13]EGPGEAIVR.E                    |
| 0.999999 | 1 R.GWLK[325.13]SNVSDAVAQSTR.I                     |
| 0.999999 | 1 K.VEAK[325.13]FINYVK.N                           |
| 0.999999 | 1 R.GWLK[325.13]SNVSDAVAQSTR.I                     |
| 0.999999 | 1 R.K[325.13]TSDFNITFLAQEGC[160.03]TK.G            |
| 0.999999 | 1 R.ALQASALK[325.13]AWGGK.K                        |
| 0.999999 | 1 R.LGQEATVGK[325.13]ATGFLK.N                      |
| 0.999999 | 1 K.LFGNMEGDC[160.03]PSDWK[325.13]TDSTC[160.03]R.I |
| 0.999999 | 1 R.TLLIK[325.13]TVETR.D                           |
| 0.999999 | 1 R.GIYAYGFVK[325.13]PSAIQQR.A                     |
| 0.999999 | 1 R.GGYGGGGPGYGNQGGGYGGGYDNYGGGNYGSGNYNDF          |
| 0.999999 | 1 R.VVDLMAHMASK[325.13]E.-                         |
| 0.999999 | 1 R.IPENNPVK[325.13]LSC[160.03]AYSFGSSPR.V         |
| 0.999999 | 1 R.K[325.13]FNALFAQGNYSEAAK.V                     |
| 0.999999 | 1 R.IPENNPVK[325.13]LSC[160.03]AYSFGSSPR.V         |
| 0.999999 | 1 R.GIYAYGFVK[325.13]PSAIQQR.A                     |
| 0.999999 | 1 R.GYFEYIEENK[325.13]YSR.A                        |
| 0.999999 | 1 R.IPENNPVK[325.13]LSC[160.03]AYSFGSSPR.V         |
| 0.999999 | 1 R.GYFEYIEENK[325.13]YSR.A                        |
| 0.999999 | 1 R.TLLIK[325.13]TVETR.D                           |
| 0.999999 | 1 R.GIYAYGFVK[325.13]PSAIQQR.A                     |
| 0.999999 | 1 R.GIYAYGFVK[325.13]PSAIQQR.A                     |
| 0.999999 | 1 R.LQDEIQNMK[325.13]EEMAR.H                       |
| 0.999999 | 1 R.K[325.13]FNALFAQGNYSEAAK.V                     |
| 0.999999 | 1 R.GALQNIIPASTGAAK[325.13]AVGK.V                  |
| 0.999999 | 1 R.IPENNPVK[325.13]LSC[160.03]AYSFGSSPR.V         |
| 0.999999 | 1 R.GALQNIIPASTGAAK[325.13]AVGK.V                  |
| 0.999999 | 1 R.K[325.13]GADIMYTGTVDC[160.03]WR.K              |
| 0.999999 | 1 K.K[325.13]LLDLVQQSC[160.03]NYK.Q                |
| 0.999999 | 1 K.SK[325.13]GIAYIEFK.T                           |
| 0.999999 | 1 K.K[325.13]LLDLVQQSC[160.03]NYK.Q                |
| 0.999999 | 1 R.LK[325.13]VGLQVVAVK.A                          |

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| 0.999999 | 1 K.IYK[325.13]IGQGYLIK.D                        |
| 0.999999 | 1 K.NVK[325.13]LTVSNVLK.E                        |
| 0.999999 | 1 R.K[325.13]EFSPFGTITSAK.V                      |
| 0.999999 | 1 K.TVMPYISTTPAK[325.13]LR.N                     |
| 0.999999 | 1 R.LDYLSSLK[325.13]VK.G                         |
| 0.999999 | 1 K.TLQLLK[325.13]VGEEDDGEYR.C                   |
| 0.999999 | 1 R.LDYLSSLK[325.13]VK.G                         |
| 0.999999 | 1 R.ETGSSK[325.13]GFGFVDFNSEEDAK.A               |
| 0.999999 | 1 R.AVLK[325.13]FAAATGATPIAGR.F                  |
| 0.999999 | 1 R.GAAK[325.13]EAAGKSSGPTSLFAVTVAPPGAR.Q        |
| 0.999999 | 1 R.ETGSSK[325.13]GFGFVDFNSEEDAK.A               |
| 0.999999 | 1 R.AVLK[325.13]FAAATGATPIAGR.F                  |
| 0.999999 | 1 R.AVLK[325.13]FAAATGATPIAGR.F                  |
| 0.999999 | 1 R.AVDDGVNTFK[325.13]VLTR.D                     |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M     |
| 0.999999 | 1 R.LK[325.13]VGLQVVAVK.A                        |
| 0.999999 | 1 R.LK[325.13]VGLQVVAVK.A                        |
| 0.999999 | 1 R.AVLK[325.13]FAAATGATPIAGR.F                  |
| 0.999999 | 1 R.GAAKEAAGK[325.13]SSGPTSLFAVTVAPPGAR.Q        |
| 0.999999 | 1 R.AVLK[325.13]FAAATGATPIAGR.F                  |
| 0.999999 | 1 R.AGDWK[325.13]C[160.03]PNPTC[160.03]ENMNFSWR. |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M     |
| 0.999999 | 1 K.ELTIGSK[325.13]LQDAEIAR.L                    |
| 0.999999 | 1 R.AVDDGVNTFK[325.13]VLTR.D                     |
| 0.999999 | 1 R.IGSSMK[325.13]SVGEVMAIGR.T                   |
| 0.999999 | 1 R.DLQQYQSQAK[325.13]QLFR.K                     |
| 0.999999 | 1 K.ELTIGSK[325.13]LQDAEIAR.L                    |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M     |
| 0.999999 | 1 R.AGDWK[325.13]C[160.03]PNPTC[160.03]ENMNFSWR. |
| 0.999999 | 1 R.DLQQYQSQAK[325.13]QLFR.K                     |
| 0.999999 | 1 R.DLQQYQSQAK[325.13]QLFR.K                     |
| 0.999999 | 1 R.IGSSMK[325.13]SVGEVMAIGR.T                   |
| 0.999999 | 1 K.TLQLLK[325.13]VGEEDDGEYR.C                   |
| 0.999999 | 1 K.TLQLLK[325.13]VGEEDDGEYR.C                   |
| 0.999999 | 1 K.SIYYITGESK[325.13]EQVANSASFVER.V             |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M     |
| 0.999999 | 1 R.DLQQYQSQAK[325.13]QLFR.K                     |
| 0.999999 | 1 R.DLQQYQSQAK[325.13]QLFR.K                     |
| 0.999999 | 1 K.TLQLLK[325.13]VGEEDDGEYR.C                   |
| 0.999999 | 1 K.M[147.04]LETK[325.13]WSLLQQQK.T              |
| 0.999999 | 1 K.TLQLLK[325.13]VGEEDDGEYR.C                   |
| 0.999999 | 1 K.GSAITGPVAK[325.13]EC[160.03]ADLWPR.I         |
| 0.999999 | 1 R.DLQQYQSQAK[325.13]QLFR.K                     |
| 0.999999 | 1 K.M[147.04]LETK[325.13]WSLLQQQK.T              |
| 0.999999 | 1 R.IK[325.13]LQLWDTAGQER.F                      |
| 0.999999 | 1 R.K[325.13]GTDIMYTGTLDLC[160.03]WR.K           |
| 0.999999 | 1 R.IK[325.13]LQLWDTAGQER.F                      |



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| 0.999999 | 1 K.YGK[325.13]SLYYYIQQDTK.G                    |
| 0.999999 | 1 R.K[325.13]GTDIMYTGTLDC[160.03]WR.K           |
| 0.999999 | 1 K.YGK[325.13]SLYYYIQQDTK.G                    |
| 0.999999 | 1 R.DLQQYQSQAK[325.13]QLFR.K                    |
| 0.999999 | 1 R.AAAEK[325.13]LFGNMEGDC[160.03]PSDWK.T       |
| 0.999999 | 1 R.GPIK[325.13]FNVWDTAGQEK.F                   |
| 0.999999 | 1 R.GK[325.13]MSSYAFFVQTC[160.03]R.E            |
| 0.999999 | 1 R.GPIK[325.13]FNVWDTAGQEK.F                   |
| 0.999999 | 1 K.TLTGK[325.13]TITLEVEPSDTIENVK.A             |
| 0.999999 | 1 K.YGK[325.13]SLYYYIQQDTK.G                    |
| 0.999999 | 1 R.DLQQYQSQAK[325.13]QLFR.K                    |
| 0.999999 | 1 R.AAAEK[325.13]LFGNMEGDC[160.03]PSDWK.T       |
| 0.999999 | 1 R.IK[325.13]LQLWDTAGQER.F                     |
| 0.999999 | 1 R.IK[325.13]LQLWDTAGQER.F                     |
| 0.999999 | 1 R.K[325.13]GTDIMYTGTLDC[160.03]WR.K           |
| 0.999999 | 1 K.YGK[325.13]SLYYYIQQDTK.G                    |
| 0.999999 | 1 K.FTASAGIQVVGDDLTVTNPK[325.13]R.I             |
| 0.999999 | 1 R.GPIK[325.13]FNVWDTAGQEK.F                   |
| 0.999999 | 1 R.GPIK[325.13]FNVWDTAGQEK.F                   |
| 0.999999 | 1 R.K[325.13]FGYVDFESAEDLEK.A                   |
| 0.999999 | 1 K.EVPNYK[325.13]LITPAVVSER.L                  |
| 0.999999 | 1 K.AVVK[325.13]TDIQIALPSGC[160.03]YGR.V        |
| 0.999999 | 1 K.EVPNYK[325.13]LITPAVVSER.L                  |
| 0.999999 | 1 R.K[325.13]FGYVDFESAEDLEK.A                   |
| 0.999999 | 1 K.TC[160.03]SLPGTALK[325.13]VSC[160.03]FNVR.F |
| 0.999999 | 1 K.K[325.13]QIPAITC[160.03]IQSQWR.G            |
| 0.999999 | 1 -.MQIFVK[325.13]TLTGK.T                       |
| 0.999999 | 1 K.EVPNYK[325.13]LITPAVVSER.L                  |
| 0.999999 | 1 R.K[325.13]FGYVDFESAEDLEK.A                   |
| 0.999999 | 1 K.AVVK[325.13]TDIQIALPSGC[160.03]YGR.V        |
| 0.999999 | 1 R.IINEPTAAAIAYGLDK[325.13]K.V                 |
| 0.999999 | 1 R.K[325.13]FGYVDFESAEDLEK.A                   |
| 0.999999 | 0.9999 K.AVELAANTK[325.13]GIC[160.03]FIR.T      |
| 0.999999 | 1 R.IINEPTAAAIAYGLDK[325.13]K.V                 |
| 0.999999 | 1 K.TC[160.03]SLPGTALK[325.13]VSC[160.03]FNVR.F |
| 0.999999 | 1 K.TLTGK[325.13]TITLEVEPSDTIENVK.A             |
| 0.999999 | 1 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I       |
| 0.999999 | 1 K.AVELAANTK[325.13]GIC[160.03]FIR.T           |
| 0.999999 | 1 -.MQIFVK[325.13]TLTGK.T                       |
| 0.999999 | 1 K.AVELAANTK[325.13]GIC[160.03]FIR.T           |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M            |
| 0.999999 | 1 K.AVELAANTK[325.13]GIC[160.03]FIR.T           |
| 0.999999 | 1 R.IINEPTAAAIAYGLDK[325.13]K.V                 |
| 0.999999 | 1 R.IINEPTAAAIAYGLDK[325.13]K.V                 |
| 0.999999 | 1 R.VINEPTAAALAYGLDK[325.13]SEDK.V              |
| 0.999999 | 1 K.AVELAANTK[325.13]GIC[160.03]FIR.T           |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M            |

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| 0.999999 | 1 K.AVELAANTK[325.13]GIC[160.03]FIR.T              |
| 0.999999 | 1 K.TIK[325.13]LQIWDTAGQER.F                       |
| 0.999999 | 1 R.GFPTIYFSPANK[325.13]K.L                        |
| 0.999999 | 1 K.MLETK[325.13]WSLLQQQK.T                        |
| 0.999999 | 1 K.YK[325.13]WC[160.03]EYGLTFTEK.W                |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M               |
| 0.999999 | 1 R.SK[325.13]GFGFVC[160.03]FSSPEEATK.A            |
| 0.999999 | 1 K.MLETK[325.13]WSLLQQQK.T                        |
| 0.999999 | 1 K.LYTLQDK[325.13]AQVADVVSRSR.W                   |
| 0.999999 | 1 R.ALANSLAC[160.03]QGK[325.13]YTPSGQAGAAAASESLFV' |
| 0.999999 | 1 K.MLETK[325.13]WSLLQQQK.T                        |
| 0.999999 | 1 R.ALANSLAC[160.03]QGK[325.13]YTPSGQAGAAAASESLFV' |
| 0.999999 | 1 R.GENSWFSTQVDTVATK[325.13]VK.D                   |
| 0.999999 | 1 R.SK[325.13]GFGFVC[160.03]FSSPEEATK.A            |
| 0.999999 | 1 K.MLETK[325.13]WSLLQQQK.T                        |
| 0.999999 | 1 R.VTLNGVPC[160.03]KVTK[325.13]FGAQLQC[160.03]VTC |
| 0.999999 | 1 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I          |
| 0.999999 | 1 K.TIK[325.13]LQIWDTAGQER.F                       |
| 0.999999 | 1 K.YK[325.13]WC[160.03]EYGLTFTEK.W                |
| 0.999999 | 1 K.LYTLQDK[325.13]AQVADVVSRSR.W                   |
| 0.999999 | 1 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I          |
| 0.999999 | 1 R.ALANSLAC[160.03]QGK[325.13]YTPSGQAGAAAASESLFV' |
| 0.999999 | 1 R.VTLNGVPC[160.03]KVTK[325.13]FGAQLQC[160.03]VTC |
| 0.999999 | 1 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I          |
| 0.999999 | 1 R.IINEPTAAAIAYGLDK[325.13]R.E                    |
| 0.999999 | 1 R.ALANSLAC[160.03]QGK[325.13]YTPSGQAGAAAASESLFV' |
| 0.999999 | 1 K.VQVEYKGETK[325.13]SFYPEEVSSMVLT.K.M            |
| 0.999999 | 1 R.VTLNGVPC[160.03]KVTK[325.13]FGAQLQC[160.03]VTC |
| 0.999999 | 1 K.VQVEYK[325.13]GETKSFYPEEVSSMVLT.K.M            |
| 0.999999 | 1 K.TLNNK[325.13]FASFIDK.V                         |
| 0.999999 | 1 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I          |
| 0.999999 | 1 R.ALANSLAC[160.03]QGK[325.13]YTPSGQAGAAAASESLFV' |
| 0.999999 | 1 R.LPAAGVGDMVMATVK[325.13]K.G                     |
| 0.999999 | 1 K.VQVEYKGETK[325.13]SFYPEEVSSMVLT.K.M            |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M               |
| 0.999999 | 1 R.AITGASLADIMAK[325.13]R.N                       |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M               |
| 0.999999 | 1 R.LK[325.13]AGVAAPATQVAQVTLQSVQR.R               |
| 0.999999 | 1 K.TLNNK[325.13]FASFIDK.V                         |
| 0.999999 | 1 R.ALGQNPTNAEVLK[325.13]VLGNPK.S                  |
| 0.999999 | 1 R.GENSWFSTQVDTVATK[325.13]VK.D                   |
| 0.999999 | 1 K.QMADTGK[325.13]LNTLLQR.A                       |
| 0.999999 | 1 R.AITGASLADIMAK[325.13]R.N                       |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M               |
| 0.999999 | 1 R.GENSWFSTQVDTVATK[325.13]VK.D                   |
| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M               |
| 0.999999 | 1 R.GENSWFSTQVDTVATK[325.13]VK.D                   |

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| 0.999999 | 1 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M                 |
| 0.999999 | 1 R.FTLTGLK[325.13]PDTTYDIK.V                        |
| 0.999999 | 1 R.FTLTGLK[325.13]PDTTYDIK.V                        |
| 0.999999 | 1 R.GENSWFSTQVDTVATK[325.13]VK.D                     |
| 0.999999 | 1 K.NQK[325.13]DDVAQTDLLQIDPNFGSK.E                  |
| 0.999999 | 1 R.GENSWFSTQVDTVATK[325.13]VK.D                     |
| 0.999999 | 1 R.SSFYVNGLTGGQK[325.13]C[160.03]SVIR.D             |
| 0.999999 | 1 K.NQK[325.13]DDVAQTDLLQIDPNFGSK.E                  |
| 0.999999 | 1 R.FTLTGLK[325.13]PDTTYDIK.V                        |
| 0.999999 | 1 R.SSFYVNGLTGGQK[325.13]C[160.03]SVIR.D             |
| 0.999999 | 1 R.FTLTGLK[325.13]PDTTYDIK.V                        |
| 0.999999 | 1 R.GENSWFSTQVDTVATK[325.13]VK.D                     |
| 0.999999 | 1 R.SSFYVNGLTGGQK[325.13]C[160.03]SVIR.D             |
| 0.999999 | 1 K.NQK[325.13]DDVAQTDLLQIDPNFGSK.E                  |
| 0.999999 | 1 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.999999 | 1 R.VLAEK[325.13]LAAIGEATR.L                         |
| 0.999999 | 1 R.K[325.13]GISLNPEQWSQLK.E                         |
| 0.999999 | 1 R.K[325.13]GISLNPEQWSQLK.E                         |
| 0.999999 | 1 R.GTQDK[325.13]TTMVTSTFTNEDLLR.G                   |
| 0.999999 | 1 R.K[325.13]GISLNPEQWSQLK.E                         |
| 0.999999 | 1 K.FIIPNVVK[325.13]YSPNC[160.03]K.L                 |
| 0.999999 | 1 R.K[325.13]GISLNPEQWSQLK.E                         |
| 0.999999 | 1 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.999999 | 1 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.999999 | 1 K.EITALAPSTMKIK[325.13]IIPPER.K                    |
| 0.999999 | 0.9996 K.EITALAPSTMKIK[325.13]IIPPER.K               |
| 0.999999 | 1 K.DC[160.03]EEC[160.03]IQLEPTFIK[325.13]GYTR.K     |
| 0.999999 | 1 K.EAAGK[325.13]SSGPTSLFAVTVAPPGAR.Q                |
| 0.999999 | 1 K.FIIPNVVK[325.13]YSPNC[160.03]K.L                 |
| 0.999999 | 1 R.LVYLVENPGGYVAYSK[325.13]AATVTGK.L                |
| 0.999999 | 1 K.ESYSVYVYK[325.13]VLK.Q                           |
| 0.999999 | 1 K.LLETK[325.13]WTLLQEQQ.S                          |
| 0.999999 | 1 K.FIIPNVVK[325.13]YSPNC[160.03]K.L                 |
| 0.999999 | 1 K.EAAGK[325.13]SSGPTSLFAVTVAPPGAR.Q                |
| 0.999999 | 1 K.LLETK[325.13]WTLLQEQQ.S                          |
| 0.999999 | 1 R.LVYLVENPGGYVAYSK[325.13]AATVTGK.L                |
| 0.999999 | 1 R.SEGVVAVLLTK[325.13]K.S                           |
| 0.999999 | 1 R.FGTK[325.13]GLAITFVSDENDAK.I                     |
| 0.999999 | 1 K.EAAGK[325.13]SSGPTSLFAVTVAPPGAR.Q                |
| 0.999999 | 1 K.ESYSVYVYK[325.13]VLK.Q                           |
| 0.999999 | 1 K.EAAGK[325.13]SSGPTSLFAVTVAPPGAR.Q                |
| 0.999999 | 1 R.FGTK[325.13]GLAITFVSDENDAK.I                     |
| 0.999999 | 1 K.EITALAPSTMK[325.13]IKIIPPER.K                    |
| 0.999999 | 1 R.VYSTALSSFLTK[325.13]R.N                          |
| 0.999999 | 1 K.YK[325.13]YGYEIPVDMLC[160.03]K.R                 |
| 0.999999 | 1 R.LDSSAVLDTGK[325.13]YVGLVR.V                      |
| 0.999999 | 1 R.TMPVEQVFAK[325.13]NFR.V                          |

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| 0.999999 | 1 K.VANVSLALYK[325.13]GK.K                        |
| 0.999999 | 1 R.VFIGNLNTLVVK[325.13]K.S                       |
| 0.999999 | 1 R.VYSTALSSFLTK[325.13]R.N                       |
| 0.999999 | 1 R.TPK[325.13]GTQGVVTNFEIFR.M                    |
| 0.999999 | 1 R.LVYLVENPPGGYVAYSK[325.13]AATVTGK.L            |
| 0.999999 | 1 R.LVYLVENPPGGYVAYSK[325.13]AATVTGK.L            |
| 0.999999 | 1 R.TMPVEQVFAK[325.13]NFR.V                       |
| 0.999999 | 1 K.SIYG EK[325.13]FEDENFILK.H                    |
| 0.999999 | 1 R.INLAQK[325.13]AFC[160.03]GFEDPR.T             |
| 0.999999 | 1 K.SIYG EK[325.13]FEDENFILK.H                    |
| 0.999999 | 1 R.LVYLVENPPGGYVAYSK[325.13]AATVTGK.L            |
| 0.999999 | 1 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                |
| 0.999999 | 1 R.LVYLVENPPGGYVAYSK[325.13]AATVTGK.L            |
| 0.999999 | 1 R.LVYLVENPPGGYVAYSK[325.13]AATVTGK.L            |
| 0.999999 | 1 R.TMPVEQVFAK[325.13]NFR.V                       |
| 0.999999 | 1 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                |
| 0.999999 | 1 K.LAQM[147.04]FSDMVLK[325.13]DGFQPSR.S          |
| 0.999999 | 1 K.SIYG EK[325.13]FEDENFILK.H                    |
| 0.999999 | 1 R.TMPVEQVFAK[325.13]NFR.V                       |
| 0.999999 | 1 K.FGEVVDC[160.03]TLK[325.13]LDPITGR.S           |
| 0.999999 | 1 K.YK[325.13]YGYEIPVDMLC[160.03]K.R              |
| 0.999999 | 1 K.SIYG EK[325.13]FEDENFILK.H                    |
| 0.999999 | 1 R.SVPTWLK[325.13]LTSDDVK.E                      |
| 0.999999 | 1 R.LVYLVENPPGGYVAYSK[325.13]AATVTGK.L            |
| 0.999999 | 1 K.YK[325.13]YGYEIPVDMLC[160.03]K.R              |
| 0.999999 | 1 K.TDK[325.13]TLVLLMGK.E                         |
| 0.999999 | 1 K.SIYG EK[325.13]FEDENFILK.H                    |
| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG |
| 0.999999 | 1 K.YK[325.13]YGYEIPVDMLC[160.03]K.R              |
| 0.999999 | 1 K.FGEVVDC[160.03]TLK[325.13]LDPITGR.S           |
| 0.999999 | 1 R.INLAQK[325.13]AFC[160.03]GFEDPR.T             |
| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG |
| 0.999999 | 1 K.TVTAM[147.04]DVVYALK[325.13]R.Q               |
| 0.999999 | 1 K.TDK[325.13]TLVLLMGK.E                         |
| 0.999999 | 1 K.TDK[325.13]TLVLLMGK.E                         |
| 0.999999 | 1 R.MIAGQVLDINLAAEPK[325.13]VNR.G                 |
| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG |
| 0.999999 | 1 K.YK[325.13]YGYEIPVDMLC[160.03]K.R              |
| 0.999999 | 1 K.FGEVVDC[160.03]TLK[325.13]LDPITGR.S           |
| 0.999999 | 1 K.YK[325.13]YGYEIPVDMLC[160.03]K.R              |
| 0.999999 | 1 R.GFAFVTFESPADAK[325.13]DAAR.D                  |
| 0.999999 | 1 K.TVTAM[147.04]DVVYALK[325.13]R.Q               |
| 0.999999 | 1 R.NYYEQWGK[325.13]LTDC[160.03]VVMR.D            |
| 0.999999 | 1 R.VSFELFADK[325.13]VPK.T                        |
| 0.999999 | 1 K.LNPK[325.13]TGLIDYNQLALTAR.L                  |
| 0.999999 | 1 R.SVPTWLK[325.13]LTSDDVK.E                      |
| 0.999999 | 1 R.GFAFVTFESPADAK[325.13]DAAR.D                  |

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| 0.999999 | 1 R.GFAFVTFESPADAK[325.13]DAAR.D                    |
| 0.999999 | 1 K.TVTAM[147.04]DVVYALK[325.13]R.Q                 |
| 0.999999 | 1 K.LNISFPATGC[160.03]QK[325.13]LIEVDDER.K          |
| 0.999999 | 1 R.NYYEQWGK[325.13]LTDC[160.03]VVMR.D              |
| 0.999999 | 1 K.LNPK[325.13]TGLIDYNQLALTAR.L                    |
| 0.999999 | 1 K.YYIEK[325.13]LFER.Y                             |
| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG   |
| 0.999999 | 1 K.TVTAM[147.04]DVVYALK[325.13]R.Q                 |
| 0.999999 | 1 R.NYYEQWGK[325.13]LTDC[160.03]VVMR.D              |
| 0.999999 | 1 K.DQLIYNLLK[325.13]EEQTPQNK.I                     |
| 0.999999 | 1 R.NTTIPTK[325.13]QTQTFTTYSNQPVGVLIQVYEGER.A       |
| 0.999999 | 1 K.ESYSIYVYK[325.13]VLK.Q                          |
| 0.999999 | 1 R.K[325.13]QVVNIPSFIVR.L                          |
| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG   |
| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG   |
| 0.999999 | 1 R.GGSVLVTC[160.03]STSC[160.03]DQPK[325.13]LLGIETP |
| 0.999999 | 1 K.TVTAM[147.04]DVVYALK[325.13]R.Q                 |
| 0.999999 | 1 R.MIAGQVLDINLAAEPK[325.13]VNR.G                   |
| 0.999999 | 1 K.EITALAPSTMKIK[325.13]IIAPPER.K                  |
| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG   |
| 0.999999 | 1 R.K[325.13]QVVNIPSFIVR.L                          |
| 0.999999 | 1 R.MIAGQVLDINLAAEPK[325.13]VNR.G                   |
| 0.999999 | 1 R.LLEDGEDFNLGDA LDSSNSMQTIQK[325.13]TTTR.R        |
| 0.999999 | 1 K.M[147.04]PILGLGTWK[325.13]SPPGQVTEAVK.V         |
| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG   |
| 0.999999 | 1 R.LLEDGEDFNLGDA LDSSNSMQTIQK[325.13]TTTR.R        |
| 0.999999 | 1 R.GGSVLVTC[160.03]STSC[160.03]DQPK[325.13]LLGIETP |
| 0.999999 | 1 R.VSFELFADK[325.13]VPK.T                          |
| 0.999999 | 1 R.AIIPC[160.03]IK[325.13]GYDVIAQAQSGTGK.T         |
| 0.999999 | 1 R.LLEDGEDFNLGDA LDSSNSMQTIQK[325.13]TTTR.R        |
| 0.999999 | 1 R.AIIPC[160.03]IK[325.13]GYDVIAQAQSGTGK.T         |
| 0.999999 | 1 R.LLEDGEDFNLGDA LDSSNSMQTIQK[325.13]TTTR.R        |
| 0.999999 | 1 R.K[325.13]TVTAMDVVYALK.R                         |
| 0.999999 | 1 R.GEVAPDAK[325.13]SFVLNLGK.D                      |
| 0.999999 | 1 R.VSFELFADK[325.13]VPK.T                          |
| 0.999999 | 1 R.GEVAPDAK[325.13]SFVLNLGK.D                      |
| 0.999999 | 1 R.AIIPC[160.03]IK[325.13]GYDVIAQAQSGTGK.T         |
| 0.999999 | 1 R.VSFELFADK[325.13]VPK.T                          |
| 0.999999 | 1 R.K[325.13]VESLQEEIAFLK.K                         |
| 0.999999 | 1 K.IVLTNPVC[160.03]TEVGEEK[325.13]IALSR.R          |
| 0.999999 | 1 R.K[325.13]TVTAMDVVYALK.R                         |
| 0.999999 | 1 R.VSFELFADK[325.13]VPK.T                          |
| 0.999999 | 1 R.K[325.13]TVTAMDVVYALK.R                         |
| 0.999999 | 1 K.TVDNFVALATGEK[325.13]GFGYK.N                    |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V                |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V                |
| 0.999999 | 1 R.K[325.13]VESLQEEIAFLK.K                         |

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| 0.999999 | 1 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG  |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 K.AAIDWFDGK[325.13]EFSGNPIK.V                    |
| 0.999999 | 1 R.GGM[147.04]GSGGLATGIAGGLAGMGGIQNEK[325.13]I    |
| 0.999999 | 1 R.AGGK[325.13]ILTFDQLALDSPK.G                    |
| 0.999999 | 1 R.AGGK[325.13]ILTFDQLALDSPK.G                    |
| 0.999999 | 1 K.AAIDWFDGK[325.13]EFSGNPIK.V                    |
| 0.999999 | 1 R.AGGK[325.13]ILTFDQLALDSPK.G                    |
| 0.999999 | 1 R.VTAQK[325.13]QVLLSLKGSQTLTV[C[160.03]PGSVQPLSS |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.YK[325.13]SYSPYDMLESIR.K                       |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.LDQELK[325.13]LIGEYGLR.N                       |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.EAGSQK[325.13]DENLALYVENQFR.E                  |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.YK[325.13]SYSPYDMLESIR.K                       |
| 0.999999 | 1 R.K[325.13]GTDVNVFNTILTTR.S                      |
| 0.999999 | 1 R.MATEVAADALGEEWK[325.13]GYVVR.I                 |
| 0.999999 | 1 R.ANTFVAELK[325.13]GLDPA.V                       |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.EAGSQK[325.13]DENLALYVENQFR.E                  |
| 0.999999 | 1 R.TFDPTTSYVVEDLK[325.13]PNTEYAFR.L               |
| 0.999999 | 1 R.K[325.13]GTDVNVFNTILTTR.S                      |
| 0.999999 | 1 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE     |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.ANTFVAELK[325.13]GLDPA.V                       |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNVTGSR.V                 |
| 0.999999 | 1 K.SGDAAIVDM[147.04]VPGK[325.13]PMC[160.03]VESFS  |
| 0.999999 | 1 R.EAGSQK[325.13]DENLALYVENQFR.E                  |
| 0.999999 | 1 R.K[325.13]GTDVNVFNTILTTR.S                      |
| 0.999999 | 1 K.SGDAAIVDM[147.04]VPGK[325.13]PMC[160.03]VESFS  |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 0.9998 R.GGMGSGGLATGIAGGLAGMGGIQNEK[325.13]ETMQSLI |
| 0.999999 | 1 K.SGDAAIVDM[147.04]VPGK[325.13]PMC[160.03]VESFS  |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.K[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGPGGFGA   |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V               |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNVTGSR.V                 |
| 0.999999 | 1 R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTTEVK.S    |
| 0.999999 | 1 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE     |
| 0.999999 | 1 R.DVFTK[325.13]GYGFGLIK.L                        |
| 0.999999 | 1 R.K[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGPGGFGA   |

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| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V              |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999999 | 1 R.GGMGSGGLATGIAGGLAGMGGIQNEK[325.13]ETMQSLI     |
| 0.999999 | 1 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE    |
| 0.999999 | 1 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE    |
| 0.999999 | 1 R.LEVNLQAMK[325.13]AQFER.D                      |
| 0.999999 | 1 K.LIVLVPPSK[325.13]PTVNIPSSATIGNR.A             |
| 0.999999 | 0.9992 K.EITALAPSTMKIK[325.13]IIAPPER.K           |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V              |
| 0.999999 | 1 R.GGMGSGGLATGIAGGLAGMGGIQNEK[325.13]ETMQSLI     |
| 0.999999 | 1 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE    |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V              |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999999 | 1 R.GGMGSGGLATGIAGGLAGMGGIQNEK[325.13]ETMQSLI     |
| 0.999999 | 1 K.IILD LISEPIK[325.13]GR.A                      |
| 0.999999 | 0.9999 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V         |
| 0.999999 | 1 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE    |
| 0.999999 | 1 K.SGDAAIVDMVPGK[325.13]PM[147.04]C[160.03]VESFS |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V              |
| 0.999999 | 1 K.SGDAAIVDMVPGK[325.13]PM[147.04]C[160.03]VESFS |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V              |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999999 | 1 K.IILD LISEPIK[325.13]GR.A                      |
| 0.999999 | 1 K.SGDAAIVDMVPGK[325.13]PM[147.04]C[160.03]VESFS |
| 0.999999 | 1 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V              |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999999 | 1 K.SGDAAIVDMVPGK[325.13]PM[147.04]C[160.03]VESFS |
| 0.999999 | 1 R.AYILNLVK[325.13]QIK.K                         |
| 0.999999 | 1 R.GTNLNK[325.13]AMTLQEAFAFVGAER.C               |
| 0.999999 | 1 K.ELAALPK[325.13]ATILD LSC[160.03]NK.L          |
| 0.999999 | 1 R.SSIAGLLLK[325.13]ATNEK.L                      |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTPVGR.V                  |
| 0.999999 | 1 R.GFK[325.13]DQIYDIFQK.L                        |
| 0.999999 | 1 R.AL GALVDSC[160.03]APGLC[160.03]PDWDSWDASK[32! |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTPVGR.V                  |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTPVGR.V                  |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999999 | 1 R.GFK[325.13]DQIYDIFQK.L                        |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L               |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTPVGR.V                  |
| 0.999999 | 1 K.LAQMFSDMVLK[325.13]DGFQPSR.S                  |
| 0.999999 | 1 R.AL GALVDSC[160.03]APGLC[160.03]PDWDSWDASK[32! |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTPVGR.V                  |
| 0.999999 | 1 R.AL GALVDSC[160.03]APGLC[160.03]PDWDSWDASK[32! |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L               |

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|----------|--------------------------------------------------|
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L              |
| 0.999999 | 1 R.LQSTLK[325.13]TLSFSFPNTVTGSER.V              |
| 0.999999 | 1 K.LAQMFSDMVLK[325.13]DGFQPSR.S                 |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                |
| 0.999999 | 1 K.LAQMFSDMVLK[325.13]DGFQPSR.S                 |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L              |
| 0.999999 | 1 K.STLTDSLVC[160.03]K[325.13]AGIIASAR.A         |
| 0.999999 | 1 R.K[325.13]ITINPGC[160.03]VVVDGMPPGVSK.A       |
| 0.999999 | 1 R.VTFLPTGITFK[325.13]SVTR.E                    |
| 0.999999 | 1 K.IVIPNEESVVIYK[325.13]IR.Q                    |
| 0.999999 | 1 K.STLTDSLVC[160.03]K[325.13]AGIIASAR.A         |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L              |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L              |
| 0.999999 | 1 R.GTNLNK[325.13]AMTLQEAFAFVGAER.C              |
| 0.999999 | 1 R.VTFLPTGITFK[325.13]SVTR.E                    |
| 0.999999 | 1 K.MPILGLGTWK[325.13]SPPGQVTEAVK.V              |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                      |
| 0.999999 | 1 K.IVIPNEESVVIYK[325.13]IR.Q                    |
| 0.999999 | 0.9997 R.LPLQDVYK[325.13]IGGIGTVPVGR.V           |
| 0.999999 | 1 K.SK[325.13]GYAFIEFASFEDAK.E                   |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                |
| 0.999999 | 1 K.MPILGLGTWK[325.13]SPPGQVTEAVK.V              |
| 0.999999 | 1 K.EVDEQMLNVQNK[325.13]NSSYFVEWIPNNVK.T         |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYPVPR.E             |
| 0.999999 | 1 K.YGGQPVPNFPSK[325.13]LQVEPAVDTSGVQC[160.03]YC |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                      |
| 0.999999 | 1 K.SK[325.13]GYAFIEFASFEDAK.E                   |
| 0.999999 | 1 R.MK[325.13]LNTQEIFDDWAR.K                     |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                      |
| 0.999999 | 1 R.NSTIPTK[325.13]QTQIFTTSDNQPGVLIQVYEGER.A     |
| 0.999999 | 1 R.GLQQQNSDWYLK[325.13]QLLSDK.Q                 |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                      |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDESLR.S                  |
| 0.999999 | 1 R.MK[325.13]LNTQEIFDDWAR.K                     |
| 0.999999 | 1 K.VAC[160.03]ITEQVLTLVNK[325.13]R.I            |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDESLR.S                  |
| 0.999999 | 1 R.FGFPEGSVELYAEK[325.13]VATR.G                 |
| 0.999999 | 1 R.FGFPEGSVELYAEK[325.13]VATR.G                 |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDESLR.S                  |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYPVPR.E             |
| 0.999999 | 1 R.FGFPEGSVELYAEK[325.13]VATR.G                 |



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|----------|----------------------------------------------|
| 0.999999 | 1 R.AEAESMYQIK[325.13]YEELQSLAGK.H           |
| 0.999999 | 1 R.FGFPEGSVELYAEK[325.13]VATR.G             |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDDESLR.S             |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 R.FGFPEGSVELYAEK[325.13]VATR.G             |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDDESLR.S             |
| 0.999999 | 1 R.AEAESMYQIK[325.13]YEELQSLAGK.H           |
| 0.999999 | 1 R.FGFPEGSVELYAEK[325.13]VATR.G             |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                  |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                  |
| 0.999999 | 1 R.IDSLSAQLSQLQK[325.13]QLAAK.E             |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDDESLR.E             |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 R.FGFPEGSVELYAEK[325.13]VATR.G             |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDDESLR.S             |
| 0.999999 | 1 K.VYEIQDIYENSWTK[325.13]LTER.F             |
| 0.999999 | 1 R.ELTGLK[325.13]ALYETELADAR.R              |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                  |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                  |
| 0.999999 | 1 K.TVTAMDVVYALK[325.13]R.Q                  |
| 0.999999 | 1 R.IDSLSAQLSQLQK[325.13]QLAAK.E             |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 R.ELTGLK[325.13]ALYETELADAR.R              |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N              |
| 0.999999 | 1 R.ADGYVLEGK[325.13]ELEFYLR.K               |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N              |
| 0.999999 | 0.9995 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 R.ELTGLK[325.13]ALYETELADAR.R              |
| 0.999999 | 1 K.ALELTGLK[325.13]VFGNEIK.L                |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N              |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N              |
| 0.999999 | 0.9994 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G |
| 0.999999 | 1 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E          |
| 0.999999 | 1 K.INEAVEC[160.03]LLSLK[325.13]AQYK.E       |
| 0.999999 | 1 R.K[325.13]EWSGLLEELAR.N                   |
| 0.999999 | 1 K.ASGPPVSELITK[325.13]AVAASK.E             |
| 0.999999 | 1 R.TWNDPSVQQDIK[325.13]FLPFK.V              |
| 0.999999 | 1 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K         |
| 0.999999 | 1 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K         |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N              |
| 0.999999 | 1 R.YTILIK[325.13]YGGDEIPFSPYR.V             |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N              |

0.999999 1 K.INEAVEC[160.03]LLSLK[325.13]AQYK.E  
0.999999 1 K.SYDYDLIIIGGSGGLAAAK[325.13]EAAQY GK.K  
0.999999 1 K.INEAVEC[160.03]LLSLK[325.13]AQYK.E  
0.999999 1 K.TFVNITPAEVGV LV GK[325.13]DR.S  
0.999999 1 K.SGDAAIVDMVPGK[325.13]PMC[160.03]VESFSDYPPLGF  
0.999999 1 K.TFVNITPAEVGV LV GK[325.13]DR.S  
0.999999 1 K.SGDAAIVDMVPGK[325.13]PMC[160.03]VESFSDYPPLGF  
0.999999 1 K.TFVNITPAEVGV LV GK[325.13]DR.S  
0.999999 1 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K  
0.999999 1 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K  
0.999999 0.9995 R.K[325.13]LFIGGLSFETTEESLR.N  
0.999999 1 R.YTILIK[325.13]YGGDEIPFSPYR.V  
0.999999 1 K.TFVNITPAEVGV LV GK[325.13]DR.S  
0.999999 1 K.SGDAAIVDMVPGK[325.13]PMC[160.03]VESFSDYPPLGF  
0.999999 1 K.NVLSLTNK[325.13]GEVFNELVGK.Q  
0.999999 1 K.SGDAAIVDMVPGK[325.13]PMC[160.03]VESFSDYPPLGF  
0.999999 1 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K  
0.999999 1 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K  
0.999999 1 K.TK[325.13]GVDEVTIVNILTNR.S  
0.999999 1 R.IITITGTQDQIQNAQYLLQNSVK[325.13]QYSGK.F  
0.999999 1 R.VETGV LK[325.13]PGMVVTFAPVNV TTEVK.S  
0.999999 1 R.GC[160.03]TATLGNFAK[325.13]ATFDAISK.T  
0.999999 1 R.IITITGTQDQIQNAQYLLQNSVK[325.13]QYSGK.F  
0.999999 1 R.IITITGTQDQIQNAQYLLQNSVK[325.13]QYSGK.F  
0.999999 1 R.GNPTVEVDLFTSK[325.13]GLFR.A  
0.999999 1 R.GNPTVEVDLFTSK[325.13]GLFR.A  
0.999999 1 R.IITITGTQDQIQNAQYLLQNSVK[325.13]QYSGK.F  
0.999999 1 R.GC[160.03]TATLGNFAK[325.13]ATFDAISK.T  
0.999999 1 K.TK[325.13]GVDEVTIVNILTNR.S  
0.999999 1 R.IGPYQPNVPVGIDYVIPK[325.13]TGFYC[160.03]K.L  
0.999999 1 R.GNPTVEVDLFTSK[325.13]GLFR.A  
0.999999 1 K.VYELSNVQEDSQPMC[160.03]YSNC[160.03]PDGQSTAK  
0.999999 1 K.LSPDAIPGK[325.13]WTSQDSLLGMEFSGR.D  
0.999999 1 R.IGPYQPNVPVGIDYVIPK[325.13]TGFYC[160.03]K.L  
0.999999 1 R.INSGGK[325.13]LPNFGFVV FDDSEPVQK.V  
0.999999 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V  
0.999999 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V  
0.999999 1 R.VLALSVETDYTFPLAEK[325.13]VK.A  
0.999999 0.9988 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G  
0.999999 1 K.NSSYFVEWIPNNVK[325.13]TAVC[160.03]DIPPR.G  
0.999999 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V  
0.999999 1 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G  
0.999999 1 K.TYSYLTPDLWK[325.13]ETVFTK.S  
0.999999 1 K.NSSYFVEWIPNNVK[325.13]TAVC[160.03]DIPPR.G  
0.999999 1 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G  
0.999999 1 K.DC[160.03]VGPEVEK[325.13]AC[160.03]ANPAAGSVILL  
0.999999 1 K.TYSYLTPDLWK[325.13]ETVFTK.S

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| 0.999999 | 1 K.DC[160.03]VGPEVEK[325.13]AC[160.03]ANPAAGSVILL  |
| 0.999999 | 1 K.DC[160.03]VGPEVEK[325.13]AC[160.03]ANPAAGSVILL  |
| 0.999999 | 1 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G             |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 1 K.DC[160.03]VGPEVEK[325.13]AC[160.03]ANPAAGSVILL  |
| 0.999999 | 1 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G             |
| 0.999999 | 1 K.DC[160.03]VGPEVEK[325.13]AC[160.03]ANPAAGSVILL  |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 0.999 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G         |
| 0.999999 | 1 K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q           |
| 0.999999 | 1 K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q           |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 1 K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q           |
| 0.999999 | 1 K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q           |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 1 R.TDITYPAGFMDVISIDK[325.13]TGENFR.L               |
| 0.999999 | 1 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                 |
| 0.999999 | 1 R.AALQEELQLC[160.03]K[325.13]GLVQALQTK.V          |
| 0.999999 | 1 R.SGSK[325.13]FPVFNMSYNPAENAVLLC[160.03]TR.A      |
| 0.999999 | 1 R.AALQEELQLC[160.03]K[325.13]GLVQALQTK.V          |
| 0.999999 | 1 K.VTIAQGGVLPNIQAVLLPK[325.13]K.T                  |
| 0.999999 | 1 K.VTIAQGGVLPNIQAVLLPK[325.13]K.T                  |
| 0.999999 | 1 R.AALQEELQLC[160.03]K[325.13]GLVQALQTK.V          |
| 0.999999 | 1 K.VTIAQGGVLPNIQAVLLPK[325.13]K.T                  |
| 0.999999 | 1 K.VTIAQGGVLPNIQAVLLPK[325.13]K.T                  |
| 0.999999 | 1 R.GFEVVYMTPEIDEC[160.03]VQQLK[325.13]EFDGK.S      |
| 0.999999 | 1 R.GFEVVYMTPEIDEC[160.03]VQQLK[325.13]EFDGK.S      |
| 0.999999 | 1 K.VTIAQGGVLPNIQAVLLPK[325.13]K.T                  |
| 0.999999 | 1 K.VTIAQGGVLPNIQAVLLPK[325.13]K.T                  |
| 0.999999 | 1 K.VTIAQGGVLPNIQAVLLPK[325.13]K.T                  |
| 0.999999 | 1 R.TDITYPAGFMDVISIDK[325.13]TGENFR.L               |
| 0.999999 | 1 R.TDITYPAGFMDVISIDK[325.13]TGENFR.L               |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                |
| 0.999999 | 1 R.YLGIPGDK[325.13]EYC[160.03]ISSDDLFLPYC[160.03]P |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                |
| 0.999999 | 1 R.K[325.13]C[160.03]GETAFIAPQC[160.03]EMPIEWVC[1  |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                |
| 0.999999 | 1 R.LAAVALINAAIQK[325.13]GVAEK.T                    |
| 0.999999 | 1 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V                |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                |
| 0.999999 | 1 R.LAAVALINAAIQK[325.13]GVAEK.T                    |

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| 0.999999 | 1 R.AEGSDVANAVLDGADC[160.03]IMLSGETAK[325.13]GD'  |
| 0.999999 | 1 R.AEGSDVANAVLDGADC[160.03]IMLSGETAK[325.13]GD'  |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T              |
| 0.999999 | 1 R.AEGSDVANAVLDGADC[160.03]IMLSGETAK[325.13]GD'  |
| 0.999999 | 1 R.AEGSDVANAVLDGADC[160.03]IMLSGETAK[325.13]GD'  |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T              |
| 0.999999 | 1 R.AEGSDVANAVLDGADC[160.03]IMLSGETAK[325.13]GD'  |
| 0.999999 | 1 R.GVLK[325.13]EYGVKVLGTSVESIMATEDR.Q            |
| 0.999999 | 1 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T              |
| 0.999999 | 1 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V              |
| 0.999999 | 1 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V              |
| 0.999999 | 1 R.K[325.13]ILGQEGDASYLASEISTWDGVIVTPSEK.A       |
| 0.999999 | 1 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V              |
| 0.999999 | 1 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V              |
| 0.999999 | 1 R.K[325.13]ILGQEGDASYLASEISTWDGVIVTPSEK.A       |
| 0.999999 | 1 K.LK[325.13]LEAELGNMQGLVEDFK.N                  |
| 0.999999 | 1 K.TIIP LISQC[160.03]TPK[325.13]VDFPQDQLTALTGR.I |
| 0.999999 | 1 K.TIIP LISQC[160.03]TPK[325.13]VDFPQDQLTALTGR.I |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                   |
| 0.999999 | 1 K.DDVAQTDLLQIDPNFGSK[325.13]EDFDSLLQSAK.K       |
| 0.999999 | 1 K.DDVAQTDLLQIDPNFGSK[325.13]EDFDSLLQSAK.K       |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                   |
| 0.999999 | 1 R.SIQFVDWC[160.03]PTGFK[325.13]VGINYQPPTVPPGGC  |
| 0.999999 | 1 K.VAQAPWK[325.13]AVNTLNEALEFAK.S                |
| 0.999999 | 1 R.AGAIAPC[160.03]EVTVPAQNTGLGPEK[325.13]TSFFQAI |
| 0.999999 | 1 R.GSNTIASAAADK[325.13]IPGLLGVFQK.L              |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                   |
| 0.999999 | 1 K.EPLFGISTGNLITGLAAGAK[325.13]TYK.M             |
| 0.999999 | 1 R.AGAIAPC[160.03]EVTVPAQNTGLGPEK[325.13]TSFFQAI |
| 0.999999 | 1 K.LFIGGLNTETNEK[325.13]ALEAVFGK.Y               |
| 0.999999 | 1 K.DDVAQTDLLQIDPNFGSK[325.13]EDFDSLLQSAK.K       |
| 0.999999 | 1 K.DDVAQTDLLQIDPNFGSK[325.13]EDFDSLLQSAK.K       |
| 0.999999 | 1 K.EPLFGISTGNLITGLAAGAK[325.13]TYK.M             |
| 0.999999 | 1 R.SIQFVDWC[160.03]PTGFK[325.13]VGINYQPPTVPPGGC  |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                   |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                   |
| 0.999999 | 1 R.ALTVP ELTQQVFD AK[325.13]NMMAAC[160.03]DPR.H  |
| 0.999999 | 0.9912 R.ADIK[325.13]EMGLSLQWLYSAR.G              |
| 0.999999 | 1 R.AGAIAPC[160.03]EVTVPAQNTGLGPEK[325.13]TSFFQAI |
| 0.999999 | 1 K.EPLFGISTGNLITGLAAGAK[325.13]TYK.M             |
| 0.999999 | 1 R.AGAIAPC[160.03]EVTVPAQNTGLGPEK[325.13]TSFFQAI |
| 0.999999 | 1 K.LEVAPISDIIAIK[325.13]SPDTFVR.T                |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                   |
| 0.999999 | 1 K.EPLFGISTGNLITGLAAGAK[325.13]TYK.M             |
| 0.999999 | 1 K.VEGTEPTTAFNLFVGNLNFNK[325.13]SAPELK.T         |
| 0.999999 | 1 R.ALTVP ELTQQVFD AK[325.13]NMMAAC[160.03]DPR.H  |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                   |

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| 0.999999 | 1 K.VEGTEPTTAFNLFVGNLNFNK[325.13]SAPELK.T          |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                    |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                    |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 K.VEGTEPTTAFNLFVGNLNFNK[325.13]SAPELK.T          |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                    |
| 0.999999 | 1 K.VEGTEPTTAFNLFVGNLNFNK[325.13]SAPELK.T          |
| 0.999999 | 1 R.DTVTPGELLK[325.13]AEIIDQDLYER.L                |
| 0.999999 | 1 R.GIFPVLC[160.03]K[325.13]DPVQEAWAEDVDLR.V       |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 R.DTVTPGELLK[325.13]AEIIDQDLYER.L                |
| 0.999999 | 1 K.VEGTEPTTAFNLFVGNLNFNK[325.13]SAPELK.T          |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 R.GIFPVLC[160.03]K[325.13]DPVQEAWAEDVDLR.V       |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.999999 | 1 R.SGVSLAALKK[325.13]ALAAAGYDVEK.N                |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.999999 | 1 K.SFIK[325.13]DYPVVSIEDPFDQDDWGAWQK.F            |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 R.SGVSLAALK[325.13]KALAAAGYDVEK.N                |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.999999 | 1 K.GIIWGEDTLMEYLENPK[325.13]K.Y                   |
| 0.999999 | 1 K.SFIK[325.13]DYPVVSIEDPFDQDDWGAWQK.F            |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.999999 | 1 K.SFIK[325.13]DYPVVSIEDPFDQDDWGAWQK.F            |
| 0.999999 | 1 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999999 | 1 K.AM[147.04]K[325.13]GLGTDEESILTLLTSR.S          |
| 0.999999 | 1 K.GSFK[325.13]TLTLPSPPLNSADEIYELR.V              |
| 0.999999 | 0.9945 R.ADIK[325.13]EMGLSLQWLYSAR.G               |
| 0.999999 | 1 R.DQLEAAQEAVPPADIVFSVK[325.13]SPPSAGYLMVSR.G     |
| 0.999999 | 1 R.ISLGLPVGAVINC[160.03]ADNTGAK[325.13]NLYIISVK.G |
| 0.999999 | 1 K.GSFK[325.13]TLTLPSPPLNSADEIYELR.V              |
| 0.999999 | 1 R.DLEK[325.13]PFLLPVEAVYSVPGR.G                  |
| 0.999999 | 1 R.ISLGLPVGAVINC[160.03]ADNTGAK[325.13]NLYIISVK.G |
| 0.999999 | 0.9986 R.ADIK[325.13]EMGLSLQWLYSAR.G               |
| 0.999999 | 1 R.DLEK[325.13]PFLLPVEAVYSVPGR.G                  |
| 0.999999 | 1 R.ISLGLPVGAVINC[160.03]ADNTGAK[325.13]NLYIISVK.G |

0.999999 1 R.ALESGDVNTVWK[325.13]QLSSSVTGLTNIEEENC[160.03]  
 0.999999 1 R.ALESGDVNTVWK[325.13]QLSSSVTGLTNIEEENC[160.03]  
 0.999999 0.9994 R.ADIK[325.13]EMGLSLQWLYSAR.G  
 0.999999 1 R.DLEK[325.13]PFLLPVEAVYSVPGR.G  
 0.999999 1 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V  
 0.999999 1 R.ALESGDVNTVWK[325.13]QLSSSVTGLTNIEEENC[160.03]  
 0.999999 1 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V  
 0.999999 1 R.AVTGYTDPYTGQQISLFQAMQK[325.13]DLIVR.E  
 0.999999 0.9962 R.ADIK[325.13]EMGLSLQWLYSAR.G  
 0.999999 1 R.SVK[325.13]GLVAVITGGASGLGLATAER.L  
 0.999999 1 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V  
 0.999999 1 K.EK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEK.S  
 0.999999 1 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V  
 0.999999 0.9996 R.ADIK[325.13]EMGLSLQWLYSAR.G  
 0.999999 1 R.SVK[325.13]GLVAVITGGASGLGLATAER.L  
 0.999999 1 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V  
 0.999999 1 K.EK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEK.S  
 0.999999 1 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V  
 0.999999 1 R.SPLSDSILGEQALAVTDDK[325.13]VSVLELR.V  
 0.999999 1 R.AVTGYTDPYTGQQISLFQAMQK[325.13]DLIVR.E  
 0.999999 1 R.FSITSQSGGGLVSLALPLDYK[325.13]LER.Q  
 0.999999 1 R.FSITSQSGGGLVSLALPLDYK[325.13]LER.Q  
 0.999999 1 R.SPLSDSILGEQALAVTDDK[325.13]VSVLELR.V  
 0.999999 1 R.SVK[325.13]GLVAVITGGASGLGLATAER.L  
 0.999999 1 R.DISEASVFDAYVLPK[325.13]LYVK.L  
 0.999999 1 R.AVTGYTDPYTGQQISLFQAMQK[325.13]DLIVR.E  
 0.999999 1 R.DISEASVFDAYVLPK[325.13]LYVK.L  
 0.999999 1 R.DISEASVFDAYVLPK[325.13]LYVK.L  
 0.999999 1 R.AVTGYTDPYTGQQISLFQAMQK[325.13]DLIVR.E  
 0.999999 1 K.TIAEC[160.03]LADELINAAK[325.13]GSSNSYAIK.K  
 0.999999 1 R.SPLSDSILGEQALAVTDDK[325.13]VSVLELR.V  
 0.999999 1 R.SPLSDSILGEQALAVTDDK[325.13]VSVLELR.V  
 0.999999 1 R.DISEASVFDAYVLPK[325.13]LYVK.L  
 0.999999 1 R.IVSLEPAYPPVFYLNK[325.13]DTGEIYTTSVTLDR.E  
 0.999999 1 R.IVSLEPAYPPVFYLNK[325.13]DTGEIYTTSVTLDR.E  
 0.999999 1 K.TIAEC[160.03]LADELINAAK[325.13]GSSNSYAIK.K  
 0.999999 1 R.AVTGYTDPYTGQQISLFQAMQK[325.13]DLIVR.E  
 0.999999 1 K.TIAEC[160.03]LADELINAAK[325.13]GSSNSYAIK.K  
 0.999999 1 R.AVTGYTDPYTGQQISLFQAMQK[325.13]DLIVR.E  
 0.999999 1 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V  
 0.999999 1 K.TIAEC[160.03]LADELINAAK[325.13]GSSNSYAIK.K  
 0.999999 1 R.K[325.13]LPIDVTEGEVISLGLPFGK.V  
 0.999999 1 R.K[325.13]LPIDVTEGEVISLGLPFGK.V  
 0.999999 0.9995 R.YISPDQLADLYK[325.13]SFIK.D  
 0.999999 1 R.K[325.13]LPIDVTEGEVISLGLPFGK.V  
 0.999999 1 R.DIENLK[325.13]DASSFLAEWQNITK.G  
 0.999999 1 R.K[325.13]LPIDVTEGEVISLGLPFGK.V

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| 0.999999 | 1 R.EVTLGQVAK[325.13]LLEAETQR.Q                    |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 K.LC[160.03]YVALDFEQEMATAASSSSLEK[325.13]SYELPD  |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.SFPFVSK[325.13]TLGVDFIDVATK.V                  |
| 0.999999 | 1 K.AMK[325.13]GLGTDEESILTLLTSR.S                  |
| 0.999999 | 0.9962 R.ADIK[325.13]EMGLSLQWLYSAR.G               |
| 0.999999 | 1 R.LAK[325.13]AAFDDAIAELDTLSEESYK.D               |
| 0.999999 | 1 K.NIILEEGK[325.13]EILVGDVGQTVDDPYATFVK.M         |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.SFPFVSK[325.13]TLGVDFIDVATK.V                  |
| 0.999999 | 1 K.LC[160.03]YVALDFEQEMATAASSSSLEK[325.13]SYELPD  |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 K.LC[160.03]YVALDFEQEMATAASSSSLEK[325.13]SYELPD  |
| 0.999999 | 1 K.SGTIFDNFLITNDEAYAEFGNETWGVTK[325.13]AAEK.Q     |
| 0.999999 | 1 K.DSPSVWAAVPGK[325.13]TFVNITPAEVGVLVGK.D         |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13 |
| 0.999999 | 1 R.VLPSITTEILK[325.13]SVVAR.F                     |
| 0.999999 | 1 R.DLVLSGDLGSLYAMTQDK[325.13]VFR.L                |
| 0.999999 | 1 K.EK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEKSYELF |
| 0.999999 | 1 K.SAALPIFSSFVSNWDEATK[325.13]R.S                 |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 K.SAALPIFSSFVSNWDEATK[325.13]R.S                 |
| 0.999999 | 1 K.DQVDIAVQELLQLK[325.13]AQYK.S                   |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 K.DQVDIAVQELLQLK[325.13]AQYK.S                   |
| 0.999999 | 1 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13 |
| 0.999999 | 1 R.NEK[325.13]APVDFGYVGIDSILEQMR.R                |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 K.DQVDIAVQELLQLK[325.13]AQYK.S                   |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.SLLVIPNTLAVNAAQSTDVLVAK[325.13]LR.A            |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 R.SLLVIPNTLAVNAAQSTDVLVAK[325.13]LR.A            |
| 0.999999 | 1 R.DVQDFWISLPGTLC[160.03]SEK[325.13]MALSTASDDR.(  |
| 0.999999 | 1 R.DPYSGSTISLFQAMQK[325.13]GLVLR.Q                |
| 0.999999 | 1 R.DVQDFWISLPGTLC[160.03]SEK[325.13]MALSTASDDR.(  |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999999 | 1 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK. |
| 0.999999 | 1 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13 |

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| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 K.ITGEAFVQFASQELA EK[325.13]ALGK.H                |
| 0.999999 | 1 K.ELASQPDVDGFLVGGASLK[325.13]PEFVDIINAK.Q         |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 K.ELASQPDVDGFLVGGASLK[325.13]PEFVDIINAK.Q         |
| 0.999999 | 1 K.DQVDIAVQELLQ LK[325.13]AQYK.S                   |
| 0.999999 | 1 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.  |
| 0.999999 | 1 R.SNILTLMYQC[160.03]MQDK[325.13]MPEVR.Q           |
| 0.999999 | 1 R.DPYSGSTISLFQAMQK[325.13]GLVLR.Q                 |
| 0.999999 | 1 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S         |
| 0.999999 | 1 R.AGMFVSK[325.13]FFGGYVPEMVLTPDDQR.L              |
| 0.999999 | 1 K.ITGEAFVQFASQELA EK[325.13]ALGK.H                |
| 0.999999 | 1 K.IK[325.13]SLEEIYLFSLPIK.E                       |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.  |
| 0.999999 | 1 K.ELASQPDVDGFLVGGASLK[325.13]PEFVDIINAK.Q         |
| 0.999999 | 1 K.ITGEAFVQFASQELA EK[325.13]ALGK.H                |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 K.LC[160.03]YVALDFEQEMATAASSSSLEK[325.13]SYELPD   |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 K.ELASQPDVDGFLVGGASLK[325.13]PEFVDIINAK.Q         |
| 0.999999 | 1 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.  |
| 0.999999 | 1 R.DPYSGSTISLFQAMQK[325.13]GLVLR.Q                 |
| 0.999999 | 1 K.IK[325.13]SLEEIYLFSLPIK.E                       |
| 0.999999 | 1 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.  |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.999999 | 1 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S         |
| 0.999999 | 1 K.EK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEKSYELF  |
| 0.999999 | 0.9996 R.YISPDQLADLYK[325.13]SFIK.D                 |
| 0.999999 | 1 R.TLQYK[325.13]LLEPVLLL GK.E                      |
| 0.999999 | 1 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.999999 | 1 R.EVTVPVFYPT EK[325.13]VWLEVEPVGM[147.04]LK.E     |
| 0.999999 | 1 K.LWK[325.13]TFTDC[160.03]FNC[160.03]LPAAIVDEK.I  |
| 0.999999 | 1 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R   |
| 0.999999 | 1 K.EK[325.13]LC[160.03]YVALDFENEM[147.04]ATAASSSSI |
| 0.999999 | 1 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.  |
| 0.999999 | 0.9996 R.YISPDQLADLYK[325.13]SFIK.D                 |
| 0.999999 | 1 K.LWK[325.13]TFTDC[160.03]FNC[160.03]LPAAIVDEK.I  |
| 0.999999 | 1 R.EVTVPVFYPT EK[325.13]VWLEVEPVGM[147.04]LK.E     |
| 0.999999 | 1 K.EK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEKSYELF  |
| 0.999999 | 1 R.ENEVLEAWK[325.13]SLLDAC[160.03]ESR.R            |
| 0.999999 | 0.9993 R.YISPDQLADLYK[325.13]SFIK.D                 |
| 0.999999 | 1 R.K[325.13]PLVIIAEDVDGEALSTLV LNR.L               |
| 0.999999 | 0.9993 R.YISPDQLADLYK[325.13]SFIK.D                 |



0.999999 1 K.EK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEKSYELF  
0.999999 1 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVLR.L  
0.999999 1 R.K[325.13]PLVIIAEDVDGEALSTLVLR.L  
0.999999 1 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVLR.L  
0.999999 1 K.NMFLVGEGDSVITQVLNK[325.13]SLAEQR.Q  
0.999999 1 R.K[325.13]PLVIIAEDVDGEALSTLVLR.L  
0.999999 1 R.K[325.13]PLVIIAEDVDGEALSTLVLR.L  
0.999999 0.9839 R.YISPDQLADLYK[325.13]SFIK.D  
0.999999 1 K.EK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEKSYELF  
0.999999 1 K.EK[325.13]LC[160.03]YVALDFENEMATAASSSSLEKSYELF  
0.999999 1 R.K[325.13]PLVIIAEDVDGEALSTLVLR.L  
0.999999 0.9995 R.YISPDQLADLYK[325.13]SFIK.D  
0.999999 1 R.K[325.13]PLVIIAEDVDGEALSTLVLR.L  
0.999999 1 R.ELLTEFGYK[325.13]GEETPVIVGSALC[160.03]ALEGR.D  
0.999999 1 K.EKLC[160.03]YVALDFENEMATAASSSSLEK[325.13]SYELF  
0.999999 1 R.ELLTEFGYK[325.13]GEETPVIVGSALC[160.03]ALEGR.D  
0.999999 1 K.GLK[325.13]EGIPALDNFLDKL.-  
0.999999 1 K.EK[325.13]LC[160.03]YVALDFENEMATAASSSSLEKSYELF  
0.999999 1 K.EK[325.13]LC[160.03]YVALDFENEMATAASSSSLEKSYELF  
0.999999 0.9853 R.YISPDQLADLYK[325.13]SFIK.D  
0.999999 1 K.GLK[325.13]EGIPALDNFLDKL.-  
0.999999 1 K.EK[325.13]LC[160.03]YVALDFENEMATAASSSSLEKSYELF  
0.999999 1 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVLR.L  
0.999999 1 K.LAK[325.13]TQGNVFATDAILATLMSC[160.03]TR.S  
0.999999 1 K.EK[325.13]LC[160.03]YVALDFENEMATAASSSSLEKSYELF  
0.999999 0.9998 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 1 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 1 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 1 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 1 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 1 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 1 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 1 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 0.9997 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK  
0.999999 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L  
0.999999 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L  
0.999999 1 K.YSLEPVAVELK[325.13]SLLGK.D  
0.999999 1 R.ILAIGLINEALDEGDAQK[325.13]TLQALQIPAAK.L  
0.999999 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L  
0.999999 1 R.K[325.13]VADLYELVQYAGNIIPR.L  
0.999999 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L  
0.999999 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L  
0.999999 1 R.SGGTEGLLAEK[325.13]LEALITQTR.A  
0.999999 1 R.SGGTEGLLAEK[325.13]LEALITQTR.A  
0.999999 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L  
0.999999 1 R.EVTVPVFYPTTEK[325.13]VWLEVEPVGMLK.E  
0.999999 1 R.EALAAVLTYAK[325.13]PDEFSALC[160.03]DLLGTR.L

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| 0.999999 | 1 R.EVTVPVFYPTK[325.13]VWLEVEPVGMLK.E            |
| 0.999999 | 1 R.NLPGLVQEGEPFSEEATLFTK[325.13]ELVLQR.E        |
| 0.999999 | 1 R.EVTVPVFYPTK[325.13]VWLEVEPVGMLK.E            |
| 0.999999 | 1 K.SQEQLAAELAETAK[325.13]IALLEEER.R             |
| 0.999999 | 1 K.SQEQLAAELAETAK[325.13]IALLEEER.R             |
| 0.999999 | 1 R.NLPGLVQEGEPFSEEATLFTK[325.13]ELVLQR.E        |
| 0.999999 | 1 K.SQEQLAAELAETAK[325.13]IALLEEER.R             |
| 0.999999 | 1 R.NLPGLVQEGEPFSEEATLFTK[325.13]ELVLQR.E        |
| 0.999999 | 1 R.IIGDPYK[325.13]VQQAC[160.03]EMVMDILR.E       |
| 0.999999 | 1 K.SQEQLAAELAETAK[325.13]IALLEEER.R             |
| 0.999999 | 1 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S      |
| 0.999999 | 1 R.NQSFC[160.03]PTVNLDK[325.13]LWTLVSEQTR.V     |
| 0.999999 | 1 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S      |
| 0.999999 | 1 R.NQSFC[160.03]PTVNLDK[325.13]LWTLVSEQTR.V     |
| 0.999999 | 1 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S      |
| 0.999999 | 1 R.NQSFC[160.03]PTVNLDK[325.13]LWTLVSEQTR.V     |
| 0.999999 | 1 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S      |
| 0.999999 | 0.9998 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 K.SLADELALVDVLEDK[325.13]LK.G                  |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 K.TGTAYTFFTPNNIK[325.13]QVSDLISVLR.E           |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.DLLVQQASQC[160.03]LSK[325.13]LVQIASR.T       |
| 0.999999 | 1 R.DLYEDELVPLFEK[325.13]AGPIWDLR.L              |
| 0.999999 | 1 R.DLYEDELVPLFEK[325.13]AGPIWDLR.L              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 1 R.DLLVQQASQC[160.03]LSK[325.13]LVQIASR.T       |
| 0.999999 | 1 R.DLLVQQASQC[160.03]LSK[325.13]LVQIASR.T       |
| 0.999999 | 1 R.DLYEDELVPLFEK[325.13]AGPIWDLR.L              |
| 0.999999 | 1 R.DLYEDELVPLFEK[325.13]AGPIWDLR.L              |
| 0.999999 | 1 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S              |
| 0.999999 | 0.9995 R.YISPDQLADLYK[325.13]SFIK.D              |
| 0.999999 | 1 K.DAIIAK[325.13]LANQAADYFGDAFK.Q               |

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| 0.999999 | 1 K.DAIIAK[325.13]LANQAADYFGDAFK.Q               |
| 0.999999 | 1 K.DQAVENILVSPVVVASSLGLVSLGGK[325.13]ATTASQAK.A |
| 0.999999 | 1 K.VPSTEAEALASSLMGLFEK[325.13]R.R               |
| 0.999999 | 1 K.DQAVENILVSPVVVASSLGLVSLGGK[325.13]ATTASQAK.A |
| 0.999999 | 1 R.LLDPEDVDVPQPDEK[325.13]SIITYVSSLYDAMPR.V     |
| 0.999999 | 1 K.VSASPLLYTLIEK[325.13]TMQNVK.H                |
| 0.999999 | 1 R.LLDPEDVDVPQPDEK[325.13]SIITYVSSLYDAMPR.V     |
| 0.999999 | 1 K.VSASPLLYTLIEK[325.13]TMQNVK.H                |
| 0.999999 | 1 R.LQLETEIEALK[325.13]EELLFM[147.04]K.K         |
| 0.999999 | 1 R.LLDPEDVDVPQPDEK[325.13]SIITYVSSLYDAMPR.V     |
| 0.999999 | 1 K.VSASPLLYTLIEK[325.13]TMQNVK.H                |
| 0.999999 | 1 K.VSASPLLYTLIEK[325.13]TMQNVK.H                |
| 0.999999 | 1 R.EAATQAQQTGSGTIDK[325.13]ATGILLYGLASR.L       |
| 0.999999 | 1 R.EAATQAQQTGSGTIDK[325.13]ATGILLYGLASR.L       |
| 0.999999 | 1 R.GYADSPSK[325.13]AGAAPYVQAFDSLLAGPVAEYLK.I    |
| 0.999999 | 1 R.GYADSPSK[325.13]AGAAPYVQAFDSLLAGPVAEYLK.I    |
| 0.999999 | 1 K.DLADELALVDVIEDK[325.13]LK.G                  |
| 0.999999 | 1 R.GYADSPSK[325.13]AGAAPYVQAFDSLLAGPVAEYLK.I    |
| 0.999999 | 1 K.DLADELALVDVIEDK[325.13]LK.G                  |
| 0.999999 | 1 R.IPADTFAALK[325.13]NPNAMLVNLEEPLASTYQDILYQAK. |
| 0.999999 | 1 R.SLDLDGIIAEVK[325.13]AQYEEMAK.C               |
| 0.999999 | 1 K.NPTLFIFAENDVVIPLK[325.13]DVSLLTQK.L          |
| 0.999999 | 1 R.SLDLDGIIAEVK[325.13]AQYEEMAK.C               |
| 0.999999 | 1 R.SLDLDGIIAEVK[325.13]AQYEEMAK.C               |
| 0.999999 | 1 K.IEK[325.13]QYDADLEQLIQWITTQC[160.03]R.K      |
| 0.999999 | 1 R.SLDLDGIIAEVK[325.13]AQYEEMAK.C               |
| 0.999999 | 1 K.IEK[325.13]QYDADLEQLIQWITTQC[160.03]R.K      |
| 0.999999 | 1 K.IEK[325.13]QYDADLEQLIQWITTQC[160.03]R.K      |
| 0.999999 | 1 K.IEK[325.13]QYDADLEQLIQWITTQC[160.03]R.K      |
| 0.999999 | 1 R.K[325.13]LIGDPNLEFVAMPALAPPEVVM DPALAAQYEH   |
| 0.999999 | 1 R.LQLETEIEALK[325.13]EELLFMK.K                 |
| 0.999999 | 1 R.LQLETEIEALK[325.13]EELLFMK.K                 |
| 0.999999 | 1 R.LQLETEIEALK[325.13]EELLFMK.K                 |
| 0.999999 | 1 R.LQLETEIEALK[325.13]EELLFMK.K                 |
| 0.999999 | 1 R.LQLETEIEALK[325.13]EELLFMK.K                 |
| 0.999999 | 1 R.LQLETEIEALK[325.13]EELLFMK.K                 |
| 0.999999 | 1 K.DGYNYTLISK[325.13]TEFLSFMNTELAFTK.N          |
| 0.999999 | 1 R.LQLETEIEALK[325.13]EELLFMK.K                 |
| 0.999999 | 1 R.VK[325.13]VFQSSANYAENFIQSIISTVEPAQR.Q        |
| 0.999999 | 1 R.VK[325.13]VFQSSANYAENFIQSIISTVEPAQR.Q        |
| 0.999999 | 1 R.LLADPTGAFGK[325.13]ETDLLDDSLVSIFGNR.R        |
| 0.999999 | 1 R.TC[160.03]ATVTIGGINIAEALVSK[325.13]GLATVIR.Y |
| 0.999999 | 1 R.TC[160.03]ATVTIGGINIAEALVSK[325.13]GLATVIR.Y |
| 0.999999 | 1 R.TC[160.03]ATVTIGGINIAEALVSK[325.13]GLATVIR.Y |
| 0.999999 | 1 R.TC[160.03]ATVTIGGINIAEALVSK[325.13]GLATVIR.Y |
| 0.999999 | 1 R.LK[325.13]GFGYAEFEDLSLSALSNEESLGNR.R         |
| 0.999999 | 1 R.TC[160.03]ATVTIGGINIAEALVSK[325.13]GLATVIR.Y |

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| 0.999999 | 1 R.TC[160.03]ATVTIGGINIAEALVSK[325.13]GLATVIR.Y    |
| 0.999999 | 1 R.LK[325.13]GFGYAEFEDLSLLSALSNEESLGNR.R           |
| 0.999999 | 1 R.LK[325.13]GFGYAEFEDLSLLSALSNEESLGNR.R           |
| 0.999999 | 1 R.YISPDQLADLYKSFIK[325.13]DYPVVSIEDPFDQDDWGAM     |
| 0.999999 | 1 R.YISPDQLADLYKSFIK[325.13]DYPVVSIEDPFDQDDWGAM     |
| 0.999999 | 1 R.AITIAGVPQSVTEC[160.03]VK[325.13]QIC[160.03]LVML |
| 0.999999 | 1 R.AITIAGVPQSVTEC[160.03]VK[325.13]QIC[160.03]LVML |
| 0.999999 | 1 R.AITIAGVPQSVTEC[160.03]VK[325.13]QIC[160.03]LVML |
| 0.999999 | 1 R.VFPDK[325.13]EVMLDAALALAAEISSK.S                |
| 0.999999 | 1 R.VFPDK[325.13]EVMLDAALALAAEISSK.S                |
| 0.999999 | 1 R.VFPDK[325.13]EVMLDAALALAAEISSK.S                |
| 0.999999 | 1 R.YISPDQLADLYK[325.13]SFIK.D                      |
| 0.999999 | 1 R.VFPDK[325.13]EVMLDAALALAAEISSK.S                |
| 0.999999 | 1 R.VFPDK[325.13]EVMLDAALALAAEISSK.S                |
| 0.999999 | 1 K.LC[160.03]YVALDFEQEMATAASSSSLEK[325.13]SYELPD   |
| 0.999999 | 1 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN     |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y             |
| 0.999999 | 1 K.SNQNGK[325.13]DSKPSSTPR.S                       |
| 0.999999 | 1 K.SNQNGK[325.13]DSKPSSTPR.S                       |
| 0.999999 | 1 K.SNQNGK[325.13]DSKPSSTPR.S                       |
| 0.999999 | 1 K.K[325.13]AEGGGGGGRPGAPAAGDGK.T                  |
| 0.999999 | 1 R.GK[325.13]SPSDC[160.03]C[160.03]HNQC[160.03]AAC |
| 0.999999 | 1 R.K[325.13]TSYAQHQQVR.Q                           |
| 0.999999 | 1 R.GK[325.13]SPSDC[160.03]C[160.03]HNQC[160.03]AAC |
| 0.999999 | 1 R.GK[325.13]SPSDC[160.03]C[160.03]HNQC[160.03]AAC |
| 0.999999 | 1 R.GK[325.13]SPSDC[160.03]C[160.03]HNQC[160.03]AAC |
| 0.999999 | 1 K.HAVSEGTK[325.13]AVTK.Y                          |
| 0.999999 | 1 R.LK[325.13]TDNAGDQHGGGGGGGGGAGAAGGGGGGEN         |
| 0.999999 | 1 K.HAVSEGTK[325.13]AVTK.Y                          |
| 0.999999 | 1 K.HAVSEGTK[325.13]AVTK.Y                          |
| 0.999999 | 1 K.HAVSEGTK[325.13]AVTK.Y                          |
| 0.999999 | 1 K.HAVSEGTK[325.13]AVTK.Y                          |
| 0.999999 | 1 K.HAVSEGTK[325.13]AVTK.Y                          |
| 0.999999 | 1 R.KTGQAPGYSYTAANK[325.13]NK.G                     |
| 0.999999 | 1 R.MVQEA EK[325.13]YKAEDEK.Q                       |
| 0.999999 | 1 R.KTGQAPGYSYTAANK[325.13]NK.G                     |
| 0.999999 | 1 R.DAVTYTEHAK[325.13]R.K                           |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEK.F                         |
| 0.999999 | 1 K.AYHLQK[325.13]STC[160.03]GK.C                   |
| 0.999999 | 1 K.AYHLQK[325.13]STC[160.03]GK.C                   |
| 0.999999 | 1 K.AYHLQK[325.13]STC[160.03]GK.C                   |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEK.F                         |
| 0.999999 | 1 K.AYHLQK[325.13]STC[160.03]GK.C                   |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEK.F                         |
| 0.999999 | 1 R.MVQEA EK[325.13]YKAEDEK.Q                       |

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| 0.999999 | 1 R.MEELHNQEVQK[325.13]R.K                           |
| 0.999999 | 1 K.IDGSANLK[325.13]SQDDRDK.F                        |
| 0.999999 | 1 R.MVQEA EK[325.13]YKAEDEK.Q                        |
| 0.999999 | 1 R.DAVTYTEHAK[325.13]R.K                            |
| 0.999999 | 1 R.EQC[160.03]C[160.03]YNC[160.03]GK[325.13]PGHLAR  |
| 0.999999 | 1 R.DAVTYTEHAK[325.13]R.K                            |
| 0.999999 | 1 R.DAVTYTEHAK[325.13]R.K                            |
| 0.999999 | 1 R.HQGVM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA      |
| 0.999999 | 0.9995 R.HQGVM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA |
| 0.999999 | 0.9995 R.HQGVM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA |
| 0.999999 | 1 R.RIVDGK[325.13]VVSETNDTK.V                        |
| 0.999999 | 1 K.YGK[325.13]IVGC[160.03]SVHK.G                    |
| 0.999999 | 1 K.DK[325.13]MMNGGHYTYSEN.R.V                       |
| 0.999999 | 1 K.YGK[325.13]IVGC[160.03]SVHK.G                    |
| 0.999999 | 1 R.MVQEA EK[325.13]YKAEDEVQR.E                      |
| 0.999999 | 1 R.MVQEA EK[325.13]YKAEDEVQR.E                      |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |
| 0.999999 | 1 K.YGK[325.13]IVGC[160.03]SVHK.G                    |
| 0.999999 | 1 K.DK[325.13]MMNGGHYTYSEN.R.V                       |
| 0.999999 | 1 R.MVQEA EK[325.13]YKAEDEVQR.E                      |
| 0.999999 | 1 K.TTWVTK[325.13]HAAENPGK.Y                         |
| 0.999999 | 1 K.VLK[325.13]QVHPDTGISSK.A                         |
| 0.999999 | 1 K.TTWVTK[325.13]HAAENPGK.Y                         |
| 0.999999 | 1 K.HELQANC[160.03]YEEVK[325.13]DR.C                 |
| 0.999999 | 1 K.TTWVTK[325.13]HAAENPGK.Y                         |
| 0.999999 | 1 K.VLK[325.13]QVHPDTGISSK.A                         |
| 0.999999 | 1 K.HELQANC[160.03]YEEVK[325.13]DR.C                 |
| 0.999999 | 1 K.VLK[325.13]QVHPDTGISSK.A                         |
| 0.999999 | 1 K.TTWVTK[325.13]HAAENPGK.Y                         |
| 0.999999 | 1 K.TTWVTK[325.13]HAAENPGK.Y                         |
| 0.999999 | 0.9992 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R   |
| 0.999999 | 1 K.VLK[325.13]QVHPDTGISSK.A                         |
| 0.999999 | 1 K.LYEEK[325.13]TGNAWHSK.N                          |
| 0.999999 | 1 R.LQAAYAGDK[325.13]ADDIQKR.E                       |
| 0.999999 | 1 R.ASGNYATVISHNPETK[325.13]K.T                      |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |
| 0.999999 | 1 R.AEVLGHK[325.13]TPEPAPR.R                         |
| 0.999999 | 1 K.FYGDEEK[325.13]DKGLQTSQDAR.F                     |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |
| 0.999999 | 1 K.IQGEYK[325.13]YTQVGPDPHNR.S                      |
| 0.999999 | 1 K.SEVQQPVHPK[325.13]PLSPDSR.A                      |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |
| 0.999999 | 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEA QSK.R        |

0.999999 1 K.ALYEHLTAK[325.13]NTK.L  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 K.IEC[160.03]EIK[325.13]INHEGEVNR.A  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEAQSK.R  
0.999999 1 K.GRPC[160.03]K[325.13]IVEMSTSK.T  
0.999999 1 K.GRPC[160.03]K[325.13]IVEMSTSK.T  
0.999999 1 K.IEC[160.03]EIK[325.13]INHEGEVNR.A  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 0.9945 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.EGQEDQGLTK[325.13]DYGNSPLHR.F  
0.999999 1 R.EGQEDQGLTK[325.13]DYGNSPLHR.F  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.EATK[325.13]GFYDKDSSGWSSSK.D  
0.999999 0.9938 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 0.9996 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.VVVTk[325.13]YC[160.03]DPDSYHR.R  
0.999999 1 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.VVVTk[325.13]YC[160.03]DPDSYHR.R  
0.999999 1 R.GYLNK[325.13]DTHDQLSEPSEVR.S  
0.999999 1 R.EGQEDQGLTK[325.13]DYGNSPLHR.F  
0.999999 1 R.EGQEDQGLTK[325.13]DYGNSPLHR.F  
0.999999 1 R.VVVTk[325.13]YC[160.03]DPDSYHR.R  
0.999999 1 R.EGQEDQGLTK[325.13]DYGNSPLHR.F  
0.999999 0.9421 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 K.VQK[325.13]HQAFAELSANQSR.I  
0.999999 1 R.EGQEDQGLTK[325.13]DYGNSPLHR.F  
0.999999 1 R.EGQEDQGLTK[325.13]DYGNSPLHR.F  
0.999999 1 K.K[325.13]LGEM[147.04]WNNTAADDKQPYEK.K  
0.999999 1 K.K[325.13]LGEM[147.04]WNNTAADDKQPYEK.K  
0.999999 1 R.LQAEEK[325.13]AHAFVQK.E  
0.999999 0.9865 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 R.KK[325.13]NLQYYDISAK.S  
0.999999 1 K.K[325.13]LGEM[147.04]WNNTAADDKQPYEK.K  
0.999999 1 R.GYLNK[325.13]DTHDQLSEPSEVR.S  
0.999999 1 K.K[325.13]LGEM[147.04]WNNTAADDKQPYEK.K  
0.999999 1 K.GAVDGLSIPHSTK[325.13]R.F  
0.999999 1 R.DHASNIYK[325.13]VEGGC[160.03]ITK.L  
0.999999 1 R.KK[325.13]NLQYYDISAK.S

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|----------|-------------------------------------------------|
| 0.999999 | 1 R.DHASNIYK[325.13]VEGGC[160.03]ITK.L          |
| 0.999999 | 1 R.K[325.13]KNLQYYDISAK.S                      |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 K.K[325.13]LGEM[147.04]WNNTAADDKQPYEK.K       |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.LEHGQATAK[325.13]DVGSLASVQR.Y               |
| 0.999999 | 1 R.GYLNK[325.13]DTHDQLSEPSEVR.S                |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.DHASNIYK[325.13]VEGGC[160.03]ITK.L          |
| 0.999999 | 1 R.DHASNIYK[325.13]VEGGC[160.03]ITK.L          |
| 0.999999 | 1 R.DHASNIYK[325.13]VEGGC[160.03]ITK.L          |
| 0.999999 | 1 R.DHASNIYK[325.13]VEGGC[160.03]ITK.L          |
| 0.999999 | 1 R.KGVAINMVTEEDK[325.13]R.T                    |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.DAGEYEC[160.03]HTPSTDK[325.13]QYFGSYSAK.M   |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K             |
| 0.999999 | 0.9948 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K        |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 K.HK[325.13]LDVTSVEDYK.A                      |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.EAILAIHK[325.13]EAQR.I                      |
| 0.999999 | 1 K.HK[325.13]LDVTSVEDYK.A                      |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.YTASGVHK[325.13]GATYVFR.L                   |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 0.999 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K         |
| 0.999999 | 1 R.EAILAIHK[325.13]EAQR.I                      |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.FNAHGDANTIVC[160.03]NSK[325.13]DGGAWGTEQR.E |
| 0.999999 | 1 R.DFTVSAMHGDMQK[325.13]ER.D                   |

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| 0.999999 | 1 R.K[325.13]GVAINMVTEEDKR.T                         |
| 0.999999 | 1 K.K[325.13]TKPYIQVDIGGGQTK.T                       |
| 0.999999 | 1 R.ENIQK[325.13]SLAGSSGPGASSGTSGDHGELVVR.I          |
| 0.999999 | 1 R.GMGSLDAMDK[325.13]HLSSQNR.Y                      |
| 0.999999 | 1 R.K[325.13]GVAINMVTEEDKR.T                         |
| 0.999999 | 1 R.DQHFKV[325.13]IQVK.D                             |
| 0.999999 | 1 R.ENIQK[325.13]SLAGSSGPGASSGTSGDHGELVVR.I          |
| 0.999999 | 1 R.ENIQK[325.13]SLAGSSGPGASSGTSGDHGELVVR.I          |
| 0.999999 | 1 K.K[325.13]EDLYLKPIQR.T                            |
| 0.999999 | 1 R.HESGASIK[325.13]IDEPLEGSEDR.I                    |
| 0.999999 | 1 R.WC[160.03]DK[325.13]SDEDDWSKPLPPSER.L            |
| 0.999999 | 1 R.DFTVSAMHGDMQK[325.13]ER.D                        |
| 0.999999 | 1 R.DFTVSAMHGDMQK[325.13]ER.D                        |
| 0.999999 | 1 K.K[325.13]LGEMWNNTAADDKQPYEK.K                    |
| 0.999999 | 1 R.WC[160.03]DK[325.13]SDEDDWSKPLPPSER.L            |
| 0.999999 | 1 K.K[325.13]LGEMWNNTAADDKQPYEK.K                    |
| 0.999999 | 1 R.HESGASIK[325.13]IDEPLEGSEDR.I                    |
| 0.999999 | 1 R.DFTVSAMHGDMQK[325.13]ER.D                        |
| 0.999999 | 1 R.WC[160.03]DK[325.13]SDEDDWSKPLPPSER.L            |
| 0.999999 | 1 K.K[325.13]HPDASVNFSEFSK.K                         |
| 0.999999 | 1 K.K[325.13]LGEMWNNTAADDKQPYEK.K                    |
| 0.999999 | 1 K.K[325.13]LGEMWNNTAADDKQPYEK.K                    |
| 0.999999 | 1 R.K[325.13]PSAPHGYTC[160.03]EC[160.03]PPNYLGPYC[1  |
| 0.999999 | 1 K.K[325.13]LGEMWNNTAADDKQPYEK.K                    |
| 0.999999 | 1 R.K[325.13]PSAPHGYTC[160.03]EC[160.03]PPNYLGPYC[1  |
| 0.999999 | 1 K.YEELQSLAGK[325.13]HGDDL.R                        |
| 0.999999 | 1 R.GENSC[160.03]K[325.13]ATGQVC[160.03]HALC[160.03] |
| 0.999999 | 1 R.MKETQK[325.13]SIYYITGESK.E                       |
| 0.999999 | 1 R.MKETQK[325.13]SIYYITGESK.E                       |
| 0.999999 | 1 K.K[325.13]LGEMWNNTAADDKQPYEK.K                    |
| 0.999999 | 1 K.K[325.13]HPDASVNFSEFSK.K                         |
| 0.999999 | 1 R.MKETQK[325.13]SIYYITGESK.E                       |
| 0.999999 | 1 K.YK[325.13]PAVNQIEC[160.03]HPYLTQEK.L             |
| 0.999999 | 1 K.K[325.13]HPDASVNFSEFSK.K                         |
| 0.999999 | 1 R.NALHK[325.13]SSVNC[160.03]PFSSQDMK.Y             |
| 0.999999 | 1 R.MKETQK[325.13]SIYYITGESK.E                       |
| 0.999999 | 1 R.K[325.13]PSAPHGYTC[160.03]EC[160.03]PPNYLGPYC[1  |
| 0.999999 | 1 R.K[325.13]PSAPHGYTC[160.03]EC[160.03]PPNYLGPYC[1  |
| 0.999999 | 1 R.DGWPAMGIHGDK[325.13]SQQER.D                      |
| 0.999999 | 1 R.DGWPAMGIHGDK[325.13]SQQER.D                      |
| 0.999999 | 1 R.GVNASAK[325.13]FATDGEGYKPC[160.03]DPQVIR.D       |
| 0.999999 | 1 R.GENSC[160.03]K[325.13]ATGQVC[160.03]HALC[160.03] |
| 0.999999 | 1 R.GENSC[160.03]K[325.13]ATGQVC[160.03]HALC[160.03] |
| 0.999999 | 1 K.K[325.13]YEDIC[160.03]PSTHNMDVPMK.R              |
| 0.999999 | 1 K.K[325.13]YEDIC[160.03]PSTHNMDVPMK.R              |
| 0.999999 | 1 R.GENSC[160.03]K[325.13]ATGQVC[160.03]HALC[160.03] |
| 0.999999 | 1 R.DGWPAMGIHGDK[325.13]SQQER.D                      |



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| 0.999999 | 1 R.GENSC[160.03]K[325.13]ATGQVC[160.03]HALC[160.03] |
| 0.999999 | 1 K.TVDLKPDPWGK[325.13]GYSR.K                        |
| 0.999999 | 1 K.TVDLKPDPWGK[325.13]GYSR.K                        |
| 0.999999 | 1 K.K[325.13]YEDIC[160.03]PSTHNMDVPMK.R              |
| 0.999999 | 1 R.GENSC[160.03]K[325.13]ATGQVC[160.03]HALC[160.03] |
| 0.999999 | 1 K.TVDLKPDPWGK[325.13]GYSR.K                        |
| 0.999999 | 1 R.GENSC[160.03]K[325.13]ATGQVC[160.03]HALC[160.03] |
| 0.999999 | 1 K.TVDLKPDPWGK[325.13]GYSR.K                        |
| 0.999999 | 1 K.TVDLKPDPWGK[325.13]GYSR.K                        |
| 0.999999 | 1 K.GSETPGATPGSK[325.13]IWDPTPSHTPAGAATPGR.G         |
| 0.999999 | 1 K.TVDLKPDPWGK[325.13]GYSR.K                        |
| 0.999999 | 1 K.AATVTGK[325.13]LVHANFGTK.K                       |
| 0.999999 | 1 K.DLSDGIHVVK[325.13]DAR.E                          |
| 0.999999 | 1 K.AQYK[325.13]SLIGVEYKPVSAEDKDK.K                  |
| 0.999999 | 1 K.LLLQVQHASK[325.13]QITADK.Q                       |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                      |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                      |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                      |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                      |
| 0.999999 | 1 R.GGSGSHNWGTVK[325.13]DELTESPK.Y                   |
| 0.999999 | 1 R.AWTSK[325.13]GSGPLSPSIQSR.T                      |
| 0.999999 | 1 K.K[325.13]IADDKYNDTFWK.E                          |
| 0.999999 | 1 R.QTVAVGVK[325.13]AVDKK.A                          |
| 0.999999 | 1 R.DGWPAMC[160.03]IHGDK[325.13]SQPER.D              |
| 0.999999 | 1 R.QTVAVGVK[325.13]AVDKK.A                          |
| 0.999999 | 1 K.KK[325.13]VWLDPNETNEIANANSR.Q                    |
| 0.999999 | 1 K.AVEHINK[325.13]TIAPALVSK.K                       |
| 0.999999 | 1 K.K[325.13]KVLDPNETNEIANANSR.Q                     |
| 0.999999 | 1 K.AVEHINK[325.13]TIAPALVSK.K                       |
| 0.999999 | 1 K.AVEHINK[325.13]TIAPALVSK.K                       |
| 0.999999 | 1 K.AVEHINK[325.13]TIAPALVSK.K                       |
| 0.999999 | 1 R.QTVAVGVK[325.13]AVDKK.A                          |
| 0.999999 | 1 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V   |
| 0.999999 | 1 K.TVDGPSGK[325.13]LWR.D                            |
| 0.999999 | 1 R.DFTVSALHGMDQK[325.13]ER.D                        |
| 0.999999 | 1 K.TVDGPSGK[325.13]LWR.D                            |
| 0.999999 | 1 K.ANPFGGASHAK[325.13]GIVLEK.V                      |
| 0.999999 | 1 R.FANYIDK[325.13]VR.F                              |
| 0.999999 | 1 K.TVDGPSGK[325.13]LWR.D                            |
| 0.999999 | 1 K.NK[325.13]GLWVPEGQR.A                            |
| 0.999999 | 1 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V   |
| 0.999999 | 1 R.VYNVTQHAVGIVVNK[325.13]QVK.G                     |
| 0.999999 | 1 R.VYNVTQHAVGIVVNK[325.13]QVK.G                     |
| 0.999999 | 1 K.VIMVTGDHPITAK[325.13]AIAK.G                      |
| 0.999999 | 1 R.FANYIDK[325.13]VR.F                              |
| 0.999999 | 1 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V   |
| 0.999999 | 1 K.NK[325.13]GLWVPEGQR.A                            |

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| 0.999999 | 1 K.VIMVTGDHPITAK[325.13]AIAK.G                      |
| 0.999999 | 1 K.VIMVTGDHPITAK[325.13]AIAK.G                      |
| 0.999999 | 1 R.K[325.13]AHEILPNLVC[160.03]C[160.03]SAK.N        |
| 0.999999 | 1 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V   |
| 0.999999 | 1 R.K[325.13]AHEILPNLVC[160.03]C[160.03]SAK.N        |
| 0.999999 | 1 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V   |
| 0.999999 | 1 R.GTK[325.13]LMC[160.03]SLC[160.03]HC[160.03]PGATI |
| 0.999999 | 1 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V   |
| 0.999999 | 1 R.C[160.03]SYC[160.03]NNK[325.13]LSLGTASYLHGR.I    |
| 0.999999 | 1 R.K[325.13]AHEILPNLVC[160.03]C[160.03]SAK.N        |
| 0.999999 | 1 K.ISK[325.13]SPDGAHLTWEPPSVTSGK.I                  |
| 0.999999 | 1 K.ISK[325.13]SPDGAHLTWEPPSVTSGK.I                  |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                        |
| 0.999999 | 1 K.DK[325.13]FNEC[160.03]GHVLYADIK.M                |
| 0.999999 | 1 K.DK[325.13]FNEC[160.03]GHVLYADIK.M                |
| 0.999999 | 1 R.GQPIYIQFSNHK[325.13]ELK.T                        |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                        |
| 0.999999 | 1 R.GQPIYIQFSNHK[325.13]ELK.T                        |
| 0.999999 | 1 R.FSGWYDADLSPAGHEEAK[325.13]R.G                    |
| 0.999999 | 1 K.DK[325.13]FNEC[160.03]GHVLYADIK.M                |
| 0.999999 | 1 R.FSGWYDADLSPAGHEEAK[325.13]R.G                    |
| 0.999999 | 1 R.AGVK[325.13]MVMIQDGPQNTGADKPLR.I                 |
| 0.999999 | 1 R.EALLSSAVDHGSDEVK[325.13]FR.Q                     |
| 0.999999 | 1 R.VVVLMGSTSDLGHC[160.03]EK[325.13]IK.K             |
| 0.999999 | 1 R.FSGWYDADLSPAGHEEAK[325.13]R.G                    |
| 0.999999 | 1 K.AGLQVYNK[325.13]C[160.03]WKFEHC[160.03]NFNDVT    |
| 0.999999 | 1 R.QGLTK[325.13]DAHNALLDIQSSGR.A                    |
| 0.999999 | 1 R.FSGWYDADLSPAGHEEAK[325.13]R.G                    |
| 0.999999 | 1 R.VAAGLQIK[325.13]NSLTSKDPDIK.A                    |
| 0.999999 | 1 K.YIDQEELNK[325.13]TKPIWTR.N                       |
| 0.999999 | 1 R.AK[325.13]VTLNGVPAQPLGPR.A                       |
| 0.999999 | 1 K.ANEVISK[325.13]LYAVHQEGNK.N                      |
| 0.999999 | 1 K.TM[147.04]QNVK[325.13]HPVTGQFLYQDSNWASK.V        |
| 0.999999 | 1 K.YIDQEELNK[325.13]TKPIWTR.N                       |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                        |
| 0.999999 | 1 K.ANEVISK[325.13]LYAVHQEGNK.N                      |
| 0.999999 | 1 R.QGLTK[325.13]DAHNALLDIQSSGR.A                    |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                        |
| 0.999999 | 1 R.AK[325.13]VTLNGVPAQPLGPR.A                       |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                        |
| 0.999999 | 1 R.GVEVTVGHEQEEGGK[325.13]WPYAGTAEAIK.A             |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                        |
| 0.999999 | 1 K.YIDQEELNK[325.13]TKPIWTR.N                       |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                        |
| 0.999999 | 1 K.K[325.13]VTHAVVTVPAYFNDAQR.Q                     |
| 0.999999 | 1 R.GVEVTVGHEQEEGGK[325.13]WPYAGTAEAIK.A             |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                        |

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| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                  |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                  |
| 0.999999 | 1 K.AEDKEWMPVTK[325.13]LGR.L                   |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                  |
| 0.999999 | 1 R.EDLQLDKPASGVK[325.13]EEWYAR.I              |
| 0.999999 | 1 K.AEDKEWMPVTK[325.13]LGR.L                   |
| 0.999999 | 1 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V          |
| 0.999999 | 1 K.AEDKEWMPVTK[325.13]LGR.L                   |
| 0.999999 | 1 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V          |
| 0.999999 | 1 R.ETNLDLPLVDTHSK[325.13]R.T                  |
| 0.999999 | 1 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V          |
| 0.999999 | 1 K.AEDKEWMPVTK[325.13]LGR.L                   |
| 0.999999 | 1 K.AEDKEWMPVTK[325.13]LGR.L                   |
| 0.999999 | 1 K.VVC[160.03]DENGSK[325.13]GYGFVHFETQEEAER.A |
| 0.999999 | 1 R.IC[160.03]K[325.13]VLAVNQENEHLMEDYEK.L     |
| 0.999999 | 1 R.AK[325.13]VTLNGVPAQPLGPR.A                 |
| 0.999999 | 1 R.AK[325.13]VTLNGVPAQPLGPR.A                 |
| 0.999999 | 1 K.GNDISSGTVLSDYVSGPPK[325.13]GTGLHR.Y        |
| 0.999999 | 1 K.HIYYITGETK[325.13]DQVANSFAVER.L            |
| 0.999999 | 1 R.KYEAQLTFK[325.13]QVSK.N                    |
| 0.999999 | 1 R.LIFAGK[325.13]QLEDGR.T                     |
| 0.999999 | 1 K.SNYNLPMHK[325.13]MINTDLR.I                 |
| 0.999999 | 1 K.K[325.13]GWLYYEAGQR.F                      |
| 0.999999 | 1 R.IAESNHIK[325.13]LSGSNPYTTVTPQIINSK.W       |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E            |
| 0.999999 | 1 K.GNDISSGTVLSDYVSGPPK[325.13]GTGLHR.Y        |
| 0.999999 | 1 K.SSK[325.13]GGPGSAVSPYPTFNPSSDVAALHK.A      |
| 0.999999 | 1 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V          |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E            |
| 0.999999 | 1 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V          |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E            |
| 0.999999 | 1 R.TTEEDRGNYC[160.03]VVSATK[325.13]QR.N       |
| 0.999999 | 1 R.VKPAPDETSFSEALLK[325.13]R.N                |
| 0.999999 | 1 R.TTEEDRGNYC[160.03]VVSATK[325.13]QR.N       |
| 0.999999 | 1 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V          |
| 0.999999 | 1 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V          |
| 0.999999 | 1 K.SSK[325.13]GGPGSAVSPYPTFNPSSDVAALHK.A      |
| 0.999999 | 1 K.VINTGIK[325.13]VWC[160.03]R.N              |
| 0.999999 | 1 R.IAESNHIK[325.13]LSGSNPYTTVTPQIINSK.W       |
| 0.999999 | 1 R.YLYTLVITDKEK[325.13]AEK.L                  |
| 0.999999 | 0.9995 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L       |
| 0.999999 | 1 K.KGATLK[325.13]ITLDNAYMEK.C                 |
| 0.999999 | 1 K.FINYVK[325.13]NC[160.03]FR.M               |
| 0.999999 | 1 R.YLYTLVITDKEK[325.13]AEK.L                  |
| 0.999999 | 1 R.YLYTLVITDKEK[325.13]AEK.L                  |
| 0.999999 | 1 K.VK[325.13]ADRDESSPYAAMLAAQDVAQR.C          |
| 0.999999 | 1 R.ALK[325.13]MIVDPVEPHGEMK.F                 |

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| 0.999999 | 1 R.ANLVK[325.13]NGC[160.03]GGEIESPASSFHVLR.S    |
| 0.999999 | 1 K.FINYVK[325.13]NC[160.03]FR.M                 |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E              |
| 0.999999 | 1 K.FINYVK[325.13]NC[160.03]FR.M                 |
| 0.999999 | 1 R.LIFAGK[325.13]QLEDGR.T                       |
| 0.999999 | 1 R.YLYTLVITDKEK[325.13]AEK.L                    |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E              |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E              |
| 0.999999 | 1 R.GYFEYIEENK[325.13]YSR.A                      |
| 0.999999 | 1 R.SYDVPPPPMEPDHPFYSNISK[325.13]DR.R            |
| 0.999999 | 1 R.GYFEYIEENK[325.13]YSR.A                      |
| 0.999999 | 1 K.KGATLK[325.13]ITLDNAYMEK.C                   |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E              |
| 0.999999 | 1 R.LIFAGK[325.13]QLEDGR.T                       |
| 0.999999 | 1 R.LIFAGK[325.13]QLEDGR.T                       |
| 0.999999 | 1 K.AFQYVETHGEVC[160.03]PANWTPDSPTIK[325.13]PSPA |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E              |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E              |
| 0.999999 | 1 K.VK[325.13]ADRDESSPYAAMLAAQDVAQR.C            |
| 0.999999 | 1 K.LSLEGDHSTPPSAYGSVK[325.13]AYTNFDAER.D        |
| 0.999999 | 1 K.LSLEGDHSTPPSAYGSVK[325.13]AYTNFDAER.D        |
| 0.999999 | 1 K.LSLEGDHSTPPSAYGSVK[325.13]AYTNFDAER.D        |
| 0.999999 | 1 R.VLADPSDDTK[325.13]GFFDPNTHENLTYR.Q           |
| 0.999999 | 1 R.HQSEIK[325.13]PGEPEPQILDFQTQQYK.L            |
| 0.999999 | 1 K.ALDVMVSTFHK[325.13]YSGK.E                    |
| 0.999999 | 1 K.VHSPSGALEEC[160.03]YVTEIDQDK[325.13]YAVR.F   |
| 0.999999 | 1 K.VHSPSGALEEC[160.03]YVTEIDQDK[325.13]YAVR.F   |
| 0.999999 | 1 K.VHSPSGALEEC[160.03]YVTEIDQDK[325.13]YAVR.F   |
| 0.999999 | 1 R.NPGGQMEGPWC[160.03]FTQNK[325.13]NVR.M        |
| 0.999999 | 1 R.GYFEYIEENK[325.13]YSR.A                      |
| 0.999999 | 1 K.ALDVMVSTFHK[325.13]YSGK.E                    |
| 0.999999 | 1 R.NPGGQMEGPWC[160.03]FTQNK[325.13]NVR.M        |
| 0.999999 | 1 K.ALDVMVSTFHK[325.13]YSGK.E                    |
| 0.999999 | 1 K.VHSPSGALEEC[160.03]YVTEIDQDK[325.13]YAVR.F   |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                       |
| 0.999999 | 1 R.GYFEYIEENK[325.13]YSR.A                      |
| 0.999999 | 1 K.LDK[325.13]SQIHDIVLVGGSTR.I                  |
| 0.999999 | 1 R.NPGGQMEGPWC[160.03]FTQNK[325.13]NVR.M        |
| 0.999999 | 1 K.LLSK[325.13]TPELNLDQFHDK.T                   |
| 0.999999 | 1 K.DPSAVAK[325.13]HFVALSTNTTK.V                 |
| 0.999999 | 1 R.AGVK[325.13]MILIQDGSQNTNVDKPLR.I             |
| 0.999999 | 1 R.AGVK[325.13]MILIQDGSQNTNVDKPLR.I             |
| 0.999999 | 1 R.VLADPSDDTK[325.13]GFFDPNTHENLTYR.Q           |
| 0.999999 | 1 K.LLSK[325.13]TPELNLDQFHDK.T                   |
| 0.999999 | 1 K.DPSAVAK[325.13]HFVALSTNTTK.V                 |
| 0.999999 | 1 R.NK[325.13]SFGSAQEFWAHDSSEYAIR.E              |
| 0.999999 | 1 R.AGVK[325.13]MILIQDGSQNTNVDKPLR.I             |

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| 0.999999 | 1 R.AGVK[325.13]MILIQDGSQNTNVDKPLR.I              |
| 0.999999 | 1 K.DPSAVAK[325.13]HFVALSTNTTK.V                  |
| 0.999999 | 1 R.NK[325.13]SFGSAQEFWAHDSSEYAIR.E               |
| 0.999999 | 1 R.VSLDVNHFAPELTVK[325.13]TK.D                   |
| 0.999999 | 1 R.YLEGTSC[160.03]IAGVLVPAK[325.13]DQPGRQEK.M    |
| 0.999999 | 1 R.NK[325.13]SFGSAQEFWAHDSSEYAIR.E               |
| 0.999999 | 1 R.KESYSVYVYK[325.13]VLK.Q                       |
| 0.999999 | 1 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V                |
| 0.999999 | 1 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V                |
| 0.999999 | 1 R.VITEEEKNFK[325.13]AFASLR.M                    |
| 0.999999 | 1 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V                |
| 0.999999 | 1 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V                |
| 0.999999 | 1 R.VITEEEKNFK[325.13]AFASLR.M                    |
| 0.999999 | 1 K.GNK[325.13]PWISLPR.G                          |
| 0.999999 | 1 K.LPDGYEFK[325.13]FPNR.L                        |
| 0.999999 | 1 K.LITEDVQGK[325.13]NC[160.03]LTNFHGMDLTR.D      |
| 0.999999 | 1 R.YESHPVC[160.03]ADLQAK[325.13]ILQC[160.03]YR.E |
| 0.999999 | 1 K.LPDGYEFK[325.13]FPNR.L                        |
| 0.999999 | 1 K.LPDGYEFK[325.13]FPNR.L                        |
| 0.999999 | 1 R.YESHPVC[160.03]ADLQAK[325.13]ILQC[160.03]YR.E |
| 0.999999 | 1 K.LITEDVQGK[325.13]NC[160.03]LTNFHGMDLTR.D      |
| 0.999999 | 1 K.LITEDVQGK[325.13]NC[160.03]LTNFHGMDLTR.D      |
| 0.999999 | 1 R.YESHPVC[160.03]ADLQAK[325.13]ILQC[160.03]YR.E |
| 0.999999 | 1 R.TK[325.13]IDC[160.03]DNLEQYFIQQGGGPDKK.G      |
| 0.999999 | 1 R.TK[325.13]IDC[160.03]DNLEQYFIQQGGGPDKK.G      |
| 0.999999 | 1 R.LK[325.13]LAQQQAALLMQQEER.A                   |
| 0.999999 | 1 R.TAPDLLPHK[325.13]PLPASAYIEDGR.F               |
| 0.999999 | 1 R.VC[160.03]ALLSC[160.03]TSHK[325.13]DYPFHEEF.- |
| 0.999999 | 1 R.IETMLGDVAVAVHPK[325.13]DTR.Y                  |
| 0.999999 | 1 R.TAPDLLPHK[325.13]PLPASAYIEDGR.F               |
| 0.999999 | 1 R.GAPLAK[325.13]VVFR.D                          |
| 0.999999 | 1 R.ALSSEGKPYVTK[325.13]EELYQNLTR.E               |
| 0.999999 | 1 R.TAPDLLPHK[325.13]PLPASAYIEDGR.F               |
| 0.999999 | 1 K.AVDIPHMDIEALK[325.13]K.L                      |
| 0.999999 | 1 R.VGSTSENITQK[325.13]VVWVEESDKR.S               |
| 0.999999 | 1 R.VGSTSENITQK[325.13]VVWVEESDKR.S               |
| 0.999999 | 1 R.GAPLAK[325.13]VVFR.D                          |
| 0.999999 | 1 R.FGLPAAAPC[160.03]PK[325.13]GSFGTAVR.H         |
| 0.999999 | 1 K.NQSQGYNQWQQGQFWGQK[325.13]PWSQHYHQGY.-        |
| 0.999999 | 1 K.NQSQGYNQWQQGQFWGQK[325.13]PWSQHYHQGY.-        |
| 0.999999 | 1 R.GK[325.13]MSSYAFFVQTC[160.03]R.E              |
| 0.999999 | 1 R.GK[325.13]MSSYAFFVQTC[160.03]R.E              |
| 0.999999 | 1 R.SPTLYGISHDDLK[325.13]GDPLLDQR.R               |
| 0.999999 | 1 R.SPTLYGISHDDLK[325.13]GDPLLDQR.R               |
| 0.999999 | 1 K.NQSQGYNQWQQGQFWGQK[325.13]PWSQHYHQGY.-        |
| 0.999999 | 1 K.NQSQGYNQWQQGQFWGQK[325.13]PWSQHYHQGY.-        |
| 0.999999 | 1 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y            |

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| 0.999999 | 1 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y               |
| 0.999999 | 1 R.LAHEVGWK[325.13]YQAVTATLEEK.R                    |
| 0.999999 | 1 R.SPTLYGISHDDLK[325.13]GDPLLDQR.R                  |
| 0.999999 | 1 R.QIYGAK[325.13]GFSLSDVPAEISGEHLR.I                |
| 0.999999 | 1 R.SPTLYGISHDDLK[325.13]GDPLLDQR.R                  |
| 0.999999 | 1 R.VFSGLVSTGLK[325.13]VR.I                          |
| 0.999999 | 1 R.DPQFQK[325.13]LQQWYR.E                           |
| 0.999999 | 1 R.LAHEVGWK[325.13]YQAVTATLEEK.R                    |
| 0.999999 | 1 R.GQK[325.13]VLDSGAPIKIPVGPETLGR.I                 |
| 0.999999 | 1 R.ASLSK[325.13]LGDVYVNDAFGTAHR.A                   |
| 0.999999 | 1 R.DPQFQK[325.13]LQQWYR.E                           |
| 0.999999 | 1 R.ASLSK[325.13]LGDVYVNDAFGTAHR.A                   |
| 0.999999 | 1 R.DVQIGDIVTVGEC[160.03]RPLSK[325.13]TVR.F          |
| 0.999999 | 1 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y               |
| 0.999999 | 1 R.DVQIGDIVTVGEC[160.03]RPLSK[325.13]TVR.F          |
| 0.999999 | 1 R.ASLSK[325.13]LGDVYVNDAFGTAHR.A                   |
| 0.999999 | 1 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y               |
| 0.999999 | 1 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y               |
| 0.999999 | 1 R.QIYGAK[325.13]GFSLSDVPAEISGEHLR.I                |
| 0.999999 | 1 R.HGK[325.13]QVLDGNSNPYDIFLK.D                     |
| 0.999999 | 1 K.SNNVEMDWVLK[325.13]HTGPNSPDTANDGFVR.L            |
| 0.999999 | 1 R.LLFNDVQTLK[325.13]DGR.H                          |
| 0.999999 | 1 R.KYGGPPPDVSYSGQQPSVGTEIFVGK[325.13]IPR.D          |
| 0.999999 | 1 K.MLETK[325.13]WSLLQQQK.T                          |
| 0.999999 | 1 K.MLETK[325.13]WSLLQQQK.T                          |
| 0.999999 | 1 K.C[160.03]DVDIRK[325.13]DLYANTVLSGGTTMYPGIADR.    |
| 0.999999 | 1 K.VLISSLQDC[160.03]LHGIESK[325.13]SYGSGSR.R        |
| 0.999999 | 1 R.QSVTYAC[160.03]NK[325.13]GFTMIGEHSIYC[160.03]T   |
| 0.999999 | 1 K.VLISSLQDC[160.03]LHGIESK[325.13]SYGSGSR.R        |
| 0.999999 | 1 K.MLETK[325.13]WSLLQQQK.T                          |
| 0.999999 | 1 K.MLETK[325.13]WSLLQQQK.T                          |
| 0.999999 | 1 K.VLISSLQDC[160.03]LHGIESK[325.13]SYGSGSR.R        |
| 0.999999 | 1 R.QSVTYAC[160.03]NK[325.13]GFTMIGEHSIYC[160.03]T   |
| 0.999999 | 1 R.QSVTYAC[160.03]NK[325.13]GFTMIGEHSIYC[160.03]T   |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                     |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                     |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                     |
| 0.999999 | 1 R.QSVTYAC[160.03]NK[325.13]GFTMIGEHSIYC[160.03]T   |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                     |
| 0.999999 | 1 K.NVNAGGHK[325.13]LGLGLEFQA.-                      |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                     |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                     |
| 0.999999 | 1 K.NVNAGGHK[325.13]LGLGLEFQA.-                      |
| 0.999999 | 1 K.LWNTLGVC[160.03]K[325.13]YTVQDESHSEWVSC[160.03]T |
| 0.999999 | 1 K.NVNAGGHK[325.13]LGLGLEFQA.-                      |
| 0.999999 | 1 K.LWNTLGVC[160.03]K[325.13]YTVQDESHSEWVSC[160.03]T |
| 0.999999 | 1 R.K[325.13]MC[160.03]LFAGFQR.K                     |

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| 0.999999 | 1 K.LWNTLGVK[160.03]K[325.13]YTVQDESHSEWVSC[160.03] |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                    |
| 0.999999 | 1 R.RLLEDGEDFNLGDALDSSNSMQTIQK[325.13]TTTR.R        |
| 0.999999 | 1 K.LWNTLGVK[160.03]K[325.13]YTVQDESHSEWVSC[160.03] |
| 0.999999 | 1 K.ETAENYLGHAK[325.13]NAVITVPAYFNDQSQR.Q           |
| 0.999999 | 1 R.RLLEDGEDFNLGDALDSSNSMQTIQK[325.13]TTTR.R        |
| 0.999999 | 1 R.VYK[325.13]APEEPNIVNPLGIPVNSKEPEEVATC[160.03]   |
| 0.999999 | 1 K.ETAENYLGHAK[325.13]NAVITVPAYFNDQSQR.Q           |
| 0.999999 | 1 R.RLLEDGEDFNLGDALDSSNSMQTIQK[325.13]TTTR.R        |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                    |
| 0.999999 | 1 K.NFINNPLAQADWAAK[325.13]K.L                      |
| 0.999999 | 1 R.LPMNK[325.13]EWPSNLDLR.K                        |
| 0.999999 | 1 K.ETAENYLGHAK[325.13]NAVITVPAYFNDQSQR.Q           |
| 0.999999 | 1 K.NFINNPLAQADWAAK[325.13]K.L                      |
| 0.999999 | 1 K.ETAENYLGHAK[325.13]NAVITVPAYFNDQSQR.Q           |
| 0.999999 | 1 R.MYAALGDPK[325.13]APGLGAFR.R                     |
| 0.999999 | 1 R.GLPLVDDGGWNTVPISK[325.13]GSRPIDTSR.L            |
| 0.999999 | 1 R.GLPLVDDGGWNTVPISK[325.13]GSRPIDTSR.L            |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                 |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                 |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                 |
| 0.999999 | 1 K.VVLAYEPVWAIGTGK[325.13]TATPQQAEVHEK.L           |
| 0.999999 | 1 K.K[325.13]VTSVVFHPSQDLVFSASPDATIR.I              |
| 0.999999 | 1 K.K[325.13]VTSVVFHPSQDLVFSASPDATIR.I              |
| 0.999999 | 1 R.GLPLVDDGGWNTVPISK[325.13]GSRPIDTSR.L            |
| 0.999999 | 1 R.MYAALGDPK[325.13]APGLGAFR.R                     |
| 0.999999 | 1 K.VVLAYEPVWAIGTGK[325.13]TATPQQAEVHEK.L           |
| 0.999999 | 1 K.DIEK[325.13]AC[160.03]QSIYPLHDVFVR.K            |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                 |
| 0.999999 | 1 K.DIEK[325.13]AC[160.03]QSIYPLHDVFVR.K            |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                 |
| 0.999999 | 1 K.VVLAYEPVWAIGTGK[325.13]TATPQQAEVHEK.L           |
| 0.999999 | 1 K.VVLAYEPVWAIGTGK[325.13]TATPQQAEVHEK.L           |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                 |
| 0.999999 | 1 K.K[325.13]VTSVVFHPSQDLVFSASPDATIR.I              |
| 0.999999 | 1 K.VVLAYEPVWAIGTGK[325.13]TATPQQAEVHEK.L           |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                 |
| 0.999999 | 1 R.LIDFLEC[160.03]GK[325.13]TNLR.R                 |
| 0.999999 | 1 K.FNVWDTAGQEK[325.13]FGGLR.D                      |
| 0.999999 | 1 K.FNVWDTAGQEK[325.13]FGGLR.D                      |
| 0.999999 | 1 K.LLTK[325.13]GLSWQPPPYTPTR.F                     |
| 0.999999 | 1 K.FNVWDTAGQEK[325.13]FGGLR.D                      |
| 0.999999 | 1 K.FNVWDTAGQEK[325.13]FGGLR.D                      |
| 0.999999 | 1 K.VLEEANQAINPK[325.13]LMQLVDHR.G                  |
| 0.999999 | 1 R.LVVFPDDISLK[325.13]C[160.03]EASGKPEVQFR.W       |
| 0.999999 | 1 R.LVVFPDDISLK[325.13]C[160.03]EASGKPEVQFR.W       |
| 0.999999 | 1 K.VLEEANQAINPK[325.13]LMQLVDHR.G                  |

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| 0.999999 | 1 K.VLEEANQAINPK[325.13]LMQLVDHR.G                   |
| 0.999999 | 1 K.TKEVYELLDSPGK[325.13]VLLQSK.D                    |
| 0.999999 | 1 R.LVVFPTDDISLK[325.13]C[160.03]EASGKPEVQFR.W       |
| 0.999999 | 1 R.KASGPPVSELITK[325.13]AVAASK.E                    |
| 0.999999 | 1 R.KASGPPVSELITK[325.13]AVAASK.E                    |
| 0.999999 | 1 K.ALANVNIGSLIC[160.03]NVGAGGPAPAAGAAPAGGPAPS       |
| 0.999999 | 1 R.LVVFPTDDISLK[325.13]C[160.03]EASGKPEVQFR.W       |
| 0.999999 | 1 R.LVVFPTDDISLK[325.13]C[160.03]EASGKPEVQFR.W       |
| 0.999999 | 1 R.KASGPPVSELITK[325.13]AVAASK.E                    |
| 0.999999 | 1 K.ALANVNIGSLIC[160.03]NVGAGGPAPAAGAAPAGGPAPS       |
| 0.999999 | 1 K.ALANVNIGSLIC[160.03]NVGAGGPAPAAGAAPAGGPAPS       |
| 0.999999 | 1 R.GC[160.03]ALQC[160.03]AILSPAFAK[325.13]VR.E      |
| 0.999999 | 1 R.EQQLVGEEK[325.13]SWVQFNSNSQLMYGLPDSSHV GK.H      |
| 0.999999 | 1 R.KATGPPVSELITK[325.13]AVAASK.E                    |
| 0.999999 | 1 R.KATGPPVSELITK[325.13]AVAASK.E                    |
| 0.999999 | 1 R.VIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I            |
| 0.999999 | 1 R.K[325.13]EAESC[160.03]DC[160.03]LQGFQLTHSLGGGT   |
| 0.999999 | 1 R.K[325.13]EAESC[160.03]DC[160.03]LQGFQLTHSLGGGT   |
| 0.999999 | 1 R.YFEITDESPYVHYLNTFSSK[325.13]EPQR.G               |
| 0.999999 | 1 R.IQEIIQLDVTTSEYEKEK[325.13]LNER.L                 |
| 0.999999 | 1 R.VIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I            |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV\ |
| 0.999999 | 1 R.K[325.13]EAESC[160.03]DC[160.03]LQGFQLTHSLGGGT   |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV\ |
| 0.999999 | 1 R.K[325.13]EAESC[160.03]DC[160.03]LQGFQLTHSLGGGT   |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV\ |
| 0.999999 | 1 R.LESGMQNM[147.04]SIHTK[325.13]TTSYGAGGLSSAYGC     |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV\ |
| 0.999999 | 1 R.K[325.13]EAESC[160.03]DC[160.03]LQGFQLTHSLGGGT   |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L              |
| 0.999999 | 1 K.YQLDPTASISAK[325.13]VNNSSLIGVGYTQTLRPGVK.L       |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L              |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV\ |
| 0.999999 | 1 K.ILLAELEQLK[325.13]GQGK.S                         |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L              |
| 0.999999 | 1 R.GFK[325.13]LPDTPQGLLGAR.M                        |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV\ |
| 0.999999 | 1 K.YQLDPTASISAK[325.13]VNNSSLIGVGYTQTLRPGVK.L       |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG     |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG     |
| 0.999999 | 1 R.NLLSVAYK[325.13]NVVGAR.R                         |
| 0.999999 | 1 K.YQLDPTASISAK[325.13]VNNSSLIGVGYTQTLRPGVK.L       |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV\ |
| 0.999999 | 1 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                 |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L              |
| 0.999999 | 1 R.APQC[160.03]LGK[325.13]FIEIAAR.K                 |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L              |



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| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPP\   |
| 0.999999 | 1 R.NLLSVAYK[325.13]NVVGAR.R                          |
| 0.999999 | 1 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                  |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG      |
| 0.999999 | 1 R.GFK[325.13]LPDTPQGGLGEAR.M                        |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPP\   |
| 0.999999 | 1 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A               |
| 0.999999 | 1 R.APQC[160.03]LGK[325.13]FIEIAAR.K                  |
| 0.999999 | 0.9999 R.APQC[160.03]LGK[325.13]FIEIAAR.K             |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPP\   |
| 0.999999 | 1 R.APQC[160.03]LGK[325.13]FIEIAAR.K                  |
| 0.999999 | 1 K.GIYQSLEGAVQAGQLK[325.13]VPPGYHPLDVEK.E            |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPP\   |
| 0.999999 | 1 R.NLLSVAYK[325.13]NVVGAR.R                          |
| 0.999999 | 1 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                  |
| 0.999999 | 1 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                  |
| 0.999999 | 1 R.IPK[325.13]EQGVLSFWR.G                            |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG      |
| 0.999999 | 1 R.NLLSVAYK[325.13]NVVGAR.R                          |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG      |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG      |
| 0.999999 | 0.9994 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG      |
| 0.999999 | 1 R.VNEVNQFAAK[325.13]LIQEQHPHEELIK.T                 |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG      |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPP\   |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPP\   |
| 0.999999 | 1 K.FLK[325.13]SGDAAIVDM[147.04]VPGKPMC[160.03]VE     |
| 0.999999 | 1 R.LAAIVAK[325.13]QVLLGR.K                           |
| 0.999999 | 1 R.VNEVNQFAAK[325.13]LIQEQHPHEELIK.T                 |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG      |
| 0.999999 | 1 R.MPK[325.13]VQQTVDLFR.A                            |
| 0.999999 | 1 R.VNEVNQFAAK[325.13]LIQEQHPHEELIK.T                 |
| 0.999999 | 1 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPP\   |
| 0.999999 | 1 K.VFQFLNAK[325.13]C[160.03]ESAFLSK.R                |
| 0.999999 | 1 R.MPK[325.13]VQQTVDLFR.A                            |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV      |
| 0.999999 | 1 R.MPK[325.13]VQQTVDLFR.A                            |
| 0.999999 | 1 R.TPEAVQK[325.13]LLEQGLR.H                          |
| 0.999999 | 1 K.IILDLESPIK[325.13]GR.A                            |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV      |
| 0.999999 | 1 R.MPK[325.13]VQQTVDLFR.A                            |
| 0.999999 | 1 R.LESGMQNMSIHTK[325.13]TTSYGAGGLSSAYGGLTSPGLS       |
| 0.999999 | 1 K.GLHVVEVTYDDVIPNSPFK[325.13]VAVTEGC[160.03]QI      |
| 0.999999 | 1 R.YLEVQYK[325.13]PQVHIQMTYPLQGLTR.E                 |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG      |
| 0.999999 | 1 R.LESGMQNMSIHTK[325.13]TTSYGAGGLSSAYGGLTSPGLS       |

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| 0.999999 | 1 R.YLEVQYK[325.13]PQVHIQMTYPLQGLTR.E               |
| 0.999999 | 1 K.AIADTGANVVVTGGK[325.13]VADMALHYANK.Y            |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.VGEPVALSEEERLK[325.13]LAQQQAALLMQQEER.A         |
| 0.999999 | 1 R.LESGMQNMSIHTK[325.13]TTSGYAGGLSSAYGGLTSPGLS     |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG    |
| 0.999999 | 1 K.EAAENSLVAYK[325.13]AASDIAMTELPPTHPIR.L          |
| 0.999999 | 1 R.YLEVQYK[325.13]PQVHIQMTYPLQGLTR.E               |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 R.LESGMQNMSIHTK[325.13]TTSGYAGGLSSAYGGLTSPGLS     |
| 0.999999 | 1 K.LAQMFSDMVLK[325.13]DGFQPSR.S                    |
| 0.999999 | 1 K.EAAENSLVAYK[325.13]AASDIAMTELPPTHPIR.L          |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 K.EAAENSLVAYK[325.13]AASDIAMTELPPTHPIR.L          |
| 0.999999 | 1 R.SSPSFSSLHYQDAGNYVC[160.03]ETALQEVEGLK[325.13]   |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 K.MK[325.13]GYSFGHPSSVAGEVVFNTGLGGYPEAITDPAYI     |
| 0.999999 | 1 R.TTSLNGGC[160.03]QYLC[160.03]LPAPQINPHSPK[325.1] |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L                 |
| 0.999999 | 1 K.EAAENSLVAYK[325.13]AASDIAMTELPPTHPIR.L          |
| 0.999999 | 1 K.IILDLISEPIK[325.13]GR.A                         |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.SNTTSK[325.13]PSHLVDAHTAEVNC[160.03]LSFNPYSEF   |
| 0.999999 | 1 R.TTSLNGGC[160.03]QYLC[160.03]LPAPQINPHSPK[325.1] |
| 0.999999 | 1 R.VTFLPTGITFK[325.13]SVTR.E                       |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 K.AVPYQK[325.13]FEAHPNDLYVEGLPENIPFR.S            |
| 0.999999 | 1 R.DGSIDLVINLPNNNTK[325.13]FVHDNYVIR.R             |
| 0.999999 | 1 R.TTSLNGGC[160.03]QYLC[160.03]LPAPQINPHSPK[325.1] |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.TTSLNGGC[160.03]QYLC[160.03]LPAPQINPHSPK[325.1] |
| 0.999999 | 1 K.MPILGLGTWK[325.13]SPPGQVTEAVK.V                 |
| 0.999999 | 0.9984 R.LPLQDVYK[325.13]IGGIGTVPVGR.V              |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L                 |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L                 |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 K.LAQMFSDMVLK[325.13]DGFQPSR.S                    |

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| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.SYSK[325.13]LLC[160.03]GLLAER.L                 |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDESLR.S                     |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                   |
| 0.999999 | 1 R.FGFPEGSVELYAEK[325.13]VATR.G                    |
| 0.999999 | 1 R.VLEC[160.03]LASGIVMPDGSGIYDPC[160.03]EK[325.13] |
| 0.999999 | 1 R.EGNDLYHEMIESGVINLK[325.13]DATSK.V               |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.VTFLPTGITFK[325.13]SVTR.E                       |
| 0.999999 | 1 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T             |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDESLR.S                     |
| 0.999999 | 1 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T             |
| 0.999999 | 1 R.VTFLPTGITFK[325.13]SVTR.E                       |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.EGNDLYHEMIESGVINLK[325.13]DATSK.V               |
| 0.999999 | 0.9994 R.LPLQDVYK[325.13]IGGIGTVPVGR.V              |
| 0.999999 | 1 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q                |
| 0.999999 | 1 K.SLGQWLQEEK[325.13]VPAIYGVDR.M                   |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T             |
| 0.999999 | 1 K.SLGQWLQEEK[325.13]VPAIYGVDR.M                   |
| 0.999999 | 1 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T             |
| 0.999999 | 1 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q                |
| 0.999999 | 1 K.SLGQWLQEEK[325.13]VPAIYGVDR.M                   |
| 0.999999 | 1 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q                |
| 0.999999 | 1 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T             |
| 0.999999 | 1 K.AK[325.13]VDEFPLC[160.03]GHMVSDEYEQLSSEALEAAI   |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                     |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                     |
| 0.999999 | 1 K.AK[325.13]VDEFPLC[160.03]GHMVSDEYEQLSSEALEAAI   |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDESLR.S                     |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV    |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTDESLR.S                     |
| 0.999999 | 0.9974 R.LPLQDVYK[325.13]IGGIGTVPVGR.V              |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                     |
| 0.999999 | 1 K.MKEIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q         |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                     |
| 0.999999 | 1 K.DLLTSSYLSDSGSTGEHTK[325.13]SLVTQYLNATGNR.W      |
| 0.999999 | 1 K.DLLTSSYLSDSGSTGEHTK[325.13]SLVTQYLNATGNR.W      |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                     |
| 0.999999 | 1 K.MKEIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q         |

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| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                      |
| 0.999999 | 1 K.MKEIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q          |
| 0.999999 | 1 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP     |
| 0.999999 | 1 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP     |
| 0.999999 | 1 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP     |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                      |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                      |
| 0.999999 | 1 K.DLLLTSSYLSDSGSTGEHTK[325.13]SLVTQYLNATGNR.W      |
| 0.999999 | 1 K.VC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M       |
| 0.999999 | 1 K.DLLLTSSYLSDSGSTGEHTK[325.13]SLVTQYLNATGNR.W      |
| 0.999999 | 1 K.K[325.13]QKVEGTEPTTAFNLFVGNLNFNK.S               |
| 0.999999 | 1 K.VC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M       |
| 0.999999 | 1 K.TKPYIQVDIGGGQTK[325.13]TFAPEEISAMVLTK.M          |
| 0.999999 | 1 R.STGEAFVQFASQEIAEK[325.13]ALKK.H                  |
| 0.999999 | 1 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP     |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                      |
| 0.999999 | 1 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP     |
| 0.999999 | 1 K.DLLLTSSYLSDSGSTGEHTK[325.13]SLVTQYLNATGNR.W      |
| 0.999999 | 1 K.VC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M       |
| 0.999999 | 1 K.K[325.13]QKVEGTEPTTAFNLFVGNLNFNK.S               |
| 0.999999 | 1 K.K[325.13]GYEVIYLTEPVDEYC[160.03]IQALPEFDGKR.F    |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                      |
| 0.999999 | 1 K.DLLLTSSYLSDSGSTGEHTK[325.13]SLVTQYLNATGNR.W      |
| 0.999999 | 1 K.K[325.13]QKVEGTEPTTAFNLFVGNLNFNK.S               |
| 0.999999 | 0.9973 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN |
| 0.999999 | 1 K.AGQVVTIWAAGAGATHSPPTDLVWK[325.13]AQNTWGC         |
| 0.999999 | 1 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP     |
| 0.999999 | 1 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP     |
| 0.999999 | 1 R.TVSLGAGAK[325.13]DELHIVEAEAMNYEGSPIK.V           |
| 0.999999 | 1 K.DLLLTSSYLSDSGSTGEHTK[325.13]SLVTQYLNATGNR.W      |
| 0.999999 | 1 K.K[325.13]QKVEGTEPTTAFNLFVGNLNFNK.S               |
| 0.999999 | 1 K.NGVK[325.13]ITLPVDFVTADKFDENAK.T                 |
| 0.999999 | 1 K.K[325.13]AQLNIGNVLPVGTMPGTVIC[160.03]C[160.03]   |
| 0.999999 | 1 K.K[325.13]AQLNIGNVLPVGTMPGTVIC[160.03]C[160.03]   |
| 0.999999 | 1 K.NQK[325.13]DDVAQTDLLQIDPNFGSKEDFDSLLQSAK.K       |
| 0.999999 | 1 K.NQK[325.13]DDVAQTDLLQIDPNFGSKEDFDSLLQSAK.K       |
| 0.999999 | 1 K.K[325.13]AQLNIGNVLPVGTMPGTVIC[160.03]C[160.03]   |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 R.LK[325.13]VPPAINQFTQALDR.Q                       |
| 0.999999 | 0.9999 R.K[325.13]LFIGGLSFETTEESLR.N                 |
| 0.999999 | 1 R.TVSLGAGAK[325.13]DELHIVEAEAMNYEGSPIK.V           |
| 0.999999 | 1 R.TLTAAAVSGAQPILSK[325.13]LEPQIASASEYHR.G          |
| 0.999999 | 1 K.NQK[325.13]DDVAQTDLLQIDPNFGSKEDFDSLLQSAK.K       |
| 0.999999 | 1 K.NQK[325.13]DDVAQTDLLQIDPNFGSKEDFDSLLQSAK.K       |
| 0.999999 | 1 R.TLTAAAVSGAQPILSK[325.13]LEPQIASASEYHR.G          |

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| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 R.TLAAAVSGAQPILSK[325.13]LEPQIASASEYHR.G           |
| 0.999999 | 1 K.SK[325.13]GLAPDLPEDLYHLIK.K                      |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 R.TVSLGAGAK[325.13]DELHIVEAEAMNYEGSPIK.V           |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 R.TVSLGAGAK[325.13]DELHIVEAEAMNYEGSPIK.V           |
| 0.999999 | 1 K.EAESC[160.03]DC[160.03]LQGFQLTHSLGGGTGSGMGTI     |
| 0.999999 | 1 K.EAESC[160.03]DC[160.03]LQGFQLTHSLGGGTGSGMGTI     |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 R.K[325.13]HGLEVIYMIPIDEYC[160.03]VQQLK.E          |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 R.TVSLGAGAK[325.13]DELHIVEAEAMNYEGSPIK.V           |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 R.TVSLGAGAK[325.13]DELHIVEAEAMNYEGSPIK.V           |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 K.TWK[325.13]FVEGLPINDFSR.E                        |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 K.TEISFRPNDPK[325.13]SYEAYVLNIVR.F                 |
| 0.999999 | 1 R.ASNGDAWVEAHGK[325.13]LYSPSQIGAFVLMK.M            |
| 0.999999 | 1 K.NQKDDVAQTDLLQIDPNFGSK[325.13]EDFDSLLQSAK.K       |
| 0.999999 | 1 R.DIFNK[325.13]GFGFGLVK.L                          |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN      |
| 0.999999 | 1 R.DIFNK[325.13]GFGFGLVK.L                          |
| 0.999999 | 1 K.NQKDDVAQTDLLQIDPNFGSK[325.13]EDFDSLLQSAK.K       |
| 0.999999 | 1 K.TEISFRPNDPK[325.13]SYEAYVLNIVR.F                 |
| 0.999999 | 1 K.TEISFRPNDPK[325.13]SYEAYVLNIVR.F                 |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 R.VLADPSDDTK[325.13]GFFDPNTHENLTYLQLLER.C          |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 0.9973 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 R.VISGVLQLGNIVFK[325.13]K.E                        |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 R.FFTVK[325.13]LPVALDPGAK.I                        |
| 0.999999 | 1 R.AK[325.13]LNWLSVDFNNWK.D                         |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.999999 | 1 K.EILVGDVGQTVDDPYATFVK[325.13]MLPKDC[160.03]F      |
| 0.999999 | 1 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L             |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |

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| 0.999999 | 1 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L           |
| 0.999999 | 1 R.HSDGNLC[160.03]VK[325.13]VTDDLVC[160.03]LVYK.T |
| 0.999999 | 1 R.FFTVK[325.13]LPVALDPGAK.I                      |
| 0.999999 | 1 R.HSDGNLC[160.03]VK[325.13]VTDDLVC[160.03]LVYK.T |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R      |
| 0.999999 | 1 K.EILVGDVGQTVDDPYATFVK[325.13]MLPDKDC[160.03]F   |
| 0.999999 | 1 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L           |
| 0.999999 | 1 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L           |
| 0.999999 | 1 R.HSDGNLC[160.03]VK[325.13]VTDDLVC[160.03]LVYK.T |
| 0.999999 | 1 K.EILVGDVGQTVDDPYATFVK[325.13]MLPDKDC[160.03]F   |
| 0.999999 | 1 K.K[325.13]GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLS   |
| 0.999999 | 1 K.KGGPSPGDVEAIK[325.13]NAIANASTLAEVER.L          |
| 0.999999 | 1 R.HSDGNLC[160.03]VK[325.13]VTDDLVC[160.03]LVYK.T |
| 0.999999 | 1 R.HSDGNLC[160.03]VK[325.13]VTDDLVC[160.03]LVYK.T |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R      |
| 0.999999 | 1 K.ILTFDQLALDSPK[325.13]GC[160.03]GTVLLSGPR.K     |
| 0.999999 | 1 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L           |
| 0.999999 | 1 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L           |
| 0.999999 | 1 R.HSDGNLC[160.03]VK[325.13]VTDDLVC[160.03]LVYK.T |
| 0.999999 | 1 K.KGGPSPGDVEAIK[325.13]NAIANASTLAEVER.L          |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R      |
| 0.999999 | 1 K.VTNVK[325.13]DGTTHQTSLELFMYLNEVAGK.H           |
| 0.999999 | 1 R.AYAPGGPAYQPVVEAFGTDILHK[325.13]DGIINR.K        |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R      |
| 0.999999 | 1 K.ISDSVLVDIKDTEPLIQTAK[325.13]TTLGSK.V           |
| 0.999999 | 1 K.ISDSVLVDIKDTEPLIQTAK[325.13]TTLGSK.V           |
| 0.999999 | 1 K.VTNVK[325.13]DGTTHQTSLELFMYLNEVAGK.H           |
| 0.999999 | 1 R.SLQAVPGAK[325.13]DGTSLOWDLLSSC[160.03]HFTEEQR  |
| 0.999999 | 1 R.SLQAVPGAK[325.13]DGTSLOWDLLSSC[160.03]HFTEEQR  |
| 0.999999 | 1 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L           |
| 0.999999 | 1 R.KQSLGELIGTLNAAK[325.13]VPADTEVVC[160.03]APPTA  |
| 0.999999 | 1 R.AFITNIPFDVK[325.13]WQSLK.D                     |
| 0.999999 | 1 K.LLDFGSLSNLQVTQPTVGMNFK[325.13]TPR.G            |
| 0.999999 | 1 K.LLDFGSLSNLQVTQPTVGMNFK[325.13]TPR.G            |
| 0.999999 | 1 R.AFITNIPFDVK[325.13]WQSLK.D                     |
| 0.999999 | 1 K.LLDFGSLSNLQVTQPTVGMNFK[325.13]TPR.G            |
| 0.999999 | 1 K.LFVGGLK[325.13]GDVAEGDLIEHFSQFGTVEK.A          |
| 0.999999 | 1 K.LLDFGSLSNLQVTQPTVGMNFK[325.13]TPR.G            |
| 0.999999 | 1 K.LGFAGLVQEISFGTTK[325.13]DK.M                   |
| 0.999999 | 1 K.ALLGSVK[325.13]DSIVQGFGWGTR.E                  |
| 0.999999 | 1 R.KYTLPPGVDPTQVSSLSPEGLTVEAPMPK[325.13]LATQ      |
| 0.999999 | 1 K.VSVYLQNWSHVLSYVSK[325.13]AESTPEIAEQR.G         |
| 0.999999 | 1 K.GVDDLDFFIGDEAIEKPTYATK[325.13]WPIR.H           |
| 0.999999 | 1 R.K[325.13]IPNPDDFFEDLEPFR.M                     |
| 0.999999 | 1 R.DSALETLQGQLEEK[325.13]AQELGHSQSALASAQR.E       |
| 0.999999 | 1 K.VSVYLQNWSHVLSYVSK[325.13]AESTPEIAEQR.G         |
| 0.999999 | 1 R.K[325.13]IPNPDDFFEDLEPFR.M                     |

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| 0.999999 | 1 K.SNYNFEK[325.13]PFLWLAR.K                         |
| 0.999999 | 1 R.K[325.13]IPNPDDFFEDLEPFR.M                       |
| 0.999999 | 1 K.AEISC[160.03]TDNQDGTCT[160.03]SVSYLPVLPDYSILVK   |
| 0.999999 | 1 R.VEFATLQEALAHALTEK[325.13]EGK.D                   |
| 0.999999 | 1 K.SNYNFEK[325.13]PFLWLAR.K                         |
| 0.999999 | 1 K.SNYNFEK[325.13]PFLWLAR.K                         |
| 0.999999 | 1 K.AEISC[160.03]TDNQDGTCT[160.03]SVSYLPVLPDYSILVK   |
| 0.999999 | 0.9998 R.FLEQQNK[325.13]ILLAELEQLK.G                 |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                      |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                      |
| 0.999999 | 1 K.IPTLEEGQLPSPTATSQLPLESDAVEC[160.03]LNYQHYK[.     |
| 0.999999 | 1 K.IPTLEEGQLPSPTATSQLPLESDAVEC[160.03]LNYQHYK[.     |
| 0.999999 | 1 K.FLPPVLLK[325.13]LSSTQEGVR.K                      |
| 0.999999 | 1 K.MAVTFIGNSTAIQELFK[325.13]R.I                     |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 K.NQLK[325.13]DMAIATGGAVFGEEGLTNLEDVQPHDLGK        |
| 0.999999 | 1 R.NTDQASMPDNTAAQK[325.13]VSHLLGINVTDFT.R.G         |
| 0.999999 | 1 K.MAVTFIGNSTAIQELFK[325.13]R.I                     |
| 0.999999 | 1 R.NTDQASMPDNTAAQK[325.13]VSHLLGINVTDFT.R.G         |
| 0.999999 | 1 R.EMAGDNK[325.13]LLGQFTLIGIPPAP.R.G                |
| 0.999999 | 1 K.FLPPVLLK[325.13]LSSTQEGVR.K                      |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 R.EMAGDNK[325.13]LLGQFTLIGIPPAP.R.G                |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                      |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                      |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                  |
| 0.999999 | 1 R.LALQALTEK[325.13]LLR.S                           |
| 0.999999 | 1 R.FLEQQNK[325.13]ILLAELEQLK.G                      |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 R.LALQALTEK[325.13]LLR.S                           |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999999 | 1 K.LIC[160.03]C[160.03]DILDVLDK[325.13]HLIPAANTGESK |
| 0.999999 | 0.9968 R.ADIK[325.13]EMGLSLQWLYSAR.G                 |
| 0.999999 | 1 K.LIC[160.03]C[160.03]DILDVLDK[325.13]HLIPAANTGESK |
| 0.999999 | 1 R.FELSC[160.03]YSLAPQIK[325.13]VIAPWR.M            |
| 0.999999 | 1 R.DAGIEPGPDYTLALLNAYA.EK[325.13]GDIDHVK.Q          |
| 0.999999 | 1 R.DAGIEPGPDYTLALLNAYA.EK[325.13]GDIDHVK.Q          |
| 0.999999 | 1 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                  |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                  |
| 0.999999 | 1 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L       |
| 0.999999 | 1 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTSR.F            |

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| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 K.IAK[325.13]AFAISGPFNVQFLVK.G                   |
| 0.999999 | 1 R.LLLNNGAK[325.13]MPILGLGTWK.S                   |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 R.NLQNLILTAIK[325.13]ADR.T                       |
| 0.999999 | 1 R.NLQNLILTAIK[325.13]ADR.T                       |
| 0.999999 | 1 R.K[325.13]EGGLGPLNIPLADVTR.R                    |
| 0.999999 | 1 R.SSSGELLEWESK[325.13]SDALETGLFLNHYQMK.N         |
| 0.999999 | 1 R.NLQNLILTAIK[325.13]ADR.T                       |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 R.LLLNNGAK[325.13]MPILGLGTWK.S                   |
| 0.999999 | 1 R.LLLNNGAK[325.13]MPILGLGTWK.S                   |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 R.SSSGELLEWESK[325.13]SDALETGLFLNHYQMK.N         |
| 0.999999 | 1 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L     |
| 0.999999 | 1 K.AVDDLNLHSYSNLPWVVK[325.13]LDMEIER.I            |
| 0.999999 | 1 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L     |
| 0.999999 | 1 R.SSSGELLEWESK[325.13]SDALETGLFLNHYQMK.N         |
| 0.999999 | 1 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L     |
| 0.999999 | 1 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L     |
| 0.999999 | 1 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L     |
| 0.999999 | 1 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L     |
| 0.999999 | 1 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L     |
| 0.999999 | 1 K.ATILDLC[160.03]NK[325.13]LTTLPDFC[160.03]GLTHI |
| 0.999999 | 1 R.K[325.13]EGGLGPLNIPLADVTR.R                    |
| 0.999999 | 1 R.K[325.13]EGGLGPLNIPLADVTR.R                    |
| 0.999999 | 1 R.AFEK[325.13]TLTPIIQEYFEHGDNEVAEMLR.D           |
| 0.999999 | 1 R.AFEK[325.13]TLTPIIQEYFEHGDNEVAEMLR.D           |
| 0.999999 | 1 K.K[325.13]VGYTPDWIFLLR.N                        |
| 0.999999 | 1 K.GYPGDYK[325.13]GVEITGFPEAQALGLEVFHAGTALK.N     |
| 0.999999 | 1 R.DHSGTLGPEEFK[325.13]AC[160.03]LISLGYDIGNDPQGE  |
| 0.999999 | 1 K.K[325.13]VGYTPDWIFLLR.N                        |
| 0.999999 | 1 K.DGNASGTTLEALDC[160.03]ILPPTPTDK[325.13]PLR.L   |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E           |
| 0.999999 | 1 K.ITPENLPQILLQLK[325.13]R.R                      |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E           |
| 0.999999 | 1 K.K[325.13]DLLPSDMAVALLEAQAGTGHIIDPAT SAR.L      |
| 0.999999 | 1 K.DGNASGTTLEALDC[160.03]ILPPTPTDK[325.13]PLR.L   |
| 0.999999 | 1 K.ITPENLPQILLQLK[325.13]R.R                      |
| 0.999999 | 1 R.SIVDYK[325.13]PNLDLLEQQHQLIQEALIFDNK.H         |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E           |
| 0.999999 | 1 K.K[325.13]VGYTPDWIFLLR.N                        |
| 0.999999 | 1 K.DGNASGTTLEALDC[160.03]ILPPTPTDK[325.13]PLR.L   |
| 0.999999 | 1 K.K[325.13]DLLPSDMAVALLEAQAGTGHIIDPAT SAR.L      |
| 0.999999 | 1 K.ITPENLPQILLQLK[325.13]R.R                      |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E           |
| 0.999999 | 1 R.SIVDYK[325.13]PNLDLLEQQHQLIQEALIFDNK.H         |



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| 0.999999 | 1 K.K[325.13]DLLPSDMAVALLEAQAGTGHIIDPATSAR.L        |
| 0.999999 | 1 R.VHIQSSQTVESSGLYTLQSILK[325.13]AQLVK.E           |
| 0.999999 | 1 K.DGNASGTTLLEALDC[160.03]ILPPTRPDK[325.13]PLR.L   |
| 0.999999 | 1 K.K[325.13]DLLPSDMAVALLEAQAGTGHIIDPATSAR.L        |
| 0.999999 | 1 R.VHIQSSQTVESSGLYTLQSILK[325.13]AQLVK.E           |
| 0.999999 | 1 R.LSK[325.13]EETVLATVQALQTASHLSQQADLR.S           |
| 0.999999 | 1 K.K[325.13]DLLPSDMAVALLEAQAGTGHIIDPATSAR.L        |
| 0.999999 | 1 K.SMTEAEQQQLIDDHFLFDK[325.13]PVSPLLLASGMAR.D      |
| 0.999999 | 1 K.SMTEAEQQQLIDDHFLFDK[325.13]PVSPLLLASGMAR.D      |
| 0.999999 | 1 R.AK[325.13]QIVWNGPVGVFWEAFAR.G                   |
| 0.999999 | 1 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.999999 | 1 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.999999 | 1 R.IASHYYITNDTVQTYNQLLK[325.13]PTLSEIELFR.V        |
| 0.999999 | 1 R.AK[325.13]QIVWNGPVGVFWEAFAR.G                   |
| 0.999999 | 1 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.999999 | 1 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.999999 | 1 R.LGGLTQAPGNPVLAVQINQDK[325.13]NFAFLEFR.S         |
| 0.999999 | 1 R.LSK[325.13]EETVLATVQALQTASHLSQQADLR.S           |
| 0.999999 | 1 K.LLGGVTIAQGGVLPNIQAVLLPK[325.13]K.T              |
| 0.999999 | 1 R.AK[325.13]QIVWNGPVGVFWEAFAR.G                   |
| 0.999999 | 1 R.AK[325.13]QIVWNGPVGVFWEAFAR.G                   |
| 0.999999 | 1 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.999999 | 1 R.LGGLTQAPGNPVLAVQINQDK[325.13]NFAFLEFR.S         |
| 0.999999 | 1 R.LSK[325.13]EETVLATVQALQTASHLSQQADLR.S           |
| 0.999999 | 1 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.999999 | 1 R.LSK[325.13]EETVLATVQALQTASHLSQQADLR.S           |
| 0.999999 | 1 R.VLPSITTEILK[325.13]SVVAR.F                      |
| 0.999999 | 1 R.AK[325.13]QIVWNGPVGVFWEAFAR.G                   |
| 0.999999 | 1 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.999999 | 1 R.VLPSITTEILK[325.13]SVVAR.F                      |
| 0.999999 | 0.9907 R.YISPDQLADLYK[325.13]SFIK.D                 |
| 0.999999 | 1 R.DPYSGTISLFQAMQK[325.13]GLVLR.Q                  |
| 0.999999 | 1 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                   |
| 0.999999 | 1 R.DPYSGTISLFQAMQK[325.13]GLVLR.Q                  |
| 0.999999 | 1 R.MSHLK[325.13]VGSAADIPINISETDLSLLTATVVPPSGR.E    |
| 0.999999 | 1 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999999 | 0.9996 R.YISPDQLADLYK[325.13]SFIK.D                 |
| 0.999999 | 1 R.MSHLK[325.13]VGSAADIPINISETDLSLLTATVVPPSGR.E    |
| 0.999999 | 0.9996 R.GVLK[325.13]VFLENVIR.D                     |
| 0.999999 | 0.9989 R.YISPDQLADLYK[325.13]SFIK.D                 |
| 0.999999 | 1 R.LLVPTQFVGAIIGK[325.13]EGATIR.N                  |
| 0.999999 | 1 K.LLGK[325.13]VTIAQGGVLPNIQAVLLPK.K               |
| 0.999999 | 1 R.LK[325.13]LLLPWLEAR.I                           |
| 0.999999 | 1 K.NFLEK[325.13]FVQGLDIGPTK.T                      |
| 0.999999 | 1 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999999 | 1 K.LLGK[325.13]VTIAQGGVLPNIQAVLLPK.K               |
| 0.999999 | 1 R.LLVPTQFVGAIIGK[325.13]EGATIR.N                  |

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| 0.999999 | 1 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                  |
| 0.999999 | 1 K.LLGK[325.13]VTIAQGGVLPNIQAVLLPK.K              |
| 0.999999 | 1 K.LLGK[325.13]VTIAQGGVLPNIQAVLLPK.K              |
| 0.999999 | 1 R.GVLK[325.13]VFLENVIR.D                         |
| 0.999999 | 1 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                  |
| 0.999999 | 1 R.AEASQLGHK[325.13]VSQMAQYFEPLTLAAVGAASK.T       |
| 0.999999 | 1 R.AEASQLGHK[325.13]VSQMAQYFEPLTLAAVGAASK.T       |
| 0.999999 | 1 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                  |
| 0.999999 | 1 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                  |
| 0.999999 | 1 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                  |
| 0.999999 | 1 R.AEASQLGHK[325.13]VSQMAQYFEPLTLAAVGAASK.T       |
| 0.999999 | 1 R.SIQLDGLVWGASK[325.13]LVPVGYGIR.K               |
| 0.999999 | 1 K.SK[325.13]DDQVTVIGAGVTLHEALAAAELLK.K           |
| 0.999999 | 1 K.SK[325.13]DDQVTVIGAGVTLHEALAAAELLK.K           |
| 0.999999 | 1 K.NAPAIIFIDELDAIAPK[325.13]R.E                   |
| 0.999999 | 1 R.SIQLDGLVWGASK[325.13]LVPVGYGIR.K               |
| 0.999999 | 1 K.NAPAIIFIDELDAIAPK[325.13]R.E                   |
| 0.999999 | 1 R.SIQLDGLVWGASK[325.13]LVPVGYGIR.K               |
| 0.999999 | 1 R.IGEWELIQESGVPLK[325.13]PLFGPGYTGIR.N           |
| 0.999999 | 1 K.SK[325.13]DDQVTVIGAGVTLHEALAAAELLK.K           |
| 0.999999 | 1 R.IGEWELIQESGVPLK[325.13]PLFGPGYTGIR.N           |
| 0.999999 | 1 R.SIQLDGLVWGASK[325.13]LVPVGYGIR.K               |
| 0.999999 | 1 R.IGEWELIQESGVPLK[325.13]PLFGPGYTGIR.N           |
| 0.999999 | 1 R.TGNK[325.13]YINVYPTYDFAC[160.03]PIVDSIEGVTHALR |
| 0.999999 | 1 R.TGNK[325.13]YINVYPTYDFAC[160.03]PIVDSIEGVTHALR |
| 0.999999 | 1 R.TGNK[325.13]YINVYPTYDFAC[160.03]PIVDSIEGVTHALR |
| 0.999999 | 1 R.THTQDAVPLTLGQEFSGYVQQVK[325.13]YAMTR.I         |
| 0.999999 | 1 R.THTQDAVPLTLGQEFSGYVQQVK[325.13]YAMTR.I         |
| 0.999999 | 1 R.THTQDAVPLTLGQEFSGYVQQVK[325.13]YAMTR.I         |
| 0.999999 | 1 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R  |
| 0.999999 | 1 R.K[325.13]PLVIIAEDVDGEALSTLV.LNR.L              |
| 0.999999 | 1 K.FVADGIFK[325.13]AELNEFLTR.E                    |
| 0.999999 | 1 R.DLDELSRYPEDK[325.13]ITPENLPQILLQLK.R           |
| 0.999999 | 1 R.DLDELSRYPEDK[325.13]ITPENLPQILLQLK.R           |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.DLDELSRYPEDK[325.13]ITPENLPQILLQLK.R           |
| 0.999999 | 1 K.FVADGIFK[325.13]AELNEFLTR.E                    |
| 0.999999 | 1 R.DLDELSRYPEDK[325.13]ITPENLPQILLQLK.R           |
| 0.999999 | 1 R.VHTVEDYQAIVDAEWNILYDK[325.13]LEK.I             |
| 0.999999 | 0.9995 K.VK[325.13]DALEFWLQAGVDGFQVR.D             |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                  |
| 0.999999 | 1 K.VDLGGFAGLFDLK[325.13]AAGFKDPLLASGTDGVBGK.L     |
| 0.999999 | 0.9992 K.VK[325.13]DALEFWLQAGVDGFQVR.D             |
| 0.999999 | 1 K.GYTGK[325.13]TITDVINIGIGSDLGPLMVTEALPKPYSSGG   |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                  |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV    |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                  |

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|----------|----------------------------------------------------|
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 K.GYTGK[325.13]TITDVINIGIGGSDLGPLMVTEALKPYSSGG   |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.LPFK[325.13]ATTPVIM[147.04]VGPGTGVAPFIGFIQER.A |
| 0.999999 | 1 R.NVNVFK[325.13]FIIPQIVK.Y                       |
| 0.999999 | 1 R.GVMLAVDAVIAELK[325.13]K.Q                      |
| 0.999999 | 1 R.NVNVFK[325.13]FIIPQIVK.Y                       |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.GVMLAVDAVIAELK[325.13]K.Q                      |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.NVNVFK[325.13]FIIPQIVK.Y                       |
| 0.999999 | 1 R.GVMLAVDAVIAELK[325.13]K.Q                      |
| 0.999999 | 1 R.GVMLAVDAVIAELK[325.13]K.Q                      |
| 0.999999 | 1 R.NVNVFK[325.13]FIIPQIVK.Y                       |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.GVMLAVDAVIAELK[325.13]K.Q                      |
| 0.999999 | 1 R.NVNIFK[325.13]FIIPNVVK.Y                       |
| 0.999999 | 1 R.NVNIFK[325.13]FIIPNVVK.Y                       |
| 0.999999 | 1 R.TDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A             |
| 0.999999 | 1 R.TDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A             |
| 0.999999 | 1 R.GVMLAVDAVIAELK[325.13]K.Q                      |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.GVMLAVDAVIAELK[325.13]K.Q                      |
| 0.999999 | 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L         |
| 0.999999 | 1 R.TDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A             |
| 0.999999 | 1 R.TDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A             |
| 0.999999 | 1 R.NVNVFK[325.13]FIIPQIVK.Y                       |
| 0.999999 | 1 R.NVNVFK[325.13]FIIPQIVK.Y                       |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.NVNIFK[325.13]FIIPNVVK.Y                       |
| 0.999999 | 1 R.NVNIFK[325.13]FIIPNVVK.Y                       |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.DLTDYLM[147.04]K[325.13]ILTER.G                |
| 0.999999 | 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L         |
| 0.999999 | 1 R.GVVQELQQAISK[325.13]LEAR.L                     |
| 0.999999 | 1 R.GVVQELQQAISK[325.13]LEAR.L                     |
| 0.999999 | 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L         |
| 0.999999 | 1 R.DLTDYLM[147.04]K[325.13]ILTER.G                |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999999 | 1 R.GVVQELQQAISK[325.13]LEAR.L                     |
| 0.999999 | 1 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLR.L         |
| 0.999999 | 1 R.GVVQELQQAISK[325.13]LEAR.L                     |
| 0.999999 | 1 R.GVVQELQQAISK[325.13]LEAR.L                     |
| 0.999999 | 1 R.FAK[325.13]NFLPILFNLYGQPVAAGDTPAPR.R           |
| 0.999999 | 1 R.GVVQELQQAISK[325.13]LEAR.L                     |

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|----------|---------------------------------------------------|
| 0.999999 | 1 K.YMNSGPVVAMVWEGLNVVK[325.13]TGR.V              |
| 0.999999 | 1 K.FALGIFAINAEVESGDVGK[325.13]TLSALR.S           |
| 0.999999 | 1 K.EGLPVALDK[325.13]HILGFDTGDAVLNEAAQILR.L       |
| 0.999999 | 1 R.DLTDYLM[147.04]K[325.13]ILTER.G               |
| 0.999999 | 1 K.EGLPVALDK[325.13]HILGFDTGDAVLNEAAQILR.L       |
| 0.999999 | 1 K.EGLPVALDK[325.13]HILGFDTGDAVLNEAAQILR.L       |
| 0.999999 | 1 K.GLGILSLK[325.13]QQEMMAALTDAIQDK.K             |
| 0.999999 | 1 K.GFQQILAGEYDHLPEQAFYMGPIEEAVAK[325.13]ADK.L    |
| 0.999999 | 1 R.LIEEK[325.13]GAVDALAAALAHISGASSFEPR.S         |
| 0.999999 | 1 R.ALM[147.04]LQGVDLLADAVAVTMGPK[325.13]GR.T     |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L            |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L            |
| 0.999999 | 1 R.ALM[147.04]LQGVDLLADAVAVTMGPK[325.13]GR.T     |
| 0.999999 | 1 R.LPFK[325.13]ATTPVIMVGPGTGVAPFIGFIQER.A        |
| 0.999999 | 1 K.IQASTMAFK[325.13]QMEQISQFLQAAER.Y             |
| 0.999999 | 1 R.LPFK[325.13]ATTPVIMVGPGTGVAPFIGFIQER.A        |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L            |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 R.LPFK[325.13]ATTPVIMVGPGTGVAPFIGFIQER.A        |
| 0.999999 | 1 R.LPFK[325.13]ATTPVIMVGPGTGVAPFIGFIQER.A        |
| 0.999999 | 1 K.NMAEQIIQEISQIQSK[325.13]K.K                   |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 K.LIEEK[325.13]GAVEALAAALAHISGATSVDQR.S         |
| 0.999999 | 1 K.NMAEQIIQEISQIQSK[325.13]K.K                   |
| 0.999999 | 1 K.NMAEQIIQEISQIQSK[325.13]K.K                   |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 K.NMAEQIIQEISQIQSK[325.13]K.K                   |
| 0.999999 | 1 K.NMAEQIIQEISQIQSK[325.13]K.K                   |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 R.WLK[325.13]GQGVYLGMPGC[160.03]LPVYDALAGEFIR.  |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 R.WLK[325.13]GQGVYLGMPGC[160.03]LPVYDALAGEFIR.  |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 K.VIQGLYSGVTTVELDTLAAETAATLTTK[325.13]HPDYAILA/ |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 K.SAILGLPQPLLELNDSPVFK[325.13]TVLER.M           |
| 0.999999 | 1 R.ENVIMSQLPC[160.03]IK[325.13]ELVSDANQHVK.S     |
| 0.999999 | 1 K.SAILGLPQPLLELNDSPVFK[325.13]TVLER.M           |
| 0.999999 | 1 R.ELAQQIQK[325.13]VVM[147.04]ALGDYMGASC[160.03] |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 R.SIFDFSALK[325.13]ELLSGPNR.L                   |
| 0.999999 | 1 R.ELAQQIQK[325.13]VVM[147.04]ALGDYMGASC[160.03] |
| 0.999999 | 1 R.NLATTVTEEILEK[325.13]SFSEFGK.L                |
| 0.999999 | 1 K.VSASPLLYTLIEK[325.13]TMQNVK.H                 |

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| 0.999999 | 1 R.NLATTVTEEILEK[325.13]SFSEFGK.L                  |
| 0.999999 | 1 R.ELAQQIQK[325.13]VVMALGDYMGASC[160.03]HAC[16     |
| 0.999999 | 1 R.TGK[325.13]PLSVELGPGIMGAIFDGIQRPLSDISSQTQSIYI   |
| 0.999999 | 1 K.VK[325.13]EFGIDPQNMFEFWDWVGGR.Y                 |
| 0.999999 | 1 R.ELAQQIQK[325.13]VVMALGDYMGASC[160.03]HAC[16     |
| 0.999999 | 1 K.VK[325.13]EFGIDPQNMFEFWDWVGGR.Y                 |
| 0.999999 | 1 K.VK[325.13]EFGIDPQNMFEFWDWVGGR.Y                 |
| 0.999999 | 1 R.ELAQQIQK[325.13]VVMALGDYMGASC[160.03]HAC[16     |
| 0.999999 | 1 R.QLSQSLLPAIVELAEDAK[325.13]WR.V                  |
| 0.999999 | 1 R.ELAQQIQK[325.13]VVMALGDYMGASC[160.03]HAC[16     |
| 0.999999 | 1 R.QLLDFSQK[325.13]LDINLLDNVNC[160.03]LYHGEGAQ     |
| 0.999999 | 1 R.QLSQSLLPAIVELAEDAK[325.13]WR.V                  |
| 0.999999 | 1 R.LNYGIPAIVK[325.13]LLNQPNQWPLVK.A                |
| 0.999999 | 1 R.DIKEK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEK.S  |
| 0.999999 | 1 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T               |
| 0.999999 | 1 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T               |
| 0.999999 | 1 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T               |
| 0.999999 | 1 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T               |
| 0.999999 | 1 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T               |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T               |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF |
| 0.999999 | 1 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T               |
| 0.999999 | 1 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.SIFSAVLDELK[325.13]VAQAPWK.A                    |
| 0.999999 | 1 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.SIFSAVLDELK[325.13]VAQAPWK.A                    |
| 0.999999 | 1 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF |
| 0.999999 | 1 R.SIFSAVLDELK[325.13]VAQAPWK.A                    |
| 0.999999 | 1 R.SIFSAVLDELK[325.13]VAQAPWK.A                    |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.DVQNTFYDIVAELGAMEHAQAVDYIK[325.13]K.L           |
| 0.999999 | 1 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.NLANTVTEEILEK[325.13]AFSQFGK.L                  |
| 0.999999 | 1 K.LFGFK[325.13]EDPFVFIPEDDPLFPPIEK.F              |
| 0.999999 | 1 R.FDDPGLMLMGFK[325.13]PLVLLK.K                    |
| 0.999999 | 1 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                         |
| 0.999999 | 1 R.NLANTVTEEILEK[325.13]AFSQFGK.L                  |

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|----------|----------------------------------------------------|
| 0.999999 | 1 R.NLANTVTEEILEK[325.13]AFSQFGK.L                 |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                        |
| 0.999999 | 1 R.FDDPGLMLMGFK[325.13]PLVLLK.K                   |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                        |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                        |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                        |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                        |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                        |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                        |
| 0.999999 | 1 K.GDLENAFLNLVQC[160.03]IQNK[325.13]PLYFADR.L     |
| 0.999999 | 1 K.GDLENAFLNLVQC[160.03]IQNK[325.13]PLYFADR.L     |
| 0.999999 | 1 R.GPTEAVGYFLYNLIDMSDSEVQAK[325.13]EEHLR.Q        |
| 0.999999 | 1 R.FNIK[325.13]LWKFTDC[160.03]FNC[160.03]LPIAAIVD |
| 0.999999 | 1 R.GPTEAVGYFLYNLIDMSDSEVQAK[325.13]EEHLR.Q        |
| 0.999999 | 1 R.DLFEDELVPLFEK[325.13]AGPIWDLR.L                |
| 0.999999 | 1 R.DLFEDELVPLFEK[325.13]AGPIWDLR.L                |
| 0.999999 | 1 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S  |
| 0.999999 | 1 K.GMTLVTPQLLLFASK[325.13]K.V                     |
| 0.999999 | 1 K.GMTLVTPQLLLFASK[325.13]K.V                     |
| 0.999999 | 1 R.LQLNGNLQLELAQVLAQERPK[325.13]LPEDPLLSGLLDSP/   |
| 0.999999 | 1 R.YISPDQLADLYKSFVK[325.13]DYPVVSIEDPFDQDDWGAW    |
| 0.999999 | 1 K.INQDPQVM[147.04]LAPLISIALK[325.13]VSQQLER.T    |
| 0.999999 | 1 K.INQDPQVM[147.04]LAPLISIALK[325.13]VSQQLER.T    |
| 0.999999 | 1 K.ITELQLK[325.13]LESALTELEQLR.K                  |
| 0.999999 | 0.9999 R.LPLQDVYK[325.13]IGGIGTVPVGR.V             |
| 0.999999 | 1 K.LPGIPIK[325.13]IVMEAIQQASVAK.K                 |
| 0.999999 | 1 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAW    |
| 0.999999 | 1 K.IWC[160.03]FGPDGTGPNILTDITK[325.13]GVQYLNEIK.C |
| 0.999999 | 1 R.VLFPATGYLSIVWK[325.13]TLAR.A                   |
| 0.999999 | 1 R.VLFPATGYLSIVWK[325.13]TLAR.A                   |
| 0.999999 | 1 R.VLFPATGYLSIVWK[325.13]TLAR.A                   |
| 0.999999 | 1 R.LLIAGTNSSDLQQILSLLESNK[325.13]DLLLTSSYLSDSGSTC |
| 0.999999 | 1 K.IAPSFAVESIEDALK[325.13]AADTIGYPVMIR.S          |
| 0.999999 | 1 R.VLFPATGYLSIVWK[325.13]TLAR.A                   |
| 0.999999 | 1 K.IAPSFAVESIEDALK[325.13]AADTIGYPVMIR.S          |
| 0.999999 | 1 K.IAPSFAVESIEDALK[325.13]AADTIGYPVMIR.S          |
| 0.999999 | 1 R.LLIAGTNSSDLQQILSLLESNK[325.13]DLLLTSSYLSDSGSTC |
| 0.999999 | 1 R.LLIAGTNSSDLQQILSLLESNK[325.13]DLLLTSSYLSDSGSTC |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG   |
| 0.999999 | 1 K.IAPSFAVESIEDALK[325.13]AADTIGYPVMIR.S          |
| 0.999999 | 1 K.IAPSFAVESIEDALK[325.13]AADTIGYPVMIR.S          |
| 0.999999 | 1 R.MFGIPVVAVNAFK[325.13]TDESELDLISR.L             |
| 0.999999 | 1 R.LESGMQNMSIHTK[325.13]TTSGYAGGLSSAYGGLTSPGLS    |
| 0.999999 | 1 K.IAPSFAVESIEDALK[325.13]AADTIGYPVMIR.S          |
| 0.999999 | 1 R.LESGMQNMSIHTK[325.13]TTSGYAGGLSSAYGGLTSPGLS    |
| 0.999999 | 1 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG   |
| 0.999999 | 1 K.IAPSFAVESIEDALK[325.13]AADTIGYPVMIR.S          |

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|----------|---------------------------------------------------|
| 0.999999 | 1 K.ILPTLEAVAALGNK[325.13]VVESLR.A                |
| 0.999999 | 1 K.TLQALQIPAAK[325.13]LEGVLA EVAQHYQDTLIR.A      |
| 0.999999 | 1 K.ILPTLEAVAALGNK[325.13]VVESLR.A                |
| 0.999999 | 1 K.ILPTLEAVAALGNK[325.13]VVESLR.A                |
| 0.999999 | 1 K.ILPTLEAVAALGNK[325.13]VVESLR.A                |
| 0.999999 | 1 K.ILPTLEAVAALGNK[325.13]VVESLR.A                |
| 0.999999 | 1 K.LTPQMFQQLMK[325.13]QVTQLAIDTEER.L             |
| 0.999999 | 1 K.ILPTLEAVAALGNK[325.13]VVESLR.A                |
| 0.999999 | 1 K.ILPTLEAVAALGNK[325.13]VVESLR.A                |
| 0.999999 | 1 K.LTPQMFQQLMK[325.13]QVTQLAIDTEER.L             |
| 0.999999 | 1 K.LTPQMFQQLMK[325.13]QVTQLAIDTEER.L             |
| 0.999999 | 1 K.LTPQMFQQLMK[325.13]QVTQLAIDTEER.L             |
| 0.999999 | 1 K.LTPQMFQQLMK[325.13]QVTQLAIDTEER.L             |
| 0.999999 | 1 R.LSFFGLEK[325.13]LLTNLGLGER.K                  |
| 0.999999 | 1 R.LSFFGLEK[325.13]LLTNLGLGER.K                  |
| 0.999999 | 1 R.YK[325.13]EVYAAAAEVLGLILR.Y                   |
| 0.999999 | 1 R.LSFFGLEK[325.13]LLTNLGLGER.K                  |
| 0.999999 | 1 R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V             |
| 0.999999 | 1 R.DPIIAK[325.13]QLFSSLFSGILK.E                  |
| 0.999999 | 1 R.DPIIAK[325.13]QLFSSLFSGILK.E                  |
| 0.999999 | 1 K.K[325.13]LDTNSDGQLDFSEFLNLIGGLAMAC[160.03]HD  |
| 0.999999 | 1 R.ALLLPDYLVTVMLSGIK[325.13]C[160.03]PTFR.R      |
| 0.999999 | 1 R.ALLLPDYLVTVMLSGIK[325.13]C[160.03]PTFR.R      |
| 0.999999 | 1 R.VVSEDFLQDVSASTK[325.13]SLQELFLAHILSPWGAEVK.A  |
| 0.999999 | 1 K.NAIQLLASFLANNPFSC[160.03]K[325.13]LSDADLAGPLQ |
| 0.999999 | 1 K.NAIQLLASFLANNPFSC[160.03]K[325.13]LSDADLAGPLQ |
| 0.999999 | 1 K.NAIQLLASFLANNPFSC[160.03]K[325.13]LSDADLAGPLQ |
| 0.999999 | 1 R.YESGDHVAVYPANDSALVNQLGK[325.13]ILGADLDVVM     |
| 0.999999 | 1 K.INQDPQVMLAPLISIALK[325.13]VSQLQER.T           |
| 0.999999 | 1 K.INQDPQVMLAPLISIALK[325.13]VSQLQER.T           |
| 0.999999 | 1 K.INQDPQVMLAPLISIALK[325.13]VSQLQER.T           |
| 0.999999 | 1 K.INQDPQVMLAPLISIALK[325.13]VSQLQER.T           |
| 0.999999 | 1 K.INQDPQVMLAPLISIALK[325.13]VSQLQER.T           |
| 0.999999 | 1 K.INQDPQVMLAPLISIALK[325.13]VSQLQER.T           |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN   |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AG AHLQGGAK.R    |
| 0.999999 | 1 R.LESGMQNMSIHTK[325.13]TTSYGAGGLSSAYGGLTSPGL    |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN   |
| 0.999999 | 1 R.K[325.13]LFIGGLSFETTEESLR.N                   |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN   |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                 |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                       |
| 0.999999 | 1 K.KEK[325.13]EHASGSGAQSEAAGR.T                  |
| 0.999999 | 1 K.NAQK[325.13]SNQNGKDSKPSSTPR.S                 |
| 0.999999 | 1 K.NAQK[325.13]SNQNGKDSKPSSTPR.S                 |

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|----------|-----------------------------------------------------|
| 0.999999 | 1 K.TATAVAHC[160.03]K[325.13]R.G                    |
| 0.999999 | 1 K.GGHGAASPSEK[325.13]GAHPSGGADDVAK.K              |
| 0.999999 | 1 K.GGHGAASPSEK[325.13]GAHPSGGADDVAK.K              |
| 0.999999 | 1 K.GGHGAASPSEK[325.13]GAHPSGGADDVAK.K              |
| 0.999999 | 1 K.GGHGAASPSEK[325.13]GAHPSGGADDVAK.K              |
| 0.999999 | 1 R.KPSAPK[325.13]KGDSSAEELK.L                      |
| 0.999999 | 1 K.HAVSEGTK[325.13]AVTKYTSSK.-                     |
| 0.999999 | 1 K.HALK[325.13]GAGTNEK.V                           |
| 0.999999 | 1 K.AGAHLQGGAK[325.13]R.V                           |
| 0.999999 | 1 K.AGAHLQGGAK[325.13]R.V                           |
| 0.999999 | 1 K.K[325.13]HGVYNPNK.I                             |
| 0.999999 | 1 K.AGAHLQGGAK[325.13]R.V                           |
| 0.999999 | 1 K.K[325.13]HGVYNPNK.I                             |
| 0.999999 | 1 K.K[325.13]HGVYNPNK.I                             |
| 0.999999 | 1 R.VHK[325.13]INNVNK.A                             |
| 0.999999 | 1 R.VHK[325.13]INNVNK.A                             |
| 0.999999 | 1 K.K[325.13]HGVYNPNK.I                             |
| 0.999999 | 1 R.GHYK[325.13]GQQIGK.V                            |
| 0.999999 | 1 R.VHK[325.13]INNVNK.A                             |
| 0.999999 | 1 R.GHYK[325.13]GQQIGK.V                            |
| 0.999999 | 1 K.FHGTVK[325.13]AENGK.L                           |
| 0.999999 | 1 K.FHGTVK[325.13]AENGK.L                           |
| 0.999999 | 1 R.GHYK[325.13]GQQIGK.V                            |
| 0.999999 | 1 K.FHGTVK[325.13]AENGK.L                           |
| 0.999999 | 1 K.FHGTVK[325.13]AENGK.L                           |
| 0.999999 | 1 R.LPSGNHMK[325.13]ESR.E                           |
| 0.999999 | 1 R.YYVGHK[325.13]GK.F                              |
| 0.999999 | 1 R.VHGPGIQSGTTNK[325.13]PNK.F                      |
| 0.999999 | 1 R.VHGPGIQSGTTNK[325.13]PNK.F                      |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R      |
| 0.999999 | 1 R.LPSGNHMK[325.13]ESR.E                           |
| 0.999999 | 1 R.YYVGHK[325.13]GK.F                              |
| 0.999999 | 1 R.VHGPGIQSGTTNK[325.13]PNK.F                      |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R      |
| 0.999999 | 1 R.ALTQTGGPHVK[325.13]AR.V                         |
| 0.999999 | 1 K.NSSNKPAVTTK[325.13]SPAVKPAAAPK.Q                |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R      |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG'   |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R      |
| 0.999999 | 1 K.NSSNKPAVTTK[325.13]SPAVKPAAAPK.Q                |
| 0.999999 | 1 R.K[325.13]AHLTNQYM[147.04]QR.V                   |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R      |
| 0.999999 | 1 R.KPNEGADGQWK[325.13]K.G                          |
| 0.999999 | 1 R.KPNEGADGQWK[325.13]K.G                          |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R      |
| 0.999999 | 1 R.KPNEGADGQWK[325.13]K.G                          |
| 0.999999 | 1 R.EQC[160.03]C[160.03]YNC[160.03]GK[325.13]PGHLAR |



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|----------|-----------------------------------------------------|
| 0.999999 | 1 R.K[325.13]AHLTNQYM[147.04]QR.V                   |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R      |
| 0.999999 | 1 R.KPNEGADGQWK[325.13]K.G                          |
| 0.999999 | 1 R.EQC[160.03]C[160.03]YNC[160.03]GK[325.13]PGHLAR |
| 0.999999 | 1 R.KPNEGADGQWK[325.13]K.G                          |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG:   |
| 0.999999 | 1 R.ALTQTGGPHVK[325.13]AR.V                         |
| 0.999999 | 1 K.HVPGGGNVQIQNK[325.13]K.V                        |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHMGGNYGDDR.R              |
| 0.999999 | 1 R.ALTQTGGPHVK[325.13]AR.V                         |
| 0.999999 | 1 R.FHVEEEGK[325.13]GK.D                            |
| 0.999999 | 1 K.NQTAEKEEFEHQK[325.13]ELEK.V                     |
| 0.999999 | 1 K.NQTAEKEEFEHQK[325.13]ELEK.V                     |
| 0.999999 | 1 R.YMAQGK[325.13]HIGK.V                            |
| 0.999999 | 1 K.MHLAGK[325.13]TEQAK.A                           |
| 0.999999 | 1 R.KGAAPAPPGK[325.13]TGPAVAK.A                     |
| 0.999999 | 1 R.YMAQGK[325.13]HIGK.V                            |
| 0.999999 | 1 R.FHVEEEGK[325.13]GK.D                            |
| 0.999999 | 1 R.EQC[160.03]C[160.03]YNC[160.03]GK[325.13]PGHLAR |
| 0.999999 | 1 K.NQTAEKEEFEHQK[325.13]ELEK.V                     |
| 0.999999 | 1 K.NQTAEKEEFEHQK[325.13]ELEK.V                     |
| 0.999999 | 1 K.MHLAGK[325.13]TEQAK.A                           |
| 0.999999 | 1 R.EQC[160.03]C[160.03]YNC[160.03]GK[325.13]PGHLAR |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHMGGNYGDDR.R              |
| 0.999999 | 1 R.LPISASHSSK[325.13]TR.S                          |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHMGGNYGDDR.R              |
| 0.999999 | 1 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T         |
| 0.999999 | 1 K.APK[325.13]PDGPGGGPGGSHMGGNYGDDR.R              |
| 0.999999 | 1 R.RIVDGK[325.13]VVSETNDTK.V                       |
| 0.999999 | 1 R.YHQIGSGK[325.13]C[160.03]EIK.V                  |
| 0.999999 | 1 R.YHQIGSGK[325.13]C[160.03]EIK.V                  |
| 0.999999 | 1 R.KIIK[325.13]DGEQHEDLNEVAK.L                     |
| 0.999999 | 1 R.HAQGEK[325.13]TAGINVR.K                         |
| 0.999999 | 1 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T         |
| 0.999999 | 1 R.KIIK[325.13]DGEQHEDLNEVAK.L                     |
| 0.999999 | 1 R.HAQGEK[325.13]TAGINVR.K                         |
| 0.999999 | 1 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T         |
| 0.999999 | 1 K.LDSEDK[325.13]DKEGKPLLK.A                       |
| 0.999999 | 1 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T         |
| 0.999999 | 1 K.VLQHMK[325.13]AVQADQER.E                        |
| 0.999999 | 1 K.K[325.13]NC[160.03]PHVVVGTPGR.I                 |
| 0.999999 | 1 R.AQHEDQVEQYKK[325.13]ELEK.T                      |
| 0.999999 | 1 R.NIK[325.13]SHLGNVHDQDN.-                        |
| 0.999999 | 1 K.VLQHMK[325.13]AVQADQER.E                        |
| 0.999999 | 1 K.K[325.13]NC[160.03]PHVVVGTPGR.I                 |
| 0.999999 | 1 K.IHK[325.13]NSSTYWEGK.A                          |
| 0.999999 | 1 K.IHK[325.13]NSSTYWEGK.A                          |

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|----------|--------|--------------------------------------------|
| 0.999999 | 0.9999 | R.HQGVM[147.04]VGMGQKDSYVGDEAQS[325.13]R.G |
| 0.999999 | 1      | K.IHK[325.13]NSSTYWEGK.A                   |
| 0.999999 | 1      | R.HIAMEK[325.13]VASR.T                     |
| 0.999999 | 1      | K.EGVHGGGLINK[325.13]K.C                   |
| 0.999999 | 1      | K.IHK[325.13]NSSTYWEGK.A                   |
| 0.999999 | 1      | K.EGVHGGGLINK[325.13]K.C                   |
| 0.999999 | 1      | K.EGVHGGGLINK[325.13]K.C                   |
| 0.999999 | 1      | K.GPNK[325.13]HTLTQIK.D                    |
| 0.999999 | 1      | K.EGVHGGGLINK[325.13]K.C                   |
| 0.999999 | 1      | K.EHIK[325.13]NPDWR.Y                      |
| 0.999999 | 1      | K.LDSEDKDKEGK[325.13]PLLK.A                |
| 0.999999 | 1      | K.LDSEDKDKEGK[325.13]PLLK.A                |
| 0.999999 | 1      | K.LDSEDKDKEGK[325.13]PLLK.A                |
| 0.999999 | 1      | K.LDSEDKDKEGK[325.13]PLLK.A                |
| 0.999999 | 1      | R.SNLPAK[325.13]AIGHR.I                    |
| 0.999999 | 1      | K.YAK[325.13]YLPHSAGR.Y                    |
| 0.999999 | 1      | R.SNLPAK[325.13]AIGHR.I                    |
| 0.999999 | 1      | K.GRPC[160.03]K[325.13]IVEMSTSK.T          |
| 0.999999 | 1      | K.YAK[325.13]YLPHSAGR.Y                    |
| 0.999999 | 1      | K.VMSQNFTNC[160.03]HTK[325.13]IR.H         |
| 0.999999 | 1      | R.SNLPAK[325.13]AIGHR.I                    |
| 0.999999 | 1      | R.EHAMLAK[325.13]TAGVK.H                   |
| 0.999999 | 1      | R.GGNRFEPYANPTK[325.13]R.Y                 |
| 0.999999 | 1      | K.VMSQNFTNC[160.03]HTK[325.13]IR.H         |
| 0.999999 | 0.998  | R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQS.R  |
| 0.999999 | 1      | K.TVFAEHISDEC[160.03]K[325.13]R.R          |
| 0.999999 | 1      | R.K[325.13]GHAVGDIPGVR.F                   |
| 0.999999 | 1      | R.K[325.13]GHAVGDIPGVR.F                   |
| 0.999999 | 1      | K.K[325.13]NC[160.03]PHIVVGTPGR.I          |
| 0.999999 | 1      | R.K[325.13]LDYGQHVVGTPGR.V                 |
| 0.999999 | 1      | R.K[325.13]LDYGQHVVGTPGR.V                 |
| 0.999999 | 1      | K.RPAEDMEEQAFK[325.13]R.S                  |
| 0.999999 | 1      | R.VTIK[325.13]AGIHAR.L                     |
| 0.999999 | 0.9976 | R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEAQS.R  |
| 0.999999 | 1      | K.GRPC[160.03]K[325.13]IVEMSTSK.T          |
| 0.999999 | 1      | K.FNK[325.13]IVHSSMTR.A                    |
| 0.999999 | 1      | K.GFVLHK[325.13]SK.S                       |
| 0.999999 | 1      | K.GRPC[160.03]K[325.13]IVEMSTSK.T          |
| 0.999999 | 1      | R.VTIK[325.13]AGIHAR.L                     |
| 0.999999 | 1      | R.K[325.13]GHAVGDIPGVR.F                   |
| 0.999999 | 0.9991 | R.HQGVMVGMGQKDSYVGDEAQS[325.13]R.G         |
| 0.999999 | 1      | K.K[325.13]NC[160.03]PHIVVGTPGR.I          |
| 0.999999 | 1      | K.WC[160.03]AHTNVELK[325.13]K.A            |
| 0.999999 | 1      | R.K[325.13]LDYGQHVVGTPGR.V                 |
| 0.999999 | 1      | K.GFVLHK[325.13]SK.S                       |
| 0.999999 | 1      | R.K[325.13]GHAVGDIPGVR.F                   |
| 0.999999 | 1      | K.TFNLEK[325.13]QNHTPR.K                   |

0.999999 1 K.WC[160.03]AHTNVELK[325.13]K.A  
0.999999 1 K.TGVAVNKPAEFTVDAK[325.13]HGGK.A  
0.999999 1 K.TGVAVNKPAEFTVDAK[325.13]HGGK.A  
0.999999 0.9994 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 1 K.GRPC[160.03]K[325.13]IVEMSTSK.T  
0.999999 1 K.TVFAEHISDEC[160.03]K[325.13]R.R  
0.999999 1 K.TFNLEK[325.13]QNHTPR.K  
0.999999 1 K.TGVAVNKPAEFTVDAK[325.13]HGGK.A  
0.999999 1 K.YHNVGLSK[325.13]C[160.03]EIK.V  
0.999999 1 K.TGVAVNKPAEFTVDAK[325.13]HGGK.A  
0.999999 1 R.RK[325.13]QEELQQLQQR.R  
0.999999 1 R.RPDQQLQGEGK[325.13]IIDR.R  
0.999999 1 K.TVFAEHISDEC[160.03]K[325.13]R.R  
0.999999 1 K.FETLQAQAGK[325.13]HGDDL.R.N  
0.999999 1 R.RPDQQLQGEGK[325.13]IIDR.R  
0.999999 1 R.GK[325.13]PLPEYHVR.I  
0.999999 0.9895 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G  
0.999999 0.9999 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 0.9989 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R  
0.999999 0.9991 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G  
0.999999 1 R.LSWGK[325.13]GSSGGSGAKPSDAASEAARPATSTLNR.F  
0.999999 1 R.LRENELTYYC[160.03]C[160.03]K[325.13]K.D  
0.999999 0.9939 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G  
0.999999 1 R.LRENELTYYC[160.03]C[160.03]K[325.13]K.D  
0.999999 1 R.LSWGK[325.13]GSSGGSGAKPSDAASEAARPATSTLNR.F  
0.999999 0.969 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G  
0.999999 1 R.LRENELTYYC[160.03]C[160.03]K[325.13]K.D  
0.999999 1 R.K[325.13]SNENSEVITPGFPPNHDQGEQYEHNR.V  
0.999999 1 R.LRENELTYYC[160.03]C[160.03]K[325.13]K.D  
0.999999 1 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G  
0.999999 1 K.FETLQAQAGK[325.13]HGDDL.R.N  
0.999999 1 K.SHLAK[325.13]EGLYQYK.N  
0.999999 1 R.K[325.13]SNENSEVITPGFPPNHDQGEQYEHNR.V  
0.999999 1 R.IYDLNKPEAEPK[325.13]EISGHTSGIK.K  
0.999999 1 K.ELFSEK[325.13]HASLQNSQR.T  
0.999999 1 K.AFGQAK[325.13]HQPTAIIAK.T  
0.999999 1 K.ELFSEK[325.13]HASLQNSQR.T  
0.999999 0.9976 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G  
0.999999 1 K.SHLAK[325.13]EGLYQYK.N  
0.999999 1 R.HEAFEK[325.13]SAATWDER.F  
0.999999 1 R.K[325.13]SNENSEVITPGFPPNHDQGEQYEHNR.V  
0.999999 1 K.AFGQAK[325.13]HQPTAIIAK.T  
0.999999 0.9993 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G  
0.999999 1 K.RGEIIAK[325.13]QGGGGGGGSPGIER.M  
0.999999 1 K.RGEIIAK[325.13]QGGGGGGGSPGIER.M  
0.999999 1 K.AFGQAK[325.13]HQPTAIIAK.T  
0.999999 1 R.VTYK[325.13]NVPNWHR.D

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|----------|--------------------------------------------|
| 0.999999 | 1 K.ELFSEK[325.13]HASLQNSQR.T              |
| 0.999999 | 1 R.THQK[325.13]FVIATSTK.I                 |
| 0.999999 | 1 K.TGKPMINLYTDK[325.13]DTGKPK.G           |
| 0.999999 | 1 R.K[325.13]SNENSEVITPGFPPNHDQGEQYEHNR.V  |
| 0.999999 | 1 K.RGEIIAK[325.13]QGGGGGGGSVPGIER.M       |
| 0.999999 | 1 R.HYGGLTGLNK[325.13]AETA.AK.H            |
| 0.999999 | 1 R.LAAVVSAC[160.03]K[325.13]QLHR.A        |
| 0.999999 | 1 R.TANDAVELHIK[325.13]NVQPSDQGHYK.C       |
| 0.999999 | 1 K.RGEIIAK[325.13]QGGGGGGGSVPGIER.M       |
| 0.999999 | 1 R.VTYK[325.13]NVPNWHR.D                  |
| 0.999999 | 1 K.AFGQAK[325.13]HQPTAIIAK.T              |
| 0.999999 | 1 K.HFVALSTNTTK[325.13]VK.E                |
| 0.999999 | 1 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G      |
| 0.999999 | 1 K.AFGQAK[325.13]HQPTAIIAK.T              |
| 0.999999 | 1 R.HYGGLTGLNK[325.13]AETA.AK.H            |
| 0.999999 | 1 R.TANDAVELHIK[325.13]NVQPSDQGHYK.C       |
| 0.999999 | 0.9928 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G |
| 0.999999 | 1 R.K[325.13]SNENSEVITPGFPPNHDQGEQYEHNR.V  |
| 0.999999 | 1 R.LNVLEK[325.13]SSPGHR.A                 |
| 0.999999 | 1 R.TANDAVELHIK[325.13]NVQPSDQGHYK.C       |
| 0.999999 | 1 R.HYGGLTGLNK[325.13]AETA.AK.H            |
| 0.999999 | 1 K.AVDALLTHC[160.03]K[325.13]SR.K         |
| 0.999999 | 1 R.TYTWLK[325.13]GHQK.S                   |
| 0.999999 | 1 R.LAAVVSAC[160.03]K[325.13]QLHR.A        |
| 0.999999 | 1 R.HYGGLTGLNK[325.13]AETA.AK.H            |
| 0.999999 | 1 R.LNVLEK[325.13]SSPGHR.A                 |
| 0.999999 | 1 R.K[325.13]SNENSEVITPGFPPNHDQGEQYEHNR.V  |
| 0.999999 | 1 R.HYGGLTGLNK[325.13]AETA.AK.H            |
| 0.999999 | 1 K.K[325.13]PPKPQLMANYYNK.V               |
| 0.999999 | 1 R.ETAQAIK[325.13]GMHIR.K                 |
| 0.999999 | 1 R.K[325.13]FLEHLSGAGK.A                  |
| 0.999999 | 0.9934 R.HQGVMVGMGQKDSYVGDEAQSK[325.13]R.G |
| 0.999999 | 1 R.RQQEGFK[325.13]GTFPDAR.E               |
| 0.999999 | 1 K.GHQK[325.13]SNGEFDWPGR.V               |
| 0.999999 | 1 R.RQQEGFK[325.13]GTFPDAR.E               |
| 0.999999 | 1 R.TYTWLK[325.13]GHQK.S                   |
| 0.999999 | 1 R.RQQEGFK[325.13]GTFPDAR.E               |
| 0.999999 | 1 R.TANDAVELHIK[325.13]NVQPSDQGHYK.C       |
| 0.999999 | 1 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R       |
| 0.999999 | 1 R.HEAFEK[325.13]SAATWDER.F               |
| 0.999999 | 1 R.EAILAIHK[325.13]EAQR.I                 |
| 0.999999 | 1 K.K[325.13]PPKPQLMANYYNK.V               |
| 0.999999 | 1 R.TANDAVELHIK[325.13]NVQPSDQGHYK.C       |
| 0.999999 | 1 R.RQQEGFK[325.13]GTFPDAR.E               |
| 0.999999 | 1 R.K[325.13]FLEHLSGAGK.A                  |
| 0.999999 | 1 R.TANDAVELHIK[325.13]NVQPSDQGHYK.C       |
| 0.999999 | 1 R.YTASGVHK[325.13]GATYVFR.L              |

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| 0.999999 | 1 R.HQGMVMGMGQK[325.13]DSYVGDEAQS.K.R          |
| 0.999999 | 1 K.YGK[325.13]AGEVFIHK.D                      |
| 0.999999 | 1 K.VEYSEEELKTHISK[325.13]GTLGK.F              |
| 0.999999 | 1 K.HGEAQVK[325.13]IWR.R                       |
| 0.999999 | 1 K.HGEAQVK[325.13]IWR.R                       |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 R.VK[325.13]GGGHVAQIYAIR.Q                   |
| 0.999999 | 1 R.IGTLEK[325.13]EHNVFQNK.I                   |
| 0.999999 | 1 R.YPMAVGLNK[325.13]GHK.V                     |
| 0.999999 | 1 R.VK[325.13]GGGHVAQIYAIR.Q                   |
| 0.999999 | 1 K.HGEAQVK[325.13]IWR.R                       |
| 0.999999 | 1 R.VK[325.13]GGGHVAQIYAIR.Q                   |
| 0.999999 | 1 R.SGK[325.13]HIGVC[160.03]ISVANNR.L          |
| 0.999999 | 1 R.EAILAIHK[325.13]EAQR.I                     |
| 0.999999 | 1 R.VK[325.13]GGGHVAQIYAIR.Q                   |
| 0.999999 | 1 K.K[325.13]WENPGLGAESHTDSL.R.N               |
| 0.999999 | 1 K.YK[325.13]DAIHFNK.S                        |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 R.TIEKFEK[325.13]EAAEMGK.G                   |
| 0.999999 | 1 R.FLMK[325.13]SYDQVHSGK.L                    |
| 0.999999 | 1 K.KLEDGPK[325.13]FLK.S                       |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 K.KLEDGPK[325.13]FLK.S                       |
| 0.999999 | 1 K.IK[325.13]GEHPGLSIGDVAK.K                  |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAM[147.04]SHEIR.L |
| 0.999999 | 1 K.IK[325.13]GEHPGLSIGDVAK.K                  |
| 0.999999 | 1 K.IK[325.13]GEHPGLSIGDVAK.K                  |
| 0.999999 | 1 K.VFGNEIK[325.13]LEKPK.G                     |
| 0.999999 | 1 K.K[325.13]QLLHLAEK.Q                        |
| 0.999999 | 1 K.IK[325.13]GEHPGLSIGDVAK.K                  |
| 0.999999 | 1 R.THINYGVK[325.13]GDVAVVR.I                  |
| 0.999999 | 1 K.NK[325.13]HEAMITDLEER.L                    |
| 0.999999 | 1 R.K[325.13]SNFAEALAAHK.Y                     |
| 0.999999 | 1 K.LLK[325.13]NHDEESLEC[160.03]LC[160.03]R.L  |
| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y          |
| 0.999999 | 1 K.K[325.13]PRPPPALGPEETSASAGLPK.K            |
| 0.999999 | 1 K.IK[325.13]GEHPGLSIGDVAK.K                  |
| 0.999999 | 1 K.IK[325.13]GEHPGLSIGDVAK.K                  |
| 0.999999 | 1 R.TYEEGLKHEANNPQLK[325.13]EGLQNMEAR.L        |
| 0.999999 | 1 K.IK[325.13]GEHPGLSIGDVAK.K                  |
| 0.999999 | 1 R.TYEEGLKHEANNPQLK[325.13]EGLQNMEAR.L        |
| 0.999999 | 1 R.DGWPAMGIHGDK[325.13]SQQER.D                |

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| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y   |
| 0.999999 | 1 K.K[325.13]LSSWDQAETPGHTPSLR.W        |
| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y   |
| 0.999999 | 1 K.DVK[325.13]GSYVSIHSSGFR.D           |
| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y   |
| 0.999999 | 1 R.LSMQK[325.13]SMQNHAAVFR.V           |
| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y   |
| 0.999999 | 1 K.K[325.13]LSSWDQAETPGHTPSLR.W        |
| 0.999999 | 1 K.K[325.13]HPDASVNFSEFSK.K            |
| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y   |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQK.D              |
| 0.999999 | 1 R.TDDVHAK[325.13]DNTRPGANSPEMWSEAIK.I |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQK.D              |
| 0.999999 | 1 K.VYIYHSSSK[325.13]GLLR.Q             |
| 0.999999 | 1 K.LQNK[325.13]EHVIEALR.R              |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQK.D              |
| 0.999999 | 1 K.KEDLYLK[325.13]PIQR.T               |
| 0.999999 | 1 R.FPGYDSESK[325.13]EFNAEVHR.K         |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQK.D              |
| 0.999999 | 1 K.VYIYHSSSK[325.13]GLLR.Q             |
| 0.999999 | 1 R.FPGYDSESK[325.13]EFNAEVHR.K         |
| 0.999999 | 1 K.VYIYHSSSK[325.13]GLLR.Q             |
| 0.999999 | 1 R.RYQK[325.13]STELLIR.K               |
| 0.999999 | 1 R.FPGYDSESK[325.13]EFNAEVHR.K         |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQK.D              |
| 0.999999 | 1 K.VYIYHSSSK[325.13]GLLR.Q             |
| 0.999999 | 1 K.KEDLYLK[325.13]PIQR.T               |
| 0.999999 | 1 K.KEDLYLK[325.13]PIQR.T               |
| 0.999999 | 1 R.IDAMHGVVGPYVK[325.13]K.I            |
| 0.999999 | 1 R.EAPHVK[325.13]NNAISLR.K             |
| 0.999999 | 1 R.FPGYDSESK[325.13]EFNAEVHR.K         |
| 0.999999 | 1 R.IDAMHGVVGPYVK[325.13]K.I            |
| 0.999999 | 1 R.FPGYDSESK[325.13]EFNAEVHR.K         |
| 0.999999 | 1 K.TVDLKP DWGK[325.13]GYSR.K           |
| 0.999999 | 1 K.LQNK[325.13]EHVIEALR.R              |
| 0.999999 | 1 R.KLLEK[325.13]C[160.03]AMTALSSK.L    |
| 0.999999 | 1 K.IPK[325.13]HLTDAYFK.K               |
| 0.999999 | 1 K.DLPEHAVLK[325.13]MK.G               |
| 0.999999 | 1 K.QGFPMK[325.13]QGVLT HGR.V           |
| 0.999999 | 1 R.K[325.13]LDALC[160.03]NIHENIR.V     |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L        |
| 0.999999 | 1 R.EAPHVK[325.13]NNAISLR.K             |
| 0.999999 | 1 R.EAPHVK[325.13]NNAISLR.K             |
| 0.999999 | 1 R.KLLEK[325.13]C[160.03]AMTALSSK.L    |
| 0.999999 | 1 K.DLPEHAVLK[325.13]MK.G               |
| 0.999999 | 1 R.AHPVFYQGTYSQALNDAK[325.13]R.E       |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L        |

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| 0.999999 | 1 R.EAPHVK[325.13]NNAISLR.K                         |
| 0.999999 | 1 K.NPIAK[325.13]IHSDLAER.G                         |
| 0.999999 | 1 K.IPK[325.13]HLTDAYFK.K                           |
| 0.999999 | 1 K.DIK[325.13]GSYVSIHSSGFR.D                       |
| 0.999999 | 1 R.SRPFTVAASFQSTSVK[325.13]SPK.T                   |
| 0.999999 | 1 R.EAPHVK[325.13]NNAISLR.K                         |
| 0.999999 | 1 R.LDHK[325.13]FDLM[147.04]YAK.R                   |
| 0.999999 | 1 K.ANPFGGASHAK[325.13]GIVLEK.V                     |
| 0.999999 | 1 K.LLLQVQHASK[325.13]QIAADK.Q                      |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L                    |
| 0.999999 | 1 R.EHPFLVK[325.13]GGEDLR.Q                         |
| 0.999999 | 1 R.AHPVIFYQGTYSQALNDAK[325.13]R.E                  |
| 0.999999 | 1 R.K[325.13]LDALC[160.03]NIHENIR.V                 |
| 0.999999 | 1 R.SRPFTVAASFQSTSVK[325.13]SPK.T                   |
| 0.999999 | 1 R.EAPHVK[325.13]NNAISLR.K                         |
| 0.999999 | 1 R.EAPHVK[325.13]NNAISLR.K                         |
| 0.999999 | 1 R.LDHK[325.13]FDLM[147.04]YAK.R                   |
| 0.999999 | 1 R.SRPFTVAASFQSTSVK[325.13]SPK.T                   |
| 0.999999 | 1 K.GIVK[325.13]DIIHDPGR.G                          |
| 0.999999 | 1 R.GEELK[325.13]GHNTLPSPWR.D                       |
| 0.999999 | 1 R.LEHAAK[325.13]QAAASATQTIAAAQHAASPK.A            |
| 0.999999 | 1 R.GEELK[325.13]GHNTLPSPWR.D                       |
| 0.999999 | 1 K.K[325.13]LASQGDSISSQLGPIHPPPR.T                 |
| 0.999999 | 1 R.K[325.13]DKFSFDLGK.G                            |
| 0.999999 | 1 K.GIVK[325.13]DIIHDPGR.G                          |
| 0.999999 | 1 R.RK[325.13]TSDFNFLAQEGC[160.03]TK.G              |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L                    |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L                    |
| 0.999999 | 1 K.K[325.13]LASQGDSISSQLGPIHPPPR.T                 |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L                    |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L                    |
| 0.999999 | 1 K.K[325.13]LASQGDSISSQLGPIHPPPR.T                 |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L                    |
| 0.999999 | 1 K.IGHAPAPNFK[325.13]ATAVM[147.04]PDGQFK.D         |
| 0.999999 | 1 R.LDSQK[325.13]HIDFSLR.S                          |
| 0.999999 | 1 K.ANPFGGASHAK[325.13]GIVLEK.V                     |
| 0.999999 | 1 R.HSEAFEALQQK[325.13]SQGLDSR.L                    |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L              |
| 0.999999 | 1 K.C[160.03]VAC[160.03]DASK[325.13]PTHKPIAEAPSAFTL |
| 0.999999 | 1 K.K[325.13]VVYENAYGQFIGPHR.I                      |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L              |
| 0.999999 | 1 R.LDSQK[325.13]HIDFSLR.S                          |
| 0.999999 | 1 R.KSGVGNVFIK[325.13]NLDK.S                        |
| 0.999999 | 1 R.GLGK[325.13]GFVPSPTSQPGGHESLVDR.W               |
| 0.999999 | 1 K.LDSPAGTALSPSGHTK[325.13]LLPR.S                  |
| 0.999999 | 1 R.LTK[325.13]ITKPGSIDSNNQLFAPGGR.L                |
| 0.999999 | 1 R.LDSQK[325.13]HIDFSLR.S                          |

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| 0.999999 | 1 R.LDSQK[325.13]HIDFSLR.S                        |
| 0.999999 | 1 R.YTLHYK[325.13]TDAPLNIR.S                      |
| 0.999999 | 1 R.FSGWYDADLSPAGHEEAK[325.13]R.G                 |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L            |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L            |
| 0.999999 | 1 R.LDSQK[325.13]HIDFSLR.S                        |
| 0.999999 | 1 R.AHIAQLC[160.03]EK[325.13]AGLLQR.A             |
| 0.999999 | 1 R.AHIAQLC[160.03]EK[325.13]AGLLQR.A             |
| 0.999999 | 1 R.GLGK[325.13]GFVPSPTSQPGGHESLVDR.W             |
| 0.999999 | 1 R.AHIAQLC[160.03]EK[325.13]AGLLQR.A             |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L            |
| 0.999999 | 1 R.LDSQK[325.13]HIDFSLR.S                        |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L            |
| 0.999999 | 1 K.HLIPAANTGESK[325.13]VFYYK.M                   |
| 0.999999 | 1 R.GLGK[325.13]GFVPSPTSQPGGHESLVDR.W             |
| 0.999999 | 1 K.LDSPAGTALSPSGHTK[325.13]LLPR.S                |
| 0.999999 | 1 R.LKAEAELLQQQK[325.13]ELAQEQAR.R                |
| 0.999999 | 1 R.AHIAQLC[160.03]EK[325.13]AGLLQR.A             |
| 0.999999 | 1 R.LKAEAELLQQQK[325.13]ELAQEQAR.R                |
| 0.999999 | 1 R.AHIAQLC[160.03]EK[325.13]AGLLQR.A             |
| 0.999999 | 1 R.AHIAQLC[160.03]EK[325.13]AGLLQR.A             |
| 0.999999 | 1 K.HLIPAANTGESK[325.13]VFYYK.M                   |
| 0.999999 | 1 K.TPQHVK[325.13]ITDFGLAK.L                      |
| 0.999999 | 1 K.SGVK[325.13]IHVSDQELQSANASVDDSRLEELK.A        |
| 0.999999 | 1 R.LKAEAELLQQQK[325.13]ELAQEQAR.R                |
| 0.999999 | 1 R.TRPAANPIQFTLNK[325.13]EK.L                    |
| 0.999999 | 1 K.AFAETHIK[325.13]GFTLNDAAANSR.L                |
| 0.999999 | 1 R.ASVFVK[325.13]LQKPNAAIR.D                     |
| 0.999999 | 1 R.LK[325.13]GSGNLEAIHIK.K                       |
| 0.999999 | 1 K.YIDQEELNK[325.13]TKPIWTR.N                    |
| 0.999999 | 1 K.YIDQEELNK[325.13]TKPIWTR.N                    |
| 0.999999 | 1 K.GKLDVQFSGLTK[325.13]GDAVR.D                   |
| 0.999999 | 1 R.ASVFVK[325.13]LQKPNAAIR.D                     |
| 0.999999 | 1 K.YIDQEELNK[325.13]TKPIWTR.N                    |
| 0.999999 | 1 K.GKLDVQFSGLTK[325.13]GDAVR.D                   |
| 0.999999 | 1 K.YIDQEELNK[325.13]TKPIWTR.N                    |
| 0.999999 | 1 K.ERQEAEEAK[325.13]EALLQASR.D                   |
| 0.999999 | 1 K.YIDQEELNK[325.13]TKPIWTR.N                    |
| 0.999999 | 1 K.VILHLK[325.13]EDQTEYLEER.W                    |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E               |
| 0.999999 | 1 K.SAEAFGK[325.13]IVAERPGTNSTGPAPMAPPR.A         |
| 0.999999 | 1 R.AHQVVEDGYEFFAK[325.13]R.Q                     |
| 0.999999 | 1 K.AFAETHIK[325.13]GFTLNDAAANSR.L                |
| 0.999999 | 1 K.AFAETHIK[325.13]GFTLNDAAANSR.L                |
| 0.999999 | 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT |
| 0.999999 | 1 K.VILHLK[325.13]EDQTEYLEER.W                    |
| 0.999999 | 1 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E               |



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| 0.999999 | 1 R.LDHK[325.13]FDLMYAK.R                         |
| 0.999999 | 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDV7 |
| 0.999999 | 1 R.AHQVVEDGYEFAK[325.13]R.Q                      |
| 0.999999 | 1 K.AFAETHIK[325.13]GFTLNDAAANSR.L                |
| 0.999999 | 1 K.SAEAFGK[325.13]IVAERPGTNSTGPAPMAPPR.A         |
| 0.999999 | 1 K.TPSSDVLVFDYTK[325.13]HPAKPDPSGEC[160.03]NPDLF |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R           |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]SAAQAR.R           |
| 0.999999 | 1 K.TPSSDVLVFDYTK[325.13]HPAKPDPSGEC[160.03]NPDLF |
| 0.999999 | 1 K.IGHPAPNFK[325.13]ATAVMPDGQFK.D                |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]SAAQAR.R           |
| 0.999999 | 1 R.LDHK[325.13]FDLMYAK.R                         |
| 0.999999 | 1 K.HGK[325.13]APILIATDVASR.G                     |
| 0.999999 | 1 K.IGHPAPNFK[325.13]ATAVMPDGQFK.D                |
| 0.999999 | 1 K.TPSSDVLVFDYTK[325.13]HPAKPDPSGEC[160.03]NPDLF |
| 0.999999 | 1 K.TPSSDVLVFDYTK[325.13]HPAKPDPSGEC[160.03]NPDLF |
| 0.999999 | 1 K.IGHPAPNFK[325.13]ATAVMPDGQFK.D                |
| 0.999999 | 1 K.AAAFEK[325.13]QVLQLQASHR.E                    |
| 0.999999 | 1 R.K[325.13]FLSDPQVHTVLVER.S                     |
| 0.999999 | 1 K.IGHPAPNFK[325.13]ATAVMPDGQFK.D                |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L            |
| 0.999999 | 1 K.AAAFEK[325.13]QVLQLQASHR.E                    |
| 0.999999 | 1 R.LVQAFQYTDEHGEVC[160.03]PAGWK[325.13]PGSDTIKI  |
| 0.999999 | 0.8176 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L          |
| 0.999999 | 1 R.KYGK[325.13]SLYYYIQQDTK.G                     |
| 0.999999 | 1 K.HGK[325.13]APILIATDVASR.G                     |
| 0.999999 | 1 K.LHIEVGTPPTGNQPFPK[325.13]K.A                  |
| 0.999999 | 1 R.K[325.13]YGKSLYYYIQQDTK.G                     |
| 0.999999 | 1 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L            |
| 0.999999 | 1 R.KYGK[325.13]SLYYYIQQDTK.G                     |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V                       |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R           |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V                       |
| 0.999999 | 1 R.KSGVGNIFIK[325.13]NLDK.S                      |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R           |
| 0.999999 | 1 R.KYGK[325.13]SLYYYIQQDTK.G                     |
| 0.999999 | 0.9995 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L          |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R           |
| 0.999999 | 1 K.AAAFEK[325.13]QVLQLQASHR.E                    |
| 0.999999 | 1 R.VVIIGAGKPAAVVLQTK[325.13]GSPESR.L             |
| 0.999999 | 1 K.LHIEVGTPPTGNQPFPK[325.13]K.A                  |
| 0.999999 | 1 K.AAAFEK[325.13]QVLQLQASHR.E                    |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L               |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]SAAQAR.R           |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R           |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R           |
| 0.999999 | 1 R.KYGK[325.13]SLYYYIQQDTK.G                     |

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| 0.999999 | 1 R.K[325.13]YGKSLYYYIQQDTK.G            |
| 0.999999 | 1 R.KYGK[325.13]SLYYYIQQDTK.G            |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R  |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R  |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]SAAQAR.R  |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]SAAQAR.R  |
| 0.999999 | 1 R.KYGK[325.13]SLYYYIQQDTK.G            |
| 0.999999 | 1 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R  |
| 0.999999 | 1 K.LK[325.13]DYAFVHFEDR.G               |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]TAAQAR.R  |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]SAAQAR.R  |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]TAAQAR.R  |
| 0.999999 | 1 R.K[325.13]LDPELHLDIK.V                |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 K.MSGK[325.13]HDVGAYMLMYK.G            |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V              |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]TAAQAR.R  |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]TAAQAR.R  |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 K.LK[325.13]DYAFVHFEDR.G               |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L      |
| 0.999999 | 1 R.GFC[160.03]FLEYEDHK[325.13]TAAQAR.R  |
| 0.999999 | 1 R.ALEHFTDLYDIK[325.13]R.A              |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V              |
| 0.999999 | 0.9996 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E |
| 0.999999 | 1 K.HPVTGQFLYQDSNWASK[325.13]VEK.L       |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V              |
| 0.999999 | 1 K.HPVTGQFLYQDSNWASK[325.13]VEK.L       |
| 0.999999 | 1 R.IGAEVYHNLK[325.13]NVIK.E             |
| 0.999999 | 1 R.REPSLSPK[325.13]LTC[160.03]LQNLK.W   |
| 0.999999 | 0.9998 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E |
| 0.999999 | 0.9991 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L |
| 0.999999 | 1 K.TEWLDGK[325.13]HVVFGK.V              |

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| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L               |
| 0.999999 | 0.9996 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E          |
| 0.999999 | 1 K.HPVTGQFLYQDSNWASK[325.13]VEK.L                |
| 0.999999 | 1 K.LLQK[325.13]GIHPTIISESFQK.A                   |
| 0.999999 | 1 K.HPVTGQFLYQDSNWASK[325.13]VEK.L                |
| 0.999999 | 1 K.FADEHVPGPSFTVK[325.13]ISGEGR.V                |
| 0.999999 | 1 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q               |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L               |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L               |
| 0.999999 | 1 R.MLQTLK[325.13]ELEAHSAEAR.A                    |
| 0.999999 | 1 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q               |
| 0.999999 | 1 K.LLQK[325.13]GIHPTIISESFQK.A                   |
| 0.999999 | 1 K.LLQK[325.13]GIHPTIISESFQK.A                   |
| 0.999999 | 1 K.AHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D   |
| 0.999999 | 1 K.TAWLDGK[325.13]HVVFGK.V                       |
| 0.999999 | 0.9953 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L          |
| 0.999999 | 1 K.FADEHVPGPSFTVK[325.13]ISGEGR.V                |
| 0.999999 | 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT |
| 0.999999 | 1 R.EHTALLK[325.13]IEGVYAR.D                      |
| 0.999999 | 1 K.LLQK[325.13]GIHPTIISESFQK.A                   |
| 0.999999 | 0.9988 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L          |
| 0.999999 | 1 K.TGGAYGEDLGADYNLSQVC[160.03]DGK[325.13]VSVHV   |
| 0.999999 | 0.9996 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L          |
| 0.999999 | 1 R.QLFHPEQLITGK[325.13]EDAANNYAR.G               |
| 0.999999 | 1 R.NK[325.13]IAGYVTHLMK.R                        |
| 0.999999 | 1 R.QLFHPEQLITGK[325.13]EDAANNYAR.G               |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H              |
| 0.999999 | 1 R.MLQTLK[325.13]ELEAHSAEAR.A                    |
| 0.999999 | 1 R.EHTALLK[325.13]IEGVYAR.D                      |
| 0.999999 | 1 R.ALEHFTDLYDIK[325.13]R.A                       |
| 0.999999 | 1 R.REPSLSPK[325.13]LTC[160.03]LQNLK.W            |
| 0.999999 | 1 K.VGLQVVAVK[325.13]APGFGDNRK.N                  |
| 0.999999 | 0.8714 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L          |
| 0.999999 | 1 K.TGGAYGEDLGADYNLSQVC[160.03]DGK[325.13]VSVHV   |
| 0.999999 | 1 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q               |
| 0.999999 | 1 R.REPSLSPK[325.13]LTC[160.03]LQNLK.W            |
| 0.999999 | 1 R.ALEHFTDLYDIK[325.13]R.A                       |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H              |
| 0.999999 | 1 R.ALEHFTDLYDIK[325.13]R.A                       |
| 0.999999 | 1 R.EHTALLK[325.13]IEGVYAR.D                      |
| 0.999999 | 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT |
| 0.999999 | 1 R.REPSLSPK[325.13]LTC[160.03]LQNLK.W            |
| 0.999999 | 1 R.EIGTHK[325.13]PLPGITVGDIGPK.F                 |
| 0.999999 | 1 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q               |
| 0.999999 | 0.787 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L           |
| 0.999999 | 1 R.REPSLSPK[325.13]LTC[160.03]LQNLK.W            |
| 0.999999 | 1 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q               |

0.999999 1 K.NVPNLHVMK[325.13]AMQSLK.S  
 0.999999 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT  
 0.999999 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT  
 0.999999 1 R.AHSIQIMK[325.13]VEEIAASK.C  
 0.999999 0.9499 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
 0.999999 1 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q  
 0.999999 1 R.IAEDDGKPRPAFSNALEPDFK[325.13]ATSITVTGSGSC[160.03]NFNDVT  
 0.999999 1 R.EIGTHK[325.13]PLPGITVGDIGPK.F  
 0.999999 1 R.IAEDDGKPRPAFSNALEPDFK[325.13]ATSITVTGSGSC[160.03]NFNDVT  
 0.999999 1 R.QLFHPEQLITGK[325.13]EDAANNYAR.G  
 0.999999 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT  
 0.999999 1 R.QLFHPEQLITGK[325.13]EDAANNYAR.G  
 0.999999 1 R.QLYHLGVVEAYSGLTK[325.13]K.K  
 0.999999 1 R.ALDTMNFDVIK[325.13]GKPVR.I  
 0.999999 1 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V  
 0.999999 1 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L  
 0.999999 1 R.ALDTMNFDVIK[325.13]GKPVR.I  
 0.999999 0.6823 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
 0.999999 1 K.K[325.13]VNAVFEWHITK.G  
 0.999999 1 R.QLFHPEQLITGK[325.13]EDAANNYAR.G  
 0.999999 1 K.NVPNLHVMK[325.13]AMQSLK.S  
 0.999999 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT  
 0.999999 1 R.QLFHPEQLITGK[325.13]EDAANNYAR.G  
 0.999999 1 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V  
 0.999999 1 R.ALDTMNFDVIK[325.13]GKPVR.I  
 0.999999 1 R.QLYHLGVVEAYSGLTK[325.13]K.K  
 0.999999 1 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L  
 0.999999 1 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L  
 0.999999 0.9867 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
 0.999999 1 R.ALDTMNFDVIK[325.13]GKPVR.I  
 0.999999 1 R.ALDTMNFDVIK[325.13]GKPVR.I  
 0.999999 1 R.GQAGGK[325.13]LHIEVGTPPTGNQPPFK.K  
 0.999999 1 R.IGKPAPDFK[325.13]ATAVVDGAFK.E  
 0.999999 1 K.IVHAFDMEDLGDK[325.13]AVYC[160.03]R.C  
 0.999999 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
 0.999999 1 R.NEMQK[325.13]LQAEAPHIIVGTPGR.V  
 0.999999 1 R.IGKPAPDFK[325.13]ATAVVDGAFK.E  
 0.999999 1 K.IAILTC[160.03]PFEPPKPK[325.13]TK.H  
 0.999999 1 K.ISMPDVLHLK[325.13]GPK.V  
 0.999999 1 K.AGLQVYNK[325.13]C[160.03]WKFEHC[160.03]NFNDVT  
 0.999999 1 R.IGKPAPDFK[325.13]ATAVVDGAFK.E  
 0.999999 1 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L  
 0.999999 1 R.FVGHTK[325.13]DVLSVAFSSDN.R  
 0.999999 1 R.IGKPAPDFK[325.13]ATAVVDGAFK.E  
 0.999999 1 K.IAILTC[160.03]PFEPPKPK[325.13]TK.H  
 0.999999 1 K.AHGPGLEGGLVGK[325.13]PAEFTIDTK.G  
 0.999999 1 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V

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| 0.999999 | 1 K.SSFTVDC[160.03]SK[325.13]AGNNMLLVGVHGPR.T       |
| 0.999999 | 1 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L              |
| 0.999999 | 1 K.ISMPDVDLHLK[325.13]GPK.V                        |
| 0.999999 | 1 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT   |
| 0.999999 | 1 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L              |
| 0.999999 | 1 R.TVVTGIEMFHK[325.13]SLER.A                       |
| 0.999999 | 1 R.FVGHTK[325.13]DVLSVAFSSDNR.Q                    |
| 0.999999 | 1 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V                  |
| 0.999999 | 1 R.VITEEEKNFK[325.13]AFASLR.M                      |
| 0.999999 | 1 K.HSQAVEELAEQLEQTK[325.13]R.V                     |
| 0.999999 | 1 K.VAGHSLGYGFVNYVTAK[325.13]DAER.A                 |
| 0.999999 | 1 K.VAGHSLGYGFVNYVTAK[325.13]DAER.A                 |
| 0.999999 | 1 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L              |
| 0.999999 | 1 K.HSQAVEELAEQLEQTK[325.13]R.V                     |
| 0.999999 | 1 K.HK[325.13]ELAPYDENWFYTR.A                       |
| 0.999999 | 1 K.IVHAFDMEDLGDK[325.13]AVYC[160.03]R.C            |
| 0.999999 | 1 K.IVHAFDMEDLGDK[325.13]AVYC[160.03]R.C            |
| 0.999999 | 1 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L              |
| 0.999999 | 1 K.VAGHSLGYGFVNYVTAK[325.13]DAER.A                 |
| 0.999999 | 1 K.KQGGLGPMNIPLVSDPK[325.13]R.T                    |
| 0.999999 | 1 R.MC[160.03]TLIDK[325.13]FDEHDGPVR.G              |
| 0.999999 | 1 K.HK[325.13]ELAPYDENWFYTR.A                       |
| 0.999999 | 1 K.IVHAFDMEDLGDK[325.13]AVYC[160.03]R.C            |
| 0.999999 | 1 K.IVHAFDMEDLGDK[325.13]AVYC[160.03]R.C            |
| 0.999999 | 1 K.M[147.04]KETAENYLGHTAK[325.13]NAVITVPAYFNDSQ    |
| 0.999999 | 1 R.LMVHTVATFNSIK[325.13]ELNER.W                    |
| 0.999999 | 1 R.K[325.13]LTATPTPLGGMTGFHMQTEDR.T                |
| 0.999999 | 1 K.IVHAFDMEDLGDK[325.13]AVYC[160.03]R.C            |
| 0.999999 | 1 K.M[147.04]KETAENYLGHTAK[325.13]NAVITVPAYFNDSQ    |
| 0.999999 | 1 K.IQQLVK[325.13]EFFNGKEPSR.G                      |
| 0.999999 | 1 R.TVVTGIEMFHK[325.13]SLER.A                       |
| 0.999999 | 1 R.K[325.13]LTATPTPLGGMTGFHMQTEDR.T                |
| 0.999999 | 1 R.TVVTGIEMFHK[325.13]SLER.A                       |
| 0.999999 | 1 K.IVGC[160.03]SVHK[325.13]GFAFVQYVNER.N           |
| 0.999999 | 1 K.IVGC[160.03]SVHK[325.13]GFAFVQYVNER.N           |
| 0.999999 | 1 R.K[325.13]LTATPTPLGGMTGFHMQTEDR.T                |
| 0.999999 | 0.9993 R.LLLPGELAK[325.13]HAVSEGTK.A                |
| 0.999999 | 1 R.TVVTGIEMFHK[325.13]SLER.A                       |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 K.LDK[325.13]AQIHDLVLVGGSTR.I                     |
| 0.999999 | 1 R.TVVTGIEMFHK[325.13]SLER.A                       |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 K.IVGC[160.03]SVHK[325.13]GFAFVQYVNER.N           |
| 0.999999 | 1 K.IVGC[160.03]SVHK[325.13]GFAFVQYVNER.N           |
| 0.999999 | 1 R.C[160.03]QK[325.13]IC[160.03]DQWDALGSLTHSR.R    |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 K.FVIHC[160.03]NSPVWGADK[325.13]C[160.03]EELLEK.T |

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| 0.999999 | 1 R.DYQGPLK[325.13]EHEVTIFVR.R                      |
| 0.999999 | 1 K.FVIHC[160.03]NSPVWGADK[325.13]C[160.03]EELLEK.T |
| 0.999999 | 1 R.SPTLYGISHDDLK[325.13]GDPLLDQR.R                 |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A              |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 R.TVVTGIEMFHK[325.13]SLER.A                       |
| 0.999999 | 1 R.TVVTGIEMFHK[325.13]SLER.A                       |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 K.VESPAK[325.13]IHVFYIDYGNR.E                     |
| 0.999999 | 1 K.IVGC[160.03]SVHK[325.13]GFAFVQYVNER.N           |
| 0.999999 | 1 K.MKETAENYLGHTAK[325.13]NAVITVPAYFNDSQR.Q         |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 K.MKETAENYLGHTAK[325.13]NAVITVPAYFNDSQR.Q         |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A              |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A              |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGM[147.04]IYDSL DYAK.K       |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 K.MKETAENYLGHTAK[325.13]NAVITVPAYFNDSQR.Q         |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 K.MKETAENYLGHTAK[325.13]NAVITVPAYFNDSQR.Q         |
| 0.999999 | 1 R.LM[147.04]AEGAPKWPK[325.13]ETVKPVEVEEGESVVL F   |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 R.EHFEK[325.13]WGTLTDC[160.03]VVMR.D              |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 R.EHFEK[325.13]WGTLTDC[160.03]VVMR.D              |
| 0.999999 | 1 R.LM[147.04]AEGAPK[325.13]WPKETVKPVEVEEGESVVL F   |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 R.EHFEK[325.13]WGTLTDC[160.03]VVMR.D              |
| 0.999999 | 1 R.LGYFSVDPDSHQGK[325.13]LVFN R.T                  |
| 0.999999 | 1 R.EHFEK[325.13]WGTLTDC[160.03]VVMR.D              |
| 0.999999 | 1 R.VAAAVD LIK[325.13]SHQGLDR.Q                     |
| 0.999999 | 1 R.LGYFSVDPDSHQGK[325.13]LVFN R.T                  |
| 0.999999 | 1 R.SPTLYGISHDDLK[325.13]GDPLLDQR.R                 |
| 0.999999 | 1 R.VAAAVD LIK[325.13]SHQGLDR.Q                     |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 R.SPPNVQFTFQQPK[325.13]PLSVEPQQGPQAGGTTLTIHG      |
| 0.999999 | 1 R.LGYFSVDPDSHQGK[325.13]LVFN R.T                  |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A              |
| 0.999999 | 1 R.VAAAVD LIK[325.13]SHQGLDR.Q                     |
| 0.999999 | 1 R.LGYFSVDPDSHQGK[325.13]LVFN R.T                  |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999999 | 1 R.GHFEAFGTLTDC[160.03]VVVVNPQTK[325.13]R.S        |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A              |
| 0.999999 | 1 R.VAAAVD LIK[325.13]SHQGLDR.Q                     |
| 0.999999 | 0.9999 R.LLLPGELAK[325.13]HAVSEGTK.A                |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTKAVTK.Y                 |

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| 0.999999 | 1 K.C[160.03]NEIINWLDK[325.13]NQTAKEEEFEHQK.E   |
| 0.999999 | 1 K.LTLHGLQQYYVK[325.13]LK.D                    |
| 0.999999 | 1 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y          |
| 0.999999 | 1 R.SPPNVQFTFQQPK[325.13]PLSVEPQQGPQAGGTTLTIHG  |
| 0.999999 | 1 R.K[325.13]FLVYVANFDEKDPR.T                   |
| 0.999999 | 1 R.HISSK[325.13]VEELSQALSQK.E                  |
| 0.999999 | 1 R.LAHEVGWK[325.13]YQAVTATLEEK.R               |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A          |
| 0.999999 | 1 R.VAAAVDLIIK[325.13]SHQGLDR.Q                 |
| 0.999999 | 1 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y          |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                 |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A          |
| 0.999999 | 1 R.VAAAVDLIIK[325.13]SHQGLDR.Q                 |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDPVLDR.I                   |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                 |
| 0.999999 | 1 K.C[160.03]NEIINWLDK[325.13]NQTAKEEEFEHQK.E   |
| 0.999999 | 1 K.LTLHGLQQYYVK[325.13]LK.D                    |
| 0.999999 | 1 R.K[325.13]FLVYVANFDEKDPR.T                   |
| 0.999999 | 1 R.LAHEVGWK[325.13]YQAVTATLEEK.R               |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGM[147.04]IYDSL DYAK.K   |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A          |
| 0.999999 | 1 R.LAHEVGWK[325.13]YQAVTATLEEK.R               |
| 0.999999 | 1 R.VHPVSTMIK[325.13]GLYGIK.D                   |
| 0.999999 | 1 R.VAAAVDLIIK[325.13]SHQGLDR.Q                 |
| 0.999999 | 1 K.TSNHAIVLAQLTK[325.13]GK.C                   |
| 0.999999 | 1 K.FAANPNQNK[325.13]NVALLS QLYHSPAR.R          |
| 0.999999 | 1 K.FAANPNQNK[325.13]NVALLS QLYHSPAR.R          |
| 0.999999 | 1 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C    |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGM[147.04]IYDSL DYAK.K   |
| 0.999999 | 1 R.VAAAVDLIIK[325.13]SHQGLDR.Q                 |
| 0.999999 | 1 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C    |
| 0.999999 | 1 R.EASIDILHSIVK[325.13]R.D                     |
| 0.999999 | 1 R.RLQEDK[325.13]EQMAQQ LAEETQGFQR.T           |
| 0.999999 | 1 R.GHFEAFGTLTDC[160.03]VVVVNPQTK[325.13]R.S    |
| 0.999999 | 1 R.DVDIIDHHDNTYTVK[325.13]YTPVQQGPVGVNV TYGGDI |
| 0.999999 | 1 R.RLQEDK[325.13]EQMAQQ LAEETQGFQR.T           |
| 0.999999 | 1 K.FAANPNQNK[325.13]NVALLS QLYHSPAR.R          |
| 0.999999 | 1 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C    |
| 0.999999 | 1 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C    |
| 0.999999 | 1 K.FAANPNQNK[325.13]NVALLS QLYHSPAR.R          |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGM[147.04]IYDSL DYAK.K   |
| 0.999999 | 1 R.GHFEAFGTLTDC[160.03]VVVVNPQTK[325.13]R.S    |
| 0.999999 | 1 R.VAAAVDLIIK[325.13]SHQGLDR.Q                 |
| 0.999999 | 1 R.DKLNNLV LFDK[325.13]ATYDK.L                 |
| 0.999999 | 1 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C    |
| 0.999999 | 1 R.EASIDILHSIVK[325.13]R.D                     |
| 0.999999 | 1 R.GHFEAFGTLTDC[160.03]VVVVNPQTK[325.13]R.S    |

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| 0.999999 | 1 R.LMAEGAPKWPK[325.13]ETVKPVEVEEGESVVLPC[160.0 |
| 0.999999 | 1 R.DVDIIDHHDNTYTVK[325.13]YTPVQQGPVGVNVYGGDI   |
| 0.999999 | 1 K.TRDENIK[325.13]VGSPFELVVSGNK.R              |
| 0.999999 | 1 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C    |
| 0.999999 | 1 R.LMAEGAPKWPK[325.13]ETVKPVEVEEGESVVLPC[160.0 |
| 0.999999 | 1 K.ILGSGISSSSVLHGMVFK[325.13]K.E               |
| 0.999999 | 1 K.TRDENIK[325.13]VGSPFELVVSGNK.R              |
| 0.999999 | 1 R.KVESLQEEIAFLK[325.13]K.L                    |
| 0.999999 | 1 K.ILGSGISSSSVLHGMVFK[325.13]K.E               |
| 0.999999 | 1 R.VAAAVDLIIK[325.13]SHQGLDR.Q                 |
| 0.999999 | 1 R.FAIGSQVSEHSIIK[325.13]DFTK.Q                |
| 0.999999 | 1 R.GHFEGFTLTDC[160.03]VVVVNPQTK[325.13]R.S     |
| 0.999999 | 1 R.KVESLQEEIAFLK[325.13]K.L                    |
| 0.999999 | 1 R.DIQQHK[325.13]EEAWVIGSVVAR.A                |
| 0.999999 | 1 R.SEFYK[325.13]HIVLSGGSTMYPGLPSR.L            |
| 0.999999 | 1 R.HGK[325.13]QVLDGNSNPYDIFLK.D                |
| 0.999999 | 1 R.SEFYK[325.13]HIVLSGGSTMYPGLPSR.L            |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                |
| 0.999999 | 1 R.HGK[325.13]QVLDGNSNPYDIFLK.D                |
| 0.999999 | 1 R.VRGEVAPDAK[325.13]SFVLNLGK.D                |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                |
| 0.999999 | 1 R.FAIGSQVSEHSIIK[325.13]DFTK.Q                |
| 0.999999 | 1 R.VSEK[325.13]VSHVLAALQAGNR.G                 |
| 0.999999 | 1 R.DIQQHK[325.13]EEAWVIGSVVAR.A                |
| 0.999999 | 1 R.VSEK[325.13]VSHVLAALQAGNR.G                 |
| 0.999999 | 1 R.IHQIEYAMEAVK[325.13]QGSATVGLK.S             |
| 0.999999 | 1 R.DIQQHK[325.13]EEAWVIGSVVAR.A                |
| 0.999999 | 1 R.HGK[325.13]QVLDGNSNPYDIFLK.D                |
| 0.999999 | 1 R.IHQIEYAMEAVK[325.13]QGSATVGLK.S             |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                |
| 0.999999 | 1 R.HGK[325.13]QVLDGNSNPYDIFLK.D                |
| 0.999999 | 1 R.DTLFC[160.03]YHK[325.13]ASEVFLQR.L          |
| 0.999999 | 1 R.FAIGSQVSEHSIIK[325.13]DFTK.Q                |
| 0.999999 | 1 R.VSEK[325.13]VSHVLAALQAGNR.G                 |
| 0.999999 | 1 K.LTLSALLDGK[325.13]NVNAGGHK.L                |
| 0.999999 | 1 R.DIQQHK[325.13]EEAWVIGSVVAR.A                |
| 0.999999 | 1 R.IHQIEYAMEAVK[325.13]QGSATVGLK.S             |
| 0.999999 | 1 R.VSEK[325.13]VSHVLAALQAGNR.G                 |
| 0.999999 | 1 K.VMTK[325.13]DGQWFTDWDAPHSR.H                |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                |
| 0.999999 | 1 K.LTLSALLDGK[325.13]NVNAGGHK.L                |
| 0.999999 | 0.9999 R.KVESLQEEIAFLK[325.13]K.L               |
| 0.999999 | 1 R.KVESLQEEIAFLK[325.13]K.L                    |
| 0.999999 | 1 R.RLEDGEDFNLGDALDSSNSMQTIQK[325.13]TTTR.R     |
| 0.999999 | 1 R.KVESLQEEIAFLK[325.13]K.L                    |
| 0.999999 | 1 R.KVESLQEEIAFLK[325.13]K.L                    |



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| 0.999999 | 1 R.HISPSAK[325.13]PFENGQYLDIYGITR.D                   |
| 0.999999 | 1 K.VLDFHNLDPGITK[325.13]TTGFC[160.03]ATR.R            |
| 0.999999 | 1 R.VRGEVAPDAK[325.13]SFVLNLGK.D                       |
| 0.999999 | 1 R.KVESLQEEIAFLK[325.13]K.L                           |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                       |
| 0.999999 | 1 K.K[325.13]HEALMSDLSAYGSSIQALR.E                     |
| 0.999999 | 1 R.KVESLQEEIAFLK[325.13]K.L                           |
| 0.999999 | 1 K.DIEK[325.13]AC[160.03]QSIYPLHDVFVR.K               |
| 0.999999 | 1 R.VRGEVAPDAK[325.13]SFVLNLGK.D                       |
| 0.999999 | 1 K.IPEISIQDMTAQVTSPSGK[325.13]THEAEIVEGENHTYC[160.03] |
| 0.999999 | 1 R.IFSAYIK[325.13]EVEERPAPTPWGSK.M                    |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                       |
| 0.999999 | 1 R.VRGEVAPDAK[325.13]SFVLNLGK.D                       |
| 0.999999 | 1 R.TLSDYNIQK[325.13]ESTLHLVLR.L                       |
| 0.999999 | 1 R.IFSAYIK[325.13]EVEERPAPTPWGSK.M                    |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                       |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                    |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                    |
| 0.999999 | 1 K.AK[325.13]FVGDPALVLNDIHK.K                         |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                       |
| 0.999999 | 1 K.AK[325.13]FVGDPALVLNDIHK.K                         |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                       |
| 0.999999 | 1 K.AGK[325.13]LDPHLVLDQLR.C                           |
| 0.999999 | 1 K.SLETEHK[325.13]ALTSEIALLQSR.L                      |
| 0.999999 | 1 K.LWNTLGVC[160.03]K[325.13]YTVQDESHSEWVSC[160.03]    |
| 0.999999 | 1 R.HISPSAK[325.13]PFENGQYLDIYGITR.D                   |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                       |
| 0.999999 | 1 K.IPEISIQDMTAQVTSPSGK[325.13]THEAEIVEGENHTYC[160.03] |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                       |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                       |
| 0.999999 | 1 K.HGIK[325.13]TVSQIISLQTLK.K                         |
| 0.999999 | 1 R.HISPSAK[325.13]PFENGQYLDIYGITR.D                   |
| 0.999999 | 1 K.SLETEHK[325.13]ALTSEIALLQSR.L                      |
| 0.999999 | 1 K.SLETEHK[325.13]ALTSEIALLQSR.L                      |
| 0.999999 | 1 R.VHFEESK[325.13]LEDLLR.K                            |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                       |
| 0.999999 | 1 R.K[325.13]FGVVLDEIKPSSAPELQAVR.M                    |
| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                    |
| 0.999999 | 1 K.HGIK[325.13]TVSQIISLQTLK.K                         |
| 0.999999 | 1 K.KAELLDNEKPAAVVAPITTYTVK[325.13]ISNYGWDQSDK         |
| 0.999999 | 1 R.K[325.13]FGVVLDEIKPSSAPELQAVR.M                    |
| 0.999999 | 1 R.K[325.13]FGVVLDEIKPSSAPELQAVR.M                    |
| 0.999999 | 1 K.DIEK[325.13]AC[160.03]QSIYPLHDVFVR.K               |
| 0.999999 | 1 R.SC[160.03]SLVLEHQPDNIK[325.13]ALFR.K               |
| 0.999999 | 1 R.NIK[325.13]VGRPSNIGQAQPIIDQLAEER.A                 |
| 0.999999 | 1 K.KAELLDNEKPAAVVAPITTYTVK[325.13]ISNYGWDQSDK         |
| 0.999999 | 1 K.NIK[325.13]HSGNITFDEIVNIAR.Q                       |

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| 0.999999 | 1 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G              |
| 0.999999 | 1 R.VSFELFADKVPK[325.13]TAENFR.A                 |
| 0.999999 | 1 R.VSFELFADKVPK[325.13]TAENFR.A                 |
| 0.999999 | 1 R.VSFELFADKVPK[325.13]TAENFR.A                 |
| 0.999999 | 1 R.KEEQEVQATLESEEVDLNAGLHGNWTLENAK[325.13]AR.I  |
| 0.999999 | 1 R.VSFELFADKVPK[325.13]TAENFR.A                 |
| 0.999999 | 1 K.LMPEIVATASK[325.13]VDIAPHVR.D                |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGMIYDSL DYAK.K            |
| 0.999999 | 1 K.VWQLGSSSPNFTLEGHEK[325.13]GVNC[160.03]IDYYS  |
| 0.999999 | 1 R.SSGPGAGLC[160.03]LFPLDK[325.13]VHAK.M        |
| 0.999999 | 1 R.LEDLLQDAQDEKEQLNEYK[325.13]GHLSGLAK.R        |
| 0.999999 | 1 R.KEEQEVQATLESEEVDLNAGLHGNWTLENAK[325.13]AR.I  |
| 0.999999 | 1 R.SSGPGAGLC[160.03]LFPLDK[325.13]VHAK.M        |
| 0.999999 | 1 R.NIK[325.13]VGRPSNIGQAQPIIDQLAEER.A           |
| 0.999999 | 1 K.ASDAFHFFQSGQAK[325.13]VQQGFLK.E              |
| 0.999999 | 1 R.VSFELFADKVPK[325.13]TAENFR.A                 |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGMIYDSL DYAK.K            |
| 0.999999 | 1 R.VSFELFADKVPK[325.13]TAENFR.A                 |
| 0.999999 | 1 K.VWQLGSSSPNFTLEGHEK[325.13]GVNC[160.03]IDYYS  |
| 0.999999 | 1 R.KYGGPPDSVYSGVQPGIGTEVFVGK[325.13]IPR.D       |
| 0.999999 | 1 R.LEDLLQDAQDEKEQLNEYK[325.13]GHLSGLAK.R        |
| 0.999999 | 1 K.ASDAFHFFQSGQAK[325.13]VQQGFLK.E              |
| 0.999999 | 1 R.KYGGPPDSVYSGVQPGIGTEVFVGK[325.13]IPR.D       |
| 0.999999 | 1 R.K[325.13]IEEIKDFLLTAR.R                      |
| 0.999999 | 1 R.NIK[325.13]VGRPSNIGQAQPIIDQLAEER.A           |
| 0.999999 | 1 R.NIK[325.13]VGRPSNIGQAQPIIDQLAEER.A           |
| 0.999999 | 1 R.SC[160.03]SLVLEHQPDNIK[325.13]ALFR.K         |
| 0.999999 | 1 K.RTDEAAFQK[325.13]LMSNLDSNR.D                 |
| 0.999999 | 1 K.NIK[325.13]HSGNITFDEIVNIAR.Q                 |
| 0.999999 | 1 K.NIK[325.13]HSGNITFDEIVNIAR.Q                 |
| 0.999999 | 1 K.APK[325.13]ISMPDFDLHLK.G                     |
| 0.999999 | 1 K.APK[325.13]ISMPDFDLHLK.G                     |
| 0.999999 | 1 R.K[325.13]IEEIKDFLLTAR.R                      |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG, |
| 0.999999 | 1 R.SC[160.03]SLVLEHQPDNIK[325.13]ALFR.K         |
| 0.999999 | 1 K.LEHEYIQNFK[325.13]ILQAGFK.R                  |
| 0.999999 | 1 K.LEHEYIQNFK[325.13]ILQAGFK.R                  |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG, |
| 0.999999 | 1 K.NIK[325.13]HSGNITFDEIVNIAR.Q                 |
| 0.999999 | 1 K.AAIDWFDGK[325.13]EFHGNIK.V                   |
| 0.999999 | 1 K.NIK[325.13]HSGNITFDEIVNIAR.Q                 |
| 0.999999 | 1 K.AAIDWFDGK[325.13]EFHGNIK.V                   |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGMIYDSL DYAK.K            |
| 0.999999 | 1 R.K[325.13]IEEIKDFLLTAR.R                      |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG, |
| 0.999999 | 1 R.KASGPPVSELITK[325.13]AVAASK.E                |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG, |

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| 0.999999 | 1 R.THFGGGK[325.13]TTGFGMIYDSL DYAK.K              |
| 0.999999 | 1 K.LEHEYIQNFK[325.13]ILQAGFK.R                    |
| 0.999999 | 0.9983 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E  |
| 0.999999 | 1 R.KTVTAMDVVYALK[325.13]R.Q                       |
| 0.999999 | 1 R.KTVTAMDVVYALK[325.13]R.Q                       |
| 0.999999 | 1 K.NIK[325.13]HSGNITFDEIVNIAR.Q                   |
| 0.999999 | 1 K.NIK[325.13]HSGNITFDEIVNIAR.Q                   |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGMIYDSL DYAK.K              |
| 0.999999 | 1 R.YFPTQALNFAFK[325.13]DKYK.Q                     |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGPGGFG,  |
| 0.999999 | 1 K.LEHEYIQNFK[325.13]ILQAGFK.R                    |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 R.K[325.13]DVYVQLYLQHLTAR.N                      |
| 0.999999 | 1 R.KTVTAMDVVYALK[325.13]R.Q                       |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 R.TGLYNYDDDEKEK[325.13]LQIVEMPLAHK.L             |
| 0.999999 | 1 R.TGLYNYDDDEKEK[325.13]LQIVEMPLAHK.L             |
| 0.999999 | 1 R.KTVTAMDVVYALK[325.13]R.Q                       |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGMIYDSL DYAK.K              |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGMIYDSL DYAK.K              |
| 0.999999 | 1 R.KTVTAMDVVYALK[325.13]R.Q                       |
| 0.999999 | 1 R.THFGGGK[325.13]TTGFGMIYDSL DYAK.K              |
| 0.999999 | 1 R.K[325.13]DVYVQLYLQHLTAR.N                      |
| 0.999999 | 1 R.YVWLVEQDRPLK[325.13]C[160.03]DEPILSNR.S        |
| 0.999999 | 1 R.SPVFLYEDHTGK[325.13]PGPEDYPLFR.G               |
| 0.999999 | 1 K.FQNVADLHLYLSAK[325.13]AQVSGQSAR.K              |
| 0.999999 | 1 R.HEMLPEFYK[325.13]TVSPALISR.F                   |
| 0.999999 | 1 R.SPVFLYEDHTGK[325.13]PGPEDYPLFR.G               |
| 0.999999 | 1 K.FQNVADLHLYLSAK[325.13]AQVSGQSAR.K              |
| 0.999999 | 1 R.SPVFLYEDHTGK[325.13]PGPEDYPLFR.G               |
| 0.999999 | 1 R.YVWLVEQDRPLK[325.13]C[160.03]DEPILSNR.S        |
| 0.999999 | 1 R.SPVFLYEDHTGK[325.13]PGPEDYPLFR.G               |
| 0.999999 | 1 R.SPVFLYEDHTGK[325.13]PGPEDYPLFR.G               |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L            |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L            |
| 0.999999 | 1 K.LNNC[160.03]GMGIGGGK[325.13]ILAAALTEC[160.03]F |
| 0.999999 | 1 K.SFVLNLGK[325.13]DSNNLC[160.03]LHFNPR.F         |
| 0.999999 | 1 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A            |
| 0.999999 | 1 R.KIEEIK[325.13]DFLLTAR.R                        |
| 0.999999 | 1 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A            |
| 0.999999 | 1 K.SFVLNLGK[325.13]DSNNLC[160.03]LHFNPR.F         |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L            |
| 0.999999 | 1 R.ALVFQPV AELK[325.13]DQTD FEHR.I                |
| 0.999999 | 1 R.KIEEIK[325.13]DFLLTAR.R                        |
| 0.999999 | 1 R.ALVFQPV AELK[325.13]DQTD FEHR.I                |
| 0.999999 | 1 K.SFVLNLGK[325.13]DSNNLC[160.03]LHFNPR.F         |
| 0.999999 | 1 R.KIEEIK[325.13]DFLLTAR.R                        |

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| 0.999999 | 1 R.C[160.03]RPDQLTGLSLLPLSEK[325.13]AAR.A      |
| 0.999999 | 1 K.SFVLNLGK[325.13]DSNNLC[160.03]LHFNPR.F      |
| 0.999999 | 1 R.C[160.03]RPDQLTGLSLLPLSEK[325.13]AAR.A      |
| 0.999999 | 1 R.KIEEIK[325.13]DFLLTAR.R                     |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L         |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L         |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L         |
| 0.999999 | 1 K.KYDAFLASESLIK[325.13]QIPR.I                 |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L         |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L         |
| 0.999999 | 1 K.KYDAFLASESLIK[325.13]QIPR.I                 |
| 0.999999 | 1 R.TFSWASVTSK[325.13]NLPPSGAVPVTGIPPHVVK.V     |
| 0.999999 | 1 R.TFSWASVTSK[325.13]NLPPSGAVPVTGIPPHVVK.V     |
| 0.999999 | 1 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A         |
| 0.999999 | 1 K.KYDAFLASESLIK[325.13]QIPR.I                 |
| 0.999999 | 1 K.FLAAGTHLGGTNLDFQMEQYIYK[325.13]R.K          |
| 0.999999 | 1 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A         |
| 0.999999 | 1 R.K[325.13]ALVTGYFMQVAHLER.T                  |
| 0.999999 | 1 R.K[325.13]ALVTGYFMQVAHLER.T                  |
| 0.999999 | 1 R.RK[325.13]DGVFLYFEDNAGVIVNNK.G              |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L         |
| 0.999999 | 1 K.KYDAFLASESLIK[325.13]QIPR.I                 |
| 0.999999 | 1 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L         |
| 0.999999 | 1 R.TFSWASVTSK[325.13]NLPPSGAVPVTGIPPHVVK.V     |
| 0.999999 | 1 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A         |
| 0.999999 | 1 K.LAGANPAVITC[160.03]DELLLGHEK[325.13]APAFR.D |
| 0.999999 | 1 K.KYDAFLASESLIK[325.13]QIPR.I                 |
| 0.999999 | 1 K.FLAAGTHLGGTNLDFQMEQYIYK[325.13]R.K          |
| 0.999999 | 1 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A         |
| 0.999999 | 1 K.FLAAGTHLGGTNLDFQMEQYIYK[325.13]R.K          |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E    |
| 0.999999 | 1 R.K[325.13]ALVTGYFMQVAHLER.T                  |
| 0.999999 | 1 R.K[325.13]ALVTGYFMQVAHLER.T                  |
| 0.999999 | 1 K.LAGANPAVITC[160.03]DELLLGHEK[325.13]APAFR.D |
| 0.999999 | 1 K.LAGANPAVITC[160.03]DELLLGHEK[325.13]APAFR.D |
| 0.999999 | 1 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A         |
| 0.999999 | 1 K.KVEELEGITTLNHK[325.13]LQDASAEVER.L          |
| 0.999999 | 1 K.KVEELEGITTLNHK[325.13]LQDASAEVER.L          |
| 0.999999 | 1 K.LAGANPAVITC[160.03]DELLLGHEK[325.13]APAFR.D |
| 0.999999 | 1 K.KVEELEGITTLNHK[325.13]LQDASAEVER.L          |
| 0.999999 | 1 R.ALFWNEEIVPQIK[325.13]EGKR.V                 |
| 0.999999 | 1 K.VTVLFAGQHIK[325.13]SPFEVYVDK.S              |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E    |
| 0.999999 | 1 R.K[325.13]NGGLGHMNIALLSDLTK.Q                |
| 0.999999 | 1 K.KVEELEGITTLNHK[325.13]LQDASAEVER.L          |
| 0.999999 | 1 K.KVEELEGITTLNHK[325.13]LQDASAEVER.L          |
| 0.999999 | 1 K.VTVLFAGQHIK[325.13]SPFEVYVDK.S              |

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| 0.999999 | 1 K.VTVLFAGQHIAK[325.13]SPFEVYVDK.S                 |
| 0.999999 | 1 R.K[325.13]NGGLGHMNIALLSDLTK.Q                    |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLYLEK.E                      |
| 0.999999 | 1 K.KVEELEGEITTLNHNK[325.13]LQDASAEVER.L            |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E        |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLYLEK.E                      |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLYLEK.E                      |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLYLEK.E                      |
| 0.999999 | 1 R.IHQC[160.03]ISINMLADK[325.13]LNMTPEEAER.W       |
| 0.999999 | 1 R.IHQC[160.03]ISINMLADK[325.13]LNMTPEEAER.W       |
| 0.999999 | 1 R.LC[160.03]IEHFDK[325.13]LLVEDINK.D              |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E        |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLYLEK.E                      |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.GHLDNISNNLLIGAINIENGK[325.13]ANSVR.N            |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLYLEK.E                      |
| 0.999999 | 1 K.K[325.13]ISSIQSIVPALEIANHR.K                    |
| 0.999999 | 1 R.EHSSWDLVGLEK[325.13]WTEYR.V                     |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLYLEK.E                      |
| 0.999999 | 0.9969 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E   |
| 0.999999 | 1 R.EHSSWDLVGLEK[325.13]WTEYR.V                     |
| 0.999999 | 1 R.HVAEVLEYTK[325.13]DEQLESFQR.T                   |
| 0.999999 | 1 R.HVAEVLEYTK[325.13]DEQLESFQR.T                   |
| 0.999999 | 1 R.LDYLSSLKVK[325.13]GLVLGPIHK.N                   |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.VTGNFK[325.13]HASPILPITEFSDIPR.R                |
| 0.999999 | 1 R.VTGNFK[325.13]HASPILPITEFSDIPR.R                |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |
| 0.999999 | 1 R.GQKPTLWALLNSEYVTEEK[325.13]K.L                  |
| 0.999999 | 1 R.LLHLLDDMPVK[325.13]PYSDGEGGIEDENR.S             |
| 0.999999 | 1 R.LLHLLDDMPVK[325.13]PYSDGEGGIEDENR.S             |
| 0.999999 | 1 R.EHSSWDLVGLEK[325.13]WTEYR.V                     |
| 0.999999 | 1 K.HSQFIGYPITLYLEK[325.13]ER.E                     |
| 0.999999 | 1 R.VANILHDDC[160.03]AFLSAFGDVSK[325.13]PER.Y       |
| 0.999999 | 1 R.EHSSWDLVGLEK[325.13]WTEYR.V                     |
| 0.999999 | 1 K.SVK[325.13]LLQALAQYQNLQEPR.K                    |
| 0.999999 | 1 K.TVSPDRLELEAAQK[325.13]FLER.A                    |
| 0.999999 | 1 R.GLGHQVATDALVAMEK[325.13]AMK.R                   |
| 0.999999 | 1 K.EVEAVIPDHC[160.03]IFASNTSALPISEIAAVSK[325.13]RP |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                  |

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| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                |
| 0.999999 | 1 R.EHSSWDLVGLEK[325.13]WTEYR.V                   |
| 0.999999 | 1 R.VTGNFK[325.13]HASPILPITEFSDIPR.R              |
| 0.999999 | 1 K.SVK[325.13]LLQALAQYQNLQEPR.K                  |
| 0.999999 | 1 R.EHSSWDLVGLEK[325.13]WTEYR.V                   |
| 0.999999 | 1 R.VTGNFK[325.13]HASPILPITEFSDIPR.R              |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                |
| 0.999999 | 1 R.EHSSWDLVGLEK[325.13]WTEYR.V                   |
| 0.999999 | 1 R.VTGNFK[325.13]HASPILPITEFSDIPR.R              |
| 0.999999 | 1 R.VTGNFK[325.13]HASPILPITEFSDIPR.R              |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                |
| 0.999999 | 0.9992 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F           |
| 0.999999 | 1 R.FVC[160.03]NDDVYSGPLK[325.13]FLHQDIDSGQGIR.N  |
| 0.999999 | 1 K.ALESPERPFLAILGGAK[325.13]VADK.I               |
| 0.999999 | 1 K.ALESPERPFLAILGGAK[325.13]VADK.I               |
| 0.999999 | 1 R.VTGNFK[325.13]HASPILPITEFSDIPR.R              |
| 0.999999 | 1 K.IWDYQNK[325.13]TC[160.03]VQTLEGHAQNVSC[160.0: |
| 0.999999 | 1 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T           |
| 0.999999 | 1 K.ALESPERPFLAILGGAK[325.13]VADK.I               |
| 0.999999 | 1 R.VTGNFK[325.13]HASPILPITEFSDIPR.R              |
| 0.999999 | 1 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T           |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                |
| 0.999999 | 1 K.ALESPERPFLAILGGAK[325.13]VADK.I               |
| 0.999999 | 1 K.ALESPERPFLAILGGAK[325.13]VADK.I               |
| 0.999999 | 0.9994 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F           |
| 0.999999 | 1 R.SC[160.03]LPQIK[325.13]LYGPTNFSPIINHVAR.F     |
| 0.999999 | 1 R.SC[160.03]LPQIK[325.13]LYGPTNFSPIINHVAR.F     |
| 0.999999 | 1 R.FVC[160.03]NDDVYSGPLK[325.13]FLHQDIDSGQGIR.N  |
| 0.999999 | 1 K.IWDYQNK[325.13]TC[160.03]VQTLEGHAQNVSC[160.0: |
| 0.999999 | 1 R.LPLQDVYK[325.13]IGGIGTPVGR.V                  |
| 0.999999 | 1 K.ALESPERPFLAILGGAK[325.13]VADK.I               |
| 0.999999 | 1 R.K[325.13]NGGLGHMNIALLSDLTK.Q                  |
| 0.999999 | 1 K.ALESPERPFLAILGGAK[325.13]VADK.I               |
| 0.999999 | 1 K.ALESPERPFLAILGGAK[325.13]VADK.I               |
| 0.999999 | 1 R.SC[160.03]LPQIK[325.13]LYGPTNFSPIINHVAR.F     |
| 0.999999 | 1 R.SC[160.03]LPQIK[325.13]LYGPTNFSPIINHVAR.F     |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I      |
| 0.999999 | 1 R.IGYPK[325.13]PALLHSTFFPALQGAQTK.M             |
| 0.999999 | 1 R.GFGFVTFDDHDPVVK[325.13]IVLQK.Y                |
| 0.999999 | 1 R.IGYPK[325.13]PALLHSTFFPALQGAQTK.M             |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I      |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I      |
| 0.999999 | 1 R.GFGFVTFDDHDPVVK[325.13]IVLQK.Y                |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLFEK.K                     |
| 0.999999 | 1 R.K[325.13]TFEDYLHNVVFPVPR.K                    |
| 0.999999 | 1 R.IGYPK[325.13]PALLHSTFFPALQGAQTK.M             |

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| 0.999999 | 1 R.AWVWNTHADFADEC[160.03]PK[325.13]PELLAIR.F     |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLFVEK.K                    |
| 0.999999 | 1 K.STANK[325.13]YQVFFFGTHETAFLGPK.D              |
| 0.999999 | 1 R.K[325.13]TFEDYLHNVVFVPR.K                     |
| 0.999999 | 1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G     |
| 0.999999 | 1 K.STANK[325.13]YQVFFFGTHETAFLGPK.D              |
| 0.999999 | 1 R.AWVWNTHADFADEC[160.03]PK[325.13]PELLAIR.F     |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLFVEK.K                    |
| 0.999999 | 1 R.K[325.13]TFEDYLHNVVFVPR.K                     |
| 0.999999 | 1 K.STANK[325.13]YQVFFFGTHETAFLGPK.D              |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G     |
| 0.999999 | 1 K.STANK[325.13]YQVFFFGTHETAFLGPK.D              |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G     |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLFVEK.K                    |
| 0.999999 | 1 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q              |
| 0.999999 | 1 R.K[325.13]TFEDYLHNVVFVPR.K                     |
| 0.999999 | 1 K.STANK[325.13]YQVFFFGTHETAFLGPK.D              |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I      |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G     |
| 0.999999 | 1 R.FSYVLPLVHSLEPTMGPK[325.13]AGGTR.I             |
| 0.999999 | 1 K.K[325.13]HSQFIGYPITLFVEK.K                    |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I      |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I      |
| 0.999999 | 1 R.AIVDC[160.03]GFEHPSEVQHEC[160.03]IPQAILGMDVLC |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I      |
| 0.999999 | 1 K.REDLVVAPAGITLK[325.13]EANEILQR.S              |
| 0.999999 | 1 K.REDLVVAPAGITLK[325.13]EANEILQR.S              |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV   |
| 0.999999 | 1 R.AIVDC[160.03]GFEHPSEVQHEC[160.03]IPQAILGMDVLC |
| 0.999999 | 1 R.FSK[325.13]SQLDIIHSLK.K                       |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV   |
| 0.999999 | 1 K.REDLVVAPAGITLK[325.13]EANEILQR.S              |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV   |
| 0.999999 | 1 R.FSK[325.13]SQLDIIHSLK.K                       |
| 0.999999 | 1 K.REDLVVAPAGITLK[325.13]EANEILQR.S              |
| 0.999999 | 1 K.K[325.13]ALIEVLQPLIAEHQAR.R                   |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV   |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV   |
| 0.999999 | 1 K.K[325.13]ALIEVLQPLIAEHQAR.R                   |
| 0.999999 | 1 K.HTGPILSM[147.04]ANAGPNTNGSQFFIC[160.03]TAK[3  |
| 0.999999 | 1 R.HVMQPYYK[325.13]DILPC[160.03]LDGYLK.T         |
| 0.999999 | 1 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D        |
| 0.999999 | 1 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN   |
| 0.999999 | 1 K.FLK[325.13]SGDAIVDMVPGKPMC[160.03]VESFSDYPP   |
| 0.999999 | 1 K.HTGPILSM[147.04]ANAGPNTNGSQFFIC[160.03]TAK[3  |
| 0.999999 | 1 R.HVMQPYYK[325.13]DILPC[160.03]LDGYLK.T         |

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| 0.999999 | 1 R.HVMQPYYK[325.13]DILPC[160.03]LDGYLK.T            |
| 0.999999 | 1 K.VLVLSQDYGK[325.13]HLLGVEDLLQK.H                  |
| 0.999999 | 1 R.K[325.13]HGLEVIYMIEPIDEYC[160.03]VQQLK.E         |
| 0.999999 | 1 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D           |
| 0.999999 | 1 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPM[147.   |
| 0.999999 | 1 K.VLVLSQDYGK[325.13]HLLGVEDLLQK.H                  |
| 0.999999 | 1 K.VLVLSQDYGK[325.13]HLLGVEDLLQK.H                  |
| 0.999999 | 1 K.VLDK[325.13]C[160.03]QEVISWLDANTLAEKDEFEHK.R     |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                 |
| 0.999999 | 1 K.IGNTGGMLDNILASK[325.13]LYRPGSVAYVSR.S            |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                 |
| 0.999999 | 1 K.VLDK[325.13]C[160.03]QEVISWLDANTLAEKDEFEHK.R     |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                 |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.SLVEIIEHGLVDEQQK[325.13]VR.T                     |
| 0.999999 | 1 R.SLVEIIEHGLVDEQQK[325.13]VR.T                     |
| 0.999999 | 1 R.YAIC[160.03]SALAASALPALVMSK[325.13]GHR.I         |
| 0.999999 | 0.9962 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.SLVEIIEHGLVDEQQK[325.13]VR.T                     |
| 0.999999 | 1 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D           |
| 0.999999 | 1 R.HK[325.13]PAFTEEDVLNIFPVVK.H                     |
| 0.999999 | 1 R.DKFPEVIINFPDPAQK[325.13]SDIVQLR.G                |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.LWK[325.13]AIHTAPVATMAFDPTSTLLATGGC[160.03]D     |
| 0.999999 | 1 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D           |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                 |
| 0.999999 | 1 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T         |
| 0.999999 | 1 R.K[325.13]LGC[160.03]EVLGVSVD SQFTHLAWINTPR.K     |
| 0.999999 | 1 R.LK[325.13]GIEEEEILPGFILC[160.03]DPNNLC[160.03]HS |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                 |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                 |
| 0.999999 | 1 R.YAIC[160.03]SALAASALPALVMSK[325.13]GHR.I         |
| 0.999999 | 1 R.K[325.13]LGC[160.03]EVLGVSVD SQFTHLAWINTPR.K     |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.YAIC[160.03]SALAASALPALVMSK[325.13]GHR.I         |
| 0.999999 | 1 R.ILK[325.13]NLIMSGYSPEHDVSGISDPFLQVR.I            |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF        |
| 0.999999 | 1 R.ILK[325.13]NLIMSGYSPEHDVSGISDPFLQVR.I            |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                 |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                 |



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| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I              |
| 0.999999 | 1 R.K[325.13]LGC[160.03]EVLGVSVDSQFTHLAWINTPR.K   |
| 0.999999 | 1 R.YAIC[160.03]SALAASALPALVMSK[325.13]GHR.I      |
| 0.999999 | 1 R.K[325.13]LGC[160.03]EVLGVSVDSQFTHLAWINTPR.K   |
| 0.999999 | 1 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T  |
| 0.999999 | 1 R.YAIC[160.03]SALAASALPALVMSK[325.13]GHR.I      |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF       |
| 0.999999 | 1 R.ILK[325.13]NLIMSGYSPEHDVSGISDPFLQVR.I         |
| 0.999999 | 1 R.KNQLK[325.13]DMAIATGGAVFGEEGLTLNLEDVQPHDLG    |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF       |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF       |
| 0.999999 | 1 R.ILK[325.13]NLIMSGYSPEHDVSGISDPFLQVR.I         |
| 0.999999 | 1 K.M[147.04]HGGGPTVTAGLPLPK[325.13]AYIQENLELVEK. |
| 0.999999 | 0.9999 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I         |
| 0.999999 | 1 R.K[325.13]LGC[160.03]EVLGVSVDSQFTHLAWINTPR.K   |
| 0.999999 | 1 R.VLSGEFQIVNPHLLK[325.13]DLTER.G                |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R     |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF       |
| 0.999999 | 1 K.M[147.04]HGGGPTVTAGLPLPK[325.13]AYIQENLELVEK. |
| 0.999999 | 1 R.GFTAAGILSAHK[325.13]IIASSPEMNLPTVSALR.K       |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R     |
| 0.999999 | 1 R.VAIEHLDK[325.13]ISDSVLVDIKDTEPLIQTAK.T        |
| 0.999999 | 1 R.K[325.13]LGC[160.03]EVLGVSVDSQFTHLAWINTPR.K   |
| 0.999999 | 1 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T      |
| 0.999999 | 1 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T      |
| 0.999999 | 1 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T      |
| 0.999999 | 1 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF       |
| 0.999999 | 1 R.GKDNK[325.13]AIIASNIMYIVGQYPR.F               |
| 0.999999 | 1 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R     |
| 0.999999 | 1 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T      |
| 0.999999 | 1 K.MHGGGPTVTAGLPLPK[325.13]AYIQENLELVEK.G        |
| 0.999999 | 1 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T      |
| 0.999999 | 1 K.VLLPEYGGTK[325.13]VVLDDKDYFLFR.D              |
| 0.999999 | 1 K.MHGGGPTVTAGLPLPK[325.13]AYIQENLELVEK.G        |
| 0.999999 | 1 K.VLIDPVSVDK[325.13]DTLSIHYLMLPR.V              |
| 0.999999 | 1 K.VLLPEYGGTK[325.13]VVLDDKDYFLFR.D              |
| 0.999999 | 1 R.VTYTPMAPGSYLISIK[325.13]YGGPYHIGGSPEK.A       |
| 0.999999 | 1 R.GFTAAGILSAHK[325.13]IIASSPEMNLPTVSALR.K       |
| 0.999999 | 1 K.VLIDPVSVDK[325.13]DTLSIHYLMLPR.V              |
| 0.999999 | 1 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T  |
| 0.999999 | 1 R.VTYTPMAPGSYLISIK[325.13]YGGPYHIGGSPEK.A       |
| 0.999999 | 1 R.GFTAAGILSAHK[325.13]IIASSPEMNLPTVSALR.K       |
| 0.999999 | 1 K.VLIDPVSVDK[325.13]DTLSIHYLMLPR.V              |
| 0.999999 | 1 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T  |
| 0.999999 | 1 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T  |
| 0.999999 | 1 K.TSFVNFTDIC[160.03]K[325.13]LLHR.Q             |
| 0.999999 | 1 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T  |

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| 0.999999 | 1 K.IVSLFAEHNDLQYAAPGGLIGVGTK[325.13]IDPTLC[160.0 |
| 0.999999 | 1 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L          |
| 0.999999 | 1 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T  |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q       |
| 0.999999 | 1 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T  |
| 0.999999 | 1 K.GLAPDLPEDLYHLIK[325.13]K.A                    |
| 0.999999 | 1 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T  |
| 0.999999 | 1 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPMDQK. |
| 0.999999 | 1 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPMDQK. |
| 0.999999 | 1 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPMDQK. |
| 0.999999 | 1 K.KEDLVFIFWAPESAPLK[325.13]SK.M                 |
| 0.999999 | 1 K.NLNTLC[160.03]WAIGSISGAMHEEDEK[325.13]R.F     |
| 0.999999 | 1 K.KEDLVFIFWAPESAPLK[325.13]SK.M                 |
| 0.999999 | 1 R.DIVEELSALK[325.13]QLTQTTHTDKVPGEDDK.G         |
| 0.999999 | 1 R.FLNK[325.13]QAPQTIHLPSGEILDVFDAAER.Y          |
| 0.999999 | 1 K.SGGVNQYVVQEVLSIK[325.13]HLPPQLR.A             |
| 0.999999 | 1 K.NLNTLC[160.03]WAIGSISGAMHEEDEK[325.13]R.F     |
| 0.999999 | 1 K.KEDLVFIFWAPESAPLK[325.13]SK.M                 |
| 0.999999 | 1 K.SGGVNQYVVQEVLSIK[325.13]HLPPQLR.A             |
| 0.999999 | 1 K.VSPVVSHK[325.13]VDLAVLAAVEIR.G                |
| 0.999999 | 1 K.SGGVNQYVVQEVLSIK[325.13]HLPPQLR.A             |
| 0.999999 | 1 R.NELHNLLDK[325.13]PQLQGIPVLVLGNK.R             |
| 0.999999 | 1 K.SGGVNQYVVQEVLSIK[325.13]HLPPQLR.A             |
| 0.999999 | 1 R.FLNK[325.13]QAPQTIHLPSGEILDVFDAAER.Y          |
| 0.999999 | 1 R.TPK[325.13]LSSIIDC[160.03]TGTASYHGFLPVLVR.N   |
| 0.999999 | 1 R.NELHNLLDK[325.13]PQLQGIPVLVLGNK.R             |
| 0.999999 | 1 R.TPK[325.13]LSSIIDC[160.03]TGTASYHGFLPVLVR.N   |
| 0.999999 | 1 R.QVLDLEDLVFTQGSHFMANK[325.13]R.C               |
| 0.999999 | 1 R.RDQLEAAQEAVPPADIVFSVK[325.13]SPPSAGYLVMMVSR.  |
| 0.999999 | 1 R.TPK[325.13]LSSIIDC[160.03]TGTASYHGFLPVLVR.N   |
| 0.999999 | 1 R.TPK[325.13]LSSIIDC[160.03]TGTASYHGFLPVLVR.N   |
| 0.999999 | 1 K.AMK[325.13]GLGTDEDTIIDIITHR.S                 |
| 0.999999 | 1 K.NLQYYDISAK[325.13]SNYNFEKPFLWLAR.K            |
| 0.999999 | 1 K.NLQYYDISAK[325.13]SNYNFEKPFLWLAR.K            |
| 0.999999 | 1 K.TK[325.13]DLPVTEAVFSALVTGHAR.A                |
| 0.999999 | 1 K.NLQYYDISAK[325.13]SNYNFEKPFLWLAR.K            |
| 0.999999 | 1 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E       |
| 0.999999 | 1 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E       |
| 0.999999 | 1 R.MK[325.13]VAC[160.03]ITEQVLTLVNKR.I           |
| 0.999999 | 1 R.VFITDDFHDMMMPK[325.13]YLNFBVK.G               |
| 0.999999 | 1 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E       |
| 0.999999 | 1 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E       |
| 0.999999 | 1 K.ELNPSLNFK[325.13]EVTYELDHPGFQIR.D             |
| 0.999999 | 1 R.GLFIIDPNGVIK[325.13]HLSVNDLPVGR.S             |
| 0.999999 | 1 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E       |
| 0.999999 | 1 R.VFITDDFHDMMMPK[325.13]YLNFBVK.G               |
| 0.999999 | 1 R.VFITDDFHDMMMPK[325.13]YLNFBVK.G               |

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| 0.999999 | 1 R.MK[325.13]VAC[160.03]ITEQVLT LVNKR.I           |
| 0.999999 | 0.9987 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E  |
| 0.999999 | 1 R.VYLFTIK[325.13]KGILGQHQFLEGPEGIENTR.F          |
| 0.999999 | 1 K.ELNPSLNFK[325.13]EVTYELDHPGFQIR.D              |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.999999 | 1 K.TFK[325.13]EFLSLDDSVDETEAVKR.Y                 |
| 0.999999 | 1 K.TFK[325.13]EFLSLDDSVDETEAVKR.Y                 |
| 0.999999 | 1 R.GLFIIDPNGVIK[325.13]HLSVNDLPVGR.S              |
| 0.999999 | 1 K.EQALSTLQLEHTSTQALVSELLPAK[325.13]HLC[160.03]Q  |
| 0.999999 | 1 R.VFITDDFHDMMMPK[325.13]YLNFKV.G                 |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.999999 | 1 R.VFITDDFHDMMMPK[325.13]YLNFKV.G                 |
| 0.999999 | 1 K.TVWDWELMNDIK[325.13]PIWQRPSK.E                 |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.999999 | 1 K.AHAFAVQQK[325.13]EQELQQT LQQEQSVLDQLR.G        |
| 0.999999 | 1 K.LVALHK[325.13]QVLMGPYNPDTC[160.03]PEVGFFDVLC   |
| 0.999999 | 1 R.VYLFTIKK[325.13]GILGQHQFLEGPEGIENTR.F          |
| 0.999999 | 1 R.VYLFTIK[325.13]KGILGQHQFLEGPEGIENTR.F          |
| 0.999999 | 1 K.LVALHK[325.13]QVLMGPYNPDTC[160.03]PEVGFFDVLC   |
| 0.999999 | 1 K.LVALHK[325.13]QVLMGPYNPDTC[160.03]PEVGFFDVLC   |
| 0.999999 | 1 R.ELAILLGMLDPAEKDEK[325.13]GMPVTAR.V             |
| 0.999999 | 1 R.FQTK[325.13]IPNIYAIGDVVAGPMLAHK.A              |
| 0.999999 | 1 K.FTLK[325.13]AGQVVTIWAAGAGATHSPPTDLVWK.A        |
| 0.999999 | 1 K.NIILGGVK[325.13]AVTLHDQGT AQWADLSSQFYLR.E      |
| 0.999999 | 1 R.ELAILLGMLDPAEKDEK[325.13]GMPVTAR.V             |
| 0.999999 | 1 R.K[325.13]FAVSQMSALLDSAHLLASSTQR.N              |
| 0.999999 | 1 R.C[160.03]PPGVVPAC[160.03]HNSK[325.13]DTVTISGPQ |
| 0.999999 | 1 R.K[325.13]FAVSQMSALLDSAHLLASSTQR.N              |
| 0.999999 | 1 R.K[325.13]ISASLQSQSPEHLLPVLIQAAQLC[160.03]R.E   |
| 0.999999 | 1 R.K[325.13]ISASLQSQSPEHLLPVLIQAAQLC[160.03]R.E   |
| 0.999999 | 1 R.FQTK[325.13]IPNIYAIGDVVAGPMLAHK.A              |
| 0.999999 | 1 R.KNILEESLC[160.03]ELVAK[325.13]QLK.Q            |
| 0.999999 | 1 R.KNILEESLC[160.03]ELVAK[325.13]QLK.Q            |
| 0.999999 | 1 K.VSNLQYLHSYLYIK[325.13]LSTAIK.R                 |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 R.FQTK[325.13]IPNIYAIGDVVAGPMLAHK.A              |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 K.VIRPLDQPSSFDATPYIK[325.13]DLFTC[160.03]TIK.R   |
| 0.999999 | 1 R.LKDLEALLNSK[325.13]EAALSTALSEK.R               |
| 0.999999 | 1 R.LKDLEALLNSK[325.13]EAALSTALSEK.R               |
| 0.999999 | 1 K.VIRPLDQPSSFDATPYIK[325.13]DLFTC[160.03]TIK.R   |
| 0.999999 | 1 R.IWDTLQK[325.13]LGAVYDVSHYNALLK.V               |
| 0.999999 | 1 R.IWDTLQK[325.13]LGAVYDVSHYNALLK.V               |
| 0.999999 | 1 R.LKDLEALLNSK[325.13]EAALSTALSEK.R               |
| 0.999999 | 1 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I              |
| 0.999999 | 1 R.TQIAPGSQTVLGIGPGPADLIDK[325.13]VTGHLK.L        |

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| 0.999999 | 1 R.LKDLEALLNSK[325.13]EAALSTALSEK.R               |
| 0.999999 | 1 R.LKDLEALLNSK[325.13]EAALSTALSEK.R               |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I              |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 K.GILADESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV    |
| 0.999999 | 1 R.LKDLEALLNSK[325.13]EAALSTALSEK.R               |
| 0.999999 | 1 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I              |
| 0.999999 | 1 R.LKDLEALLNSK[325.13]EAALSTALSEK.R               |
| 0.999999 | 1 K.FLDGNELTLADC[160.03]NLLPK[325.13]LHIVQVVC[160. |
| 0.999999 | 1 R.GHNC[160.03]PK[325.13]PVLNFYEANFPANVMDVIAR.C   |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 K.FLDGNELTLADC[160.03]NLLPK[325.13]LHIVQVVC[160. |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 R.GHNC[160.03]PK[325.13]PVLNFYEANFPANVMDVIAR.C   |
| 0.999999 | 1 K.FLDGNELTLADC[160.03]NLLPK[325.13]LHIVQVVC[160. |
| 0.999999 | 1 R.GHNC[160.03]PK[325.13]PVLNFYEANFPANVMDVIAR.C   |
| 0.999999 | 1 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L          |
| 0.999999 | 1 R.TQIAPGSQTVLGIGPGPADLIDK[325.13]VTGHLK.L        |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 R.GHNC[160.03]PK[325.13]PVLNFYEANFPANVMDVIAR.C   |
| 0.999999 | 1 R.GHNC[160.03]PK[325.13]PVLNFYEANFPANVMDVIAR.C   |
| 0.999999 | 1 R.TQIAPGSQTVLGIGPGPADLIDK[325.13]VTGHLK.L        |
| 0.999999 | 1 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999999 | 1 K.VAHALAEGLGVIAC[160.03]IGEK[325.13]LDER.E       |
| 0.999999 | 1 R.TQIAPGSQTVLGIGPGPADLIDK[325.13]VTGHLK.L        |
| 0.999999 | 1 K.VAHALAEGLGVIAC[160.03]IGEK[325.13]LDER.E       |
| 0.999999 | 1 R.TQIAPGSQTVLGIGPGPADLIDK[325.13]VTGHLK.L        |
| 0.999999 | 1 K.VAHALAEGLGVIAC[160.03]IGEK[325.13]LDER.E       |
| 0.999999 | 1 K.VAHALAEGLGVIAC[160.03]IGEK[325.13]LDER.E       |
| 0.999999 | 1 K.VAHALAEGLGVIAC[160.03]IGEK[325.13]LDER.E       |
| 0.999999 | 1 R.LKETK[325.13]DGMFLTDQSYIDVLPFR.D               |
| 0.999999 | 1 R.LK[325.13]ETKDGFMFLTDQSYIDVLPFR.D              |
| 0.999999 | 1 R.K[325.13]LAKTQGNVFATDAILATLMSC[160.03]TR.S     |
| 0.999999 | 1 R.K[325.13]LAKTQGNVFATDAILATLMSC[160.03]TR.S     |
| 0.999999 | 1 R.LKETK[325.13]DGMFLTDQSYIDVLPFR.D               |
| 0.999999 | 1 R.K[325.13]LAKTQGNVFATDAILATLMSC[160.03]TR.S     |
| 0.999999 | 1 R.K[325.13]LAKTQGNVFATDAILATLMSC[160.03]TR.S     |
| 0.999999 | 0.9818 R.DALSDLALHFLNK[325.13]M[147.04]K.I         |
| 0.999999 | 1 K.LKPQYLEELPGQLK[325.13]QFSMFLGK.F               |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |

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| 0.999999 | 1 R.AHQLVLPPC[160.03]DVVIK[325.13]AVADYVR.N                    |
| 0.999999 | 1 R.FEYLLK[325.13]QTELFHFQIPAAQK.T                             |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 K.EAGELKPEEEITVGPVQK[325.13]LVTEMGTATQSALSSSF                |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 K.K[325.13]LISPESTMMLLEAQAATGGIIDPHR.N                       |
| 0.999999 | 1 K.EAGELKPEEEITVGPVQK[325.13]LVTEMGTATQSALSSSF                |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 K.EAGELKPEEEITVGPVQK[325.13]LVTEMGTATQSALSSSF                |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 K.VSYFPTVPGVYIVSTK[325.13]FADEHVPGPSFTVK.I                   |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 R.VEAVNMAEGIIHDTETK[325.13]MEEFKDQLPADEC[160.03]M[147.04]K.I |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 K.HNQLPLVIEFTEQTAPK[325.13]IFGGEIK.T                         |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 R.TPGVTYSDSFDLQC[160.03]IHK[325.13]PHYPAWVPVSVT              |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 K.HNQLPLVIEFTEQTAPK[325.13]IFGGEIK.T                         |
| 0.999999 | 1 R.TPGVTYSDSFDLQC[160.03]IHK[325.13]PHYPAWVPVSVT              |
| 0.999999 | 1 R.DLLDDLKSELTGK[325.13]FEK.L                                 |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 R.DLLDDLKSELTGK[325.13]FEK.L                                 |
| 0.999999 | 1 K.HNQLPLVIEFTEQTAPK[325.13]IFGGEIK.T                         |
| 0.999999 | 1 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E                       |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 R.TPGVTYSDSFDLQC[160.03]IHK[325.13]PHYPAWVPVSVT              |
| 0.999999 | 1 R.DLLDDLKSELTGK[325.13]FEK.L                                 |
| 0.999999 | 1 K.HNQLPLVIEFTEQTAPK[325.13]IFGGEIK.T                         |
| 0.999999 | 1 R.VYYTM[147.04]EPEHPVGNWQK[325.13]HNVDDSLLTTV                |
| 0.999999 | 1 R.DLLDDLKSELTGK[325.13]FEK.L                                 |
| 0.999999 | 0.9993 R.DALSDLALHFLNK[325.13]M[147.04]K.I                     |
| 0.999999 | 1 R.RSDNVVTSELLAVMDGDWTLK[325.13]YGER.S                        |
| 0.999999 | 1 R.VYYTM[147.04]EPEHPVGNWQK[325.13]HNVDDSLLTTV                |
| 0.999999 | 1 R.RSDNVVTSELLAVMDGDWTLK[325.13]YGER.S                        |
| 0.999999 | 1 R.GVLK[325.13]VFLENVIR.D                                     |
| 0.999999 | 1 K.IAALQAFADQLIAAGHYAK[325.13]GDISSR.R                        |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I                          |
| 0.999999 | 1 R.VYYTM[147.04]EPEHPVGNWQK[325.13]HNVDDSLLTTV                |
| 0.999999 | 1 K.IAALQAFADQLIAAGHYAK[325.13]GDISSR.R                        |
| 0.999999 | 1 K.HELLQPFNVLYEK[325.13]EGEFVAQFK.F                           |

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| 0.999999 | 1 K.IAALQAFADQLIAAGHYAK[325.13]GDISSR.R             |
| 0.999999 | 1 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999999 | 1 K.HELLQPFNVLYEK[325.13]EGEFVAQFK.F                |
| 0.999999 | 1 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I               |
| 0.999999 | 1 K.IAALQAFADQLIAAGHYAK[325.13]GDISSR.R             |
| 0.999999 | 1 K.DIHTLAQLISAYSLVDPEK[325.13]AK.A                 |
| 0.999999 | 1 K.HELLQPFNVLYEK[325.13]EGEFVAQFK.F                |
| 0.999999 | 1 R.RIPADTFAALK[325.13]NPNAM[147.04]LVNLEEPLASTYC   |
| 0.999999 | 1 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999999 | 1 K.IAALQAFADQLIAAGHYAK[325.13]GDISSR.R             |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I    |
| 0.999999 | 1 K.DKQFVAK[325.13]VMQVLNADAIVVK.L                  |
| 0.999999 | 1 K.DIHTLAQLISAYSLVDPEK[325.13]AK.A                 |
| 0.999999 | 1 R.VYYTM[147.04]EPEHPVGNWQK[325.13]HNVDDSLTTV      |
| 0.999999 | 1 K.DIHTLAQLISAYSLVDPEK[325.13]AK.A                 |
| 0.999999 | 1 R.VYYTMEPEHPVGNWQK[325.13]HNVDDSLTTVGSLLEDI       |
| 0.999999 | 1 K.TTQLIEMLHADMNVPFPEGFVIANDVDNK[325.13]R.C        |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIM[147.04]NSFVNDIFER.I    |
| 0.999999 | 0.9995 R.DALSDLALHFLNK[325.13]M[147.04]K.I          |
| 0.999999 | 1 K.GISDLVLK[325.13]EYLDNVQLGHILER.E                |
| 0.999999 | 1 K.GISDLVLK[325.13]EYLDNVQLGHILER.E                |
| 0.999999 | 1 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999999 | 1 K.TTQLIEMLHADMNVPFPEGFVIANDVDNK[325.13]R.C        |
| 0.999999 | 0.9859 R.DALSDLALHFLNK[325.13]M[147.04]K.I          |
| 0.999999 | 1 K.AK[325.13]GPVTIPYPLFQSHVEDLYVEGLPEGIPFR.R       |
| 0.999999 | 1 K.GISDLVLK[325.13]EYLDNVQLGHILER.E                |
| 0.999999 | 1 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999999 | 1 K.GISDLVLK[325.13]EYLDNVQLGHILER.E                |
| 0.999999 | 0.9992 R.LLLPGELAK[325.13]HAVSEGTK.A                |
| 0.999999 | 1 R.VYYTMEPEHPVGNWQK[325.13]HNVDDSLTTVGSLLEDI       |
| 0.999999 | 0.9984 R.DALSDLALHFLNK[325.13]M[147.04]K.I          |
| 0.999999 | 0.9946 R.LLLPGELAK[325.13]HAVSEGTK.A                |
| 0.999999 | 1 R.VYYTMEPEHPVGNWQK[325.13]HNVDDSLTTVGSLLEDI       |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I               |
| 0.999999 | 1 R.LTHVDSPLAPAGPLGQVK[325.13]LTLWYYSEER.K          |
| 0.999999 | 1 K.GLGILSLK[325.13]QQEMMAALTDAIQDKK.N              |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I               |
| 0.999999 | 0.9957 R.DALSDLALHFLNK[325.13]M[147.04]K.I          |
| 0.999999 | 1 R.GVQDIVVGEGTHFLIPWVQK[325.13]PIIFDC[160.03]R.S   |
| 0.999999 | 1 R.DSTLGK[325.13]AFHITNDEIPFWTFLSR.I               |
| 0.999999 | 1 R.YAHWVVSQPPDTYLK[325.13]PLMTELLK.R               |
| 0.999999 | 1 R.YAHWVVSQPPDTYLK[325.13]PLMTELLK.R               |
| 0.999999 | 1 R.GVQDIVVGEGTHFLIPWVQK[325.13]PIIFDC[160.03]R.S   |
| 0.999999 | 1 R.K[325.13]FDVNTSAVQVLEHIGNLDR.A                  |
| 0.999999 | 1 R.K[325.13]FDVNTSAVQVLEHIGNLDR.A                  |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I               |

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| 0.999999 | 1 R.GVQDIVVGEGTHFLIPWVQK[325.13]PIIFDC[160.03]R.S |
| 0.999999 | 1 R.YAHWVVSQPPDTYLK[325.13]PLMTELLK.R             |
| 0.999999 | 1 R.DSTLGGK[325.13]AFHITNDEPIPFWTFLSR.I           |
| 0.999999 | 1 R.K[325.13]FDVNTSAVQVLEHIGNLDR.A                |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I             |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  |
| 0.999999 | 1 R.YAHWVVSQPPDTYLK[325.13]PLMTELLK.R             |
| 0.999999 | 1 R.DSTLGGK[325.13]AFHITNDEPIPFWTFLSR.I           |
| 0.999999 | 1 R.YAHWVVSQPPDTYLK[325.13]PLMTELLK.R             |
| 0.999999 | 1 R.DALSDLALHFLNK[325.13]M[147.04]K.I             |
| 0.999999 | 1 K.NMAEQIIQEISQIQSK[325.13]KK.I                  |
| 0.999999 | 1 R.TGVVK[325.13]EGDQIVGATIYFDNLQSGEVTQLLNTMGH    |
| 0.999999 | 1 R.ITK[325.13]VLNMKPPEILSMIEEAAGTR.M             |
| 0.999999 | 1 R.DDPIISTHLAK[325.13]LYDNLLEQNLR.V              |
| 0.999999 | 0.9996 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |
| 0.999999 | 1 K.NMAEQIIQEISQIQSK[325.13]KK.I                  |
| 0.999999 | 1 R.VLGEAQT[325.13]AQHQQALSSLELLNVLFR.T           |
| 0.999999 | 1 K.MKDAILAK[325.13]LANQAADYFGDAFK.Q              |
| 0.999999 | 1 R.ITK[325.13]VLNMKPPEILSMIEEAAGTR.M             |
| 0.999999 | 0.9793 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |
| 0.999999 | 1 R.VLGEAQT[325.13]AQHQQALSSLELLNVLFR.T           |
| 0.999999 | 1 R.VLGEAQT[325.13]AQHQQALSSLELLNVLFR.T           |
| 0.999999 | 1 K.MKDAILAK[325.13]LANQAADYFGDAFK.Q              |
| 0.999999 | 0.9508 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |
| 0.999999 | 1 R.VLGEAQT[325.13]AQHQQALSSLELLNVLFR.T           |
| 0.999999 | 1 R.VLGEAQT[325.13]AQHQQALSSLELLNVLFR.T           |
| 0.999999 | 0.9973 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  |
| 0.999999 | 0.9645 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |
| 0.999999 | 1 R.DFQQALYELSYHVIK[325.13]GNLK.H                 |
| 0.999999 | 0.9853 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |
| 0.999999 | 1 R.LQLETEIEALKEELFMK[325.13]K.N                  |
| 0.999999 | 1 R.LQLETEIEALKEELFMK[325.13]K.N                  |
| 0.999999 | 1 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A         |
| 0.999999 | 1 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A         |
| 0.999999 | 0.9954 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |
| 0.999999 | 1 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A         |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                 |
| 0.999999 | 1 R.TDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A            |
| 0.999999 | 1 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A         |
| 0.999999 | 1 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A         |
| 0.999999 | 0.9687 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |
| 0.999999 | 1 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A         |
| 0.999999 | 1 K.VK[325.13]DALEFWLQAGVDGFQVR.D                 |
| 0.999999 | 1 R.TDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A            |
| 0.999999 | 1 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A         |
| 0.999999 | 0.9994 R.DALSDLALHFLNK[325.13]M[147.04]K.I        |

0.999999 1 R.LQLETEIEALKEELLFMK[325.13]K.N  
0.999999 1 R.RM[147.04]PQAPPSLC[160.03]VTPYPEPSEC[160.03]SW  
0.999999 1 R.LQLETEIEALKEELLFMK[325.13]K.N  
0.999999 1 R.LQLETEIEALKEELLFMK[325.13]K.N  
0.999999 0.9965 R.DALSDLALHFLNK[325.13]M[147.04]K.I  
0.999999 1 R.RM[147.04]PQAPPSLC[160.03]VTPYPEPSEC[160.03]SW  
0.999999 0.9972 R.DALSDLALHFLNK[325.13]M[147.04]K.I  
0.999999 0.9996 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 0.992 R.DALSDLALHFLNK[325.13]M[147.04]K.I  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 0.9919 R.DALSDLALHFLNK[325.13]M[147.04]K.I  
0.999999 1 K.QVHPDTGISSK[325.13]AMGIM[147.04]NSFVNDIFER.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 0.9999 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
0.999999 1 K.AYAALAALEK[325.13]LFPDTPLALDANKK.K  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 K.AYAALAALEK[325.13]LFPDTPLALDANKK.K  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
0.999999 0.9971 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I  
0.999999 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
0.999999 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I  
0.999999 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I  
0.999999 1 K.AIHYALNC[160.03]C[160.03]GLAGGVEQFISDIC[160.03]  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I



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|----------|-----------------------------------------------------|
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 K.AIHyalNC[160.03]C[160.03]GLAGGVEQFISDIC[160.03] |
| 0.999999 | 1 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR.   |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 R.SVFK[325.13]PIVQIAVIENSESLDC[160.03]QLLAVTHAGV  |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 R.SIPAYLAETLYYAMK[325.13]GAGTDDHTLIR.V            |
| 0.999999 | 1 R.GRDPVNPEK[325.13]LLVITVATAETEGYLR.F             |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 R.SVFK[325.13]PIVQIAVIENSESLDC[160.03]QLLAVTHAGV  |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 R.GRDPVNPEK[325.13]LLVITVATAETEGYLR.F             |
| 0.999999 | 1 R.GRDPVNPEK[325.13]LLVITVATAETEGYLR.F             |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.999999 | 1 R.SVFK[325.13]PIVQIAVIENSESLDC[160.03]QLLAVTHAGV  |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.999999 | 1 R.SIPAYLAETLYYAMK[325.13]GAGTDDHTLIR.V            |
| 0.999999 | 1 R.SIPAYLAETLYYAMK[325.13]GAGTDDHTLIR.V            |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.999999 | 1 R.SIPAYLAETLYYAMK[325.13]GAGTDDHTLIR.V            |
| 0.999999 | 1 R.SIPAYLAETLYYAMK[325.13]GAGTDDHTLIR.V            |
| 0.999999 | 1 R.RIPADTFAALK[325.13]NPNAMLVNLEEPLASTYQDILYQA     |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y             |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y             |
| 0.999999 | 1 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.999999 | 1 R.RIPADTFAALK[325.13]NPNAMLVNLEEPLASTYQDILYQA     |
| 0.999999 | 1 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y             |
| 0.999999 | 0.9992 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I       |
| 0.999999 | 1 K.ASLDRPFTNLESAFYSLGLSSSLGAQVPDAK[325.13]K.A      |
| 0.999999 | 1 R.FQSSAVM[147.04]ALQEAC[160.03]EAYLVGLFEDTNLC[1   |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 1 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999999 | 0.9969 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I       |
| 0.999999 | 1 K.TGAFSIPVIQIVYETLKDQQEGK[325.13]K.G              |
| 0.999999 | 1 K.GILADESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV     |
| 0.999999 | 1 K.DNTIEHLLPLFLAQLK[325.13]DEC[160.03]PEVR.L       |
| 0.999999 | 1 K.DNTIEHLLPLFLAQLK[325.13]DEC[160.03]PEVR.L       |
| 0.999999 | 1 K.GILADESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV     |
| 0.999999 | 1 K.DNTIEHLLPLFLAQLK[325.13]DEC[160.03]PEVR.L       |

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| 0.999999 | 1 R.LADLK[325.13]QLWGGLIEETEK.R.H                  |
| 0.999999 | 1 K.GILADEDESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV  |
| 0.999999 | 1 R.ELAQQIQK[325.13]VVMALGDYMGASC[160.03]HAC[16    |
| 0.999999 | 1 K.GILADEDESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV  |
| 0.999999 | 1 R.LADLK[325.13]QLWGGLIEETEK.R.H                  |
| 0.999999 | 1 R.LADLK[325.13]QLWGGLIEETEK.R.H                  |
| 0.999999 | 1 K.GILADEDESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV  |
| 0.999999 | 1 R.ELAQQIQK[325.13]VVMALGDYMGASC[160.03]HAC[16    |
| 0.999999 | 1 R.LGHAETDEQLQNIISK[325.13]FLPPVLLK.L             |
| 0.999999 | 1 K.EVK[325.13]GDLENAFLNLVQC[160.03]IQNKPLYFADR.L  |
| 0.999999 | 1 K.EVK[325.13]GDLENAFLNLVQC[160.03]IQNKPLYFADR.L  |
| 0.999999 | 1 K.EVK[325.13]GDLENAFLNLVQC[160.03]IQNKPLYFADR.L  |
| 0.999999 | 1 K.EVK[325.13]GDLENAFLNLVQC[160.03]IQNKPLYFADR.L  |
| 0.999999 | 1 R.HTDNVIQWLNAMDEIGLPK[325.13]IFYPETTDIYDR.K      |
| 0.999999 | 1 R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK[325.13]YESLEL    |
| 0.999999 | 1 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T              |
| 0.999999 | 1 R.LAEPSQLLK[325.13]SAIVHLINYQDDAELATR.A          |
| 0.999999 | 1 R.LAEPSQLLK[325.13]SAIVHLINYQDDAELATR.A          |
| 0.999999 | 1 K.LLLQGEADQSLTIFDK[325.13]AMHGELQK.A             |
| 0.999999 | 1 R.LAEPSQLLK[325.13]SAIVHLINYQDDAELATR.A          |
| 0.999999 | 1 K.LLLQGEADQSLTIFDK[325.13]AMHGELQK.A             |
| 0.999999 | 1 K.LLLQGEADQSLTIFDK[325.13]AMHGELQK.A             |
| 0.999999 | 1 R.QREELGQGLQGVEQK[325.13]VQSLQATFGTFESILR.S      |
| 0.999999 | 1 R.LAEPSQLLK[325.13]SAIVHLINYQDDAELATR.A          |
| 0.999999 | 1 R.LAEPSQLLK[325.13]SAIVHLINYQDDAELATR.A          |
| 0.999999 | 1 R.DIK[325.13]EKLC[160.03]YVALDFENEMATAASSSSLEK.S |
| 0.999999 | 1 K.SLEGDLEDLKDQIAQLEASLAAAK[325.13]K.Q            |
| 0.999999 | 1 R.FQSAAIGALQEASEAYLVGLFEDTNLC[160.03]AIHAK[325.  |
| 0.999999 | 1 K.SLEGDLEDLKDQIAQLEASLAAAK[325.13]K.Q            |
| 0.999999 | 1 K.SLEGDLEDLKDQIAQLEASLAAAK[325.13]K.Q            |
| 0.999999 | 1 K.SLEGDLEDLKDQIAQLEASLAAAK[325.13]K.Q            |
| 0.999999 | 1 R.FQSAAIGALQEASEAYLVGLFEDTNLC[160.03]AIHAK[325.  |
| 0.999999 | 1 K.SLEGDLEDLKDQIAQLEASLAAAK[325.13]K.Q            |
| 0.999999 | 1 R.DIKEK[325.13]LC[160.03]YVALDFENEMATAASSSSLEK.S |
| 0.999999 | 1 R.FQSAAIGALQEASEAYLVGLFEDTNLC[160.03]AIHAK[325.  |
| 0.999999 | 1 R.FQSAAIGALQEASEAYLVGLFEDTNLC[160.03]AIHAK[325.  |
| 0.999999 | 1 R.KLPIDVTEGEVISLGLPFGK[325.13]VTNLLMLK.G         |
| 0.999999 | 1 R.DLTDYLMK[325.13]ILTER.G                        |
| 0.999999 | 1 R.KLPIDVTEGEVISLGLPFGK[325.13]VTNLLMLK.G         |
| 0.999999 | 1 R.ALGLGVEQLPVVFEDVVLHQATILPK[325.13]TGTVSLEVR.   |
| 0.999999 | 1 R.ALGLGVEQLPVVFEDVVLHQATILPK[325.13]TGTVSLEVR.   |
| 0.999999 | 1 R.ALGLGVEQLPVVFEDVVLHQATILPK[325.13]TGTVSLEVR.   |
| 0.999999 | 1 R.ALGLGVEQLPVVFEDVVLHQATILPK[325.13]TGTVSLEVR.   |
| 0.999999 | 1 R.GIHSIDASQTPDVVFASILAAFSK[325.13]ATC[160.03]K.I |
| 0.999999 | 1 R.GIHSIDASQTPDVVFASILAAFSK[325.13]ATC[160.03]K.I |
| 0.999999 | 1 R.GIHSIDASQTPDVVFASILAAFSK[325.13]ATC[160.03]K.I |
| 0.999999 | 1 R.GIHSIDASQTPDVVFASILAAFSK[325.13]ATC[160.03]K.I |

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| 0.999999 | 1 R.LQLNGNLQLELAQVLAQERPK[325.13]LPEDPLLSGLLDSP/   |
| 0.999999 | 1 R.GIHSIDASQTPDVVFASILAAFSK[325.13]ATC[160.03]K.I |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K         |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K         |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K         |
| 0.999999 | 1 K.ELASALK[325.13]SALSGHLETVILGLLK.T              |
| 0.999999 | 1 K.ELASALK[325.13]SALSGHLETVILGLLK.T              |
| 0.999999 | 1 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A             |
| 0.999999 | 1 R.SSK[325.13]QHYN[160.03]EHSK.I                  |
| 0.999999 | 1 K.KAK[325.13]KPAAAAGAK.K                         |
| 0.999999 | 1 K.KAK[325.13]KPAAAAGAK.K                         |
| 0.999999 | 1 K.KAK[325.13]KPAAAAGAK.K                         |
| 0.999999 | 1 K.KPAPEK[325.13]KPAEK.K                          |
| 0.999999 | 1 K.K[325.13]KAEGGGGGGRPGAPAAGDGK.T                |
| 0.999999 | 1 K.K[325.13]KAEGGGGGGRPGAPAAGDGK.T                |
| 0.999999 | 1 K.KPAPEK[325.13]KPAEK.K                          |
| 0.999999 | 1 K.AGGTKPK[325.13]KPVGAAG.K                       |
| 0.999999 | 1 K.KK[325.13]AEGGGGGGRPGAPAAGDGK.T                |
| 0.999999 | 1 K.AGGTKPK[325.13]KPVGAAG.K                       |
| 0.999999 | 1 K.KAK[325.13]KPAAATVTK.K                         |
| 0.999999 | 1 K.KAK[325.13]KPAAATVTK.K                         |
| 0.999999 | 1 R.GGHIK[325.13]DC[160.03]KEPK.R                  |
| 0.999999 | 1 K.KAK[325.13]KPAAATVTK.K                         |
| 0.999999 | 1 K.KAEGGGGGGRPGAPAAGDGK[325.13]TEQK.G             |
| 0.999999 | 1 R.GGHIK[325.13]DC[160.03]KEPK.R                  |
| 0.999999 | 1 R.KPSAPK[325.13]KGDSSAEELK.L                     |
| 0.999999 | 1 K.K[325.13]HGVYNPNK.I                            |
| 0.999999 | 1 K.K[325.13]HGVYNPNK.I                            |
| 0.999999 | 1 K.KVSYSHIQSK[325.13]C[160.03]GSK.D               |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG:  |
| 0.999999 | 1 R.K[325.13]VAHSDKPGSTSTASFR.D                    |
| 0.999999 | 1 R.K[325.13]VAHSDKPGSTSTASFR.D                    |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG:  |
| 0.999999 | 1 R.K[325.13]VAHSDKPGSTSTASFR.D                    |
| 0.999999 | 1 R.HLVYESDKNK[325.13]DEK.L                        |
| 0.999999 | 1 R.HLVYESDKNK[325.13]DEK.L                        |
| 0.999999 | 1 R.DMHSAYK[325.13]HADGK.K                         |
| 0.999999 | 1 R.FHVEEEGKGK[325.13]DASGNK.V                     |
| 0.999999 | 1 R.FHVEEEGKGK[325.13]DASGNK.V                     |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG:  |
| 0.999999 | 1 R.K[325.13]VAHSDKPGSTSTASFR.D                    |
| 0.999999 | 1 R.K[325.13]VAHSDKPGSTSTASFR.D                    |
| 0.999999 | 1 R.K[325.13]VAHSDKPGSTSTASFR.D                    |
| 0.999999 | 1 R.K[325.13]VAHSDKPGSTSTASFR.D                    |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG:  |
| 0.999999 | 1 R.FHVEEEGKGK[325.13]DASGNK.V                     |
| 0.999999 | 1 R.DMHSAYK[325.13]HADGK.K                         |

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|----------|-----------------------------------------------------|
| 0.999999 | 1 R.DMHSAYK[325.13]HADGK.K                          |
| 0.999999 | 1 R.LPSGNHMK[325.13]ESR.E                           |
| 0.999999 | 1 R.FHVEEEGKGK[325.13]DASGNK.V                      |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 R.HLVYESDK[325.13]NKDEK.L                         |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 K.VHLDK[325.13]AQQNNVEHK.V                        |
| 0.999999 | 1 R.FHVEEEGK[325.13]GKDASGNK.V                      |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 R.HLVYESDK[325.13]NKDEK.L                         |
| 0.999999 | 1 R.FHVEEEGK[325.13]GKDASGNK.V                      |
| 0.999999 | 1 R.C[160.03]YEC[160.03]GEK[325.13]GHYAYDC[160.03]H |
| 0.999999 | 1 R.FHVEEEGK[325.13]GKDASGNK.V                      |
| 0.999999 | 1 R.C[160.03]YEC[160.03]GEK[325.13]GHYAYDC[160.03]H |
| 0.999999 | 1 K.KQPHGGQQK[325.13]PSYGSYGQSHQGQQQSYNQSPYSI       |
| 0.999999 | 1 K.AC[160.03]VK[325.13]TYHYHC[160.03]GVQDK.A       |
| 0.999999 | 1 K.AC[160.03]VK[325.13]TYHYHC[160.03]GVQDK.A       |
| 0.999999 | 1 K.RDPALNSGVSQKDPK[325.13]TK.N                     |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 K.AC[160.03]VK[325.13]TYHYHC[160.03]GVQDK.A       |
| 0.999999 | 1 K.K[325.13]QPHGGQQKPSYGSYGQSHQGQQQSYNQSPYSI       |
| 0.999999 | 1 K.GYEK[325.13]KPYC[160.03]NAHYPK.Q                |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 K.K[325.13]QPHGGQQKPSYGSYGQSHQGQQQSYNQSPYSI       |
| 0.999999 | 1 R.NQHLVSQQK[325.13]DPDTEEYRK.L                    |
| 0.999999 | 1 R.NQHLVSQQK[325.13]DPDTEEYRK.L                    |
| 0.999999 | 1 R.C[160.03]YEC[160.03]GEK[325.13]GHYAYDC[160.03]H |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 R.C[160.03]YEC[160.03]GEK[325.13]GHYAYDC[160.03]H |
| 0.999999 | 1 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG!   |
| 0.999999 | 1 K.K[325.13]QPHGGQQKPSYGSYGQSHQGQQQSYNQSPYSI       |
| 0.999999 | 1 K.K[325.13]QPHGGQQKPSYGSYGQSHQGQQQSYNQSPYSI       |
| 0.999999 | 1 R.C[160.03]YEC[160.03]GEK[325.13]GHYAYDC[160.03]H |
| 0.999999 | 1 K.KQPHGGQQK[325.13]PSYGSYGQSHQGQQQSYNQSPYSI       |
| 0.999999 | 1 R.C[160.03]YEC[160.03]GEK[325.13]GHYAYDC[160.03]H |
| 0.999999 | 1 R.C[160.03]YEC[160.03]GEK[325.13]GHYAYDC[160.03]H |
| 0.999999 | 1 K.GATYGK[325.13]PVHHGVNQLK.F                      |
| 0.999999 | 1 K.GATYGK[325.13]PVHHGVNQLK.F                      |
| 0.999999 | 1 K.GATYGK[325.13]PVHHGVNQLK.F                      |
| 0.999999 | 1 K.GATYGK[325.13]PVHHGVNQLK.F                      |
| 0.999999 | 1 K.GATYGK[325.13]PVHHGVNQLK.F                      |
| 0.999999 | 1 R.LEKPAK[325.13]YDDIKK.V                          |
| 0.999999 | 1 R.LEKPAK[325.13]YDDIKK.V                          |
| 0.999999 | 1 K.KQPHGGQQK[325.13]PSYGSYGQSHQGQQQSYNQSPYSI       |

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| 0.999999 | 1 R.LEKPAK[325.13]YDDIKK.V                           |
| 0.999999 | 1 R.LQVK[325.13]EHQHHEIQNVR.N                        |
| 0.999999 | 1 K.KQPHGGQK[325.13]PSYSGYQSHQGQQSYNQSPYSI           |
| 0.999999 | 1 K.K[325.13]TTHFVEGGDAGNREDQINR.L                   |
| 0.999999 | 1 R.K[325.13]GSEHQAIVQHLEK.S                         |
| 0.999999 | 1 R.K[325.13]REDC[160.03]SPADKPYIDEAR.R              |
| 0.999999 | 1 R.K[325.13]REDC[160.03]SPADKPYIDEAR.R              |
| 0.999999 | 1 R.LEK[325.13]PAKYDDIKK.V                           |
| 0.999999 | 1 R.LQVK[325.13]EHQHHEIQNVR.N                        |
| 0.999999 | 0.7211 R.HQVGM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA |
| 0.999999 | 1 K.LHQAMK[325.13]GVGTR.H                            |
| 0.999999 | 1 R.EDSVKPGAHLTVK[325.13]K.I                         |
| 0.999999 | 1 R.LEK[325.13]PAKYDDIKK.V                           |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.K[325.13]REDC[160.03]SPADKPYIDEAR.R              |
| 0.999999 | 1 K.LHQAMK[325.13]GVGTR.H                            |
| 0.999999 | 1 K.LHQAMK[325.13]GVGTR.H                            |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.TSSAQVEGGVHSLHSYEK[325.13]R.L                    |
| 0.999999 | 1 R.TSSAQVEGGVHSLHSYEK[325.13]R.L                    |
| 0.999999 | 1 R.LGNDFHTNK[325.13]R.V                             |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.LGNDFHTNK[325.13]R.V                             |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.TSSAQVEGGVHSLHSYEK[325.13]R.L                    |
| 0.999999 | 1 K.TKDGVEITGK[325.13]HEER.Q                         |
| 0.999999 | 1 K.TKDGVEITGK[325.13]HEER.Q                         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.TSSAQVEGGVHSLHSYEK[325.13]R.L                    |
| 0.999999 | 1 R.KIIK[325.13]DGEQHEDLNEVAK.L                      |
| 0.999999 | 1 R.TSSAQVEGGVHSLHSYEK[325.13]R.L                    |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 K.TKDGVEITGK[325.13]HEER.Q                         |
| 0.999999 | 1 K.TKDGVEITGK[325.13]HEER.Q                         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |
| 0.999999 | 1 R.LSHYLQK[325.13]GC[160.03]R.L                     |
| 0.999999 | 1 R.TSSAQVEGGVHSLHSYEK[325.13]R.L                    |
| 0.999999 | 1 R.LSHYLQK[325.13]GC[160.03]R.L                     |
| 0.999999 | 1 K.K[325.13]IKDPDASKPEDWDER.A                       |
| 0.999999 | 1 K.K[325.13]IKDPDASKPEDWDER.A                       |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L        |

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| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.KIIK[325.13]DGEQHEDLNEVAK.L                       |
| 0.999999 | 1 R.LSHYLQK[325.13]GC[160.03]R.L                      |
| 0.999999 | 1 R.KIIK[325.13]DGEQHEDLNEVAK.L                       |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 K.K[325.13]IKDPDASKPEDWDER.A                        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 K.GISVHISNAEPK[325.13]HNSNR.Q                       |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 0.9157 R.HQGVMM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA |
| 0.999999 | 1 K.K[325.13]IKDPDASKPEDWDER.A                        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 K.GISVHISNAEPK[325.13]HNSNR.Q                       |
| 0.999999 | 1 R.HQGVMMVGM[147.04]GQK[325.13]DSYVGDEAQSKR.G        |
| 0.999999 | 1 R.HQGVMMVGM[147.04]GQK[325.13]DSYVGDEAQSKR.G        |
| 0.999999 | 1 R.HQGVMMVGM[147.04]GQK[325.13]DSYVGDEAQSKR.G        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 K.TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK[3             |
| 0.999999 | 1 K.TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK[3             |
| 0.999999 | 1 K.TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK[3             |
| 0.999999 | 1 R.HQGVMM[147.04]VGMGQK[325.13]DSYVGDEAQSKR.G        |
| 0.999999 | 1 R.HQGVMM[147.04]VGMGQK[325.13]DSYVGDEAQSKR.G        |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 R.VSVADHSLHLSK[325.13]AK.I                          |
| 0.999999 | 1 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L         |
| 0.999999 | 1 K.LAQSHHVK[325.13]QVLVAPGNAGTAC[160.03]SEK.I        |
| 0.999999 | 1 K.LAQSHHVK[325.13]QVLVAPGNAGTAC[160.03]SEK.I        |
| 0.999999 | 1 R.VSVADHSLHLSK[325.13]AK.I                          |
| 0.999999 | 1 K.LAQSHHVK[325.13]QVLVAPGNAGTAC[160.03]SEK.I        |
| 0.999999 | 1 K.LAQSHHVK[325.13]QVLVAPGNAGTAC[160.03]SEK.I        |
| 0.999999 | 0.994 R.HQGVMMVGMGQK[325.13]DSYVGDEAQSKR.G            |
| 0.999999 | 1 R.MKENQK[325.13]HIYYITGETK.D                        |
| 0.999999 | 1 R.MKENQK[325.13]HIYYITGETK.D                        |
| 0.999999 | 1 R.HQGVMMVGMGQK[325.13]DSYVGDEAQSKR.G                |
| 0.999999 | 1 R.MKENQK[325.13]HIYYITGETK.D                        |
| 0.999999 | 1 R.MKENQK[325.13]HIYYITGETK.D                        |
| 0.999999 | 1 R.IFAPNHVVAK[325.13]SR.F                            |
| 0.999999 | 1 K.TLHPDLGTDK[325.13]DKEQWK.E                        |
| 0.999999 | 1 K.TLHPDLGTDK[325.13]DKEQWK.E                        |

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| 0.999999 | 1 K.TKHK[325.13]LDVTSVEDYK.A                          |
| 0.999999 | 1 R.ARENIQK[325.13]SLAGSSGPGASSGTSGDHGELVVR.I         |
| 0.999999 | 1 K.TLHPDLGTDK[325.13]DKEQWK.E                        |
| 0.999999 | 1 K.TLHPDLGTDK[325.13]DKEQWK.E                        |
| 0.999999 | 1 R.HQGVMVGMGQK[325.13]DSYVGDEAQSKR.G                 |
| 0.999999 | 1 R.IC[160.03]SKPVVLPK[325.13]GPESESEDHR.A            |
| 0.999999 | 1 R.HQGVMVGMGQK[325.13]DSYVGDEAQSKR.G                 |
| 0.999999 | 1 K.TKHK[325.13]LDVTSVEDYK.A                          |
| 0.999999 | 1 K.TKHK[325.13]LDVTSVEDYK.A                          |
| 0.999999 | 1 R.HYC[160.03]GK[325.13]C[160.03]C[160.03]LTYC[160.0 |
| 0.999999 | 1 K.KAEVEGK[325.13]DLPEHAVLK.M                        |
| 0.999999 | 1 K.KAEVEGK[325.13]DLPEHAVLK.M                        |
| 0.999999 | 1 R.HQGVMVGMGQK[325.13]DSYVGDEAQSKR.G                 |
| 0.999999 | 1 R.IFAPNHVVAK[325.13]SR.F                            |
| 0.999999 | 1 R.IFAPNHVVAK[325.13]SR.F                            |
| 0.999999 | 1 R.ASEEHLK[325.13]QHYIDLK.D                          |
| 0.999999 | 1 R.ASEEHLK[325.13]QHYIDLK.D                          |
| 0.999999 | 1 R.ARENIQK[325.13]SLAGSSGPGASSGTSGDHGELVVR.I         |
| 0.999999 | 1 R.ASEEHLK[325.13]QHYIDLK.D                          |
| 0.999999 | 1 R.IFAPNHVVAK[325.13]SR.F                            |
| 0.999999 | 1 R.GITGVEDK[325.13]ESWHGKPLPK.N                      |
| 0.999999 | 1 K.GFGYK[325.13]GSC[160.03]FHR.I                     |
| 0.999999 | 1 R.GITGVEDK[325.13]ESWHGKPLPK.N                      |
| 0.999999 | 1 R.MNK[325.13]AGQVMC[160.03]VAQGSNGTHSVGTVC[1        |
| 0.999999 | 1 R.ARENIQK[325.13]SLAGSSGPGASSGTSGDHGELVVR.I         |
| 0.999999 | 1 R.ARENIQK[325.13]SLAGSSGPGASSGTSGDHGELVVR.I         |
| 0.999999 | 1 R.GITGVEDK[325.13]ESWHGKPLPK.N                      |
| 0.999999 | 1 R.HYC[160.03]GK[325.13]C[160.03]C[160.03]LTYC[160.0 |
| 0.999999 | 1 R.GITGVEDK[325.13]ESWHGKPLPK.N                      |
| 0.999999 | 1 R.HYC[160.03]GK[325.13]C[160.03]C[160.03]LTYC[160.0 |
| 0.999999 | 1 R.ALVDHENVISC[160.03]PHLGASTK[325.13]EAQSR.C        |
| 0.999999 | 1 R.K[325.13]SNENSEVITPGFPPNHDQGEQYEHNR.V             |
| 0.999999 | 1 R.HYC[160.03]GK[325.13]C[160.03]C[160.03]LTYC[160.0 |
| 0.999999 | 1 R.HYC[160.03]GK[325.13]C[160.03]C[160.03]LTYC[160.0 |
| 0.999999 | 1 R.TGVELGKPTHFTVNAK[325.13]AAGK.G                    |
| 0.999999 | 1 R.GITGVEDKESWHGK[325.13]PLPK.N                      |
| 0.999999 | 1 R.AK[325.13]IDDPTDSKPEDWDKPEHIPDPDAK.K              |
| 0.999999 | 1 K.HGEVC[160.03]PAGWKPGSDTIK[325.13]PDVQK.S          |
| 0.999999 | 1 R.AK[325.13]IDDPTDSKPEDWDKPEHIPDPDAK.K              |
| 0.999999 | 1 R.GITGVEDKESWHGK[325.13]PLPK.N                      |
| 0.999999 | 1 R.GITGVEDKESWHGK[325.13]PLPK.N                      |
| 0.999999 | 1 K.HGEVC[160.03]PAGWKPGSDTIK[325.13]PDVQK.S          |
| 0.999999 | 1 K.YEELQSLAGK[325.13]HGDDLRR.T                       |
| 0.999999 | 1 K.YEELQSLAGK[325.13]HGDDLRR.T                       |
| 0.999999 | 1 R.ALVDHENVISC[160.03]PHLGASTK[325.13]EAQSR.C        |
| 0.999999 | 1 R.AK[325.13]IDDPTDSKPEDWDKPEHIPDPDAK.K              |
| 0.999999 | 1 R.ALVDHENVISC[160.03]PHLGASTK[325.13]EAQSR.C        |

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| 0.999999 | 1 K.HGEVC[160.03]PAGWKPGSDTIK[325.13]PDVQK.S   |
| 0.999999 | 1 R.AK[325.13]IDDPDTSKPEDWDKPEHIPDPDAK.K       |
| 0.999999 | 1 K.K[325.13]QLLC[160.03]GAAIGTHEDDKYR.L       |
| 0.999999 | 1 R.ALVDHENVISC[160.03]PHLGASTK[325.13]EAQSR.C |
| 0.999999 | 1 K.HGEVC[160.03]PAGWK[325.13]PGSDTIKPDVQK.S   |
| 0.999999 | 1 K.HGEVC[160.03]PAGWK[325.13]PGSDTIKPDVQK.S   |
| 0.999999 | 1 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T            |
| 0.999999 | 1 K.YEELQSLAGK[325.13]HGDDLRR.T                |
| 0.999999 | 1 R.ALVDHENVISC[160.03]PHLGASTK[325.13]EAQSR.C |
| 0.999999 | 1 K.K[325.13]KDQVTAQEIFQDNHEDGPTAK.K           |
| 0.999999 | 1 K.K[325.13]QLLC[160.03]GAAIGTHEDDKYR.L       |
| 0.999999 | 1 K.K[325.13]QLLC[160.03]GAAIGTHEDDKYR.L       |
| 0.999999 | 1 K.K[325.13]KDQVTAQEIFQDNHEDGPTAK.K           |
| 0.999999 | 1 R.ALVDHENVISC[160.03]PHLGASTK[325.13]EAQSR.C |
| 0.999999 | 1 K.HGEVC[160.03]PAGWK[325.13]PGSDTIKPDVQK.S   |
| 0.999999 | 1 K.HGEVC[160.03]PAGWK[325.13]PGSDTIKPDVQK.S   |
| 0.999999 | 1 K.K[325.13]QLLC[160.03]GAAIGTHEDDKYR.L       |
| 0.999999 | 1 K.HGEVC[160.03]PAGWK[325.13]PGSDTIKPDVQK.S   |
| 0.999999 | 1 K.FIDTTSK[325.13]FGHGR.F                     |
| 0.999999 | 1 K.LTGIK[325.13]HELQANC[160.03]YEEVKDR.C      |
| 0.999999 | 1 K.LTGIK[325.13]HELQANC[160.03]YEEVKDR.C      |
| 0.999999 | 1 R.M[147.04]HAPGK[325.13]GLSQSALPYR.R         |
| 0.999999 | 1 K.LTGIK[325.13]HELQANC[160.03]YEEVKDR.C      |
| 0.999999 | 1 K.LTGIK[325.13]HELQANC[160.03]YEEVKDR.C      |
| 0.999999 | 1 R.M[147.04]HAPGK[325.13]GLSQSALPYR.R         |
| 0.999999 | 1 K.KYEDIC[160.03]PSTHNMDVPNIK[325.13]R.N      |
| 0.999999 | 1 K.VHSPSGAVEEC[160.03]HVSELEPDK[325.13]YAVR.F |
| 0.999999 | 1 K.VHSPSGAVEEC[160.03]HVSELEPDK[325.13]YAVR.F |
| 0.999999 | 1 K.VHSPSGAVEEC[160.03]HVSELEPDK[325.13]YAVR.F |
| 0.999999 | 1 R.LREK[325.13]LQEEMLQR.E                     |
| 0.999999 | 1 K.VHSPSGAVEEC[160.03]HVSELEPDK[325.13]YAVR.F |
| 0.999999 | 1 R.K[325.13]VAC[160.03]IGAWHPAR.V             |
| 0.999999 | 1 R.MHAPGK[325.13]GLSQSALPYR.R                 |
| 0.999999 | 1 R.K[325.13]VAC[160.03]IGAWHPAR.V             |
| 0.999999 | 1 R.K[325.13]VAC[160.03]IGAWHPAR.V             |
| 0.999999 | 1 K.YGGPNHIVGSPFK[325.13]AK.V                  |
| 0.999999 | 1 K.AATKK[325.13]PVVNIITPSHVEER.G              |
| 0.999999 | 1 R.LLSDATVEKDESHAGK[325.13]VVLR.S             |
| 0.999999 | 1 R.ITLSK[325.13]HQNVLPR.E                     |
| 0.999999 | 1 R.LLSDATVEKDESHAGK[325.13]VVLR.S             |
| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y          |
| 0.999999 | 1 K.YGGPNHIVGSPFK[325.13]AK.V                  |
| 0.999999 | 1 R.K[325.13]VAC[160.03]IGAWHPAR.V             |
| 0.999999 | 1 R.K[325.13]VAC[160.03]IGAWHPAR.V             |
| 0.999999 | 1 R.LLSDATVEKDESHAGK[325.13]VVLR.S             |
| 0.999999 | 1 R.LLSDATVEKDESHAGK[325.13]VVLR.S             |
| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y          |



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|----------|---------------------------------------------------|
| 0.999999 | 1 R.K[325.13]VAC[160.03]IGAWHPAR.V                |
| 0.999999 | 1 R.K[325.13]VAC[160.03]IGAWHPAR.V                |
| 0.999999 | 1 R.LLSDATVEKDESHAGK[325.13]VVLR.S                |
| 0.999999 | 1 R.MHAPGK[325.13]GLSQSALPYR.R                    |
| 0.999999 | 1 R.LLSDATVEKDESHAGK[325.13]VVLR.S                |
| 0.999999 | 1 R.LREK[325.13]LQEEMLQR.E                        |
| 0.999999 | 1 R.MHAPGK[325.13]GLSQSALPYR.R                    |
| 0.999999 | 1 R.MHAPGK[325.13]GLSQSALPYR.R                    |
| 0.999999 | 1 R.HQEGEIFDTEK[325.13]EKYEITEQR.K                |
| 0.999999 | 1 R.LREK[325.13]LQEEMLQR.E                        |
| 0.999999 | 1 R.LREK[325.13]LQEEMLQR.E                        |
| 0.999999 | 1 R.K[325.13]TFTAWC[160.03]NSHLR.K                |
| 0.999999 | 1 R.MHAPGK[325.13]GLSQSALPYR.R                    |
| 0.999999 | 0.9999 K.GLVLGPIHK[325.13]NQK.D                   |
| 0.999999 | 1 R.GINLSDGK[325.13]WHR.I                         |
| 0.999999 | 1 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y             |
| 0.999999 | 1 K.DYHFK[325.13]VDNDENEHQLSLR.T                  |
| 0.999999 | 1 R.K[325.13]TFTAWC[160.03]NSHLR.K                |
| 0.999999 | 1 R.SKVDEAVAVLQAHQAK[325.13]EAAQK.A               |
| 0.999999 | 1 R.SKVDEAVAVLQAHQAK[325.13]EAAQK.A               |
| 0.999999 | 0.9999 R.K[325.13]TFTAWC[160.03]NSHLR.K           |
| 0.999999 | 1 K.NVIIWGNHSSTQYPDVNHAK[325.13]VK.L              |
| 0.999999 | 1 K.YGGPYHIGGSPFK[325.13]AK.V                     |
| 0.999999 | 1 R.K[325.13]TFTAWC[160.03]NSHLR.K                |
| 0.999999 | 1 R.LLM[147.04]HGK[325.13]EVGSIIGK.K              |
| 0.999999 | 1 K.LK[325.13]TNHIGHTGYLNTVTVSPDGSLC[160.03]ASGGK |
| 0.999999 | 1 R.SKVDEAVAVLQAHQAK[325.13]EAAQK.A               |
| 0.999999 | 1 R.SKVDEAVAVLQAHQAK[325.13]EAAQK.A               |
| 0.999999 | 1 K.LK[325.13]TNHIGHTGYLNTVTVSPDGSLC[160.03]ASGGK |
| 0.999999 | 1 R.K[325.13]TFTAWC[160.03]NSHLR.K                |
| 0.999999 | 1 K.NVIIWGNHSSTQYPDVNHAK[325.13]VK.L              |
| 0.999999 | 1 K.NVIIWGNHSSTQYPDVNHAK[325.13]VK.L              |
| 0.999999 | 1 R.HQEGEIFDTEKEK[325.13]YEITEQR.K                |
| 0.999999 | 1 K.INEEISVK[325.13]HLPSTEPDPHVVR.I               |
| 0.999999 | 1 K.YGGPYHIGGSPFK[325.13]AK.V                     |
| 0.999999 | 1 R.HQEGEIFDTEKEK[325.13]YEITEQR.K                |
| 0.999999 | 1 R.SLHDALC[160.03]VVK[325.13]R.V                 |
| 0.999999 | 1 K.LK[325.13]TNHIGHTGYLNTVTVSPDGSLC[160.03]ASGGK |
| 0.999999 | 1 K.INEEISVK[325.13]HLPSTEPDPHVVR.I               |
| 0.999999 | 1 R.QLYVLGHEAMK[325.13]R.L                        |
| 0.999999 | 1 K.KEELVAEQAIK[325.13]HLK.Q                      |
| 0.999999 | 1 R.QLYVLGHEAMK[325.13]R.L                        |
| 0.999999 | 1 K.FSGK[325.13]HVVFIAQR.R                        |
| 0.999999 | 1 R.K[325.13]NVLGHMQQGGAPSPFDR.N                  |
| 0.999999 | 1 K.QGFPMK[325.13]QGVLTGHR.V                      |
| 0.999999 | 1 K.FSGK[325.13]HVVFIAQR.R                        |
| 0.999999 | 1 R.SVPHLQK[325.13]VFDR.Y                         |

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|----------|-------------------------------------------------|
| 0.999999 | 1 K.FSGK[325.13]HVVFIAQR.R                      |
| 0.999999 | 1 R.K[325.13]NVLGHMQQGGAPSPFDR.N                |
| 0.999999 | 0.9999 R.SVPHLQK[325.13]VFDR.Y                  |
| 0.999999 | 1 R.SVPHLQK[325.13]VFDR.Y                       |
| 0.999999 | 1 K.NVIHK[325.13]IFSK.F                         |
| 0.999999 | 1 K.LK[325.13]HYGPGWVSMANAGK.D                  |
| 0.999999 | 1 R.NRPPLPAGTNSK[325.13]GPPDFSSDEEREPTPVLGSGAAA |
| 0.999999 | 1 K.LK[325.13]HYGPGWVSMANAGK.D                  |
| 0.999999 | 1 R.SVPHLQK[325.13]VFDR.Y                       |
| 0.999999 | 1 R.NRPPLPAGTNSK[325.13]GPPDFSSDEEREPTPVLGSGAAA |
| 0.999999 | 1 K.KEELVAEQAQK[325.13]HLK.Q                    |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 R.NALQQENHIIDGVK[325.13]VQVHTR.R              |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 K.KPYC[160.03]NAHYPK[325.13]QSFTMVADTPENLR.L  |
| 0.999999 | 1 R.LVNHFVEEFK[325.13]R.K                       |
| 0.999999 | 1 R.K[325.13]KNGPLEVAGAAVSAGHGLPAK.F            |
| 0.999999 | 1 R.GTK[325.13]VILHLKEDQTEYLEER.R               |
| 0.999999 | 1 R.EGDYVLFHHEGGVDVGDDAK[325.13]AQK.L           |
| 0.999999 | 1 K.VAVPSTIHC[160.03]DHLIEAQVGGEK[325.13]DLR.R  |
| 0.999999 | 1 R.RLELGPKE[325.13]PEVAQQTR.K                  |
| 0.999999 | 1 R.GTK[325.13]VILHLKEDQTEYLEER.R               |
| 0.999999 | 1 R.GPVLQLHDLK[325.13]R.E                       |
| 0.999999 | 1 K.VK[325.13]GLVLGPIHK.N                       |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 R.AHIAQLC[160.03]EK[325.13]AGLLQR.A           |
| 0.999999 | 0.9996 R.M[147.04]VNHFAIEFK[325.13]R.K          |
| 0.999999 | 1 R.GPVLQLHDLK[325.13]R.E                       |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 R.DDSFFGETSHNYHK[325.13]FDSEYER.M             |
| 0.999999 | 1 R.DDSFFGETSHNYHK[325.13]FDSEYER.M             |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 R.M[147.04]VNHFAIEFK[325.13]R.K               |
| 0.999999 | 1 R.LVNHFVEEFK[325.13]R.K                       |
| 0.999999 | 1 K.FAGGLHFSGPK[325.13]VEGGVK.G                 |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 R.DDSFFGETSHNYHK[325.13]FDSEYER.M             |
| 0.999999 | 1 R.DDSFFGETSHNYHK[325.13]FDSEYER.M             |
| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G      |
| 0.999999 | 1 R.LLMHGK[325.13]EVGSIIGK.K                    |
| 0.999999 | 1 R.LLMHGK[325.13]EVGSIIGK.K                    |
| 0.999999 | 1 R.LVNHFVEEFK[325.13]R.K                       |
| 0.999999 | 1 K.KVQAAQSEAK[325.13]VVSQYHELVVQAR.D           |
| 0.999999 | 1 R.LLMHGK[325.13]EVGSIIGK.K                    |
| 0.999999 | 1 R.VHIPNDDAQFDASHC[160.03]DSDK[325.13]GEFGGFGS |

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| 0.999999 | 1 R.HGK[325.13]YMAC[160.03]C[160.03]LLYR.G          |
| 0.999999 | 1 K.VGAVDADK[325.13]HHS LGGQYGVQGFPTIK.I            |
| 0.999999 | 1 R.MTLK[325.13]NLPLADQGSSHHITVK.I                  |
| 0.999999 | 1 R.M[147.04]VNH FIAEFK[325.13]R.K                  |
| 0.999999 | 1 R.LLMHGK[325.13]EVGSIIGK.K                        |
| 0.999999 | 1 K.LDSGK[325.13]ELHINLIPNKQDR.T                    |
| 0.999999 | 1 R.VHIPNDDAQFDASHC[160.03]DSDK[325.13]GEFGGFGSV    |
| 0.999999 | 1 R.VHIPNDDAQFDASHC[160.03]DSDK[325.13]GEFGGFGSV    |
| 0.999999 | 1 R.MTLK[325.13]NLPLADQGSSHHITVK.I                  |
| 0.999999 | 1 K.VGAVDADK[325.13]HHS LGGQYGVQGFPTIK.I            |
| 0.999999 | 1 R.LLMHGK[325.13]EVGSIIGK.K                        |
| 0.999999 | 1 R.AHIAQLC[160.03]EK[325.13]AGLLQR.A               |
| 0.999999 | 1 K.VK[325.13]GLVLGPIHK.N                           |
| 0.999999 | 1 K.LDSGK[325.13]ELHINLIPNKQDR.T                    |
| 0.999999 | 1 R.DC[160.03]QLNAHK[325.13]DHQYQFLEDAVR.N          |
| 0.999999 | 1 R.DC[160.03]QLNAHK[325.13]DHQYQFLEDAVR.N          |
| 0.999999 | 1 R.DAK[325.13]LDKSIHQDIVLVGGSTR.I                  |
| 0.999999 | 1 R.K[325.13]HGVVPLATYMR.I                          |
| 0.999999 | 1 K.AVIVK[325.13]NIDDGTS DRPYSHALVAGIDR.Y           |
| 0.999999 | 1 R.NMSVIAHVDHGK[325.13]STLTDSLVC[160.03]K.A        |
| 0.999999 | 1 R.NMSVIAHVDHGK[325.13]STLTDSLVC[160.03]K.A        |
| 0.999999 | 1 R.IGNFIVK[325.13]KPMVLGHEASGTVEK.V                |
| 0.999999 | 1 K.VK[325.13]GLVLGPIHK.N                           |
| 0.999999 | 1 K.VK[325.13]GLVLGPIHK.N                           |
| 0.999999 | 1 R.DC[160.03]QLNAHK[325.13]DHQYQFLEDAVR.N          |
| 0.999999 | 1 R.DC[160.03]QLNAHK[325.13]DHQYQFLEDAVR.N          |
| 0.999999 | 1 R.IGNFIVK[325.13]KPMVLGHEASGTVEK.V                |
| 0.999999 | 1 K.VK[325.13]GLVLGPIHK.N                           |
| 0.999999 | 1 R.DC[160.03]QLNAHK[325.13]DHQYQFLEDAVR.N          |
| 0.999999 | 1 R.K[325.13]HGVVPLATYMR.I                          |
| 0.999999 | 1 K.YKPAVNQIEC[160.03]HPYLTQEK[325.13]LIQYC[160.03] |
| 0.999999 | 1 R.GNTAAQLSK[325.13]TFHFNTVEEVHSR.F                |
| 0.999999 | 1 K.AVIVK[325.13]NIDDGTS DRPYSHALVAGIDR.Y           |
| 0.999999 | 1 K.AVIVK[325.13]NIDDGTS DRPYSHALVAGIDR.Y           |
| 0.999999 | 1 K.AVIVK[325.13]NIDDGTS DRPYSHALVAGIDR.Y           |
| 0.999999 | 1 R.GNTAAQLSK[325.13]TFHFNTVEEVHSR.F                |
| 0.999999 | 1 K.AVIVK[325.13]NIDDGTS DRPYSHALVAGIDR.Y           |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                 |
| 0.999999 | 1 R.SK[325.13]VDEAVAVLQAHHAK.K                      |
| 0.999999 | 1 K.LHIIEVGTPPTGNQPFPK[325.13]K.A                   |
| 0.999999 | 1 R.LDHK[325.13]FDLMYAK.R                           |
| 0.999999 | 1 R.MVNH FIAEFK[325.13]R.K                          |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                 |
| 0.999999 | 1 R.MVNH FIAEFK[325.13]R.K                          |
| 0.999999 | 1 R.LDHK[325.13]FDLMYAK.R                           |
| 0.999999 | 1 R.LGGHGPSFPLK[325.13]GITEQQK.E                    |

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| 0.999999 | 1 R.MVNHFAIEFK[325.13]R.K                        |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H             |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H             |
| 0.999999 | 0.9972 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L         |
| 0.999999 | 1 R.LGGHGPSFPLK[325.13]GITEQQK.E                 |
| 0.999999 | 1 K.RVTIMPK[325.13]DIQLAR.R                      |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H             |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 K.RVTIMPK[325.13]DIQLAR.R                      |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.DAK[325.13]LDKAQIHDLVLVGGSTR.I               |
| 0.999999 | 1 K.RVTIMPK[325.13]DIQLAR.R                      |
| 0.999999 | 1 K.LHIIEVGTPPTGNQPFPK[325.13]K.A                |
| 0.999999 | 1 K.LHIIEVGTPPTGNQPFPK[325.13]K.A                |
| 0.999999 | 1 K.VDWLTEK[325.13]MHAR.D                        |
| 0.999999 | 1 R.HDK[325.13]VEDALNLKEEFDR.L                   |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H             |
| 0.999999 | 1 R.IFHELTQTDK[325.13]ALFNR.L                    |
| 0.999999 | 1 K.VDWLTEK[325.13]MHAR.D                        |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H             |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.LVQAFQYTDEHGEVC[160.03]PAGWK[325.13]PGSDTIKF |
| 0.999999 | 1 R.LVQAFQYTDEHGEVC[160.03]PAGWK[325.13]PGSDTIKF |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 0.9992 R.LK[325.13]LEPHEGLLLR.F                  |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                       |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L              |
| 0.999999 | 1 R.LAQFVEHWK[325.13]ELK.Q                       |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                       |
| 0.999999 | 1 R.AC[160.03]K[325.13]AVGHFPFVIQLGR.I           |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                       |
| 0.999999 | 0.9945 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L         |
| 0.999999 | 0.999 R.LK[325.13]LEPHEGLLLR.F                   |
| 0.999999 | 0.9753 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L         |

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| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 0.9914 R.LLLPGELAK[325.13]HAVSEGTK.A                |
| 0.999999 | 1 K.IWFDKFK[325.13]YDDAER.R                         |
| 0.999999 | 1 K.IWFDKFK[325.13]YDDAER.R                         |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.SQHDILQMIC[160.03]SK[325.13]R.R                 |
| 0.999999 | 1 R.SQHDILQMIC[160.03]SK[325.13]R.R                 |
| 0.999999 | 1 K.IWFDKFK[325.13]YDDAER.R                         |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.LYVHEAVK[325.13]AGVVGPPELHEQLLSAEK.A            |
| 0.999999 | 1 K.LPNLTHLNLSGNK[325.13]LK.D                       |
| 0.999999 | 1 K.FLDAGHK[325.13]LNFAVASR.K                       |
| 0.999999 | 1 R.GAGM[147.04]PGQHGQITQQELDTVVK[325.13]TQHEIL     |
| 0.999999 | 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160 |
| 0.999999 | 1 R.LLIHQSLAGGIIGVK[325.13]GAK.I                    |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.SQHDILQMIC[160.03]SK[325.13]R.R                 |
| 0.999999 | 1 K.IWFDKFK[325.13]YDDAER.R                         |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.LYVHEAVK[325.13]AGVVGPPELHEQLLSAEK.A            |
| 0.999999 | 1 K.LPNLTHLNLSGNK[325.13]LK.D                       |
| 0.999999 | 1 K.IWFDKFK[325.13]YDDAER.R                         |
| 0.999999 | 1 R.LLIHQSLAGGIIGVK[325.13]GAK.I                    |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 K.KPLPDHVSIVEPK[325.13]DEILPTTPISEQK.G            |
| 0.999999 | 1 R.TVYC[160.03]NVHK[325.13]HEPLVLFC[160.03]ESC[160 |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 0.9996 R.LLLPGELAK[325.13]HAVSEGTK.A                |
| 0.999999 | 1 K.LPNLTHLNLSGNK[325.13]LK.D                       |
| 0.999999 | 1 R.GAGM[147.04]PGQHGQITQQELDTVVK[325.13]TQHEIL     |
| 0.999999 | 1 R.LFTK[325.13]VKPLLQVSR.Q                         |
| 0.999999 | 0.9999 R.LK[325.13]LEPHEGLLLR.F                     |
| 0.999999 | 1 R.GAGM[147.04]PGQHGQITQQELDTVVK[325.13]TQHEIL     |
| 0.999999 | 1 R.VGSHITGGDIYGIVSENSLIK[325.13]HK.I               |
| 0.999999 | 1 R.HIQQVDC[160.03]SGNDLEQLHIK[325.13]VTSLC[160.03  |
| 0.999999 | 1 R.LFTK[325.13]VKPLLQVSR.Q                         |
| 0.999999 | 1 R.GAGM[147.04]PGQHGQITQQELDTVVK[325.13]TQHEIL     |
| 0.999999 | 1 R.HIQQVDC[160.03]SGNDLEQLHIK[325.13]VTSLC[160.03  |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999999 | 1 R.HIQQVDC[160.03]SGNDLEQLHIK[325.13]VTSLC[160.03  |
| 0.999999 | 1 R.GAGM[147.04]PGQHGQITQQELDTVVK[325.13]TQHEIL     |
| 0.999999 | 1 K.AHDGGIYAISWSPDSTHLLSASGDK[325.13]TSK.I          |
| 0.999999 | 0.9996 R.LK[325.13]LEPHEGLLLR.F                     |

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| 0.999999 | 1 R.LLIHQSLAGGIIGVK[325.13]GAK.I                 |
| 0.999999 | 0.9992 R.LK[325.13]LEPHEGLLLR.F                  |
| 0.999999 | 1 R.LLIHQSLAGGIIGVK[325.13]GAK.I                 |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                       |
| 0.999999 | 1 K.AHDGGIYAIWSPDSTHLLSASGDK[325.13]TSK.I        |
| 0.999999 | 1 R.LLIHQSLAGGIIGVK[325.13]GAK.I                 |
| 0.999999 | 1 K.K[325.13]LKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFR.V |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                       |
| 0.999999 | 1 R.LLIHQSLAGGIIGVK[325.13]GAK.I                 |
| 0.999999 | 0.9997 R.LLLPGELAK[325.13]HAVSEGTK.A             |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 K.K[325.13]LKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFR.V |
| 0.999999 | 1 R.VGTVIGSNK[325.13]LEQMPSKEDAIEHFMK.L          |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.SENKNEGQDATMYC[160.03]K[325.13]SVGYPHPDWIW   |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.SENKNEGQDATMYC[160.03]K[325.13]SVGYPHPDWIW   |
| 0.999999 | 1 R.EK[325.13]LC[160.03]FLDKVEPHATIAEIK.N        |
| 0.999999 | 0.9992 R.LLLPGELAK[325.13]HAVSEGTK.A             |
| 0.999999 | 1 K.VDIDAPDVDVHGPDWHLK[325.13]MPK.M              |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 K.IVGC[160.03]SVHK[325.13]GFAFVQYVNER.N        |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 K.ARPFFNEFQGADSEIK[325.13]FAK.T                |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.HQAC[160.03]LLLQK[325.13]TLSMR.E             |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.AK[325.13]VAMSHFEPNEYIHYDLLEK.N              |
| 0.999999 | 1 R.HQAC[160.03]LLLQK[325.13]TLSMR.E             |
| 0.999999 | 1 R.LLLPGELAK[325.13]HAVSEGTK.A                  |
| 0.999999 | 1 R.HQAC[160.03]LLLQK[325.13]TLSMR.E             |
| 0.999999 | 1 R.AK[325.13]VAMSHFEPNEYIHYDLLEK.N              |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                    |
| 0.999999 | 1 R.HQAC[160.03]LLLQK[325.13]TLSMR.E             |
| 0.999999 | 1 K.ARPFFNEFQGADSEIK[325.13]FAK.T                |
| 0.999999 | 1 R.HQAC[160.03]LLLQK[325.13]TLSMR.E             |
| 0.999999 | 1 K.KLYDIDVAK[325.13]VNTLIRPDGEK.K               |
| 0.999999 | 1 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C     |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                    |
| 0.999999 | 1 K.KLYDIDVAK[325.13]VNTLIRPDGEK.K               |
| 0.999999 | 0.9996 R.ELPAQK[325.13]WWHTGALYR.I               |
| 0.999999 | 1 R.K[325.13]AHQLWLSVEALK.Y                      |

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| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.K[325.13]NLNYLHLDYNFNLPVK.T                     |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 K.LGETYKDHENIVIAK[325.13]MDSTANEVEAVK.V           |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 K.KPEDWDEEMDGEWEPPIQNPEYK[325.13]GEWKPR.Q         |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999999 | 1 K.KPEDWDEEMDGEWEPPIQNPEYK[325.13]GEWKPR.Q         |
| 0.999999 | 1 K.TNHIGHTGYLNTVTVSPDGLC[160.03]ASGGK[325.13]D     |
| 0.999999 | 1 R.STKK[325.13]EVFNILQAAYVSKPGAQLAR.Q              |
| 0.999999 | 1 K.K[325.13]GADSLEDFLYHEGYAC[160.03]TSIHGDR.S      |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                    |
| 0.999999 | 1 R.STKK[325.13]EVFNILQAAYVSKPGAQLAR.Q              |
| 0.999999 | 1 K.GK[325.13]C[160.03]YGLHAFIVPIR.E                |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                    |
| 0.999999 | 1 K.K[325.13]GADSLEDFLYHEGYAC[160.03]TSIHGDR.S      |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                    |
| 0.999999 | 1 R.RQQEQQVPILEK[325.13]FC[160.03]FTPHTEEGC[160.03] |
| 0.999999 | 1 K.K[325.13]GADSLEDFLYHEGYAC[160.03]TSIHGDR.S      |
| 0.999999 | 1 K.C[160.03]GEDYK[325.13]LHFIFR.H                  |
| 0.999999 | 1 K.VHLVGIDIFTGK[325.13]K.Y                         |
| 0.999999 | 1 K.C[160.03]GEDYK[325.13]LHFIFR.H                  |
| 0.999999 | 1 K.VHLVGIDIFTGK[325.13]K.Y                         |
| 0.999999 | 1 K.DRPQEADGIDSIVVVDNVPQVGPDRLEK[325.13]LK.N        |
| 0.999999 | 1 K.FKGPFTDVVTTNLK[325.13]LR.N                      |
| 0.999999 | 1 K.EK[325.13]ISMFC[160.03]HVEPEQVIC[160.03]VHDVSSI |
| 0.999999 | 1 K.FKGPFTDVVTTNLK[325.13]LR.N                      |
| 0.999999 | 1 K.VHLVGIDIFTGK[325.13]K.Y                         |
| 0.999999 | 1 K.VHLVGIDIFTGK[325.13]K.Y                         |
| 0.999999 | 1 K.VHLVGIDIFTGK[325.13]K.Y                         |
| 0.999999 | 1 K.DRPQEADGIDSIVVVDNVPQVGPDRLEK[325.13]LK.N        |
| 0.999999 | 1 K.FKGPFTDVVTTNLK[325.13]LR.N                      |
| 0.999999 | 1 R.VEYHFLSPYVSPK[325.13]ESPFR.H                    |
| 0.999999 | 1 R.RQQEQQVPILEK[325.13]FC[160.03]FTPHTEEGC[160.03] |
| 0.999999 | 1 R.RQQEQQVPILEK[325.13]FC[160.03]FTPHTEEGC[160.03] |
| 0.999999 | 1 K.WK[325.13]PPMIDNPSYQGIWKPR.K                    |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E        |
| 0.999999 | 1 K.VHSFPTLK[325.13]FFPASADR.T                      |
| 0.999999 | 1 K.K[325.13]SAEFLHMLK.N                            |

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| 0.999999 | 1 K.VHSFPTLK[325.13]FFPASADR.T                     |
| 0.999999 | 1 R.NLGSIAK[325.13]MLQHAASNK.M                     |
| 0.999999 | 1 K.FGDPVVQSDMK[325.13]HWPQVINDGDKPK.V             |
| 0.999999 | 0.9989 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E  |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.YAQVKPDGTYVKPLSNK[325.13]LTYGTMVFVR.S          |
| 0.999999 | 1 K.YAQVKPDGTYVKPLSNK[325.13]LTYGTMVFVR.S          |
| 0.999999 | 1 R.NLGSIAK[325.13]MLQHAASNK.M                     |
| 0.999999 | 1 R.NLGSIAK[325.13]MLQHAASNK.M                     |
| 0.999999 | 1 R.HQVK[325.13]YLGLLENLR.V                        |
| 0.999999 | 1 R.HQVK[325.13]YLGLLENLR.V                        |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.K[325.13]WTTLNQLHGLQLR.I                       |
| 0.999999 | 1 K.K[325.13]WTTLNQLHGLQLR.I                       |
| 0.999999 | 1 K.K[325.13]SAEFLHMLK.N                           |
| 0.999999 | 1 K.K[325.13]WTTLNQLHGLQLR.I                       |
| 0.999999 | 1 K.HVVFVK[325.13]VLEGMEVVR.K                      |
| 0.999999 | 1 R.HQVK[325.13]YLGLLENLR.V                        |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.HVVFVK[325.13]VLEGMEVVR.K                      |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG,   |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG,   |
| 0.999999 | 1 K.K[325.13]WTTLNQLHGLQLR.I                       |
| 0.999999 | 1 K.K[325.13]WTTLNQLHGLQLR.I                       |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG,   |
| 0.999999 | 1 R.KEAAENSLVAYK[325.13]AASDIAMTELPPTHPIR.L        |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG,   |
| 0.999999 | 1 K.K[325.13]WTTLNQLHGLQLR.I                       |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG,   |
| 0.999999 | 1 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG,   |
| 0.999999 | 1 R.NLGSIAK[325.13]MLQHAASNK.M                     |
| 0.999999 | 1 R.HQVK[325.13]YLGLLENLR.V                        |
| 0.999999 | 1 K.K[325.13]WTTLNQLHGLQLR.I                       |
| 0.999999 | 1 R.NLGSIAK[325.13]MLQHAASNK.M                     |
| 0.999999 | 1 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999999 | 1 K.HVVFVK[325.13]VLEGMEVVR.K                      |
| 0.999999 | 1 K.LMDALK[325.13]HASNMLGELR.T                     |
| 0.999999 | 1 K.K[325.13]PGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V     |
| 0.999999 | 1 K.VM[147.04]IGENVDEK[325.13]HLPTLDHPIIPADYVAIK.A |
| 0.999999 | 1 K.KGGSWIQEINVAEK[325.13]NWYPR.Q                  |
| 0.999999 | 1 R.GIDIHGVYPYVINVTLPDEK[325.13]QNYVHR.I           |
| 0.999999 | 1 K.SFVLNLGK[325.13]DSNNLC[160.03]LHFNPR.F         |
| 0.999999 | 1 R.TIC[160.03]SHVQNMNIK[325.13]GVTLGFR.Y          |
| 0.999999 | 1 K.VM[147.04]IGENVDEK[325.13]HLPTLDHPIIPADYVAIK.A |
| 0.999999 | 1 K.VM[147.04]IGENVDEK[325.13]HLPTLDHPIIPADYVAIK.A |



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| 0.999999 | 1 K.DHFTK[325.13]LAVEAVLR.L                        |
| 0.999999 | 1 K.SFVLNLGK[325.13]DSNNLC[160.03]LHFNPR.F         |
| 0.999999 | 1 R.TIC[160.03]SHVQNMNIK[325.13]GVTLGFR.Y          |
| 0.999999 | 1 R.TIC[160.03]SHVQNMNIK[325.13]GVTLGFR.Y          |
| 0.999999 | 1 R.TIC[160.03]SHVQNMNIK[325.13]GVTLGFR.Y          |
| 0.999999 | 1 K.SFVLNLGK[325.13]DSNNLC[160.03]LHFNPR.F         |
| 0.999999 | 1 K.ILSAC[160.03]EK[325.13]NPTDAYQLNYDMHNPFDIC[16  |
| 0.999999 | 1 R.TIC[160.03]SHVQNMNIK[325.13]GVTLGFR.Y          |
| 0.999999 | 1 R.TIC[160.03]SHVQNMNIK[325.13]GVTLGFR.Y          |
| 0.999999 | 1 R.TIC[160.03]SHVQNMNIK[325.13]GVTLGFR.Y          |
| 0.999999 | 1 K.KVEELEGEITTLNHK[325.13]LQDASAEVER.L            |
| 0.999999 | 1 K.VMIGENVDEK[325.13]HLPTLDHPIIPADYVAIK.A         |
| 0.999999 | 1 K.VMIGENVDEK[325.13]HLPTLDHPIIPADYVAIK.A         |
| 0.999999 | 1 R.RGPFELEAFYSDPQGVPEAK[325.13]IGR.F              |
| 0.999999 | 1 R.RGPFELEAFYSDPQGVPEAK[325.13]IGR.F              |
| 0.999999 | 1 K.QLAPIWDK[325.13]LGETYKDHENIVIAK.M              |
| 0.999999 | 1 R.LAAFGQLHK[325.13]VLGMDPLPSK.M                  |
| 0.999999 | 1 K.AKLEQLFQDEVAK[325.13]AQQLR.E                   |
| 0.999999 | 1 K.HQILEQAVEDYAETVHQLSK[325.13]TSR.A              |
| 0.999999 | 1 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E |
| 0.999999 | 1 R.KEAESC[160.03]DC[160.03]LQGFQLTHSLGGGTGSGMG    |
| 0.999999 | 1 R.SSFDWLTGSSTDPLVDHTSPSSD SLLFAHK[325.13]R.S     |
| 0.999999 | 1 R.SSFDWLTGSSTDPLVDHTSPSSD SLLFAHK[325.13]R.S     |
| 0.999999 | 1 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E |
| 0.999999 | 1 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E |
| 0.999999 | 1 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E |
| 0.999999 | 1 K.HSQFIGYPITLYLEK[325.13]ER.E                    |
| 0.999999 | 1 R.SSFDWLTGSSTDPLVDHTSPSSD SLLFAHK[325.13]R.S     |
| 0.999999 | 1 R.SSFDWLTGSSTDPLVDHTSPSSD SLLFAHK[325.13]R.S     |
| 0.999999 | 1 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E |
| 0.999999 | 1 R.C[160.03]K[325.13]DDEFTHLYTLIVRPDNTYEVK.I      |
| 0.999999 | 0.9993 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F            |
| 0.999999 | 1 K.K[325.13]GDVVIVLTGWRPGSGFTNTMR.V               |
| 0.999999 | 1 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E |
| 0.999999 | 1 K.K[325.13]GDVVIVLTGWRPGSGFTNTMR.V               |
| 0.999999 | 1 R.LQALDTGWNELHK[325.13]MWENR.Q                   |
| 0.999999 | 1 R.LQALDTGWNELHK[325.13]MWENR.Q                   |
| 0.999999 | 1 R.KEAESC[160.03]DC[160.03]LQGFQLTHSLGGGTGSGMG    |
| 0.999999 | 1 K.K[325.13]GDVVIVLTGWRPGSGFTNTMR.V               |
| 0.999999 | 1 R.KEAESC[160.03]DC[160.03]LQGFQLTHSLGGGTGSGMG    |
| 0.999999 | 1 R.K[325.13]HPEVDVLINFASLR.S                      |
| 0.999999 | 1 K.SRLDQELK[325.13]LIGEYGLR.N                     |
| 0.999999 | 1 R.RPFTK[325.13]NLGLEELGIELDPR.G                  |
| 0.999999 | 1 R.K[325.13]HPEVDVLINFASLR.S                      |
| 0.999999 | 1 R.RPFTK[325.13]NLGLEELGIELDPR.G                  |
| 0.999999 | 1 R.C[160.03]EAFGWHAIIVDGHSVEELC[160.03]K[325.13]A |
| 0.999999 | 1 R.DMFC[160.03]K[325.13]ILHGFK.N                  |

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| 0.999999 | 1 R.K[325.13]HPEVDVLINFASLR.S                       |
| 0.999999 | 1 K.FFGNLMASK[325.13]LSLC[160.03]GEESFGTGSDHIR.E    |
| 0.999999 | 1 R.RPFTK[325.13]NLGLEELGIELDPR.G                   |
| 0.999999 | 1 K.LHEEEIQELQAQIQEQHVQIDVDVSK[325.13]PDLTAALR.L    |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G       |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G       |
| 0.999999 | 1 K.LHEEEIQELQAQIQEQHVQIDVDVSK[325.13]PDLTAALR.L    |
| 0.999999 | 1 K.LHEEEIQELQAQIQEQHVQIDVDVSK[325.13]PDLTAALR.L    |
| 0.999999 | 1 R.LTLYDIAHTPGVAADLSHIETK[325.13]AAVK.G            |
| 0.999999 | 1 K.FFGNLMASK[325.13]LSLC[160.03]GEESFGTGSDHIR.E    |
| 0.999999 | 1 R.LTLYDIAHTPGVAADLSHIETK[325.13]AAVK.G            |
| 0.999999 | 1 K.LHEEEIQELQAQIQEQHVQIDVDVSK[325.13]PDLTAALR.L    |
| 0.999999 | 1 R.RQFASQANVVGPIQTK[325.13]MEEIGR.I                |
| 0.999999 | 1 K.LPEKWESVK[325.13]LLFVK.T                        |
| 0.999999 | 1 K.IPGLNSPIESC[160.03]SFGYHAGGWGK[325.13]PPVDET    |
| 0.999999 | 1 K.SIVNYKPK[325.13]IDQLEGDHQLIQEALIFDNK.H          |
| 0.999999 | 1 K.IPGLNSPIESC[160.03]SFGYHAGGWGK[325.13]PPVDET    |
| 0.999999 | 1 R.VFVHYTGWLLDGTK[325.13]FDSSLDR.K                 |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G       |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G       |
| 0.999999 | 1 R.HPAENGK[325.13]SNFLNC[160.03]YVSGFHPSDIEVDLLK   |
| 0.999999 | 1 K.K[325.13]LRPLYDIPYMFEAR.E                       |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G       |
| 0.999999 | 1 K.ILVDISNNLK[325.13]INQYPESNAEYLAHLVPGAHVVK.A     |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G       |
| 0.999999 | 1 K.K[325.13]LRPLYDIPYMFEAR.E                       |
| 0.999999 | 1 R.LSNIFVIGK[325.13]GNKPWISLPR.G                   |
| 0.999999 | 1 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHVR.G       |
| 0.999999 | 1 K.K[325.13]LRPLYDIPYMFEAR.E                       |
| 0.999999 | 1 R.LSNIFVIGK[325.13]GNKPWISLPR.G                   |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV     |
| 0.999999 | 1 K.HSQFIGYPITLFVEK[325.13]ER.D                     |
| 0.999999 | 1 K.HSQFIGYPITLFVEK[325.13]ER.D                     |
| 0.999999 | 1 R.LSNIFVIGK[325.13]GNKPWISLPR.G                   |
| 0.999999 | 1 R.AIVDC[160.03]GFEHPSEVQHEC[160.03]IPQAILGMDVLC   |
| 0.999999 | 1 K.ALSVGNIDDALQC[160.03]YSEAIK[325.13]LDPHNHVLYS   |
| 0.999999 | 1 K.LTFSC[160.03]LGGSDNFK[325.13]HLNEIDLFHC[160.03] |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV     |
| 0.999999 | 1 R.HPAENGK[325.13]SNFLNC[160.03]YVSGFHPSDIEVDLLK   |
| 0.999999 | 1 K.LTGLHK[325.13]MWEVLESTTQTK.A                    |
| 0.999999 | 1 K.LTGLHK[325.13]MWEVLESTTQTK.A                    |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV     |
| 0.999999 | 1 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T             |
| 0.999999 | 1 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV     |
| 0.999999 | 1 R.HPAENGK[325.13]SNFLNC[160.03]YVSGFHPSDIEVDLLK   |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSDFNSDTHSSTFDAG      |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSDFNSDTHSSTFDAG      |

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| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG |
| 0.999999 | 1 K.HK[325.13]FMVQTIFAPPNTSDMEAVWK.E            |
| 0.999999 | 1 K.HK[325.13]FMVQTIFAPPNTSDMEAVWK.E            |
| 0.999999 | 1 R.DPVWK[325.13]YLQTVQYGVHGNFPR.L              |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG |
| 0.999999 | 1 R.FTVAELK[325.13]QLVARPDVVEMHDVTAQDPK.L       |
| 0.999999 | 1 K.HK[325.13]FMVQTIFAPPNTSDMEAVWK.E            |
| 0.999999 | 1 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T         |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG |
| 0.999999 | 1 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T         |
| 0.999999 | 1 R.SLGEISALTSK[325.13]LADLRR.Q                 |
| 0.999999 | 1 K.HK[325.13]FMVQTIFAPPNTSDMEAVWK.E            |
| 0.999999 | 1 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T         |
| 0.999999 | 1 K.KPPVPALPSK[325.13]LPTFGAPEQLVDLK.Q          |
| 0.999999 | 1 R.NLLQELK[325.13]VIQENEHALQK.D                |
| 0.999999 | 1 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T         |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG |
| 0.999999 | 1 K.NISFTVWDVGGQDK[325.13]IRPLWR.H              |
| 0.999999 | 1 R.TGQLFLK[325.13]IIHTSVWAGQK.R                |
| 0.999999 | 1 K.GMSVSDLADK[325.13]LSTDDLNSLIAHAHR.R         |
| 0.999999 | 1 R.TGQLFLK[325.13]IIHTSVWAGQK.R                |
| 0.999999 | 1 K.GMSVSDLADK[325.13]LSTDDLNSLIAHAHR.R         |
| 0.999999 | 1 K.GMSVSDLADK[325.13]LSTDDLNSLIAHAHR.R         |
| 0.999999 | 1 R.TGQLFLK[325.13]IIHTSVWAGQK.R                |
| 0.999999 | 1 R.TGQLFLK[325.13]IIHTSVWAGQK.R                |
| 0.999999 | 1 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I            |
| 0.999999 | 1 R.KIAK[325.13]AFAISGPFNVQFLVK.G               |
| 0.999999 | 1 R.HNLEIHK[325.13]TLVEC[160.03]WK.D            |
| 0.999999 | 1 R.KNQLK[325.13]DMAIATGGAVFGEEGLTLNLEDVQPHDLC  |
| 0.999999 | 1 R.KLNVNAK[325.13]PFVPNVHAAEFVPSFLR.G          |
| 0.999999 | 1 R.KLNVNAK[325.13]PFVPNVHAAEFVPSFLR.G          |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q     |
| 0.999999 | 1 R.ALETLTGALFQRPPLIAAVK[325.13]R.Q             |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q     |
| 0.999999 | 1 R.KLNVNAK[325.13]PFVPNVHAAEFVPSFLR.G          |
| 0.999999 | 1 R.K[325.13]LNVNAKPFVPNVHAAEFVPSFLR.G          |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q     |
| 0.999999 | 1 R.ALETLTGALFQRPPLIAAVK[325.13]R.Q             |
| 0.999999 | 1 R.ALETLTGALFQRPPLIAAVK[325.13]R.Q             |
| 0.999999 | 1 R.LK[325.13]LEPHEGLLLR.F                      |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q     |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q     |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q     |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q     |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q     |
| 0.999999 | 1 K.MVINHLEK[325.13]LFVTNDAATILR.E              |

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| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPPDDYLDC[160.03]LGK.Q          |
| 0.999999 | 1 K.MVINHLEK[325.13]LFVTNDAATILR.E                    |
| 0.999999 | 1 R.EEFWEMFDGSLYHK[325.13]LR.E                        |
| 0.999999 | 1 K.SPVTTLLEC[160.03]MHK[325.13]LGNSC[160.03]EFR.L    |
| 0.999999 | 1 K.SPVTTLLEC[160.03]MHK[325.13]LGNSC[160.03]EFR.L    |
| 0.999999 | 1 K.NKPK[325.13]WLLQGIFSTTVLC[160.03]QK.L             |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPPDDYLDC[160.03]LGK.Q          |
| 0.999999 | 1 R.LFK[325.13]QLHPQLLLPPDDYLDC[160.03]LGK.Q          |
| 0.999999 | 1 R.EEFWEMFDGSLYHK[325.13]LR.E                        |
| 0.999999 | 1 K.SPVTTLLEC[160.03]MHK[325.13]LGNSC[160.03]EFR.L    |
| 0.999999 | 1 R.LLDHMQNTPGFMKY[325.13]NLQC[160.03]LVIDEADR.I      |
| 0.999999 | 0.9992 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLR. |
| 0.999999 | 1 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLR.      |
| 0.999999 | 1 K.MVINHLEK[325.13]LFVTNDAATILR.E                    |
| 0.999999 | 1 K.TFNQVEIK[325.13]PEMIGHYLGFEFSITYKPVK.H            |
| 0.999999 | 1 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLR.      |
| 0.999999 | 1 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLR.      |
| 0.999999 | 1 K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK[325.13]YHH\       |
| 0.999999 | 1 R.LLDHMQNTPGFMKY[325.13]NLQC[160.03]LVIDEADR.I      |
| 0.999999 | 1 K.TFNQVEIK[325.13]PEMIGHYLGFEFSITYKPVK.H            |
| 0.999999 | 1 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLR.      |
| 0.999999 | 1 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLR.      |
| 0.999999 | 1 K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK[325.13]YHH\       |
| 0.999999 | 1 K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK[325.13]YHH\       |
| 0.999999 | 1 K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK[325.13]YHH\       |
| 0.999999 | 1 K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK[325.13]YHH\       |
| 0.999999 | 1 K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK[325.13]YHH\       |
| 0.999999 | 1 K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK[325.13]YHH\       |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 R.EK[325.13]EISGLWNELDLSDKDAVEHQR.K                 |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 R.VPELQGLVTEHVFLDK[325.13]C[160.03]LR.E             |
| 0.999999 | 1 R.K[325.13]DGNASGTTLEALDC[160.03]ILPPTRPDKPLR.      |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 R.EK[325.13]EISGLWNELDLSDKDAVEHQR.K                 |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 R.GGGVGGFLPAMK[325.13]QIGNVAALPGIVHR.S              |
| 0.999999 | 1 R.VPELQGLVTEHVFLDK[325.13]C[160.03]LR.E             |
| 0.999999 | 1 K.K[325.13]FISDKDASIVGFFDDSFSEAHSEFLK.A             |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 K.SAEFLHMLK[325.13]NAESNAELK.G                      |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |
| 0.999999 | 1 R.IC[160.03]FELLELLK[325.13]AHK.K                   |
| 0.999999 | 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                    |

0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.  
0.999999 1 R.TVSLGAGAKDELHIVEAEAMNYEGSPIK[325.13]VTLATLK.  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.GLDISNVK[325.13]HVINFDLPSDIEEYVHR.I  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.TVSLGAGAKDELHIVEAEAMNYEGSPIK[325.13]VTLATLK.  
0.999999 1 R.TVSLGAGAKDELHIVEAEAMNYEGSPIK[325.13]VTLATLK.  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.GLDISNVK[325.13]HVINFDLPSDIEEYVHR.I  
0.999999 0.9964 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.GLDISNVK[325.13]HVINFDLPSDIEEYVHR.I  
0.999999 1 R.GLDISNVK[325.13]HVINFDLPSDIEEYVHR.I  
0.999999 1 K.SK[325.13]DDQVTIGAGVTLHEALAAELLKK.E  
0.999999 1 K.FSDSYASVIK[325.13]ALEHSALAINHK.L  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.LPLQDVYK[325.13]IGGIGTVPVGRVETGVLPKPGMVVTF  
0.999999 1 K.FSDSYASVIK[325.13]ALEHSALAINHK.L  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.  
0.999999 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.  
0.999999 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.  
0.999999 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C  
0.999999 1 R.VAYVSFGPHAGK[325.13]LVAIVDVIDQNR.A  
0.999999 1 R.EHALLAYTLGVK[325.13]QLIVGVNK.M  
0.999999 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.  
0.999999 1 R.VAYVSFGPHAGK[325.13]LVAIVDVIDQNR.A  
0.999999 1 R.VAYVSFGPHAGK[325.13]LVAIVDVIDQNR.A  
0.999999 1 R.FGWDC[160.03]HGLPVEYEIDK[325.13]TLGIR.G  
0.999999 1 R.FGWDC[160.03]HGLPVEYEIDK[325.13]TLGIR.G  
0.999999 1 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR.  
0.999999 1 R.DWSHYFK[325.13]IIEDLR.A  
0.999999 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C  
0.999999 1 R.VAYVSFGPHAGK[325.13]LVAIVDVIDQNR.A  
0.999999 1 K.SKDDQVTIGAGVTLHEALAAELLK[325.13]K.E  
0.999999 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C  
0.999999 1 R.DWSHYFK[325.13]IIEDLR.A  
0.999999 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L  
0.999999 1 K.YMHSGPVVAMVWEGLNVVK[325.13]TGR.V  
0.999999 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L  
0.999999 1 R.FGWDC[160.03]HGLPVEYEIDK[325.13]TLGIR.G  
0.999999 1 R.FGWDC[160.03]HGLPVEYEIDK[325.13]TLGIR.G  
0.999999 1 R.DWSHYFK[325.13]IIEDLR.A

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| 0.999999 | 1 K.YMHSGPVVAMVWEGLVVVK[325.13]TGR.V             |
| 0.999999 | 1 K.SKDDQVTVIGAGVTLHEALAAELLK[325.13]K.E         |
| 0.999999 | 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C         |
| 0.999999 | 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L       |
| 0.999999 | 0.9995 R.EHALLAYTLGVK[325.13]QLIVGVNK.M          |
| 0.999999 | 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L       |
| 0.999999 | 1 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I            |
| 0.999999 | 1 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I            |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C         |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 0.9695 R.EHALLAYTLGVK[325.13]QLIVGVNK.M          |
| 0.999999 | 1 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I            |
| 0.999999 | 1 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I            |
| 0.999999 | 1 R.DWSHYFK[325.13]IIEDLR.A                      |
| 0.999999 | 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C         |
| 0.999999 | 1 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I            |
| 0.999999 | 1 R.EVC[160.03]DEVK[325.13]AHLLADMAHISGLVAAK.V   |
| 0.999999 | 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L       |
| 0.999999 | 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L       |
| 0.999999 | 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L       |
| 0.999999 | 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L       |
| 0.999999 | 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L       |
| 0.999999 | 1 R.K[325.13]GLIAAIC[160.03]AGPTALLAHEIGFGSK.V   |
| 0.999999 | 1 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L       |
| 0.999999 | 1 R.K[325.13]GLIAAIC[160.03]AGPTALLAHEIGFGSK.V   |
| 0.999999 | 1 K.K[325.13]GIIRPGTAFELLEQAATGYVIDPIK.G         |
| 0.999999 | 1 K.K[325.13]GIIRPGTAFELLEQAATGYVIDPIK.G         |
| 0.999999 | 1 R.K[325.13]GLIAAIC[160.03]AGPTALLAHEIGFGSK.V   |
| 0.999999 | 1 R.K[325.13]GLIAAIC[160.03]AGPTALLAHEIGFGSK.V   |
| 0.999999 | 1 K.IVKPNGEKPDEFESGISQALLELEMNSDLK[325.13]AQLR.E |
| 0.999999 | 1 K.K[325.13]GIIRPGTAFELLEQAATGYVIDPIK.G         |
| 0.999999 | 1 K.K[325.13]GIIRPGTAFELLEQAATGYVIDPIK.G         |
| 0.999999 | 1 R.K[325.13]GLIAAIC[160.03]AGPTALLAHEIGFGSK.V   |
| 0.999999 | 1 R.K[325.13]GLIAAIC[160.03]AGPTALLAHEIGFGSK.V   |
| 0.999999 | 1 R.GLFIIDPNGVIK[325.13]HLSVNDLPVGR.S            |
| 0.999999 | 1 R.GLFIIDPNGVIK[325.13]HLSVNDLPVGR.S            |
| 0.999999 | 1 K.VLDFEHFLPMLQTVAK[325.13]NK.D                 |
| 0.999999 | 1 K.VLDFEHFLPMLQTVAK[325.13]NK.D                 |
| 0.999999 | 1 R.GLFIIDPNGVIK[325.13]HLSVNDLPVGR.S            |
| 0.999999 | 1 R.GLFIIDPNGVIK[325.13]HLSVNDLPVGR.S            |
| 0.999999 | 1 K.VLDFEHFLPMLQTVAK[325.13]NK.D                 |
| 0.999999 | 1 K.VLDFEHFLPMLQTVAK[325.13]NK.D                 |
| 0.999999 | 1 K.VLDFEHFLPMLQTVAK[325.13]NK.D                 |
| 0.999999 | 1 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D     |
| 0.999999 | 1 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D     |

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| 0.999999 | 1 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D     |
| 0.999999 | 1 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D     |
| 0.999999 | 1 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D     |
| 0.999999 | 1 R.EIFNFVLK[325.13]AIRPQIDLK.R                  |
| 0.999999 | 1 R.EIFNFVLK[325.13]AIRPQIDLK.R                  |
| 0.999999 | 1 R.ISSNPVAK[325.13]IYGDVPTFLPHLPR.K             |
| 0.999999 | 1 R.EIFNFVLK[325.13]AIRPQIDLK.R                  |
| 0.999999 | 1 K.HNQLPLVIEFTEQTAPK[325.13]IFGGEIK.T           |
| 0.999999 | 1 R.ISSNPVAK[325.13]IYGDVPTFLPHLPR.K             |
| 0.999999 | 1 R.EIFNFVLK[325.13]AIRPQIDLK.R                  |
| 0.999999 | 1 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTGSFGTS |
| 0.999999 | 1 R.EIFNFVLK[325.13]AIRPQIDLK.R                  |
| 0.999999 | 1 K.HNQLPLVIEFTEQTAPK[325.13]IFGGEIK.T           |
| 0.999999 | 1 K.LGLVGVNLTLDGVK[325.13]SWLKPR.L               |
| 0.999999 | 1 R.EIFNFVLK[325.13]AIRPQIDLK.R                  |
| 0.999999 | 1 R.HLILPEK[325.13]YPPPTELLDLQPLVSALR.N          |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 K.LGLVGVNLTLDGVK[325.13]SWLKPR.L               |
| 0.999999 | 1 K.LGLVGVNLTLDGVK[325.13]SWLKPR.L               |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.TGGMAFHSYFMEAIAPLLQELK[325.13]K.V            |
| 0.999999 | 1 R.TGGMAFHSYFMEAIAPLLQELK[325.13]K.V            |
| 0.999999 | 1 R.HLILPEK[325.13]YPPPTELLDLQPLVSALR.N          |
| 0.999999 | 1 R.HLILPEK[325.13]YPPPTELLDLQPLVSALR.N          |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 K.LGLVGVNLTLDGVK[325.13]SWLKPR.L               |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 K.TFSFAIPLIEK[325.13]LHGELQDR.K                |
| 0.999999 | 1 R.GHYTIGK[325.13]EIDLVLDR.I                    |
| 0.999999 | 1 R.FLSQPFQVAEVFTGHMGK[325.13]LVPLK.E            |
| 0.999999 | 1 R.K[325.13]MDADGFLPITLIASFHR.V                 |
| 0.999999 | 1 K.RQELVTK[325.13]IDHILDAL.-                    |
| 0.999999 | 1 R.K[325.13]MDADGFLPITLIASFHR.V                 |
| 0.999999 | 1 R.K[325.13]MDADGFLPITLIASFHR.V                 |
| 0.999999 | 1 R.LTHVDSPLEAPAGPLQVK[325.13]LTLWYYSEER.K       |
| 0.999999 | 1 R.LVNQLHLDLLNNK[325.13]LVTLPVSFAQLK.N          |
| 0.999999 | 1 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTGSFGTS |
| 0.999999 | 1 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTGSFGTS |
| 0.999999 | 1 R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H           |
| 0.999999 | 1 R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H           |
| 0.999999 | 1 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTGSFGTS |

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| 0.999999 | 1 R.FLQPVHK[325.13]IDMNLTDLLGELQR.D               |
| 0.999999 | 1 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTGSGFTS  |
| 0.999999 | 1 R.LLGAALPLLTk[325.13]EQLHLVMQGDVIR.H            |
| 0.999999 | 1 R.FLQPVHK[325.13]IDMNLTDLLGELQR.D               |
| 0.999999 | 1 R.LLGAALPLLTk[325.13]EQLHLVMQGDVIR.H            |
| 0.999999 | 1 R.LVNLQHLDLLNNK[325.13]LVTLPVSFQALK.N           |
| 0.999999 | 1 R.FLQPVHK[325.13]IDMNLTDLLGELQR.D               |
| 0.999999 | 1 R.LVNLQHLDLLNNK[325.13]LVTLPVSFQALK.N           |
| 0.999999 | 1 R.LLGAALPLLTk[325.13]EQLHLVMQGDVIR.H            |
| 0.999999 | 1 R.LVNLQHLDLLNNK[325.13]LVTLPVSFQALK.N           |
| 0.999999 | 1 R.LVNLQHLDLLNNK[325.13]LVTLPVSFQALK.N           |
| 0.999999 | 1 R.QHFPATPLLDYALEVEK[325.13]ITTSK.K              |
| 0.999999 | 1 K.ELNYFAK[325.13]ALESPERPFLAILGGAK.V            |
| 0.999999 | 1 K.DGNASGTTLEALDC[160.03]ILPPTRPDTK[325.13]PLRLP |
| 0.999999 | 1 K.ELNYFAK[325.13]ALESPERPFLAILGGAK.V            |
| 0.999999 | 1 K.YGIIC[160.03]MEDLIHEIYTVGK[325.13]R.F         |
| 0.999999 | 1 K.YGIIC[160.03]MEDLIHEIYTVGK[325.13]R.F         |
| 0.999999 | 1 K.RDELTLEGIK[325.13]QFFVAVER.E                  |
| 0.999999 | 1 K.ELNYFAK[325.13]ALESPERPFLAILGGAK.V            |
| 0.999999 | 1 K.LDVGK[325.13]VLQASVLDDWFPLQGGQGQVHLR.L        |
| 0.999999 | 1 R.LRPEDPVLK[325.13]DLYLSWGTVLER.D               |
| 0.999999 | 1 K.LDVGK[325.13]VLQASVLDDWFPLQGGQGQVHLR.L        |
| 0.999999 | 1 K.K[325.13]ALTGHLEEVVLALLK.T                    |
| 0.999999 | 1 R.DLANDIMTLMSHTK[325.13]PYIR.K                  |
| 0.999999 | 1 K.K[325.13]ALTGHLEEVVLALLK.T                    |
| 0.999999 | 1 K.RPWITGDESIVGLMK[325.13]DIVGANER.E             |
| 0.999999 | 1 R.LRPEDPVLK[325.13]DLYLSWGTVLER.D               |
| 0.999999 | 1 K.LDVGK[325.13]VLQASVLDDWFPLQGGQGQVHLR.L        |
| 0.999999 | 1 K.K[325.13]ALTGHLEEVVLALLK.T                    |
| 0.999999 | 1 K.K[325.13]ALTGHLEEVVLALLK.T                    |
| 0.999999 | 1 K.LDVGK[325.13]VLQASVLDDWFPLQGGQGQVHLR.L        |
| 0.999999 | 1 R.GAVGALLVYDIK[325.13]HLYENVER.W                |
| 0.999999 | 1 K.RPWITGDESIVGLMK[325.13]DIVGANER.E             |
| 0.999999 | 1 R.DLANDIMTLMSHTK[325.13]PYIR.K                  |
| 0.999999 | 1 R.GAVGALLVYDIK[325.13]HLYENVER.W                |
| 0.999999 | 1 R.KLGEK[325.13]ILPEIIPILEEGLR.S                 |
| 0.999999 | 1 K.K[325.13]ALTGHLEEVVLALLK.T                    |
| 0.999999 | 1 R.GAVGALLVYDIK[325.13]HLYENVER.W                |
| 0.999999 | 1 R.KLGEK[325.13]ILPEIIPILEEGLR.S                 |
| 0.999999 | 1 R.KLGEK[325.13]ILPEIIPILEEGLR.S                 |
| 0.999999 | 1 K.K[325.13]ALTGHLEEVVLALLK.T                    |
| 0.999999 | 1 K.HLVMGDIPA AVNAFQEAASLLGK[325.13]K.Y           |
| 0.999999 | 1 K.HLVMGDIPA AVNAFQEAASLLGK[325.13]K.Y           |
| 0.999999 | 1 R.FLGVAEQLHNEGFK[325.13]LFATEATSDWLNANNVPATP    |
| 0.999999 | 1 R.GAVGALLVYDIK[325.13]HLYENVER.W                |
| 0.999999 | 1 R.KLGEK[325.13]ILPEIIPILEEGLR.S                 |
| 0.999999 | 1 R.GAVGALLVYDIK[325.13]HLYENVER.W                |



0.999999 1 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A  
0.999999 1 R.KLGEK[325.13]ILPEIIPILEEGLR.S  
0.999999 0.9999 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W  
0.999999 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W  
0.999999 0.9999 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A  
0.999999 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W  
0.999999 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W  
0.999999 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W  
0.999999 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W  
0.999999 1 R.GAVGALLVYDIAK[325.13]HLTYENVER.W  
0.999999 0.9994 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I  
0.999999 1 R.VPLAIVNK[325.13]AHQANQLYPFAISLIESVR.T  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.VPLAIVNK[325.13]AHQANQLYPFAISLIESVR.T  
0.999999 1 R.VPLAIVNK[325.13]AHQANQLYPFAISLIESVR.T  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.VPLAIVNK[325.13]AHQANQLYPFAISLIESVR.T  
0.999999 1 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 K.SLQELFLAHILSPWGAEVK[325.13]AEPVEVVAPR.G  
0.999999 1 R.DALSDLALHFLNK[325.13]MK.I  
0.999999 1 R.DGMLDDEEFALASHLIEAK[325.13]LEGHGLPANLPR.R  
0.999999 0.9969 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I  
0.999999 1 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I  
0.999999 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ  
0.999999 1 R.LPLATIVK[325.13]DLVAQAPLKPK.T  
0.999999 1 R.LPLATIVK[325.13]DLVAQAPLKPK.T  
0.999999 1 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I  
0.999999 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ  
0.999999 1 R.LPLATIVK[325.13]DLVAQAPLKPK.T  
0.999999 1 R.LPLATIVK[325.13]DLVAQAPLKPK.T  
0.999999 1 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I  
0.999999 1 R.LPLATIVK[325.13]DLVAQAPLKPK.T  
0.999999 1 R.LPLATIVK[325.13]DLVAQAPLKPK.T  
0.999999 1 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I  
0.999999 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ  
0.999999 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ  
0.999999 1 R.AMQK[325.13]VMATTGGM[147.04]GM[147.04]GPGGI  
0.999999 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ

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| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.LGGIGQFLAK[325.13]AIEPPPLDAVIEAEHTLR.E         |
| 0.999999 | 1 R.LGGIGQFLAK[325.13]AIEPPPLDAVIEAEHTLR.E         |
| 0.999999 | 1 R.LGGIGQFLAK[325.13]AIEPPPLDAVIEAEHTLR.E         |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I        |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.LGGIGQFLAK[325.13]AIEPPPLDAVIEAEHTLR.E         |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 K.ANIVHMLLSSPEQIQK[325.13]QLSDAISIIGR.E          |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 K.MLDAEDIVGTARPDEK[325.13]AIMTYVSSFYHAFSGAQK.    |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 K.ANIVHMLLSSPEQIQK[325.13]QLSDAISIIGR.E          |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 K.GILADESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV    |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.KIWC[160.03]FGPDGTGPNILTDITK[325.13]GVQYLNEIK. |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 K.GILADESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV    |
| 0.999999 | 1 R.KIWC[160.03]FGPDGTGPNILTDITK[325.13]GVQYLNEIK. |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.KIWC[160.03]FGPDGTGPNILTDITK[325.13]GVQYLNEIK. |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 K.GILADESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV    |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.RPAEK[325.13]FLESVEGNQNYPLLLLTLEK.S            |
| 0.999999 | 1 R.RPAEK[325.13]FLESVEGNQNYPLLLLTLEK.S            |
| 0.999999 | 1 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999999 | 1 R.LGHAETDEQLQNIISK[325.13]FLPPVLLK.L             |
| 0.999999 | 1 R.RPAEK[325.13]FLESVEGNQNYPLLLLTLEK.S            |
| 0.999999 | 1 R.LGHAETDEQLQNIISK[325.13]FLPPVLLK.L             |
| 0.999999 | 1 R.RPAEK[325.13]FLESVEGNQNYPLLLLTLEK.S            |
| 0.999999 | 1 R.LGHAETDEQLQNIISK[325.13]FLPPVLLK.L             |
| 0.999999 | 1 R.LGHAETDEQLQNIISK[325.13]FLPPVLLK.L             |
| 0.999999 | 1 K.LLGLGQK[325.13]HLVMGDIPA AVNAFQEAASLLGK.K      |
| 0.999999 | 1 R.IHPVSTMVK[325.13]GMYGIENEVFLSLPC[160.03]ILNAR  |

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| 0.999999 | 1 K.ILNIFGVK[325.13]GFVEPDHYVVVGAQR.D                |
| 0.999999 | 1 K.LLGLGQK[325.13]HLVMGDIPAAVNAFQEAASLLGK.K         |
| 0.999999 | 1 R.IHPVSTMVK[325.13]GMYGIENEVFLSLPC[160.03]ILNAR    |
| 0.999999 | 1 K.ILNIFGVK[325.13]GFVEPDHYVVVGAQR.D                |
| 0.999999 | 1 K.LLGLGQK[325.13]HLVMGDIPAAVNAFQEAASLLGK.K         |
| 0.999999 | 1 R.IHPVSTMVK[325.13]GMYGIENEVFLSLPC[160.03]ILNAR    |
| 0.999999 | 1 K.NFIEK[325.13]VEALTKEELEFEVPFR.D                  |
| 0.999999 | 1 K.ILNIFGVK[325.13]GFVEPDHYVVVGAQR.D                |
| 0.999999 | 1 K.LLGLGQK[325.13]HLVMGDIPAAVNAFQEAASLLGK.K         |
| 0.999999 | 1 R.IHPVSTMVK[325.13]GMYGIENEVFLSLPC[160.03]ILNAR    |
| 0.999999 | 1 K.LLGLGQK[325.13]HLVMGDIPAAVNAFQEAASLLGK.K         |
| 0.999999 | 1 K.MLDAEDIVNTARPDEK[325.13]AIMTYVSSFYHAFSGAQK.      |
| 0.999999 | 1 K.MLDAEDIVNTARPDEK[325.13]AIMTYVSSFYHAFSGAQK.      |
| 0.999999 | 1 R.IHPVSTMVK[325.13]GMYGIENEVFLSLPC[160.03]ILNAR    |
| 0.999999 | 1 K.ILNIFGVK[325.13]GFVEPDHYVVVGAQR.D                |
| 0.999999 | 1 K.ILNIFGVK[325.13]GFVEPDHYVVVGAQR.D                |
| 0.999999 | 1 K.ILNIFGVK[325.13]GFVEPDHYVVVGAQR.D                |
| 0.999999 | 1 K.ILNIFGVK[325.13]GFVEPDHYVVVGAQR.D                |
| 0.999999 | 1 K.ILNIFGVK[325.13]GFVEPDHYVVVGAQR.D                |
| 0.999999 | 1 R.GIHSIDASQTPDVVFASILAAFSK[325.13]ATC[160.03]K.I   |
| 0.999999 | 1 R.GIHSIDASQTPDVVFASILAAFSK[325.13]ATC[160.03]K.I   |
| 0.999999 | 1 R.NPPIDDLIK[325.13]SGILPILVHC[160.03]LER.D         |
| 0.999999 | 1 R.GIHSIDASQTPDVVFASILAAFSK[325.13]ATC[160.03]K.I   |
| 0.999999 | 1 R.K[325.13]NIVSLLSMLGHDEDNTR.I                     |
| 0.999999 | 1 R.K[325.13]NIVSLLSMLGHDEDNTR.I                     |
| 0.999999 | 1 R.K[325.13]NIVSLLSMLGHDEDNTR.I                     |
| 0.999999 | 1 R.K[325.13]NIVSLLSMLGHDEDNTR.I                     |
| 0.999999 | 1 R.K[325.13]NIVSLLSMLGHDEDNTR.I                     |
| 0.999999 | 1 R.K[325.13]NIVSLLSMLGHDEDNTR.I                     |
| 0.999999 | 1 K.KLDTNSDGQLDFSEFLNLIGGLAMAC[160.03]HDSFLK[325.13] |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K           |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K           |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K           |
| 0.999999 | 1 K.SLTGVVNAQALTSAFSPHTK[325.13]PWIGLAEALGTLMR.      |
| 0.999999 | 1 K.SLTGVVNAQALTSAFSPHTK[325.13]PWIGLAEALGTLMR.      |
| 0.999999 | 1 K.SLTGVVNAQALTSAFSPHTK[325.13]PWIGLAEALGTLMR.      |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K           |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K           |
| 0.999999 | 1 K.SLTGVVNAQALTSAFSPHTK[325.13]PWIGLAEALGTLMR.      |
| 0.999999 | 1 K.SLTGVVNAQALTSAFSPHTK[325.13]PWIGLAEALGTLMR.      |
| 0.999999 | 1 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K           |
| 0.999999 | 1 K.VHAELADVLTEAVVDSILAIK[325.13]K.Q                 |
| 0.999999 | 1 K.IISNASC[160.03]TTNC[160.03]LAPLAK[325.13]VIHDNFC |
| 0.999999 | 1 K.EIRPALELLEPIEQK[325.13]FVSISDLLVPK.D             |
| 0.999999 | 1 K.EIRPALELLEPIEQK[325.13]FVSISDLLVPK.D             |
| 0.999999 | 1 K.QASEGPLK[325.13]GILGYTEHQVVSDFNSDTHSSTFDAG       |
| 0.999999 | 0.9996 R.EHALLAYTLGVK[325.13]QLIVGVNK.M              |

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| 0.999999 | 0.9716 | R.LK[325.13]LEPHEGLLLR.F                           |
| 0.999999 | 0.9888 | R.EHALLAYTLGVK[325.13]QLIVGVNK.M                   |
| 0.999999 | 0.9909 | R.EHALLAYTLGVK[325.13]QLIVGVNK.M                   |
| 0.999999 | 0.9962 | R.EHALLAYTLGVK[325.13]QLIVGVNK.M                   |
| 0.999999 | 0.9628 | R.LK[325.13]LEPHEGLLLR.F                           |
| 0.999999 | 1      | K.QASEGPLK[325.13]GILGYTEHQVVSSDFNSDTHSSTFDAG      |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.HSTC[160.03]K[325.13]DSGHAGAR.D                  |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.IVQK[325.13]HPHTGDTKEEK.D                        |
| 0.999998 | 1      | R.SK[325.13]C[160.03]HGHGVC[160.03]DSNR.H          |
| 0.999998 | 1      | R.YGQNC[160.03]HK[325.13]GPPHSK.S                  |
| 0.999998 | 1      | R.YGQNC[160.03]HK[325.13]GPPHSK.S                  |
| 0.999998 | 1      | R.YGQNC[160.03]HK[325.13]GPPHSK.S                  |
| 0.999998 | 1      | K.KPLKPC[160.03]C[160.03]AC[160.03]PETK[325.13]K.A |
| 0.999998 | 1      | K.KPLKPC[160.03]C[160.03]AC[160.03]PETK[325.13]K.A |
| 0.999998 | 1      | K.KPLKPC[160.03]C[160.03]AC[160.03]PETK[325.13]K.A |
| 0.999998 | 1      | R.AGSQGLPGYQHHAQPK[325.13]R.K                      |
| 0.999998 | 1      | R.SK[325.13]SYSFHQSQHR.K                           |
| 0.999998 | 1      | R.SK[325.13]SYSFHQSQHR.K                           |
| 0.999998 | 1      | K.HLTHAQSTLDAK[325.13]ATK.A                        |
| 0.999998 | 1      | K.HLTHAQSTLDAK[325.13]ATK.A                        |
| 0.999998 | 1      | K.HLTHAQSTLDAK[325.13]ATK.A                        |
| 0.999998 | 1      | R.K[325.13]EWHGPPSQGPSYHDTR.R                      |
| 0.999998 | 1      | R.K[325.13]EWHGPPSQGPSYHDTR.R                      |
| 0.999998 | 1      | R.K[325.13]EWHGPPSQGPSYHDTR.R                      |
| 0.999998 | 1      | R.K[325.13]EWHGPPSQGPSYHDTR.R                      |
| 0.999998 | 1      | R.K[325.13]EWHGPPSQGPSYHDTR.R                      |
| 0.999998 | 1      | R.K[325.13]EWHGPPSQGPSYHDTR.R                      |
| 0.999998 | 1      | R.K[325.13]YC[160.03]QRPC[160.03]DNLHLC[160.03]K.L |
| 0.999998 | 1      | K.GELHSK[325.13]LISGGHDNR.V                        |
| 0.999998 | 1      | K.GELHSK[325.13]LISGGHDNR.V                        |
| 0.999998 | 1      | K.GELHSK[325.13]LISGGHDNR.V                        |
| 0.999998 | 1      | K.GELHSK[325.13]LISGGHDNR.V                        |
| 0.999998 | 1      | K.GELHSK[325.13]LISGGHDNR.V                        |
| 0.999998 | 1      | K.GELHSK[325.13]LISGGHDNR.V                        |
| 0.999998 | 1      | R.TMSAQIEGGVHGLHSYEK[325.13]R.L                    |
| 0.999998 | 1      | R.TMSAQIEGGVHGLHSYEK[325.13]R.L                    |
| 0.999998 | 1      | R.HLSDSINQK[325.13]HFEQAIER.V                      |
| 0.999998 | 1      | K.LTK[325.13]ASVHC[160.03]LETGEYTHIR.N             |
| 0.999998 | 1      | K.LTK[325.13]ASVHC[160.03]LETGEYTHIR.N             |

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| 0.999998 | 1 R.SHLK[325.13]ITDSAGHILYSK.E                      |
| 0.999998 | 1 R.SHLK[325.13]ITDSAGHILYSK.E                      |
| 0.999998 | 1 R.SHLK[325.13]ITDSAGHILYSK.E                      |
| 0.999998 | 1 R.SHLK[325.13]ITDSAGHILYSK.E                      |
| 0.999998 | 1 R.SHLK[325.13]ITDSAGHILYSK.E                      |
| 0.999998 | 1 R.SLENYHFVDEHGK[325.13]DQGINIR.Q                  |
| 0.999998 | 1 R.VLHK[325.13]LTTLHVYEEDPR.E                      |
| 0.999998 | 1 K.LNK[325.13]QQTDIAVNWAGGLHHAK.K                  |
| 0.999998 | 0.9994 R.M[147.04]VNHFAIEFK[325.13]R.K              |
| 0.999998 | 1 K.THTMEGK[325.13]LHDPEGMGIIPR.I                   |
| 0.999998 | 1 R.HQK[325.13]VVEIAPAAHLDPQLR.T                    |
| 0.999998 | 1 R.HQK[325.13]VVEIAPAAHLDPQLR.T                    |
| 0.999998 | 0.9995 R.M[147.04]VNHFAIEFK[325.13]R.K              |
| 0.999998 | 1 R.KLVAIVDPHIK[325.13]VDSGYR.V                     |
| 0.999998 | 0.9995 R.MVNHFAIEFK[325.13]R.K                      |
| 0.999998 | 1 R.GVSEHDFAYQDPK[325.13]VHSIFPAR.G                 |
| 0.999998 | 1 R.GVSEHDFAYQDPK[325.13]VHSIFPAR.G                 |
| 0.999998 | 1 K.K[325.13]PPVKPPTPIGFDLEIEKR.I                   |
| 0.999998 | 1 R.K[325.13]SKNILFVITKPDVYK.S                      |
| 0.999998 | 1 R.K[325.13]SKNILFVITKPDVYK.S                      |
| 0.999998 | 0.9991 R.ELPAQK[325.13]WWHTGALYR.I                  |
| 0.999998 | 1 K.FRGPFTDVVTTNLK[325.13]LGNPTDR.N                 |
| 0.999998 | 1 K.FRGPFTDVVTTNLK[325.13]LGNPTDR.N                 |
| 0.999998 | 1 R.DRDVDVLSAALK[325.13]EQLSHSR.Q                   |
| 0.999998 | 1 R.DRDVDVLSAALK[325.13]EQLSHSR.Q                   |
| 0.999998 | 1 R.DRDVDVLSAALK[325.13]EQLSHSR.Q                   |
| 0.999998 | 1 K.ASLASLPPLHVAK[325.13]LSHEGPGSELPAALYR.K         |
| 0.999998 | 1 R.DVFLPK[325.13]PTWGNHTPIFR.D                     |
| 0.999998 | 1 R.DVFLPK[325.13]PTWGNHTPIFR.D                     |
| 0.999998 | 1 R.FPAEDEFPDLSAHNNHMAK[325.13]VLTPELYAELR.A        |
| 0.999998 | 1 R.ESGYAGK[325.13]ISQMPVILTPLHFDRDPLQK.Q           |
| 0.999998 | 1 R.HGK[325.13]LWSNFWGALSPDEYYAR.S                  |
| 0.999998 | 1 R.AFGFSHLEALLDDSK[325.13]ELQR.F                   |
| 0.999998 | 1 R.NSLK[325.13]ELWLVIHGR.V                         |
| 0.999998 | 1 R.NSLK[325.13]ELWLVIHGR.V                         |
| 0.999998 | 1 R.NSLK[325.13]ELWLVIHGR.V                         |
| 0.999998 | 1 R.NSLK[325.13]ELWLVIHGR.V                         |
| 0.999998 | 0.9996 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR |
| 0.999998 | 1 R.NSLK[325.13]ELWLVIHGR.V                         |
| 0.999998 | 1 R.SPAHYAGYWK[325.13]AVQELWLR.L                    |
| 0.999998 | 1 R.SPAHYAGYWK[325.13]AVQELWLR.L                    |
| 0.999998 | 1 R.SPAHYAGYWK[325.13]AVQELWLR.L                    |
| 0.999998 | 1 R.SSPK[325.13]ALNFGGIGVVVGHELTHAFDDQGR.E          |
| 0.999998 | 1 R.SSPK[325.13]ALNFGGIGVVVGHELTHAFDDQGR.E          |
| 0.999998 | 1 R.SSPK[325.13]ALNFGGIGVVVGHELTHAFDDQGR.E          |
| 0.999998 | 1 R.M[147.04]VLAAAGGVEHQQLDLAQK[325.13]HLGGIPW      |
| 0.999998 | 1 R.M[147.04]VLAAAGGVEHQQLDLAQK[325.13]HLGGIPW      |

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| 0.999998 | 0.9984 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTTRPTDKPLR. |
| 0.999998 | 1 K.FLVHNVK[325.13]ELEVLLMC[160.03]NK.S                  |
| 0.999998 | 1 K.STLLLLLTGK[325.13]LTPTHGEMR.K                        |
| 0.999998 | 1 K.LFNHLSAVSESIQALGWVAMAPK[325.13]PGPYVK.E              |
| 0.999998 | 1 K.LFNHLSAVSESIQALGWVAMAPK[325.13]PGPYVK.E              |
| 0.999998 | 1 R.AIAIAAGVPVPGTDAPITSLHEAHEFSNTYGFPIIFK[325.13]        |
| 0.999998 | 1 R.VQLIK[325.13]ALLALPIRPATR.R                          |
| 0.999998 | 1 K.AIHyalNC[160.03]C[160.03]GLAGGVEQFISDIC[160.03]      |
| 0.999998 | 1 R.IREPALLSK[325.13]QDIVLTTYNILTHDYGTK.G                |
| 0.999998 | 1 R.APVLSIDPPVHEVEEQGIDAK[325.13]WSLALGLPLPLGEHA         |
| 0.999998 | 1 R.APVLSIDPPVHEVEEQGIDAK[325.13]WSLALGLPLPLGEHA         |
| 0.999998 | 1 K.MIQLGK[325.13]TVHYLPILFIDQLSNR.V                     |
| 0.999998 | 1 K.MIQLGK[325.13]TVHYLPILFIDQLSNR.V                     |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                         |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                         |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                         |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                         |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                         |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                         |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                         |
| 0.999998 | 1 R.HGEEVTPEDVLSAAMYDPVFAHFK[325.13]DFTATFGPLD           |
| 0.999998 | 1 K.SAHLTNPWNEHKPVK[325.13]IGR.D                         |
| 0.999998 | 1 K.ILK[325.13]SLHHPNIVGYR.A                             |
| 0.999998 | 1 K.ILK[325.13]SLHHPNIVGYR.A                             |
| 0.999998 | 1 R.LALK[325.13]FHPDKNHAPGATEAFK.A                       |
| 0.999998 | 1 K.TLVMNK[325.13]HVGHLR.T                               |
| 0.999998 | 1 K.TLVMNK[325.13]HVGHLR.T                               |
| 0.999998 | 1 R.FGLESHAHTIQIC[160.03]K[325.13]LSGGQK.A               |
| 0.999998 | 1 R.FGLESHAHTIQIC[160.03]K[325.13]LSGGQK.A               |
| 0.999998 | 1 R.TSHGEVISVPHK[325.13]IITHLR.K                         |
| 0.999998 | 1 R.TSHGEVISVPHK[325.13]IITHLR.K                         |
| 0.999998 | 1 R.GHLAK[325.13]IYAMHWGTDSR.L                           |
| 0.999998 | 1 R.K[325.13]FIC[160.03]HVVGITYQHIDR.W                   |
| 0.999998 | 1 R.VFHAGFGVVLGEDKK[325.13]K.F                           |
| 0.999998 | 1 R.K[325.13]FIC[160.03]HVVGITYQHIDR.W                   |
| 0.999998 | 1 R.K[325.13]FIC[160.03]HVVGITYQHIDR.W                   |
| 0.999998 | 1 K.ATIAGGGVIPHIHK[325.13]SLIGK.K                        |
| 0.999998 | 1 R.GKDQVVILHHMLSK[325.13]ATVK.A                         |
| 0.999998 | 1 K.ATIAGGGVIPHIHK[325.13]SLIGK.K                        |
| 0.999998 | 1 R.HAGGHGIEFAPMYK[325.13]INYSR.D                        |
| 0.999998 | 1 R.LQFHDVAGDIFHQQC[160.03]K[325.13]R.N                  |
| 0.999998 | 1 R.LQFHDVAGDIFHQQC[160.03]K[325.13]R.N                  |
| 0.999998 | 1 R.HAGGHGIEFAPMYK[325.13]INYSR.D                        |
| 0.999998 | 1 R.HAGGHGIEFAPMYK[325.13]INYSR.D                        |
| 0.999998 | 1 K.LDLIHESILHK[325.13]C[160.03]IK.T                     |
| 0.999998 | 1 R.HIGK[325.13]PLLGGPFSLTHTGER.K                        |

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| 0.999998 | 1 R.HIGK[325.13]PLLGGPFSLTTHHTGER.K                |
| 0.999998 | 1 R.GHTK[325.13]LAFPSFPGHLSEGFHSR.W                |
| 0.999998 | 1 R.GHTK[325.13]LAFPSFPGHLSEGFHSR.W                |
| 0.999998 | 1 R.HIGK[325.13]PLLGGPFSLTTHHTGER.K                |
| 0.999998 | 1 R.GHTK[325.13]LAFPSFPGHLSEGFHSR.W                |
| 0.999998 | 1 K.VIVDFSSPNIK[325.13]EMHVGHLR.S                  |
| 0.999998 | 1 K.VIVDFSSPNIK[325.13]EMHVGHLR.S                  |
| 0.999998 | 1 R.HEVININLK[325.13]NKPEWFFK.K                    |
| 0.999998 | 1 R.HEVININLK[325.13]NKPEWFFK.K                    |
| 0.999998 | 1 K.LFGYEPTIYYPKRPNK[325.13]PLFTALVTQC[160.03]QK.M |
| 0.999998 | 1 K.NEEVLAVLGHELGHWK[325.13]LGHTVK.N               |
| 0.999998 | 1 R.ALKDPNAFLFDHLLTLK[325.13]PVK.F                 |
| 0.999998 | 1 R.ALKDPNAFLFDHLLTLK[325.13]PVK.F                 |
| 0.999998 | 1 R.ALK[325.13]DPNAFLFDHLLTLKPVK.F                 |
| 0.999998 | 1 R.ALK[325.13]DPNAFLFDHLLTLKPVK.F                 |
| 0.999998 | 1 R.AGGPLGLSIVGGSDHSSHPFQVQEPGVFISK[325.13]VLPR.   |
| 0.999998 | 1 K.HYLDQLNHILGILGSPSQEDLNC[160.03]IINLK[325.13]AR |
| 0.999998 | 1 K.HYLDQLNHILGILGSPSQEDLNC[160.03]IINLK[325.13]AR |
| 0.999998 | 1 K.HYLDQLNHILGILGSPSQEDLNC[160.03]IINLK[325.13]AR |
| 0.999998 | 1 K.LRTDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A           |
| 0.999998 | 1 R.KLDPELHLDIK[325.13]VLQSALAAIR.H                |
| 0.999998 | 1 R.KLDPELHLDIK[325.13]VLQSALAAIR.H                |
| 0.999998 | 1 R.LSGDWNPLHIDPNFASLAGFDK[325.13]PILHGLC[160.03]  |
| 0.999998 | 1 R.LSGDWNPLHIDPNFASLAGFDK[325.13]PILHGLC[160.03]  |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                   |
| 0.999998 | 1 K.ERPPNPIEFLASYLLK[325.13]NK.A                   |
| 0.999998 | 1 K.K[325.13]LPPLPLTLALGAFLNHR.K                   |
| 0.999998 | 1 K.K[325.13]LPPLPLTLALGAFLNHR.K                   |
| 0.999998 | 1 K.K[325.13]LPPLPLTLALGAFLNHR.K                   |
| 0.999998 | 1 K.K[325.13]LPPLPLTLALGAFLNHR.K                   |
| 0.999998 | 1 R.K[325.13]TGQAPGYSYTAANK.N                      |
| 0.999998 | 1 K.VGEFSGANK[325.13]EK.L                          |
| 0.999998 | 1 K.VGEFSGANK[325.13]EK.L                          |
| 0.999998 | 1 K.AQAAAPASVPAQAPK[325.13]R.T                     |
| 0.999998 | 1 K.AQAAAPASVPAQAPK[325.13]R.T                     |
| 0.999998 | 1 K.VVGAK[325.13]VVTNAR.S                          |
| 0.999998 | 1 K.IGEGTYGVVYK[325.13]GR.H                        |
| 0.999998 | 1 R.IQQESGC[160.03]K[325.13]IQIAPDSGGLPER.S        |
| 0.999998 | 1 R.IQQESGC[160.03]K[325.13]IQIAPDSGGLPER.S        |
| 0.999998 | 1 R.LVVPASQC[160.03]GSLIGK[325.13]GGC[160.03]K.I   |
| 0.999998 | 1 R.VAAGLQIK[325.13]NSLTSK.D                       |
| 0.999998 | 1 R.YALYDASFETK[325.13]ESR.K                       |
| 0.999998 | 1 R.K[325.13]ASPPSGLWSPAYASH.-                     |
| 0.999998 | 1 K.K[325.13]LLDLVQQSC[160.03]NYK.Q                |
| 0.999998 | 1 K.ELTIGSK[325.13]LQDAEIAR.L                      |
| 0.999998 | 1 K.AVVK[325.13]TDIQIALPSGC[160.03]YGR.V           |
| 0.999998 | 1 K.SDGIYIINLK[325.13]R.T                          |

0.999998 1 R.ASDTEAGK[325.13]YQC[160.03]VAELWR.K  
0.999998 1 K.K[325.13]QIWTLEQPPDEAGSAAVC[160.03]LR.S  
0.999998 1 K.TIK[325.13]LQIWDTAGQER.F  
0.999998 1 K.K[325.13]QIWTLEQPPDEAGSAAVC[160.03]LR.S  
0.999998 1 R.AAK[325.13]VLEQLTGQTPVFSK.A  
0.999998 1 R.STPAITLESPIK[325.13]YPLR.L  
0.999998 1 R.SVLISLK[325.13]QAPLVH.-  
0.999998 1 R.SVLISLK[325.13]QAPLVH.-  
0.999998 1 R.DFGSAAVSLQVAAPYSK[325.13]PSMTLEPNK.D  
0.999998 1 R.DFGSAAVSLQVAAPYSK[325.13]PSMTLEPNK.D  
0.999998 1 K.IVIPNEESVVIYK[325.13]IR.Q  
0.999998 0.9991 R.K[325.13]LFIGGLSFETTEESLR.N  
0.999998 1 K.VGK[325.13]DELFALEQSC[160.03]AQVVLQAANER.N  
0.999998 1 R.TGLK[325.13]ITSLTEVVC[160.03]GLDLC[160.03]NQGN:  
0.999998 1 K.AIQLNSNSVQALLK[325.13]GAALR.N  
0.999998 1 K.AIQLNSNSVQALLK[325.13]GAALR.N  
0.999998 0.9999 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T  
0.999998 1 K.LEVAPISDIIAK[325.13]SPDTFVR.T  
0.999998 1 R.M[147.04]YQK[325.13]GQETSTNPIASIFAWTR.G  
0.999998 1 R.SVK[325.13]GLVAVITGGASGLGLATAER.L  
0.999998 0.9802 R.ADIK[325.13]EMGLSLQWLYSAR.G  
0.999998 1 K.LQTYK[325.13]TAVETAVLLLR.I  
0.999998 0.9995 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S  
0.999998 1 K.K[325.13]DILLPFQGLDSIPVSNPSC[160.03]PMIPLYR.N  
0.999998 0.9999 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R  
0.999998 1 K.ILDPNTGEPAPVLSPPPADVSTFLAFPSPEK[325.13]LLR.L  
0.999998 1 K.LLSATGESEK[325.13]QFQEAIIVFQEEFK.C  
0.999998 1 K.LLSATGESEK[325.13]QFQEAIIVFQEEFK.C  
0.999998 1 K.LLSATGESEK[325.13]QFQEAIIVFQEEFK.C  
0.999998 1 R.VVYIFGPPVK[325.13]EPPTDVTPTFLTGTGLSTLR.Q  
0.999998 1 R.VVYIFGPPVK[325.13]EPPTDVTPTFLTGTGLSTLR.Q  
0.999998 1 K.GQLTTDQVFPYPSVLNEEQTQFLK[325.13]ELVEPVSR.F  
0.999998 1 R.TEPTAQQLALQLAEK[325.13]LGSLVENNER.V  
0.999998 0.9993 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S  
0.999998 1 K.AC[160.03]SLAK[325.13]TAFDEAIAELDTLSEESYK.D  
0.999998 1 R.VLSTAGPSEALQPLVYPLAQVIIGC[160.03]IK[325.13]LIPT  
0.999998 1 R.K[325.13]SNIHC[160.03]NTIAPNAGSR.M  
0.999998 1 R.FTSYQK[325.13]ATEEHSTR.Q  
0.999998 1 R.NEK[325.13]IAVHC[160.03]TVR.G  
0.999998 1 K.K[325.13]VLTGVAGEDAEC[160.03]HAAK.L  
0.999998 1 K.K[325.13]VLTGVAGEDAEC[160.03]HAAK.L  
0.999998 1 K.MVSGMVK[325.13]HITGSYK.V  
0.999998 1 K.MVSGMVK[325.13]HITGSYK.V  
0.999998 1 R.K[325.13]AIVIC[160.03]PTDEDLKDR.T  
0.999998 1 R.THTGK[325.13]YWTLTATGGVQSTASSK.N  
0.999998 1 R.THTGK[325.13]YWTLTATGGVQSTASSK.N  
0.999998 1 K.YGPK[325.13]GYGYGQGAGTLSTDKGESLGIK.H



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| 0.999998 | 1 K.YGPK[325.13]GYGYGQGAGTLSTDKGESLGIK.H                 |
| 0.999998 | 1 R.THTGK[325.13]YWTLTATGGVQSTASSK.N                     |
| 0.999998 | 1 K.YGPK[325.13]GYGYGQGAGTLSTDKGESLGIK.H                 |
| 0.999998 | 1 K.NVVHK[325.13]TGGYLTESGYVNLQR.V                       |
| 0.999998 | 1 R.IFGSNK[325.13]WTTEQQQR.F                             |
| 0.999998 | 1 R.IFGSNK[325.13]WTTEQQQR.F                             |
| 0.999998 | 1 R.AVLLGPPGAGK[325.13]GTQAPR.L                          |
| 0.999998 | 1 R.VFQSLPHENK[325.13]PLTLSNYQTNK.A                      |
| 0.999998 | 1 R.VLAKPQNTAEVQK[325.13]VQLTGEPVPMAR.C                  |
| 0.999998 | 1 R.VLAKPQNTAEVQK[325.13]VQLTGEPVPMAR.C                  |
| 0.999998 | 1 R.VLAKPQNTAEVQK[325.13]VQLTGEPVPMAR.C                  |
| 0.999998 | 1 R.VLAKPQNTAEVQK[325.13]VQLTGEPVPMAR.C                  |
| 0.999998 | 1 R.VLAKPQNTAEVQK[325.13]VQLTGEPVPMAR.C                  |
| 0.999998 | 1 R.VLAKPQNTAEVQK[325.13]VQLTGEPVPMAR.C                  |
| 0.999998 | 1 R.VLAKPQNTAEVQK[325.13]VQLTGEPVPMAR.C                  |
| 0.999998 | 1 K.LTALDYHNPAGFNC[160.03]K[325.13]DETEFR.N              |
| 0.999998 | 1 R.VK[325.13]TTGIVETHFTFK.D                             |
| 0.999998 | 1 R.AGIK[325.13]VTVAGLAGKDPVQC[160.03]SR.D               |
| 0.999998 | 1 R.AGIK[325.13]VTVAGLAGKDPVQC[160.03]SR.D               |
| 0.999998 | 1 K.GFVEFAAK[325.13]PPAR.K                               |
| 0.999998 | 1 R.ISGASEK[325.13]DIVHSGLAYTMER.S                       |
| 0.999998 | 1 R.ISGASEK[325.13]DIVHSGLAYTMER.S                       |
| 0.999998 | 1 R.ISGASEK[325.13]DIVHSGLAYTMER.S                       |
| 0.999998 | 1 R.ISGASEK[325.13]DIVHSGLAYTMER.S                       |
| 0.999998 | 1 K.IDSK[325.13]LGHVVMGNNVSPYQQVIEK.T                    |
| 0.999998 | 1 K.IDSK[325.13]LGHVVMGNNVSPYQQVIEK.T                    |
| 0.999998 | 1 K.DNPK[325.13]IVHAFDMEDLGDK.A                          |
| 0.999998 | 1 R.K[325.13]FYGPEGPYGVFAGR.D                            |
| 0.999998 | 1 R.K[325.13]FYGPEGPYGVFAGR.D                            |
| 0.999998 | 1 R.EQVPSLGSNVAC[160.03]GLAYTDYHK[325.13]AAMGLG.         |
| 0.999998 | 1 R.K[325.13]WC[160.03]ELIPGAEFR.C                       |
| 0.999998 | 1 K.SK[325.13]NILFVITKPDVYK.S                            |
| 0.999998 | 1 R.TGAHYILFPC[160.03]ASSLC[160.03]GC[160.03]SVK[325.13] |
| 0.999998 | 1 R.K[325.13]WC[160.03]ELIPGAEFR.C                       |
| 0.999998 | 1 R.K[325.13]WC[160.03]ELIPGAEFR.C                       |
| 0.999998 | 1 R.VPDSC[160.03]C[160.03]LEFSESC[160.03]GLHAPGTWV       |
| 0.999998 | 1 R.TGAHYILFPC[160.03]ASSLC[160.03]GC[160.03]SVK[325.13] |
| 0.999998 | 1 R.VPDSC[160.03]C[160.03]LEFSESC[160.03]GLHAPGTWV       |
| 0.999998 | 1 R.VPDSC[160.03]C[160.03]LEFSESC[160.03]GLHAPGTWV       |
| 0.999998 | 1 R.VLMEK[325.13]EFPGFLENQKDPLAVDK.I                     |
| 0.999998 | 1 R.VLMEK[325.13]EFPGFLENQKDPLAVDK.I                     |
| 0.999998 | 1 R.VLMEK[325.13]EFPGFLENQKDPLAVDK.I                     |
| 0.999998 | 1 R.VLMEK[325.13]EFPGFLENQKDPLAVDK.I                     |
| 0.999998 | 1 R.GVEVDPSLIK[325.13]DTWHQVYR.R                         |
| 0.999998 | 1 R.GVEVDPSLIK[325.13]DTWHQVYR.R                         |
| 0.999998 | 1 R.TWEK[325.13]LLLAAR.A                                 |
| 0.999998 | 1 R.GVEVDPSLIK[325.13]DTWHQVYR.R                         |

0.999998 0.9999 K.IILDLISESPIK[325.13]GR.A  
0.999998 1 K.VEELEGEITTLNHNK[325.13]LQDASAEVER.L  
0.999998 1 K.VEELEGEITTLNHNK[325.13]LQDASAEVER.L  
0.999998 0.9994 R.K[325.13]LFIGGLSFETTEESLR.N  
0.999998 1 K.VEELEGEITTLNHNK[325.13]LQDASAEVER.L  
0.999998 0.9992 R.K[325.13]LFIGGLSFETTEESLR.N  
0.999998 0.9999 R.LK[325.13]VPPAINQFTQALDR.Q  
0.999998 0.9993 R.K[325.13]LFIGGLSFETTEESLR.N  
0.999998 1 R.NFLVFQGAVESIAMK[325.13]NPK.E  
0.999998 0.9947 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN  
0.999998 1 K.SSMSVTSLEAELQAK[325.13]IQESHPELR.R  
0.999998 1 R.VLFLIPK[325.13]NNPPTLVGDFTK.S  
0.999998 1 R.SLGEISALTSK[325.13]LADLR.R  
0.999998 1 R.EFALQSTSEPVAGLGPALAWK[325.13]PSGSLIASTQDKPN  
0.999998 1 R.EFALQSTSEPVAGLGPALAWK[325.13]PSGSLIASTQDKPN  
0.999998 1 R.TC[160.03]LITFK[325.13]PGAFIPGAPVQPVVLR.Y  
0.999998 1 R.TGIIVTSEAVLLQLVADK[325.13]DHPK.F  
0.999998 1 R.TGIIVTSEAVLLQLVADK[325.13]DHPK.F  
0.999998 1 R.TGIIVTSEAVLLQLVADK[325.13]DHPK.F  
0.999998 1 R.AANPVDFLSK[325.13]ASEIMVDDEELAQHPATTEDIR.V  
0.999998 0.9998 K.VK[325.13]DALEFWLQAGVDGFQVR.D  
0.999998 1 R.DISILQC[160.03]HGDC[160.03]DPLVPLMFGSLTVEK[325.13]IR.A  
0.999998 1 R.DISILQC[160.03]HGDC[160.03]DPLVPLMFGSLTVEK[325.13]IR.A  
0.999998 1 R.DISILQC[160.03]HGDC[160.03]DPLVPLMFGSLTVEK[325.13]IR.A  
0.999998 1 R.MQEAMTQEVSDVFSDDTTPIK[325.13]LLAVAATAPPDAP  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.GQLDK[325.13]DTLDTLTAIFYPGYLC[160.03]SLSPEELSSV  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
0.999998 1 K.TFHETLDC[160.03]C[160.03]GSSTLTALTTSVLK[325.13]IR.A  
0.999998 1 R.DPLLLAIIPK[325.13]YLR.A  
0.999998 1 R.LIEEK[325.13]GAVDALAAALAHISGASSFEPR.S  
0.999998 1 R.DPLLLAIIPK[325.13]YLR.A  
0.999998 0.9983 K.VK[325.13]DALEFWLQAGVDGFQVR.D  
0.999998 1 R.LAAVQLLQFLAPK[325.13]IR.A  
0.999998 1 R.WLK[325.13]GQGVYLGMPGC[160.03]LPVYDALAGEFIR.  
0.999998 0.9985 K.VK[325.13]DALEFWLQAGVDGFQVR.D  
0.999998 0.9997 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y  
0.999998 1 R.GLPFQANAQDIINFFAPLK[325.13]PVR.I  
0.999998 1 R.GLPFQANAQDIINFFAPLK[325.13]PVR.I  
0.999998 1 R.LLPPLLQIVC[160.03]K[325.13]GLEDPSQVVR.N  
0.999998 1 R.LLPPLLQIVC[160.03]K[325.13]GLEDPSQVVR.N

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| 0.999998 | 1 R.LLPPLLQIVC[160.03]K[325.13]GLEDPSQVVR.N         |
| 0.999998 | 1 R.LLPPLLQIVC[160.03]K[325.13]GLEDPSQVVR.N         |
| 0.999998 | 0.9996 R.DLTDYLMK[325.13]ILTER.G                    |
| 0.999998 | 1 R.LADSPPPQVWQLISK[325.13]VLAR.H                   |
| 0.999998 | 1 R.LADSPPPQVWQLISK[325.13]VLAR.H                   |
| 0.999998 | 1 R.LADSPPPQVWQLISK[325.13]VLAR.H                   |
| 0.999998 | 1 R.LADSPPPQVWQLISK[325.13]VLAR.H                   |
| 0.999998 | 1 R.LADSPPPQVWQLISK[325.13]VLAR.H                   |
| 0.999998 | 1 R.LADSPPPQVWQLISK[325.13]VLAR.H                   |
| 0.999998 | 1 R.ILALEK[325.13]LGAVFNQVAFPLQYTPR.K               |
| 0.999998 | 1 R.AYEAASALQIATHTAFAVAK[325.13]AMQADISQAAQILSS     |
| 0.999998 | 1 K.LPGIPIK[325.13]IVMEAIQQASVAK.K                  |
| 0.999998 | 1 R.NLDFQDVLDK[325.13]LADMGIAIR.V                   |
| 0.999998 | 1 R.NLDFQDVLDK[325.13]LADMGIAIR.V                   |
| 0.999998 | 1 R.VM[147.04]TIAPGLFGTPLLTSLEK[325.13]VC[160.03]N  |
| 0.999998 | 1 R.VM[147.04]TIAPGLFGTPLLTSLEK[325.13]VC[160.03]N  |
| 0.999998 | 1 R.VM[147.04]TIAPGLFGTPLLTSLEK[325.13]VC[160.03]N  |
| 0.999998 | 1 R.VM[147.04]TIAPGLFGTPLLTSLEK[325.13]VC[160.03]N  |
| 0.999998 | 1 R.LFAQLAGDDMEVSATELMNILNK[325.13]VVTR.H           |
| 0.999998 | 1 R.LFAQLAGDDMEVSATELMNILNK[325.13]VVTR.H           |
| 0.999998 | 1 K.MHLAGK[325.13]TEQAK.A                           |
| 0.999998 | 1 K.MHLAGK[325.13]TEQAK.A                           |
| 0.999998 | 1 R.K[325.13]RPAPQQIQVQQQAVQNR.N                    |
| 0.999998 | 1 R.K[325.13]RPAPQQIQVQQQAVQNR.N                    |
| 0.999998 | 1 R.K[325.13]RPAPQQIQVQQQAVQNR.N                    |
| 0.999998 | 1 R.K[325.13]RPAPQQIQVQQQAVQNR.N                    |
| 0.999998 | 1 R.TIQGHLQSENFK[325.13]QR.V                        |
| 0.999998 | 1 R.DC[160.03]DHADEQK[325.13]C[160.03]YSC[160.03]GE |
| 0.999998 | 1 R.TIQGHLQSENFK[325.13]QR.V                        |
| 0.999998 | 1 R.TIQGHLQSENFK[325.13]QR.V                        |
| 0.999998 | 1 R.DC[160.03]DHADEQK[325.13]C[160.03]YSC[160.03]GE |
| 0.999998 | 1 R.K[325.13]SDLHPTLPAGR.Y                          |
| 0.999998 | 1 R.AHVTGPVEDNEK[325.13]C[160.03]YPPPSVQSC[160.03]  |
| 0.999998 | 1 R.K[325.13]SDLHPTLPAGR.Y                          |
| 0.999998 | 1 R.K[325.13]SDLHPTLPAGR.Y                          |
| 0.999998 | 1 K.TTWAIK[325.13]HAASNPSK.K                        |
| 0.999998 | 1 R.AHVTGPVEDNEK[325.13]C[160.03]YPPPSVQSC[160.03]  |
| 0.999998 | 0.9516 R.HQGVMMVGMGQKDSYVGDEAQSK[325.13]R.G         |
| 0.999998 | 1 K.LHVGNISPTC[160.03]TNK[325.13]ELR.A              |
| 0.999998 | 1 K.IGEEIQKPEEK[325.13]VTWDGHSGLMAR.T               |
| 0.999998 | 1 R.K[325.13]NVLGHMQQGSPTPFDR.N                     |
| 0.999998 | 1 R.K[325.13]NVLGHMQQGSPTPFDR.N                     |
| 0.999998 | 1 K.AQITQK[325.13]IGVHAFQQR.L                       |
| 0.999998 | 1 R.AHPVFYQGTYSQALNDAK[325.13]R.E                   |
| 0.999998 | 1 R.C[160.03]VK[325.13]IFQGNVHNFEK.N                |
| 0.999998 | 1 R.AHPVFYQGTYSQALNDAK[325.13]R.E                   |
| 0.999998 | 1 R.TLSVSSK[325.13]NISLHGDGPLR.L                    |
| 0.999998 | 1 R.LLGLTGSTK[325.13]QVAQASHSYR.V                   |

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| 0.999998 | 1 R.LLGLTGSTK[325.13]QVAQASHSYR.V                     |
| 0.999998 | 1 R.LLGLTGSTK[325.13]QVAQASHSYR.V                     |
| 0.999998 | 1 R.LLGLTGSTK[325.13]QVAQASHSYR.V                     |
| 0.999998 | 1 R.TLSVSSK[325.13]NISLHGDGPLR.L                      |
| 0.999998 | 1 R.TLSVSSK[325.13]NISLHGDGPLR.L                      |
| 0.999998 | 1 R.DAVHNK[325.13]LWLQR.R                             |
| 0.999998 | 1 K.FQAK[325.13]LEHEYIQNFK.I                          |
| 0.999998 | 1 K.FQAK[325.13]LEHEYIQNFK.I                          |
| 0.999998 | 1 R.LAQQPHQNQAK[325.13]LVVALSR.T                      |
| 0.999998 | 1 K.EFHTTGLAWSK[325.13]TGPVAK.E                       |
| 0.999998 | 1 R.LAQQPHQNQAK[325.13]LVVALSR.T                      |
| 0.999998 | 1 K.EFHTTGLAWSK[325.13]TGPVAK.E                       |
| 0.999998 | 1 R.K[325.13]VFIQHITLSDEER.K                          |
| 0.999998 | 1 R.LAQQPHQNQAK[325.13]LVVALSR.T                      |
| 0.999998 | 1 R.INFDK[325.13]YHPGYFGK.V                           |
| 0.999998 | 1 R.INFDK[325.13]YHPGYFGK.V                           |
| 0.999998 | 1 R.INFDK[325.13]YHPGYFGK.V                           |
| 0.999998 | 0.9994 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E              |
| 0.999998 | 1 R.GFYLNQSTAYHFNPK[325.13]PASPR.F                    |
| 0.999998 | 1 R.VK[325.13]TTGIVETHFTFK.D                          |
| 0.999998 | 1 R.GFYLNQSTAYHFNPK[325.13]PASPR.F                    |
| 0.999998 | 1 R.FAAHLIAGAPSEGSALK[325.13]PELSR.R                  |
| 0.999998 | 1 R.AGVHIK[325.13]LPNLGK.H                            |
| 0.999998 | 1 R.FAAHLIAGAPSEGSALK[325.13]PELSR.R                  |
| 0.999998 | 1 R.FAAHLIAGAPSEGSALK[325.13]PELSR.R                  |
| 0.999998 | 1 R.AGVHIK[325.13]LPNLGK.H                            |
| 0.999998 | 1 R.FAAHLIAGAPSEGSALK[325.13]PELSR.R                  |
| 0.999998 | 1 K.YHSDEYIK[325.13]FLR.S                             |
| 0.999998 | 1 R.KSDGIYIINLK[325.13]R.T                            |
| 0.999998 | 1 R.KSDGIYIINLK[325.13]R.T                            |
| 0.999998 | 1 R.LNAIQNNLTK[325.13]SHIEIIR.G                       |
| 0.999998 | 1 R.LNAIQNNLTK[325.13]SHIEIIR.G                       |
| 0.999998 | 1 R.LNAIQNNLTK[325.13]SHIEIIR.G                       |
| 0.999998 | 1 R.GLAVNMVDSK[325.13]HSMNILNR.I                      |
| 0.999998 | 1 R.GLAVNMVDSK[325.13]HSMNILNR.I                      |
| 0.999998 | 1 K.TAGVK[325.13]HLIVLINK.M                           |
| 0.999998 | 1 K.RPAC[160.03]TLK[325.13]PEC[160.03]VQQLLVC[160.03] |
| 0.999998 | 1 K.RPAC[160.03]TLK[325.13]PEC[160.03]VQQLLVC[160.03] |
| 0.999998 | 1 R.LVK[325.13]AFQYVETHGEVC[160.03]PANWTPDSPTIKP.     |
| 0.999998 | 1 K.LLAHEIFEK[325.13]SNAAGVPC[160.03]DLVTGEER.V       |
| 0.999998 | 1 R.ELVGHK[325.13]VNLQMVDYSPLC[160.03]R.L             |
| 0.999998 | 1 R.ELVGHK[325.13]VNLQMVDYSPLC[160.03]R.L             |
| 0.999998 | 1 R.ELVGHK[325.13]VNLQMVDYSPLC[160.03]R.L             |
| 0.999998 | 1 K.GAGAFGYFEVTHDITK[325.13]YSK.A                     |
| 0.999998 | 1 R.VVVSGLPPSGSWQDLK[325.13]DHMR.E                    |
| 0.999998 | 1 R.HISPSAK[325.13]PFENGQYLDIYGITR.D                  |
| 0.999998 | 1 R.ATNWAK[325.13]FTATASLGVIHK.G                      |

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| 0.999998 | 1 R.SC[160.03]SLVLEHQPDNIK[325.13]ALFR.K            |
| 0.999998 | 1 K.AHVLAASVEQATENFLEK[325.13]GDK.I                 |
| 0.999998 | 1 R.SC[160.03]SLVLEHQPDNIK[325.13]ALFR.K            |
| 0.999998 | 1 R.IAAK[325.13]FITHAPPGEFNEVFNDVR.L                |
| 0.999998 | 1 R.IAAK[325.13]FITHAPPGEFNEVFNDVR.L                |
| 0.999998 | 1 R.SLK[325.13]SVQLYGPTNFAPVINHVAR.Y                |
| 0.999998 | 1 R.SLK[325.13]SVQLYGPTNFAPVINHVAR.Y                |
| 0.999998 | 1 R.SLK[325.13]SVQLYGPTNFAPVINHVAR.Y                |
| 0.999998 | 1 K.LLASADDFGK[325.13]VHLFSYPC[160.03]C[160.03]QPR. |
| 0.999998 | 1 R.EILTLLQGVBHQGAGFQDIPK[325.13]R.C                |
| 0.999998 | 1 R.HVDLLEVAQETDGFSGSDLK[325.13]EMC[160.03]R.D      |
| 0.999998 | 1 R.HVDLLEVAQETDGFSGSDLK[325.13]EMC[160.03]R.D      |
| 0.999998 | 1 R.EILTLLQGVBHQGAGFQDIPK[325.13]R.C                |
| 0.999998 | 1 R.HVDLLEVAQETDGFSGSDLK[325.13]EMC[160.03]R.D      |
| 0.999998 | 1 R.HVDLLEVAQETDGFSGSDLK[325.13]EMC[160.03]R.D      |
| 0.999998 | 1 R.TVLEHYALEDPLAAFK[325.13]QR.Q                    |
| 0.999998 | 1 R.TAAQC[160.03]LEHYEFLLDK[325.13]AAQR.D           |
| 0.999998 | 1 K.NLVLAGIK[325.13]AVTIHDTEK.C                     |
| 0.999998 | 1 R.DLISHDEMFSDIYK[325.13]IR.E                      |
| 0.999998 | 1 R.DLISHDEMFSDIYK[325.13]IR.E                      |
| 0.999998 | 1 K.LIIWDSYTTNK[325.13]VHAIPLR.S                    |
| 0.999998 | 1 K.NLVLAGIK[325.13]AVTIHDTEK.C                     |
| 0.999998 | 1 R.DFNHINVELSLLGK[325.13]K.K                       |
| 0.999998 | 1 R.DLISHDEMFSDIYK[325.13]IR.E                      |
| 0.999998 | 1 R.DLISHDEMFSDIYK[325.13]IR.E                      |
| 0.999998 | 1 K.DHPAVAATLNNLAVLYGK[325.13]R.G                   |
| 0.999998 | 1 K.DHPAVAATLNNLAVLYGK[325.13]R.G                   |
| 0.999998 | 1 K.DHPAVAATLNNLAVLYGK[325.13]R.G                   |
| 0.999998 | 1 R.TVLEHYALEDPLAAFK[325.13]QR.Q                    |
| 0.999998 | 1 K.DHPAVAATLNNLAVLYGK[325.13]R.G                   |
| 0.999998 | 1 R.YPSLSLHGIEGAFSGSGAK[325.13]TVIPR.K              |
| 0.999998 | 1 R.TVLEHYALEDPLAAFK[325.13]QR.Q                    |
| 0.999998 | 1 R.TVLEHYALEDPLAAFK[325.13]QR.Q                    |
| 0.999998 | 1 R.GIYQK[325.13]AIEVLSDEHAR.E                      |
| 0.999998 | 1 R.VADLADFVK[325.13]IAHPEPAFR.E                    |
| 0.999998 | 1 R.SHDTTSNTLAQLLAK[325.13]AER.V                    |
| 0.999998 | 1 R.EHALTSGTIK[325.13]AMLSGPGQFAENETNEVNFR.E        |
| 0.999998 | 1 R.EHALTSGTIK[325.13]AMLSGPGQFAENETNEVNFR.E        |
| 0.999998 | 1 R.VADLADFVK[325.13]IAHPEPAFR.E                    |
| 0.999998 | 1 K.LILEYVK[325.13]ASEAGEVPFNHEILR.E                |
| 0.999998 | 1 K.LILEYVK[325.13]ASEAGEVPFNHEILR.E                |
| 0.999998 | 1 R.EIPSHVLSK[325.13]VC[160.03]MYFTYK.V             |
| 0.999998 | 1 K.SIAK[325.13]FFDHSGTLVMDAYEPEISR.L               |
| 0.999998 | 1 K.SIAK[325.13]FFDHSGTLVMDAYEPEISR.L               |
| 0.999998 | 1 K.SIAK[325.13]FFDHSGTLVMDAYEPEISR.L               |
| 0.999998 | 1 R.FIK[325.13]PLSNAYHELAQVYSTNNPSEL.R.N            |
| 0.999998 | 1 K.K[325.13]VPTVSRPYSFIEFDTFIQK.T                  |

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| 0.999998 | 1 R.FIK[325.13]PLSNAYHELAQVYSTNNPSEL.R.N              |
| 0.999998 | 1 R.FIK[325.13]PLSNAYHELAQVYSTNNPSEL.R.N              |
| 0.999998 | 1 R.LYWVDSK[325.13]LHQLSSIDFSGGNR.K                   |
| 0.999998 | 1 R.FIK[325.13]PLSNAYHELAQVYSTNNPSEL.R.N              |
| 0.999998 | 1 R.LYWVDSK[325.13]LHQLSSIDFSGGNR.K                   |
| 0.999998 | 1 R.HC[160.03]NMVLENVK[325.13]EMWTEVPK.S              |
| 0.999998 | 1 R.HC[160.03]NMVLENVK[325.13]EMWTEVPK.S              |
| 0.999998 | 1 R.HC[160.03]NMVLENVK[325.13]EMWTEVPK.S              |
| 0.999998 | 1 K.IVSK[325.13]DLTNSHFFLDFQK.T                       |
| 0.999998 | 1 K.IVSK[325.13]DLTNSHFFLDFQK.T                       |
| 0.999998 | 1 R.LYPWGVVEVENPEHNDFLK[325.13]LR.T                   |
| 0.999998 | 1 R.K[325.13]VDPMAIVVFHQADIGEYVR.H                    |
| 0.999998 | 1 K.IVSK[325.13]DLTNSHFFLDFQK.T                       |
| 0.999998 | 1 R.K[325.13]VDPMAIVVFHQADIGEYVR.H                    |
| 0.999998 | 1 R.EHGLIFMETSAK[325.13]TASNVEEAFINTAK.E              |
| 0.999998 | 1 R.EHGLIFMETSAK[325.13]TASNVEEAFINTAK.E              |
| 0.999998 | 1 R.EHGLIFMETSAK[325.13]TASNVEEAFINTAK.E              |
| 0.999998 | 1 R.EHGLIFMETSAK[325.13]TASNVEEAFINTAK.E              |
| 0.999998 | 1 R.IEINFPAEYPPFKPPK[325.13]ITFK.T                    |
| 0.999998 | 1 R.HEIVQTLCLK[325.13]DGLIPLEIR.F                     |
| 0.999998 | 1 R.HEIVQTLCLK[325.13]DGLIPLEIR.F                     |
| 0.999998 | 1 R.EAVELPLTHFELYK[325.13]QIGIDPPR.G                  |
| 0.999998 | 1 R.EAVELPLTHFELYK[325.13]QIGIDPPR.G                  |
| 0.999998 | 0.9999 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T |
| 0.999998 | 1 K.NLMK[325.13]HGYP LIYDVFPDAC[160.03]K.E            |
| 0.999998 | 1 R.GFTAAGILSAHK[325.13]IIASSPEMNLPTVSALR.K           |
| 0.999998 | 1 R.FLNK[325.13]QAPQTIHLPSGEILDVFDAAER.Y              |
| 0.999998 | 1 R.DAVSGMGVIVHIEK[325.13]DK.I                        |
| 0.999998 | 1 R.SAHFSTLAIK[325.13]QNPLLAEAYSNLGNVYK.E             |
| 0.999998 | 1 R.SAHFSTLAIK[325.13]QNPLLAEAYSNLGNVYK.E             |
| 0.999998 | 1 R.TLQEDLVK[325.13]DVLSNAHIQNELER.E                  |
| 0.999998 | 1 K.ATGRPEC[160.03]FLTQIEGLASK[325.13]FTSLTK.V        |
| 0.999998 | 1 K.GSIQK[325.13]FVPYLIAGIQHGC[160.03]QDIGAR.S        |
| 0.999998 | 1 K.GSIQK[325.13]FVPYLIAGIQHGC[160.03]QDIGAR.S        |
| 0.999998 | 1 R.ALAHQLGLAEDEDVLFTVFAQGQK[325.13]NR.V              |
| 0.999998 | 1 R.DWIVK[325.13]HVNTNPLC[160.03]DLTPIFK.D            |
| 0.999998 | 1 R.DWIVK[325.13]HVNTNPLC[160.03]DLTPIFK.D            |
| 0.999998 | 1 R.K[325.13]TLISSTDFLSHPFGIADFEDK.V                  |
| 0.999998 | 1 R.DWIVK[325.13]HVNTNPLC[160.03]DLTPIFK.D            |
| 0.999998 | 1 R.K[325.13]TLISSTDFLSHPFGIADFEDK.V                  |
| 0.999998 | 1 R.YFEITEPPYIHFLNTFTSK[325.13]EPQR.G                 |
| 0.999998 | 1 R.DWIVK[325.13]HVNTNPLC[160.03]DLTPIFK.D            |
| 0.999998 | 1 R.YFEITEPPYIHFLNTFTSK[325.13]EPQR.G                 |
| 0.999998 | 1 R.LVPGPVFGSK[325.13]DNFHGLAIFLDTPNDETER.V           |
| 0.999998 | 1 R.LVPGPVFGSK[325.13]DNFHGLAIFLDTPNDETER.V           |
| 0.999998 | 1 R.ILEDQEENPLPAALVQPHTGK[325.13]LC[160.03]WFLDE/     |
| 0.999998 | 1 K.EILTLK[325.13]EVFQIASNDHDAAINR.Y                  |

0.999998 1 R.ILEDQEENPLPAALVQPHTGK[325.13]LC[160.03]WFLDE/  
 0.999998 1 R.AVPEDAK[325.13]QLASFLHGNASLLFR.R  
 0.999998 1 R.AVPEDAK[325.13]QLASFLHGNASLLFR.R  
 0.999998 1 K.FLEVIK[325.13]PFC[160.03]VILPEIQKPER.K  
 0.999998 1 R.GLQTVHINENFAK[325.13]LAEALYIADR.K  
 0.999998 1 K.FLEVIK[325.13]PFC[160.03]VILPEIQKPER.K  
 0.999998 1 K.GSQGPLPFHEK[325.13]VLLGSVSGLAGGFVGT PADLVNVI  
 0.999998 1 K.GSQGPLPFHEK[325.13]VLLGSVSGLAGGFVGT PADLVNVI  
 0.999998 1 K.GSQGPLPFHEK[325.13]VLLGSVSGLAGGFVGT PADLVNVI  
 0.999998 1 K.LMQITSLHSLNAFLPIK[325.13]TVGVQGDC[160.03]R.S  
 0.999998 0.9994 R.GVLK[325.13]VFLENVIR.D  
 0.999998 0.9998 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
 0.999998 1 R.DQPQK[325.13]EEDLGPAVHHVYELINQGPSSISQGVLELS  
 0.999998 1 R.DSTLGGK[325.13]AFHITNDEPIFWTFLSR.I  
 0.999998 1 R.DQPQK[325.13]EEDLGPAVHHVYELINQGPSSISQGVLELS  
 0.999998 1 R.DQPQK[325.13]EEDLGPAVHHVYELINQGPSSISQGVLELS  
 0.999998 1 R.LLM[147.04]TEVAWTK[325.13]DELKEALDDVTLPR.L  
 0.999998 1 R.LLM[147.04]TEVAWTK[325.13]DELKEALDDVTLPR.L  
 0.999998 1 R.NLSK[325.13]ILPALC[160.03]HDITDWVVGTR.V  
 0.999998 1 K.GFDALQYQEHLDEIISLNPEFNK[325.13]AVIR.V  
 0.999998 1 R.LLM[147.04]TEVAWTK[325.13]DELKEALDDVTLPR.L  
 0.999998 1 K.NVQDIK[325.13]NVVLQTLEGHLR.S  
 0.999998 1 K.NVQDIK[325.13]NVVLQTLEGHLR.S  
 0.999998 1 K.NVQDIK[325.13]NVVLQTLEGHLR.S  
 0.999998 1 R.DISILQC[160.03]HGDC[160.03]DPLVPLMFGSLTVEK[325.13]  
 0.999998 1 R.ETGYPLAVK[325.13]LGTITPDGADVSYDEDDMVLDPSLA  
 0.999998 0.9999 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
 0.999998 1 K.GLLPEELTPLILATQK[325.13]QFNYTHIC[160.03]AGASAF  
 0.999998 1 K.GLLPEELTPLILATQK[325.13]QFNYTHIC[160.03]AGASAF  
 0.999998 1 K.VK[325.13]AIANLYGPLMALNHMVQQDYFPK.A  
 0.999998 1 R.LLM[147.04]TEVAWTK[325.13]DELKEALDDVTLPR.L  
 0.999998 1 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G  
 0.999998 1 K.DGPLNMILDDGGDLTNLIHTK[325.13]YPQLPGIR.G  
 0.999998 1 K.DGPLNMILDDGGDLTNLIHTK[325.13]YPQLPGIR.G  
 0.999998 1 K.NSTIVFPLPIDMLQGIIGAK[325.13]HSHLG.-  
 0.999998 1 R.LVFVPLLLC[160.03]NIK[325.13]PR.R  
 0.999998 1 R.LVFVPLLLC[160.03]NIK[325.13]PR.R  
 0.999998 1 R.LVFVPLLLC[160.03]NIK[325.13]PR.R  
 0.999998 1 R.LVFVPLLLC[160.03]NIK[325.13]PR.R  
 0.999998 1 R.LVFVPLLLC[160.03]NIK[325.13]PR.R  
 0.999998 1 R.LVFVPLLLC[160.03]NIK[325.13]PR.R  
 0.999998 1 R.LVFVPLLLC[160.03]NIK[325.13]PR.R  
 0.999998 1 R.LVFVPLLLC[160.03]NIK[325.13]PR.R  
 0.999998 1 K.K[325.13]HEEEEEAKAER.E  
 0.999998 1 K.K[325.13]HEEEEEAKAER.E  
 0.999998 0.9999 R.LAHYNK[325.13]R.S  
 0.999998 1 K.VVVTMEHSAK[325.13]GNAHK.I

0.999998 1 K.VVVTMEHSAK[325.13]GNAHK.I  
0.999998 1 K.VVVTMEHSAK[325.13]GNAHK.I  
0.999998 1 R.SPSDEYKDNLHQVSK[325.13]R.L  
0.999998 1 R.SPSDEYKDNLHQVSK[325.13]R.L  
0.999998 1 R.SPSDEYKDNLHQVSK[325.13]R.L  
0.999998 1 R.LQVK[325.13]EHQHEEIQNVR.N  
0.999998 0.6972 R.HQGVMM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA  
0.999998 1 R.GHGADVK[325.13]C[160.03]VDWHPTK.G  
0.999998 1 R.GHGADVK[325.13]C[160.03]VDWHPTK.G  
0.999998 1 R.GHGADVK[325.13]C[160.03]VDWHPTK.G  
0.999998 1 R.GHGADVK[325.13]C[160.03]VDWHPTK.G  
0.999998 0.9999 R.IFAPNHVVAK[325.13]SR.F  
0.999998 1 R.K[325.13]AHSVYNFEKPVVMK.A  
0.999998 1 R.K[325.13]AHSVYNFEKPVVMK.A  
0.999998 1 R.K[325.13]LALQLHPDRNPDDPQAEK.F  
0.999998 1 R.K[325.13]AHSVYNFEKPVVMK.A  
0.999998 1 R.K[325.13]AHSVYNFEKPVVMK.A  
0.999998 1 K.LK[325.13]LEQIDGHIAEHNSK.I  
0.999998 1 K.EVSMDDHK[325.13]LSLDELHR.K  
0.999998 1 R.KPGVIDK[325.13]FTSDTKPIINK.V  
0.999998 1 R.KPGVIDK[325.13]FTSDTKPIINK.V  
0.999998 0.9999 R.HSEAFEALQQK[325.13]SQGLDSR.L  
0.999998 0.9993 R.M[147.04]VNHFIAEFK[325.13]R.K  
0.999998 0.9995 R.MVNHFIAEFK[325.13]R.K  
0.999998 1 R.SYHEEFNPPK[325.13]EPMKDDITGEPLIR.R  
0.999998 1 R.SPFLQK[325.13]QLTQPETHFGR.E  
0.999998 1 R.SPFLQK[325.13]QLTQPETHFGR.E  
0.999998 0.9999 K.RVTIMPK[325.13]DIQLAR.R  
0.999998 1 K.VLSVC[160.03]PSNKP AIVEAGGMQALGK[325.13]HLTSN  
0.999998 0.955 R.LK[325.13]LEPHEGLLLR.F  
0.999998 1 R.LC[160.03]YSSDHEK[325.13]LKPQYLEELPGQLK.Q  
0.999998 1 R.NIHSSDWPK[325.13]FFEK.Y  
0.999998 1 K.THLPGFVEQAEALK[325.13]AK.G  
0.999998 1 K.FGK[325.13]HGGTIPIVPTAEFQDR.I  
0.999998 1 R.SIFDHIK[325.13]LPQASK.S  
0.999998 0.9978 R.LLLPGELAK[325.13]HAVSEGTK.A  
0.999998 1 R.K[325.13]PGINVASDWSIHLR.-  
0.999998 1 R.FDSKDEILLTLEK[325.13]HGGIC[160.03]DC[160.03]QTSI  
0.999998 1 K.NHAAPFSK[325.13]VLTIFYR.K  
0.999998 1 K.NHAAPFSK[325.13]VLTIFYR.K  
0.999998 1 R.SPEEQC[160.03]LDVVTHWIQEGEEGRPK[325.13]DDR.H  
0.999998 1 R.SPEEQC[160.03]LDVVTHWIQEGEEGRPK[325.13]DDR.H  
0.999998 0.9947 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E  
0.999998 1 R.SPEEQC[160.03]LDVVTHWIQEGEEGRPK[325.13]DDR.H  
0.999998 1 K.VSQAAADLK[325.13]QFC[160.03]LQNAQHDPLLTGVSSS  
0.999998 1 K.VSQAAADLK[325.13]QFC[160.03]LQNAQHDPLLTGVSSS  
0.999998 1 K.VSQAAADLK[325.13]QFC[160.03]LQNAQHDPLLTGVSSS



|          |                                                     |
|----------|-----------------------------------------------------|
| 0.999998 | 1 K.KPALVAK[325.13]SSILLDVKPWDEETDMAK.L             |
| 0.999998 | 1 R.VMDGLLVIAMNK[325.13]HR.E                        |
| 0.999998 | 1 K.EILK[325.13]WEALHAAEC[160.03]PC[160.03]GPSLIR.F |
| 0.999998 | 1 K.KPALVAK[325.13]SSILLDVKPWDEETDMAK.L             |
| 0.999998 | 1 R.IVVEHIIMK[325.13]PAC[160.03]PLFVR.R             |
| 0.999998 | 1 R.IVVEHIIMK[325.13]PAC[160.03]PLFVR.R             |
| 0.999998 | 1 R.IVVEHIIMK[325.13]PAC[160.03]PLFVR.R             |
| 0.999998 | 1 R.IVVEHIIMK[325.13]PAC[160.03]PLFVR.R             |
| 0.999998 | 1 R.DVFLPK[325.13]PTWGNHTPIFR.D                     |
| 0.999998 | 1 R.HK[325.13]IPVMALVGNDAGWTQISR.E                  |
| 0.999998 | 1 R.LHPELSGPGVAAK[325.13]VLAASVR.R                  |
| 0.999998 | 1 K.TLLPHDPTADVFTPAEEKPIEQWVK[325.13]PEPK.V         |
| 0.999998 | 1 K.SLVHDLFQK[325.13]VEEAK.S                        |
| 0.999998 | 1 K.TLLPHDPTADVFTPAEEKPIEQWVK[325.13]PEPK.V         |
| 0.999998 | 1 R.K[325.13]TSQLETLNQLSTHTHVVDITR.T                |
| 0.999998 | 1 R.K[325.13]TSQLETLNQLSTHTHVVDITR.T                |
| 0.999998 | 1 R.IVDPEIALK[325.13]ILHR.Q                         |
| 0.999998 | 1 R.IVDPEIALK[325.13]ILHR.Q                         |
| 0.999998 | 1 K.NDWHGGAIVSALSQTGSLFK[325.13]PR.K                |
| 0.999998 | 1 K.NDWHGGAIVSALSQTGSLFK[325.13]PR.K                |
| 0.999998 | 1 K.NDWHGGAIVSALSQTGSLFK[325.13]PR.K                |
| 0.999998 | 1 R.LNHQK[325.13]NLVELSFLPGDTGKPDVLSASLEGQLTK.Q     |
| 0.999998 | 1 R.ALSSVGLHMTK[325.13]GLALWEAYR.E                  |
| 0.999998 | 1 R.ALSSVGLHMTK[325.13]GLALWEAYR.E                  |
| 0.999998 | 1 R.K[325.13]LYGKSPLFGQYFVLENPGTIK.V                |
| 0.999998 | 1 R.KLYGK[325.13]SPLFGQYFVLENPGTIK.V                |
| 0.999998 | 1 R.AK[325.13]EMDLVGLGLHPLFSSR.F                    |
| 0.999998 | 1 R.TTIHEMFLSTLDPK[325.13]TISFR.S                   |
| 0.999998 | 1 K.LTFSC[160.03]LGGSDNFK[325.13]HLNEIDLFHC[160.03] |
| 0.999998 | 1 R.IRVESLLVTAISK[325.13]ASAQQR.A                   |
| 0.999998 | 1 K.DNQVVQLHPSTVLDHK[325.13]PEWVLYNEFVLTTK.N        |
| 0.999998 | 1 K.DNQVVQLHPSTVLDHK[325.13]PEWVLYNEFVLTTK.N        |
| 0.999998 | 0.9466 R.DALSDLALHFLNK[325.13]M[147.04]K.I          |
| 0.999998 | 1 R.LSAFFEEHISVLSDYK[325.13]SALR.F                  |
| 0.999998 | 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C            |
| 0.999998 | 1 K.STLLLLLTGK[325.13]LTPTHGEMR.K                   |
| 0.999998 | 1 R.RAIEK[325.13]LAVEALSSLDGDLAGR.Y                 |
| 0.999998 | 1 K.STLLLLLTGK[325.13]LTPTHGEMR.K                   |
| 0.999998 | 0.9611 R.EHALLAYTLGVK[325.13]QLIVGVNK.M             |
| 0.999998 | 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C            |
| 0.999998 | 1 K.K[325.13]GLHLYGTQGNVGLTNAWSIIQTDFR.C            |
| 0.999998 | 1 K.FEQLTLDGHNLPVLVC[160.03]VITGK[325.13]GPLR.E     |
| 0.999998 | 1 R.QAHLIC[160.03]VLASNC[160.03]DEPMYVK[325.13]LVE/ |
| 0.999998 | 1 K.VIK[325.13]GAEILEVLHSLPAVR.Q                    |
| 0.999998 | 1 K.VIK[325.13]GAEILEVLHSLPAVR.Q                    |
| 0.999998 | 1 R.QAHLIC[160.03]VLASNC[160.03]DEPMYVK[325.13]LVE/ |
| 0.999998 | 1 K.VIK[325.13]GAEILEVLHSLPAVR.Q                    |

0.999998 1 K.VIK[325.13]GAEILEVLHSLPAVR.Q  
 0.999998 1 K.AIHyalNC[160.03]C[160.03]GLAGGVEQFISDIC[160.03]  
 0.999998 1 K.AIHyalNC[160.03]C[160.03]GLAGGVEQFISDIC[160.03]  
 0.999998 1 R.C[160.03]SSILLHGK[325.13]EQPLDEELKDAFQNAYLELG  
 0.999998 1 R.C[160.03]SSILLHGK[325.13]EQPLDEELKDAFQNAYLELG  
 0.999998 1 R.LPVVVPLHSLDEK[325.13]TLVQILTEPR.N  
 0.999998 1 R.LPVVVPLHSLDEK[325.13]TLVQILTEPR.N  
 0.999998 1 R.LPVVVPLHSLDEK[325.13]TLVQILTEPR.N  
 0.999998 1 R.IFGGLDMLAEK[325.13]LPNLTHLNLSGNK.L  
 0.999998 1 R.IFGGLDMLAEK[325.13]LPNLTHLNLSGNK.L  
 0.999998 1 R.IFGGLDMLAEK[325.13]LPNLTHLNLSGNK.L  
 0.999998 1 K.HLK[325.13]QYSPLLAFTTQGQSELTLKK.I  
 0.999998 1 K.HLK[325.13]QYSPLLAFTTQGQSELTLKK.I  
 0.999998 1 K.GTK[325.13]PFKPLEQLMGVFPAASGNFLPPSWR.K  
 0.999998 1 K.GTKPFK[325.13]PLEQLMGVFPAASGNFLPPSWR.K  
 0.999998 1 R.EVIQALHPETLISC[160.03]QSQFK[325.13]PAVDFFPSQD  
 0.999998 1 R.EVIQALHPETLISC[160.03]QSQFK[325.13]PAVDFFPSQD  
 0.999998 1 K.NSTIVFPLPIDMLQGIIGAK[325.13]HSHLG.-  
 0.999998 1 K.NSTIVFPLPIDMLQGIIGAK[325.13]HSHLG.-  
 0.999998 1 K.NSTIVFPLPIDMLQGIIGAK[325.13]HSHLG.-  
 0.999998 1 K.NSTIVFPLPIDMLQGIIGAK[325.13]HSHLG.-  
 0.999998 1 K.NSTIVFPLPIDMLQGIIGAK[325.13]HSHLG.-  
 0.999998 1 R.NPPIDDLIK[325.13]SGILPILVHC[160.03]LER.D  
 0.999997 0.9998 K.SVHELEKSK[325.13]R.A  
 0.999997 1 K.TEHAFLHC[160.03]K[325.13]SK.K  
 0.999997 0.9998 R.HGESGSM[147.04]AVFHQTQGSPSYSESK[325.13]R.L  
 0.999997 1 R.EHFQHVAAPYIAK[325.13]AGEK.S  
 0.999997 1 R.EHFQHVAAPYIAK[325.13]AGEK.S  
 0.999997 1 K.TVK[325.13]HGAPSPSHPIAPQAAAAAALR.R  
 0.999997 1 R.TELLNVC[160.03]MNAK[325.13]HHK.E  
 0.999997 0.9998 R.HWGGNVLGPK[325.13]SVAR.I  
 0.999997 1 K.SESGDWHC[160.03]TASWK[325.13]THSGSVWR.V  
 0.999997 1 R.SLDTHVTK[325.13]SLHSIIR.H  
 0.999997 0.9991 R.M[147.04]VNHFAIEFK[325.13]R.K  
 0.999997 1 R.GHAGNPRDPTDEGIFISK[325.13]VSPTGAAGR.D  
 0.999997 0.9992 R.MVNHFAIEFK[325.13]R.K  
 0.999997 1 R.THYILIQDGGALHIGAEK[325.13]C[160.03]R.Y  
 0.999997 0.9948 R.LK[325.13]LEPHEGLLLR.F  
 0.999997 1 K.RYESHPVC[160.03]ADLQAK[325.13]ILQC[160.03]YR.E  
 0.999997 1 R.SQSIYLQVLTDK[325.13]HAPEHYR.V  
 0.999997 1 R.HGIPNNQK[325.13]DTVC[160.03]EDMTFSTWTPPPGVH  
 0.999997 1 R.HGIPNNQK[325.13]DTVC[160.03]EDMTFSTWTPPPGVH  
 0.999997 1 R.GIC[160.03]IHTLTK[325.13]HQEPVYSVAFSPDGR.Y  
 0.999997 1 R.GIC[160.03]IHTLTK[325.13]HQEPVYSVAFSPDGR.Y  
 0.999997 1 R.IDIHSC[160.03]NHEAEK[325.13]LGC[160.03]SASNFFVA  
 0.999997 1 R.HGIPNNQK[325.13]DTVC[160.03]EDMTFSTWTPPPGVH  
 0.999997 1 R.IDIHSC[160.03]NHEAEK[325.13]LGC[160.03]SASNFFVA

0.999997 1 R.HGIPNNQK[325.13]DTVC[160.03]EDMTFSTWTPPPGVH  
0.999997 1 K.LPGHAGSINEVAFHPDEPIIISASSDK[325.13]R.L  
0.999997 1 K.LPGHAGSINEVAFHPDEPIIISASSDK[325.13]R.L  
0.999997 0.9981 R.ELPAQK[325.13]WWHTGALYR.I  
0.999997 1 R.VLK[325.13]EFHQAGKPIGLC[160.03]C[160.03]IAPVLAA  
0.999997 1 K.YSFK[325.13]GPHLVQSDGTVPFWAHAGNAIPSSDQIR.V  
0.999997 1 K.YSFK[325.13]GPHLVQSDGTVPFWAHAGNAIPSSDQIR.V  
0.999997 1 K.KYDVDTLDMVFLDHWK[325.13]DR.Y  
0.999997 1 K.K[325.13]KYDVDTLDMVFLDHWK.D  
0.999997 1 K.HFTVMNYDPDVVLK[325.13]QVHC[160.03]EEFIPEFEK.C  
0.999997 1 R.AFGFSHLEALLDDSK[325.13]ELQR.F  
0.999997 1 R.FIAEAAAASGAK[325.13]C[160.03]VLTHSPTWIIDPIDGTC  
0.999997 1 K.DKLDGTGVALK[325.13]VIHELNER.W  
0.999997 1 R.QATDHQELVEIPTRPLLTK[325.13]LSLITAPR.R  
0.999997 1 K.SDLFFHDYSIAPLFVQENYIHVK[325.13]PVAAGGDMK.K  
0.999997 0.9991 R.GHYTIGK[325.13]EIIDLVLDR.I  
0.999997 1 R.RSQVEQQQLITVEK[325.13]ALAILSQPTPSLVVDHER.L  
0.999997 1 K.TK[325.13]THYHAMHADC[160.03]LQELR.R  
0.999997 1 R.YTIHSQLEHLQSK[325.13]YIGTGHADTTK.W  
0.999997 1 R.HPYK[325.13]MNLASEPQEV LHIGSAHNR.S  
0.999997 1 R.KLIHLEIK[325.13]PAIR.N  
0.999997 1 R.KLIHLEIK[325.13]PAIR.N  
0.999997 1 R.K[325.13]LIHLEIKPAIR.N  
0.999997 1 R.K[325.13]LIHLEIKPAIR.N  
0.999997 1 K.HK[325.13]WVPLQIDMKPEVPR.E  
0.999997 1 K.KQDIENILHWNVTQHK[325.13]NIEVPFKPAR.V  
0.999997 1 K.GK[325.13]FGHEFLEFEFRPDGK.L  
0.999997 1 R.YHPK[325.13]SQPFVDHVFTFTILDNR.I  
0.999997 1 K.ALYEQSLHIK[325.13]SAIPHPLIMGVIR.E  
0.999997 1 K.ALYEQSLHIK[325.13]SAIPHPLIMGVIR.E  
0.999997 1 R.GK[325.13]SVILDC[160.03]TPTGTHDHYMLEWFLTDR.S  
0.999997 1 R.GK[325.13]SVILDC[160.03]TPTGTHDHYMLEWFLTDR.S  
0.999997 1 K.HRPQVAIIC[160.03]GSGLGGLTDK[325.13]LTQAQIFDYG  
0.999997 1 K.TLC[160.03]PLC[160.03]FSILK[325.13]GPISDALAHHLR.I  
0.999997 1 R.FVHSENQHLVSPEALDFLDK[325.13]LLR.Y  
0.999997 1 R.FVHSENQHLVSPEALDFLDK[325.13]LLR.Y  
0.999997 1 K.K[325.13]LLGLGQKHLVMGDIPA AVNAFQEAASLLGK.K  
0.999997 1 R.ALSSSK[325.13]QSSSSR.D  
0.999997 1 R.ALSSSK[325.13]QSSSSR.D  
0.999997 0.9997 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M  
0.999997 0.9996 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M  
0.999997 1 K.AK[325.13]LVILANNC[160.03]PALR.K  
0.999997 1 R.MNYFQVAK[325.13]TVAQR.L  
0.999997 1 R.VLNVPLC[160.03]K[325.13]EDC[160.03]EQWWEDC[16  
0.999997 1 R.VLNVPLC[160.03]K[325.13]EDC[160.03]EQWWEDC[16  
0.999997 1 R.GDPGYPK[325.13]PISVWQGIPASPK.G  
0.999997 1 R.GDPGYPK[325.13]PISVWQGIPASPK.G

|          |        |                                                 |
|----------|--------|-------------------------------------------------|
| 0.999997 | 0.9987 | K.EITALAPSTMK[325.13]IKIIPPER.K                 |
| 0.999997 | 1      | K.TLVK[325.13]NC[160.03]IVLIDSTPYR.Q            |
| 0.999997 | 0.9994 | R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999997 | 1      | R.VLQK[325.13]LGADAVGMSTVPEVIVAR.H              |
| 0.999997 | 1      | R.VLQK[325.13]LGADAVGMSTVPEVIVAR.H              |
| 0.999997 | 0.9998 | R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999997 | 0.9994 | R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V              |
| 0.999997 | 1      | R.FQQVPTDALANK[325.13]LFGAPEPSTIAR.S            |
| 0.999997 | 1      | R.SIQADGLVWGSSK[325.13]LVPVGYGIK.K              |
| 0.999997 | 0.9995 | K.LDSTDFTGTIK[325.13]LLNENSYVPR.E               |
| 0.999997 | 1      | K.LSSDVLTLIK[325.13]QYC[160.03]R.E              |
| 0.999997 | 0.9715 | R.ADIK[325.13]EMGLSLQWLYSAR.G                   |
| 0.999997 | 1      | K.NIEDVIAQGIGK[325.13]LASVPAGGAVAVSAAPGSAAPAA   |
| 0.999997 | 0.9731 | R.ADIK[325.13]EMGLSLQWLYSAR.G                   |
| 0.999997 | 0.9994 | R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S       |
| 0.999997 | 0.9993 | R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S       |
| 0.999997 | 1      | R.SIATLAITTLK[325.13]TGSESSIDR.L                |
| 0.999997 | 0.9994 | R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S       |
| 0.999997 | 1      | K.AAGVNVFPFWPGLFAK[325.13]ALANVNIGSLIC[160.03]I |
| 0.999997 | 1      | K.SYC[160.03]AEIAHNVSSEK[325.13]NR.K            |
| 0.999997 | 1      | K.IGK[325.13]VDC[160.03]TQHYELC[160.03]SGNQVR.G |
| 0.999997 | 1      | R.IEK[325.13]VEHSDLSFSK.D                       |
| 0.999997 | 1      | R.ASC[160.03]ESDVLHFTSTTTSK[325.13]NR.I         |
| 0.999997 | 1      | R.IK[325.13]ATVMDVKPVDYR.E                      |
| 0.999997 | 1      | R.IK[325.13]ATVMDVKPVDYR.E                      |
| 0.999997 | 1      | R.SGDSEVYQLGDVSQK[325.13]TTWHR.I                |
| 0.999997 | 1      | R.EIVSGMK[325.13]YIQHTYR.K                      |
| 0.999997 | 1      | R.LYTLK[325.13]VEAENTHVDPR.F                    |
| 0.999997 | 1      | K.K[325.13]ILDSVGIEADDDRLNK.V                   |
| 0.999997 | 1      | K.K[325.13]ILDSVGIEADDDRLNK.V                   |
| 0.999997 | 1      | R.SGDSEVYQLGDVSQK[325.13]TTWHR.I                |
| 0.999997 | 1      | R.SGDSEVYQLGDVSQK[325.13]TTWHR.I                |
| 0.999997 | 1      | R.SGDSEVYQLGDVSQK[325.13]TTWHR.I                |
| 0.999997 | 1      | K.LVLSK[325.13]LYEEGSNKR.L                      |
| 0.999997 | 0.9998 | K.YIDQEELNKTK[325.13]PIWTR.N                    |
| 0.999997 | 1      | K.FYK[325.13]ELQAHGADELLK.R                     |
| 0.999997 | 1      | K.FYK[325.13]ELQAHGADELLK.R                     |
| 0.999997 | 1      | R.ADLTEYLSTHYK[325.13]APR.M                     |
| 0.999997 | 1      | R.EAMEHPYFYTIVK[325.13]DQAR.M                   |
| 0.999997 | 0.9999 | R.ALK[325.13]MIVDPVEPHGEMK.F                    |
| 0.999997 | 1      | K.SLNLSTEFISSTK[325.13]RPYAK.E                  |
| 0.999997 | 1      | R.YPPWPGK[325.13]IVNPPK.D                       |
| 0.999997 | 1      | K.VLVADK[325.13]SGDVYSFVLEPHGC[160.03]GR.L      |
| 0.999997 | 1      | K.LQGK[325.13]EVGVYEALKDDSWLK.G                 |
| 0.999997 | 0.9996 | R.APQC[160.03]LGK[325.13]FIEIAAR.K              |
| 0.999997 | 0.9998 | R.LESGMQNMSIHTK[325.13]TTSYGAGGLSSAYGGLTSPGLS   |
| 0.999997 | 1      | K.IITYKDPDNPEYLEFLK[325.13]QLK.H                |

0.999997 0.998 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAW  
0.999997 0.9999 R.LK[325.13]VPPAINQFTQALDR.Q  
0.999997 1 R.IMLFTGGPPTQGPMMVVGDELK[325.13]IPIR.S  
0.999997 0.9998 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVLR.L  
0.999997 0.9996 R.DLTDYLM[147.04]K[325.13]ILTER.G  
0.999997 1 R.SQVEQQQLITVEK[325.13]ALAILSQPTPSLVVDHER.L  
0.999997 1 R.LGLIPLISDDIVDK[325.13]LQYSR.D  
0.999997 1 K.TFHETLDC[160.03]C[160.03]GSSTLTALTTSVLK[325.13]I  
0.999997 1 R.LGLIPLISDDIVDK[325.13]LQYSR.D  
0.999997 1 K.ILTDIMWPPIAK[325.13]LAR.E  
0.999997 1 K.ELAC[160.03]K[325.13]MALELLTQEFGIPIER.L  
0.999997 1 R.VMTIAPGLFGTPLLTSLEPK[325.13]VC[160.03]NFLASQVI  
0.999997 1 R.VMTIAPGLFGTPLLTSLEPK[325.13]VC[160.03]NFLASQVI  
0.999997 1 K.GQLGHGDTK[325.13]R.V  
0.999997 0.9999 K.AGAHLQGGAK[325.13]R.V  
0.999997 1 R.NQIHVK[325.13]SPPR.E  
0.999997 0.9999 R.K[325.13]GHAVGDIPGVR.F  
0.999997 0.9999 R.K[325.13]LDYGQHVVAGTPGR.V  
0.999997 0.9941 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQS.K  
0.999997 1 R.K[325.13]LHGTAQQLQDSK.T  
0.999997 1 R.VTK[325.13]QYLPHVAR.L  
0.999997 1 R.HVFGQAVK[325.13]NDQC[160.03]YDDIR.V  
0.999997 1 R.HVFGQAVK[325.13]NDQC[160.03]YDDIR.V  
0.999997 1 R.K[325.13]YGTC[160.03]PHGGYGLGLER.F  
0.999997 1 R.DLIHGAPVGK[325.13]PAANR.A  
0.999997 1 R.HGNQYIQVNEPWK[325.13]R.I  
0.999997 1 R.HGNQYIQVNEPWK[325.13]R.I  
0.999997 1 R.LSQQLDK[325.13]VVTNNYKPVANHQYNIEYER.K  
0.999997 1 R.LSQQLDK[325.13]VVTNNYKPVANHQYNIEYER.K  
0.999997 1 K.K[325.13]NNPAIVIIGNNGQIHYDHQNDGASQALASC[160  
0.999997 1 K.LAAK[325.13]LIHTLDDR.T  
0.999997 1 R.RGPLVK[325.13]YSSDYFQAPSDYR.Y  
0.999997 0.9996 K.LHIEVGTPPTGNQPFPK[325.13]K.A  
0.999997 1 R.K[325.13]QMVIDVLHPGK.A  
0.999997 1 K.GTINFLHADC[160.03]DK[325.13]FR.H  
0.999997 1 R.FSVGGMTDVAEIK[325.13]GHR.R  
0.999997 0.9999 K.TAWLDGK[325.13]HVVFGK.V  
0.999997 0.9998 R.ALEHFTDLYDIK[325.13]R.A  
0.999997 1 R.NVFHC[160.03]EPANILYIC[160.03]ENQPLK[325.13]K.L  
0.999997 1 R.FQEYHIQQNEALAAK[325.13]AGLLGQPR.-  
0.999997 1 R.FQEYHIQQNEALAAK[325.13]AGLLGQPR.-  
0.999997 1 K.LAAAILGGVDQIHIK[325.13]PGAK.V  
0.999997 1 R.ALFGLYMSASHIASNPK[325.13]ASAK.T  
0.999997 1 K.IGPK[325.13]ANLLNNEAHITMQVTK.S  
0.999997 1 R.MIAPEGSLVFHEK[325.13]AWNAYPYC[160.03]R.T  
0.999997 0.9929 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E  
0.999997 1 R.YPSLSLHGIEGAFSGSGAK[325.13]TVIPR.K

0.999997 1 R.SHLEK[325.13]AWLISQQIPQFEDVK.F  
 0.999997 1 R.GIYQK[325.13]AIEVLSDEHAR.E  
 0.999997 0.9985 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F  
 0.999997 1 R.NSSHAGAFVIVTEEAIK[325.13]GIR.R  
 0.999997 1 K.SGVPVLAVSLALEGK[325.13]ASHR.E  
 0.999997 1 K.IVSK[325.13]DLTNSHFFLDFQK.T  
 0.999997 1 K.IVSK[325.13]DLTNSHFFLDFQK.T  
 0.999997 0.9996 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPMQDK.  
 0.999997 1 R.IPDIVLWPTC[160.03]HDDVVK[325.13]IVNLAC[160.03]I  
 0.999997 1 R.IPDIVLWPTC[160.03]HDDVVK[325.13]IVNLAC[160.03]I  
 0.999997 1 R.YSIK[325.13]DLLNHAFQEETGVR.V  
 0.999997 1 R.ILEDQEENPLPAALVQPHTGK[325.13]LC[160.03]WFLDE/  
 0.999997 1 K.FLEVIK[325.13]PFC[160.03]VILPEIQKPER.K  
 0.999997 1 K.FLALK[325.13]QTPDFHTVIGDVTGLLER.C  
 0.999997 1 R.TPALVFEHVNNTDFK[325.13]QLYQTLTDYDIR.F  
 0.999997 0.999 R.GVLK[325.13]VFLENVIR.D  
 0.999997 1 R.SLDLSGLELLSEHDPK[325.13]LLC[160.03]R.L  
 0.999997 1 K.ISAILHPSTYLNK[325.13]JLLGSEQGSLQLWNVK.S  
 0.999997 1 R.SLDLSGLELLSEHDPK[325.13]LLC[160.03]R.L  
 0.999997 1 K.ISAILHPSTYLNK[325.13]JLLGSEQGSLQLWNVK.S  
 0.999997 1 K.DTHEDHDTSTENTDESNHDPQFEPVSLPEQEIK[325.13]TI  
 0.999997 1 K.DTHEDHDTSTENTDESNHDPQFEPVSLPEQEIK[325.13]TI  
 0.999997 0.9999 R.VSGPYFPTLLGLSLQVLEPPQHGAHQK[325.13]EDGPQAR.  
 0.999997 0.9996 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
 0.999997 1 K.NNTVGLIQLNRPK[325.13]ALNALC[160.03]DGLIDELNQ/  
 0.999997 1 K.NNTVGLIQLNRPK[325.13]ALNALC[160.03]DGLIDELNQ/  
 0.999997 1 R.GHVTQDAPIPGSPLYTIK[325.13]AFIPAIDSFGFETDLR.T  
 0.999997 1 R.GHVTQDAPIPGSPLYTIK[325.13]AFIPAIDSFGFETDLR.T  
 0.999997 0.999 R.GVLK[325.13]VFLENVIR.D  
 0.999997 1 K.SHAAGSK[325.13]QHESIPGK.A  
 0.999997 1 K.SHAAGSK[325.13]QHESIPGK.A  
 0.999997 0.9999 R.K[325.13]GHAVGDIPGVR.F  
 0.999997 1 R.FNWNHC[160.03]GEMAPAC[160.03]K[325.13]R.H  
 0.999997 1 R.FNWNHC[160.03]GEMAPAC[160.03]K[325.13]R.H  
 0.999997 1 R.SEHK[325.13]VWSPLVTEEGKR.H  
 0.999997 1 R.SEHK[325.13]VWSPLVTEEGKR.H  
 0.999997 1 R.ANATAK[325.13]ATVAFAASEGHSHPR.V  
 0.999997 1 K.C[160.03]WK[325.13]FEHC[160.03]NFNDVTTR.L  
 0.999997 1 K.C[160.03]WK[325.13]FEHC[160.03]NFNDVTTR.L  
 0.999997 0.9991 R.M[147.04]VNHFAIEFK[325.13]R.K  
 0.999997 0.9991 R.M[147.04]VNHFAIEFK[325.13]R.K  
 0.999997 1 R.RQQEVETELK[325.13]MWDPHNDPNAQGDAFK.T  
 0.999997 0.9927 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
 0.999997 1 R.HGIPNNQK[325.13]DTVC[160.03]EDMTFSTWTPPPGVH  
 0.999997 1 R.GHDDLGDHYLDC[160.03]GDLSNALK[325.13]C[160.03]  
 0.999997 1 R.HGIPNNQK[325.13]DTVC[160.03]EDMTFSTWTPPPGVH  
 0.999997 1 K.KDDEENYLDLFSHK[325.13]NMK.L

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| 0.999997 | 0.9663 | R.LLLPGELAK[325.13]HAVSEGTK.A                      |
| 0.999997 | 0.9999 | R.LLIHQSLAGGIIGVK[325.13]GAK.I                     |
| 0.999997 | 1      | R.SLLSQMLHYDPNK[325.13]R.I                         |
| 0.999997 | 0.9928 | K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E         |
| 0.999997 | 1      | R.LQLLSNLFHGMMDK[325.13]NTPVR.Y                    |
| 0.999997 | 1      | K.HFTVMNYDPDVVLK[325.13]QVHC[160.03]EEFIPEFEK.C    |
| 0.999997 | 0.9906 | R.K[325.13]DGNASGTTLEALDC[160.03]ILPPTRPDKPLR.     |
| 0.999997 | 0.9999 | R.GLDISNVK[325.13]HVINFDLPSDIEEYVHR.I              |
| 0.999997 | 1      | K.NQMSK[325.13]LISEMHSFIQIK.K                      |
| 0.999997 | 1      | R.LALHELK[325.13]NLTQYSWLLDGFPR.T                  |
| 0.999997 | 1      | R.KGNTMQQFLQK[325.13]ALEILR.K                      |
| 0.999996 | 0.9997 | K.SVHELEK[325.13]SKR.A                             |
| 0.999996 | 0.9999 | K.GFGYK[325.13]GSC[160.03]FHR.I                    |
| 0.999996 | 1      | R.VC[160.03]K[325.13]SHLLNC[160.03]C[160.03]PHDVLS |
| 0.999996 | 1      | K.TLVPHYC[160.03]ELVGANPK[325.13]VRPNPAR.F         |
| 0.999996 | 1      | R.MHPHLSK[325.13]GYAYVEFENPDEAEK.A                 |
| 0.999996 | 1      | R.MHPHLSK[325.13]GYAYVEFENPDEAEK.A                 |
| 0.999996 | 1      | R.VREEVPLELVEAHVK[325.13]K.V                       |
| 0.999996 | 1      | K.KVPDK[325.13]LLDSSTVTHLFK.I                      |
| 0.999996 | 1      | R.HLVGLWTADNATATNLLK[325.13]R.I                    |
| 0.999996 | 1      | R.HLVGLWTADNATATNLLK[325.13]R.I                    |
| 0.999996 | 1      | R.K[325.13]LVGFISAIPANIHIYDTEKK.M                  |
| 0.999996 | 1      | R.LFDPQLK[325.13]EKPEESLAAPTWLVLHQQVER.Q           |
| 0.999996 | 0.9999 | R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V            |
| 0.999996 | 1      | K.EKDNIDITLQWLIQHSK[325.13]SR.R                    |
| 0.999996 | 1      | R.NHPQMIAVLVDK[325.13]MIR.T                        |
| 0.999996 | 1      | K.YHYELLNYIDLPLAIHGK[325.13]QK.Q                   |
| 0.999996 | 1      | K.YHYELLNYIDLPLAIHGK[325.13]QK.Q                   |
| 0.999996 | 1      | R.LIAEK[325.13]VQAERPDTMLGVVC[160.03]GALHVADVS     |
| 0.999996 | 1      | R.VVHLLNDQHLGVVTAATSLITLAQK[325.13]NPEEFK.T        |
| 0.999996 | 1      | K.LGYLTLILC[160.03]TAHTLVYGGK[325.13]R.F           |
| 0.999996 | 1      | K.LGYLTLILC[160.03]TAHTLVYGGK[325.13]R.F           |
| 0.999996 | 1      | K.AHIAAK[325.13]TVFHLAHR.H                         |
| 0.999996 | 1      | R.SIAADHK[325.13]DLIHDVSFDFHGR.R                   |
| 0.999996 | 1      | R.FHWEQDQIAHMK[325.13]NYIAR.F                      |
| 0.999996 | 1      | R.TPAIPFASYGLHHTSLLK[325.13]R.H                    |
| 0.999996 | 1      | K.SFSHSFSALAK[325.13]FHEVFK.T                      |
| 0.999996 | 1      | K.SFSHSFSALAK[325.13]FHEVFK.T                      |
| 0.999996 | 1      | R.LADHFGGK[325.13]LHLGFIEIR.E                      |
| 0.999996 | 1      | R.LADHFGGK[325.13]LHLGFIEIR.E                      |
| 0.999996 | 1      | R.FKDIFQEIFDK[325.13]HYK.T                         |
| 0.999996 | 1      | R.LLGHWEEAAHDLALAC[160.03]K[325.13]LDYDEDASAM      |
| 0.999996 | 1      | K.HC[160.03]VDPTSFLKPIAK[325.13]LFSVIK.N           |
| 0.999996 | 0.9996 | R.ISVYYNEATGGK[325.13]YVPR.A                       |
| 0.999996 | 1      | R.VLYAYGYTGEPK[325.13]R.S                          |
| 0.999996 | 1      | K.TIK[325.13]AQIWDTAGQER.Y                         |
| 0.999996 | 0.9995 | R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M         |

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|----------|--------|----------------------------------------------------|
| 0.999996 | 0.9999 | K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.999996 | 0.9996 | R.GENSWFSTQVDTVATK[325.13]VK.D                     |
| 0.999996 | 0.9992 | R.LQSTLK[325.13]TLSFSFPNTVTGSER.V                  |
| 0.999996 | 0.9998 | R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTVEVK.S      |
| 0.999996 | 0.9992 | R.LQSTLK[325.13]TLSFSFPNTVTGSER.V                  |
| 0.999996 | 0.9993 | K.LDSTDFTGTIK[325.13]LLNENSYVPR.E                  |
| 0.999996 | 1      | K.LWEEQLAAAK[325.13]AQQEQELAADAFK.E                |
| 0.999996 | 0.9996 | K.TVTAMDVVYALK[325.13]R.Q                          |
| 0.999996 | 0.9964 | R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G              |
| 0.999996 | 0.9964 | R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G              |
| 0.999996 | 0.9996 | K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI     |
| 0.999996 | 0.9862 | K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I             |
| 0.999996 | 1      | R.DYVLNC[160.03]SILNPLLTLTK[325.13]STR.L           |
| 0.999996 | 1      | R.DYVLNC[160.03]SILNPLLTLTK[325.13]STR.L           |
| 0.999996 | 1      | K.GK[325.13]VAAQC[160.03]SHAAVSAYK.Q               |
| 0.999996 | 0.9984 | R.HQGVM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA      |
| 0.999996 | 0.778  | R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R                 |
| 0.999996 | 1      | R.VAGC[160.03]SVHK[325.13]GYAFVQYSNER.H            |
| 0.999996 | 1      | K.GVK[325.13]IDKTDYMGVSYGPR.A                      |
| 0.999996 | 1      | R.TGAVYLC[160.03]PLTAHK[325.13]DDC[160.03]ER.M     |
| 0.999996 | 1      | R.TGAVYLC[160.03]PLTAHK[325.13]DDC[160.03]ER.M     |
| 0.999996 | 1      | R.LWK[325.13]DSGVQAC[160.03]FNR.S                  |
| 0.999996 | 1      | R.FGDVSVK[325.13]ISHLSGSGSGDER.V                   |
| 0.999996 | 0.9999 | K.TM[147.04]QNVK[325.13]HPVTGQFLYQDSNWASK.V        |
| 0.999996 | 1      | R.AAPSK[325.13]AC[160.03]MLTTATAHDGDVNVISWSR.R     |
| 0.999996 | 1      | K.TSVQFQNFSPVTVHPGDLQTLAVQTK[325.13]R.V            |
| 0.999996 | 0.9999 | R.VIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I            |
| 0.999996 | 1      | K.K[325.13]VTHVALNPC[160.03]C[160.03]DWFLATASVDI   |
| 0.999996 | 1      | R.DHADSNIVIMLVGNK[325.13]SDLR.H                    |
| 0.999996 | 1      | K.LPAELQELPGLSHQYWSAPSDK[325.13]EGYSGVGLLSR.Q      |
| 0.999996 | 0.9994 | K.WGDAGAIEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R       |
| 0.999996 | 0.9999 | R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999996 | 1      | K.LK[325.13]FGIGDGNLQYYLYNWK.C                     |
| 0.999996 | 0.9996 | R.NLQNLLILTAIK[325.13]ADR.T                        |
| 0.999996 | 1      | R.EALDHMVEYVAQNTPVTWLVGPFAPGITEK[325.13]APEE       |
| 0.999996 | 0.9998 | R.GVMLAVDAVIAELK[325.13]K.Q                        |
| 0.999996 | 0.9994 | R.DLTDYLM[147.04]K[325.13]ILTER.G                  |
| 0.999996 | 0.9993 | R.DLTDYLM[147.04]K[325.13]ILTER.G                  |
| 0.999996 | 1      | R.K[325.13]PFGAILNLVPLAESVVK.L                     |
| 0.999996 | 1      | R.K[325.13]PFGAILNLVPLAESVVK.L                     |
| 0.999996 | 0.9962 | K.VK[325.13]DALEFWLQAGVDGFQVR.D                    |
| 0.999996 | 1      | R.GSPK[325.13]ALALEYALC[160.03]LTGDGLAHLQATDPQI    |
| 0.999996 | 1      | R.GLSNLFLSC[160.03]PIPK[325.13]LLLLAGVDR.L         |
| 0.999996 | 0.9974 | K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV      |
| 0.999996 | 1      | R.DYVLNC[160.03]SILNPLLTLTK[325.13]STR.L           |
| 0.999996 | 1      | K.QHQQQK[325.13]ALQSGPPQSR.R                       |
| 0.999996 | 1      | K.QHQQQK[325.13]ALQSGPPQSR.R                       |



0.999996 0.9924 R.HQGV[147.04]VGMGQK[325.13]DSYVGDEAQS.R  
 0.999996 1 K.K[325.13]GPSGYGFNLHSDK.S  
 0.999996 1 R.FHC[160.03]K[325.13]LC[160.03]EC[160.03]SFNDPNAK  
 0.999996 1 K.K[325.13]GPSGYGFNLHSDK.S  
 0.999996 1 K.NYFLHK[325.13]SAQEAYK.S  
 0.999996 1 K.K[325.13]GPSGYGFNLHSDK.S  
 0.999996 1 R.GLC[160.03]GAIHSSIAK[325.13]QMK.S  
 0.999996 1 R.GLC[160.03]GAIHSSIAK[325.13]QMK.S  
 0.999996 1 R.AK[325.13]SLLHC[160.03]FQC[160.03]C[160.03]GAK.V  
 0.999996 1 R.AK[325.13]SLLHC[160.03]FQC[160.03]C[160.03]GAK.V  
 0.999996 1 K.WK[325.13]GFSEHNTWEPEK.N  
 0.999996 1 K.GGHFYSAK[325.13]PEILR.A  
 0.999996 1 R.LWAHVYAGAPVSSPEYTK[325.13]K.I  
 0.999996 1 R.HPQLLYESK[325.13]LYK.I  
 0.999996 1 R.K[325.13]LEELIQGAQC[160.03]VHSPR.F  
 0.999996 1 K.GC[160.03]WDSIHVVEVQEK[325.13]SSGR.T  
 0.999996 1 R.VIHVAGK[325.13]ETTNIFSNC[160.03]GC[160.03]VR.A  
 0.999996 1 K.GC[160.03]WDSIHVVEVQEK[325.13]SSGR.T  
 0.999996 1 R.LGVHTK[325.13]GADIDALC[160.03]VAPR.H  
 0.999996 1 R.TEVVK[325.13]NNLNPVWRPFK.I  
 0.999996 1 R.SNFGYNIPLK[325.13]HLADR.V  
 0.999996 1 R.MDLGEC[160.03]LK[325.13]VHDLALR.A  
 0.999996 1 R.THSDQFLVAFK[325.13]EVGR.K  
 0.999996 1 R.THSDQFLVAFK[325.13]EVGR.K  
 0.999996 1 R.THSDQFLVAFK[325.13]EVGR.K  
 0.999996 1 K.DIVAAIQHNYK[325.13]MSAFK.E  
 0.999996 1 K.DIVAAIQHNYK[325.13]MSAFK.E  
 0.999996 1 K.HAASTVQILGAEK[325.13]ALFR.A  
 0.999996 1 K.HAASTVQILGAEK[325.13]ALFR.A  
 0.999996 1 R.NVTK[325.13]DHIMEIFSTYGK.I  
 0.999996 1 R.NVTK[325.13]DHIMEIFSTYGK.I  
 0.999996 1 R.K[325.13]LVGFISAIPANIHIYDTEK.K  
 0.999996 0.9996 R.VTGALQFGELQK[325.13]QGAGGVEGAEWATQAFHQF  
 0.999996 0.9996 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I  
 0.999996 0.9995 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I  
 0.999996 1 K.K[325.13]C[160.03]PELLQGLAHFPETIAGSDAPSLATVAG  
 0.999996 1 R.GVNAIVYMIDAADREK[325.13]IEASR.N  
 0.999996 1 R.GVNAIVYMIDAADREK[325.13]IEASR.N  
 0.999996 1 R.MHC[160.03]AVDGEWLVPIGQC[160.03]LC[160.03]QA  
 0.999996 0.9999 K.VAHALAEGLGVIAC[160.03]IGEK[325.13]LDER.E  
 0.999996 1 R.RLPPQQIEK[325.13]NLSDLIDLVPVSLC[160.03]EDLLSSVDI  
 0.999996 1 R.RLPPQQIEK[325.13]NLSDLIDLVPVSLC[160.03]EDLLSSVDI  
 0.999996 1 R.RLPPQQIEK[325.13]NLSDLIDLVPVSLC[160.03]EDLLSSVDI  
 0.999996 1 R.RLPPQQIEK[325.13]NLSDLIDLVPVSLC[160.03]EDLLSSVDI  
 0.999996 0.9996 R.LEKPAK[325.13]YDDIKK.V  
 0.999996 1 K.TGRPAGK[325.13]GSITISAEIKDNR.V  
 0.999996 1 K.VHK[325.13]EDDGVPVIC[160.03]QVEHPAVTGNLQTQR.

0.999996 0.9995 K.LHIEVGTPPTGNQPFPK[325.13]K.A  
 0.999996 1 R.NLGFTAIPLHGQMSQSK[325.13]R.L  
 0.999996 1 R.LNVDFALHK[325.13]ER.K  
 0.999996 1 R.IK[325.13]IQHMELQLIK.K  
 0.999996 1 R.FTDDDKTDHLSWEWNLTIK[325.13]K.D  
 0.999996 1 K.K[325.13]PLFHGDSEIDQLFR.I  
 0.999996 1 K.K[325.13]PLFHGDSEIDQLFR.I  
 0.999996 1 R.K[325.13]DLGHAQMVVDELFSHSDLDSDSELDR.A  
 0.999996 1 R.K[325.13]DLGHAQMVVDELFSHSDLDSDSELDR.A  
 0.999996 1 R.HC[160.03]NK[325.13]LFLIDFGLAK.K  
 0.999996 1 R.HC[160.03]NK[325.13]LFLIDFGLAK.K  
 0.999996 0.999 R.GHYTIGK[325.13]EIIDLVLDR.I  
 0.999996 0.9979 R.KDGNASGTTLEALDC[160.03]ILPPTRPDTK[325.13]PLR.  
 0.999996 1 K.VFAQPNLAEMIQK[325.13]GEQLFLEPELVIPHR.Q  
 0.999995 0.9996 K.SPAKPK[325.13]AVKPK.A  
 0.999995 1 R.AHAYGDPNAGLNSQLHYK[325.13]R.Q  
 0.999995 1 K.TGKPLPFGTLGVHK[325.13]K.A  
 0.999995 1 K.VLQHYQESDKGEELGPGNVQK[325.13]EVSSSFDHVIK.E  
 0.999995 0.8726 R.LK[325.13]LEPHEGLLLR.F  
 0.999995 0.9487 R.LLLPGELAK[325.13]HAVSEGTK.A  
 0.999995 0.9991 R.ELPAQK[325.13]WWHTGALYR.I  
 0.999995 1 K.DAHSIHGTNPQYLVEK[325.13]IIR.T  
 0.999995 1 K.K[325.13]IKLTAEAEELKPFFMK.E  
 0.999995 1 K.FTRPLFK[325.13]DLAAFDK.S  
 0.999995 1 K.KIK[325.13]LTAEAEELKPFFMK.E  
 0.999995 1 K.FIVDGWHEMDAENPLHQSPSLNK[325.13]LVAENK.F  
 0.999995 1 K.FTRPLFK[325.13]DLAAFDK.S  
 0.999995 0.9999 R.FHK[325.13]LQNVQIALDYLR.H  
 0.999995 1 R.VLGHFKEK[325.13]PLFLELC[160.03]R.H  
 0.999995 1 R.K[325.13]PPMLQPLALPPGLSVHQALER.V  
 0.999995 1 R.K[325.13]PPMLQPLALPPGLSVHQALER.V  
 0.999995 1 R.IQHYAGK[325.13]VLYQVEGFVDKNNDLLYR.D  
 0.999995 1 R.IDDIADGAVKPPPNK[325.13]YPIFFFGTHETAFLGPK.D  
 0.999995 1 R.IDDIADGAVKPPPNK[325.13]YPIFFFGTHETAFLGPK.D  
 0.999995 0.9974 R.KDGNASGTTLEALDC[160.03]ILPPTRPDTK[325.13]PLR.  
 0.999995 1 K.AYDHLFK[325.13]LLLIGDSGVGK.T  
 0.999995 1 R.LTRPGSSYFNLNPFEVLQIDPEVTDEEIKK[325.13]R.F  
 0.999995 1 K.DQHSFELDEK[325.13]ALASILLQDHIR.D  
 0.999995 1 R.LALHK[325.13]PPLHHQSK.V  
 0.999995 1 R.VK[325.13]GHFGPINSVAFHPDGK.S  
 0.999995 1 K.SVVFLNSPHPLVWHLK[325.13]TER.L  
 0.999995 1 R.SHAHFFFLTK[325.13]ELALGQDR.I  
 0.999995 1 R.SHAHFFFLTK[325.13]ELALGQDR.I  
 0.999995 0.9996 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V  
 0.999995 1 R.VGAGLHNLGNTC[160.03]FLNATIQC[160.03]LTYTPPLAN  
 0.999995 0.9995 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR.  
 0.999995 1 R.M[147.04]GFPPGAAQALVLQVFK[325.13]TFDHMAR.Q

0.999995 1 R.MGFPPGAAQALVLQVFK[325.13]TFDHMAR.Q  
 0.999995 0.9999 K.EITALAPSTM[147.04]K[325.13]IK.I  
 0.999995 1 R.K[325.13]VPGVTAIELDEDTGTFR.I  
 0.999995 0.9999 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I  
 0.999995 1 R.DGEDQTQDTELVEPTRPAGDGTFFQK[325.13]WAAVVVPSC  
 0.999995 1 R.EVFSK[325.13]YGPIADVSIVYDQQSR.R  
 0.999995 1 R.EVFSK[325.13]YGPIADVSIVYDQQSR.R  
 0.999995 0.9995 K.TVTAMDVVYALK[325.13]R.Q  
 0.999995 1 R.DLDGNGYPDLIVGSFGVVK[325.13]AVVYR.G  
 0.999995 0.9999 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T  
 0.999995 0.9622 R.ADIK[325.13]EMGLSLQWLYSAR.G  
 0.999995 1 K.AVSGASAGDYSDAIELLLTAIAVIK[325.13]QSR.V  
 0.999995 0.998 R.HQGVMM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA  
 0.999995 1 R.K[325.13]SMSVYC[160.03]TPNKPSR.T  
 0.999995 1 R.K[325.13]SMSVYC[160.03]TPNKPSR.T  
 0.999995 1 R.AGK[325.13]VEAQHILASAPTDR.N  
 0.999995 0.9999 R.K[325.13]VSQPIEGHAASFAQFK.M  
 0.999995 1 K.AC[160.03]VGNAYHK[325.13]QLAALNC[160.03]SVR.D  
 0.999995 1 K.AC[160.03]VGNAYHK[325.13]QLAALNC[160.03]SVR.D  
 0.999995 1 K.AC[160.03]VGNAYHK[325.13]QLAALNC[160.03]SVR.D  
 0.999995 1 K.AC[160.03]VGNAYHK[325.13]QLAALNC[160.03]SVR.D  
 0.999995 0.9998 K.TVDLKPDPWGK[325.13]GYSR.K  
 0.999995 1 R.YSYQYTVANK[325.13]EYVAYSHTGR.I  
 0.999995 0.9996 R.QTVAVGVK[325.13]AVDKK.A  
 0.999995 1 R.APGSLIK[325.13]LQGC[160.03]R.E  
 0.999995 1 K.SNK[325.13]IFVGGIPHNC[160.03]GETELR.E  
 0.999995 1 K.SNK[325.13]IFVGGIPHNC[160.03]GETELR.E  
 0.999995 1 K.SNK[325.13]IFVGGIPHNC[160.03]GETELR.E  
 0.999995 1 K.GVNTVFHC[160.03]ASPPSSNNK[325.13]ELFYR.V  
 0.999995 1 K.GVNTVFHC[160.03]ASPPSSNNK[325.13]ELFYR.V  
 0.999995 1 K.GKDAFPVAGQK[325.13]LIYAGK.I  
 0.999995 1 K.GKDAFPVAGQK[325.13]LIYAGK.I  
 0.999995 1 R.VLISSLK[325.13]DC[160.03]LHGIEAK.S  
 0.999995 1 R.SNNTSK[325.13]PSHSVDAHTAEVNC[160.03]LSFNYPYSEF  
 0.999995 0.9972 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV  
 0.999995 0.9992 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R  
 0.999995 1 R.GQAFVIFK[325.13]EVSSATNALR.S  
 0.999995 1 R.GQAFVIFK[325.13]EVSSATNALR.S  
 0.999995 1 R.VAILVDDMADTC[160.03]GTIC[160.03]HAADK[325.13]I  
 0.999995 1 R.K[325.13]YVFFLDPC[160.03]NLDLINR.K  
 0.999995 0.9999 K.LLGK[325.13]VTIAQGGVLPNIQAVLLPK.K  
 0.999995 0.9992 R.DLTDYLM[147.04]K[325.13]ILTER.G  
 0.999995 1 K.TGVVPQLVK[325.13]LLGASELPIVTPALR.A  
 0.999995 1 R.VPNEEDPSLDRPFISEGTTLK[325.13]DLIYDMTTSGSGSGL  
 0.999995 1 R.TPIGSFLGSLLPATK[325.13]LGSIAIQGAIEK.A  
 0.999995 1 R.AAC[160.03]HLK[325.13]DGNC[160.03]R.D  
 0.999995 1 R.AAC[160.03]HLK[325.13]DGNC[160.03]R.D

0.999995 1 K.IHMGSC[160.03]AENTAK[325.13]K.L  
0.999995 1 K.K[325.13]ASGQPAGPDNKENC[160.03]PVPGKPGEAFAA  
0.999995 1 K.K[325.13]ASGQPAGPDNKENC[160.03]PVPGKPGEAFAA  
0.999995 1 K.NPSDSAVHSPFTK[325.13]R.Q  
0.999995 1 R.DRPFVC[160.03]APSSK[325.13]TGSVTTTYC[160.03]C[1  
0.999995 1 K.NPSDSAVHSPFTK[325.13]R.Q  
0.999995 1 R.DRPFVC[160.03]APSSK[325.13]TGSVTTTYC[160.03]C[1  
0.999995 1 R.ALIESLNQK[325.13]PQTAGDQPPPTDTTHATHR.K  
0.999995 1 R.ALIESLNQK[325.13]PQTAGDQPPPTDTTHATHR.K  
0.999995 1 R.AK[325.13]SDLLGKPLGPR.T  
0.999995 1 K.K[325.13]IYQNIQDGSGLDLNAAESGVQHKPSAPQGGR.L  
0.999995 1 R.FC[160.03]LSKPGVYK[325.13]VTPR.S  
0.999995 0.9999 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L  
0.999995 1 K.MDK[325.13]EETKDWILPSDYDHAEAEAR.H  
0.999995 1 K.MDKEETK[325.13]DWILPSDYDHAEAEAR.H  
0.999995 1 K.TPSSDVLVFDYTK[325.13]HPSKPDPSGEC[160.03]NPDLR  
0.999995 1 R.K[325.13]DHPFGFVAVPTK.N  
0.999995 1 K.K[325.13]FMADC[160.03]PHTIGVEFGTR.I  
0.999995 1 R.IHNQNNQAWK[325.13]EILK.W  
0.999995 1 R.VAIHYINPPNPAK[325.13]DNFTFK.C  
0.999995 0.9455 R.LLLPGELAK[325.13]HAVSEGK.A  
0.999995 1 R.KYAVLYQPLFDK[325.13]R.F  
0.999995 1 K.VEPITK[325.13]HIGLVYSGMGPDYR.V  
0.999995 1 R.QYYTLLNK[325.13]APEYLHR.F  
0.999995 1 K.AQVARPGGDTIFGK[325.13]IIR.K  
0.999995 1 K.AFDK[325.13]HMNLILC[160.03]DC[160.03]DEFR.K  
0.999995 1 R.KK[325.13]PALVSIPEDVVQAEAGGMHTVC[160.03]LSK.S  
0.999995 1 R.LGPLK[325.13]LTLEQGQQLVAEGHPGASQASAR.A  
0.999995 1 R.LGPLK[325.13]LTLEQGQQLVAEGHPGASQASAR.A  
0.999995 0.9996 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L  
0.999995 1 R.TIQVENSHLITGAGALNK[325.13]VLGR.E  
0.999995 1 R.ILQEK[325.13]VQADVPPEILNNVGALHFR.L  
0.999995 1 R.IATK[325.13]ASHLLETLLC[160.03]K.H  
0.999995 1 K.VLPGDYEILATHPTWALK[325.13]EASTTVR.V  
0.999995 1 R.IATK[325.13]ASHLLETLLC[160.03]K.H  
0.999995 1 R.IATK[325.13]ASHLLETLLC[160.03]K.H  
0.999995 1 R.HVK[325.13]MIDNVYNPAAIAVDWVYK.T  
0.999995 1 R.TAIHEVMEQQTISIAK[325.13]AGILTTLNAR.C  
0.999995 1 R.TGVK[325.13]IGEMPLTDSILC[160.03]DGLTDAFHNC[16  
0.999995 1 R.TGVK[325.13]IGEMPLTDSILC[160.03]DGLTDAFHNC[16  
0.999995 1 R.SIATLMTDEIFHDVAYK[325.13]AK.D  
0.999995 1 K.RLETEASTGQQLNSLNLSSPFDLNFPLPGEK[325.13]GPAC[  
0.999995 0.9996 K.IAALQAFADQLIAAGHYAK[325.13]GDISSR.R  
0.999995 0.8429 R.DALSDALHFLNK[325.13]M[147.04]K.I  
0.999995 1 R.LAQDPFPLYPGEVLEK[325.13]DITPLQVVLNPTALHLK.A  
0.999995 1 R.NENTFLDLTVQQIEHLNK[325.13]TYNTDVPLVLMNSFNTI  
0.999995 1 K.HVLVEYPMTLSLAAAQELWELAEQK[325.13]GK.V

0.999995 1 K.K[325.13]THQPSDEVGTSIEHPR.E  
 0.999995 1 R.TK[325.13]LHQLSGSDQLESTASR.I  
 0.999995 1 R.LAHLASAQK[325.13]EPEAAAPAPGTGGDSVC[160.03]G  
 0.999995 1 R.LAHLASAQK[325.13]EPEAAAPAPGTGGDSVC[160.03]G  
 0.999995 1 R.VLSTVHTHSSVK[325.13]SVPENLLK.C  
 0.999995 1 R.VLSTVHTHSSVK[325.13]SVPENLLK.C  
 0.999995 1 R.K[325.13]EVVHTVSLHEIDVINSR.T  
 0.999995 0.9996 K.VK[325.13]GLVLGPIHK.N  
 0.999995 1 R.SENKNEGQDATM[147.04]YC[160.03]K[325.13]SVGYPH  
 0.999995 1 R.SENKNEGQDATM[147.04]YC[160.03]K[325.13]SVGYPH  
 0.999995 0.9997 R.LLIHQSLAGGIIGVK[325.13]GAK.I  
 0.999995 1 K.VHK[325.13]ISNPWQSPSGTLPALR.T  
 0.999995 1 K.VHK[325.13]ISNPWQSPSGTLPALR.T  
 0.999995 1 R.GGFC[160.03]NFMHLK[325.13]PISR.E  
 0.999995 1 R.GGFC[160.03]NFMHLK[325.13]PISR.E  
 0.999995 1 R.GGFC[160.03]NFMHLK[325.13]PISR.E  
 0.999995 1 R.LHC[160.03]LK[325.13]LQPLSPVPSDIEISR.G  
 0.999995 1 R.LHC[160.03]LK[325.13]LQPLSPVPSDIEISR.G  
 0.999995 1 R.LHC[160.03]LK[325.13]LQPLSPVPSDIEISR.G  
 0.999995 0.9999 R.FHK[325.13]LQNVQIALDYLR.H  
 0.999995 1 K.EAWPHIK[325.13]TIFQGIAAK.V  
 0.999995 1 R.ILK[325.13]SLGELGLEHFQAPLVR.F  
 0.999995 1 K.HANAKPFEVPFLK[325.13]F.-  
 0.999995 1 K.HANAKPFEVPFLK[325.13]F.-  
 0.999995 1 R.GSLAAVAHAQSLVEAQPNDK[325.13]LVEDHLAVQSLIR.  
 0.999995 0.9994 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I  
 0.999995 0.997 R.KDGNASGTTLEALDC[160.03]ILPPTRPDTK[325.13]PLR.  
 0.999995 1 R.K[325.13]HMOVFLGGAVLADIMK.D  
 0.999995 1 R.FINVPPQIALPMYQQLQK[325.13]ELAGHR.T  
 0.999995 1 R.FINVPPQIALPMYQQLQK[325.13]ELAGHR.T  
 0.999995 1 R.ALSAVHSPTFC[160.03]QLAC[160.03]GQDQQLK[325.13]  
 0.999995 0.9999 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I  
 0.999995 1 K.HK[325.13]GFAFVEYEVPEAAQLALEQMNSVMLGGR.N  
 0.999994 1 K.RRPASQK[325.13]DSGAASEQATAAPNPC[160.03]SSSSR  
 0.999994 1 R.THSTHPDDEDSGPYK[325.13]HISPGDTK.V  
 0.999994 1 R.THSTHPDDEDSGPYK[325.13]HISPGDTK.V  
 0.999994 1 R.RQPQEEVVHEDQGK[325.13]KPQDQLVIER.E  
 0.999994 1 K.HSK[325.13]ALNTLSSPGQSSFSHGTR.N  
 0.999994 1 K.LC[160.03]LTLHNNEGSYLAHTQGK[325.13]K.H  
 0.999994 1 R.NWLK[325.13]EGHPVTSEPSRPEPAVFK.A  
 0.999994 1 K.GHFGPINSVAFHPDGK[325.13]SYSSGGEDGYVR.I  
 0.999994 1 R.SFLHGPELDK[325.13]GQLR.I  
 0.999994 1 R.SFGTGTHVK[325.13]LPGPAPDKPNVYDFK.T  
 0.999994 1 R.SFGTGTHVK[325.13]LPGPAPDKPNVYDFK.T  
 0.999994 0.9999 R.HFLLEEDK[325.13]PEEPTAHAFVSTLTR.G  
 0.999994 0.999 R.ELPAQK[325.13]WWHTGALYR.I  
 0.999994 1 R.VRPDYTAQNLDHGK[325.13]AWGILTFK.G

0.999994 1 R.RPASHQTFPLQQESGQTVEC[160.03]TVAQYFK[325.13]D  
 0.999994 1 K.HDDPALTLVAGLTSNKPTDK[325.13]LR.A  
 0.999994 1 K.VPSGFYVGSYVHGAMQSPSLHK[325.13]LVLGK.Y  
 0.999994 1 R.SLPGPAPC[160.03]LK[325.13]HFPLDLR.T  
 0.999994 1 R.AQFVTC[160.03]GQDK[325.13]LVHLWSSDSHQPLWSR.I  
 0.999994 1 R.HNLITEMVALNPDFK[325.13]PPADYKPPATR.V  
 0.999994 1 R.HNLITEMVALNPDFKPPADYK[325.13]PPATR.V  
 0.999994 1 K.VTLPC[160.03]HHQLGLPEK[325.13]DTLDIEWLLTDNEG  
 0.999994 1 R.EKEHYC[160.03]LADLASLMDK[325.13]TFER.K  
 0.999994 1 R.DC[160.03]YASVFK[325.13]ALEHSALAINHK.L  
 0.999994 1 R.DC[160.03]YASVFK[325.13]ALEHSALAINHK.L  
 0.999994 1 K.NIDHMLWLEQPENIATC[160.03]IALRPYPK[325.13]EEVC  
 0.999994 1 K.K[325.13]ATRPEELLELLGGSHDLDSNQAAMVLIR.L  
 0.999994 1 R.GDEELDSLK[325.13]ATIAGGGVIPHIHK.S  
 0.999994 1 K.LNPNFLVDFGK[325.13]EPLGPALAHCLR.Y  
 0.999994 1 K.K[325.13]LKQSMWSLLTALSGK.E  
 0.999994 1 R.AALEAC[160.03]HK[325.13]GWGVSVVVGVAASGEEIATF  
 0.999994 0.9957 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSK.L  
 0.999994 1 R.DVPIDHSDLVADLLK[325.13]ELSNHNER.V  
 0.999994 1 K.TPELRDDDFLGGAEC[160.03]SLGQIVSSQVLTPLMLKPGI  
 0.999994 1 K.K[325.13]HLVSAGYVHVNR.D  
 0.999994 1 R.K[325.13]HAGPIVSVWHR.E  
 0.999994 1 R.K[325.13]HAGPIVSVWHR.E  
 0.999994 1 R.HFIQSLSK[325.13]FPHESAR.L  
 0.999994 1 K.K[325.13]LYTGPGLAHC[160.03]MQVHK.E  
 0.999994 1 R.K[325.13]HTGFLEISQHSQEFINR.L  
 0.999994 1 R.K[325.13]HTGFLEISQHSQEFINR.L  
 0.999994 1 R.VISK[325.13]HDLGHFMLR.C  
 0.999994 1 R.HSAESQILK[325.13]HLLK.N  
 0.999994 1 R.HHSK[325.13]LLVSGFWGVAR.H  
 0.999994 1 R.HHSK[325.13]LLVSGFWGVAR.H  
 0.999994 1 K.KLLVPGK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E  
 0.999994 1 R.HLC[160.03]AVYYNK[325.13]NPGFEIHHGLLDR.I  
 0.999994 1 R.K[325.13]DLSQAPFSWPAGALVAQAC[160.03]HAATAAL  
 0.999994 1 R.K[325.13]ATAAVIFLHGLGDTGHGWAEAFAGIR.S  
 0.999994 1 R.SHK[325.13]IQTQLNLIHPDIFPLTSFR.C  
 0.999994 1 R.VKPFMTGAAEQIK[325.13]HILANFK.N  
 0.999994 1 R.SHK[325.13]IQTQLNLIHPDIFPLTSFR.C  
 0.999994 1 R.VKPFMTGAAEQIK[325.13]HILANFK.N  
 0.999994 1 K.DSK[325.13]AEPHFLSILQHLLLV.R.N  
 0.999994 1 R.DSK[325.13]SQAPGQPGASQWGS.R.V  
 0.999994 0.9999 K.FAAK[325.13]GEGQLGPAER.A  
 0.999994 0.9999 R.LQAEIEGLK[325.13]GQR.A  
 0.999994 1 R.LC[160.03]AAAASILGK[325.13]PADR.V  
 0.999994 0.9996 R.TLLIK[325.13]TVETR.D  
 0.999994 1 R.LVK[325.13]DVFISAAER.D  
 0.999994 0.9994 K.NQK[325.13]DDVAQTDLLQIDPNFGSK.E

0.999994 1 K.VTDDLVC[160.03]LVYK[325.13]TDQAQDV.K  
 0.999994 0.9963 K.EITALAPSTMKIK[325.13]IIAPPER.K  
 0.999994 0.9473 R.ADIK[325.13]EMGLSLQWLYSAR.G  
 0.999994 1 K.ESDTGLAPPALWDLAADK[325.13]QTLQSEQPLQVAR.C  
 0.999994 0.9999 R.AVTGYTDPYTGGQISLFQAMQK[325.13]DLIVR.E  
 0.999994 1 K.LVDQALLTMDTYLGQFPDIK[325.13]SR.I  
 0.999994 0.9999 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13]  
 0.999994 0.9999 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.  
 0.999994 0.9996 K.EK[325.13]LC[160.03]YVALDFENEMATAASSSSLEKSYELF  
 0.999994 1 R.RGPALEDC[160.03]DC[160.03]AQDENC[160.03]K[325.13]  
 0.999994 1 R.NDSPTYGQQGHPNTWK[325.13]R.E  
 0.999994 1 R.WK[325.13]C[160.03]DGD PDC[160.03]EDGSDESPEQC[  
 0.999994 1 R.IIGAK[325.13]DHASI QMNVAEVDK.V  
 0.999994 1 R.IIGAK[325.13]DHASI QMNVAEVDK.V  
 0.999994 1 R.EFLEDTC[160.03]VQYVQK[325.13]HISAENTK.G  
 0.999994 1 R.EFLEDTC[160.03]VQYVQK[325.13]HISAENTK.G  
 0.999994 1 R.DLSHIGDAVVISC[160.03]AK[325.13]DGVK.F  
 0.999994 1 K.INEVQTDVGVDTK[325.13]HQT LQGVAFPISR.E  
 0.999994 0.9376 R.LLLPGELAK[325.13]HAVSEG.TK.A  
 0.999994 0.9993 R.APQC[160.03]LGK[325.13]FIEIAAR.K  
 0.999994 1 K.EGNELFK[325.13]C[160.03]GDYGGALAAAYTQALGLDATP  
 0.999994 1 R.TVIEDMLAMPK[325.13]AALLNDC[160.03]VC[160.03]D  
 0.999994 1 K.HSTVLENTDGK[325.13]TLPSWGQALLSQDFELLC[160.03]  
 0.999994 1 K.HSTVLENTDGK[325.13]TLPSWGQALLSQDFELLC[160.03]  
 0.999994 1 R.MPILISK[325.13]IFPGLAADQSR.A  
 0.999994 0.9996 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R  
 0.999994 1 R.YNVPFLTFINK[325.13]LDR.M  
 0.999994 1 K.VPEDPTQC[160.03]FLLFANQTEK[325.13]DIILREDLEELQ  
 0.999994 0.9991 R.DLTDYLM[147.04]K[325.13]ILTER.G  
 0.999994 0.999 R.DLTDYLM[147.04]K[325.13]ILTER.G  
 0.999994 1 K.EPESILQVLSQMEK[325.13]IVR.I  
 0.999994 0.9999 K.NAQK[325.13]SNQNGKDSKPSSTPR.S  
 0.999994 1 R.K[325.13]EVDSKPV SQKPPPPSEK.V  
 0.999994 1 K.HISAENTK[325.13]GSQTSR.S  
 0.999994 1 K.HISAENTK[325.13]GSQTSR.S  
 0.999994 1 K.HISAENTK[325.13]GSQTSR.S  
 0.999994 1 R.VTQEEIK[325.13]KEPEKPIDR.E  
 0.999994 0.9999 R.FHVEEEGK[325.13]GK.D  
 0.999994 1 R.LGK[325.13]HDVTC[160.03]TVSGGGR.S  
 0.999994 1 R.YWAAHDK[325.13]EEAANR.V  
 0.999994 1 R.I LHENTQTDK[325.13]ALYNR.L  
 0.999994 1 K.YC[160.03]RPESQEHPEADPGSAAPYLK[325.13]TK.F  
 0.999994 1 K.YC[160.03]RPESQEHPEADPGSAAPYLK[325.13]TK.F  
 0.999994 1 R.K[325.13]GHFEC[160.03]PPYNSSTIR.S  
 0.999994 1 R.K[325.13]GHFEC[160.03]PPYNSSTIR.S  
 0.999994 1 K.VQFSNK[325.13]SANMDHWQQR.F  
 0.999994 1 K.VQFSNK[325.13]SANMDHWQQR.F

0.999994 1 R.HVFGQPVK[325.13]NDQC[160.03]YEDIR.V  
0.999994 1 R.SEIK[325.13]GFYDPPRR.L  
0.999994 1 R.LQHLEK[325.13]SNIYSK.F  
0.999994 0.9999 K.VFGNEIK[325.13]LEKPK.G  
0.999994 1 R.C[160.03]GAHYK[325.13]LVPQQLAH.-  
0.999994 1 K.NK[325.13]QLPTAAPDKTEVTGDHIPTPQDLPQR.K  
0.999994 1 K.NIK[325.13]QNAHIVEWSPR.G  
0.999994 1 R.QHLNPPGGK[325.13]TSDIFGSPVTATSR.L  
0.999994 1 R.QHLNPPGGK[325.13]TSDIFGSPVTATSR.L  
0.999994 1 R.K[325.13]GVHC[160.03]VMSLGVPGPATLAK.A  
0.999994 1 K.LATELYHQK[325.13]SVLIMGR.G  
0.999994 1 R.KDPGVPNSAPFK[325.13]EALLR.E  
0.999994 1 K.SQLK[325.13]VLSHNL[160.03]TVLK.V  
0.999994 1 K.IDQLQEELLHTQLK[325.13]YQR.I  
0.999994 1 K.SSGPWNK[325.13]TAPVQAPPAPVIVTETPEPAMTSGVYR  
0.999994 1 R.LHVTALDYLAPYAK[325.13]YK.V  
0.999994 1 R.DFGSAAVSLQVAAPYSK[325.13]PSMTLEPNKDLRPGDTV  
0.999994 0.9999 K.LAGANPAVITC[160.03]DELLLGHEK[325.13]APAFR.D  
0.999994 1 R.KQAAAK[325.13]FYSFLVLK.K  
0.999994 1 K.WTPEVK[325.13]HFC[160.03]PNVPIILVGNK.K  
0.999994 1 K.WTPEVK[325.13]HFC[160.03]PNVPIILVGNK.K  
0.999994 0.9999 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I  
0.999994 0.9973 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP  
0.999994 1 R.NDLEAFIHFHMGK[325.13]GAAAER.F  
0.999994 1 R.DIKPENLLLGLK[325.13]GELK.I  
0.999994 1 R.DIKPENLLLGLK[325.13]GELK.I  
0.999994 1 R.KPVAGALDVSNK[325.13]FIPLSEPAPVPPIPNEQQLAR.L  
0.999994 0.815 R.DALSDALHFLNK[325.13]M[147.04]K.I  
0.999994 1 R.LTRPGSSYFNLNPFVQLIDPEVTDEEIK[325.13]K.R  
0.999994 1 K.VEAVVEK[325.13]LGVPFQVLVATHAGLYR.K  
0.999994 1 K.VGLTSEILNSFEHEFLSK[325.13]R.L  
0.999994 1 K.VGLTSEILNSFEHEFLSK[325.13]R.L  
0.999994 1 R.AWRDPDEPVLLEPVVLALAEK[325.13]YGR.S  
0.999994 1 R.ESLKDQLALAIGK[325.13]LGENMILK.R  
0.999994 1 K.K[325.13]LLDQC[160.03]ENQELEAPGGIATPPVYGQLLAL  
0.999994 1 R.ESDTGLWLHNK[325.13]LGATDELWAPPSIASLLTAAVIDN  
0.999994 1 R.ESDTGLWLHNK[325.13]LGATDELWAPPSIASLLTAAVIDN  
0.999994 1 R.LSAKPAPPK[325.13]PEPKPK.K  
0.999994 1 R.IC[160.03]K[325.13]SSVHQPGSHYC[160.03]QGC[160.0  
0.999994 0.9998 R.K[325.13]GHAVGDIPGVR.F  
0.999994 1 R.HSGSSHLPQQLK[325.13]FTTSDSC[160.03]DR.I  
0.999994 1 R.HSGSSHLPQQLK[325.13]FTTSDSC[160.03]DR.I  
0.999994 1 R.FHEIC[160.03]SNLVK[325.13]TR.R  
0.999994 1 R.GVK[325.13]YNQATPNFHQWR.D  
0.999994 1 R.GVK[325.13]YNQATPNFHQWR.D  
0.999994 1 R.FGQVYTEAK[325.13]RPPGFDR.V  
0.999994 1 R.FGQVYTEAK[325.13]RPPGFDR.V



0.999994 1 R.SFLHGPELKD[325.13]GQLR.I  
 0.999994 1 R.KTPQGPPEIYSDTQFPSLQSTAK[325.13]HVESR.K  
 0.999994 0.9996 R.LLIHQSLAGGIIGVK[325.13]GAK.I  
 0.999994 1 R.K[325.13]SWLWQHDEPC[160.03]YWR.L  
 0.999994 1 K.IYHPNIDEK[325.13]GQVC[160.03]LPVISAENWKPATK.T  
 0.999994 1 R.ALVAIGTHDLDTLSPFTYTAK[325.13]RPSDIK.F  
 0.999994 0.9991 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E  
 0.999994 1 R.TK[325.13]HLLNVINENFGTLAFC[160.03]R.R  
 0.999994 1 R.RQLASLLEGTSDQSVVIPNLFPK[325.13]YIR.A  
 0.999994 1 K.AGPHK[325.13]EIYPYVIQELRPTLNELGISTPEELGLDKV.-  
 0.999994 1 K.AGPHK[325.13]EIYPYVIQELRPTLNELGISTPEELGLDKV.-  
 0.999994 1 R.DQYLGHLLQYVAAYQQLTSEK[325.13]EVLHNQLLLQTQL  
 0.999994 1 R.RLEDQLAGLQQELAALALK[325.13]QSSVAEEVGLLPQQIQ  
 0.999993 0.9994 K.SPAKPK[325.13]AVKPK.A  
 0.999993 1 R.ERPQIGGTIK[325.13]QPPSNPPRPPAEAR.K  
 0.999993 1 R.ITTTFGEHLNAVQASAEHQK[325.13]R.L  
 0.999993 1 K.IADLGNAC[160.03]WVHK[325.13]HFTEDIQTR.Q  
 0.999993 1 R.DC[160.03]HYLK[325.13]MSIAQC[160.03]TSSHPIIR.Q  
 0.999993 1 R.KNELEQK[325.13]MLLNLHK.K  
 0.999993 1 R.HLPNLQTHK[325.13]ENPVLDVVSNEQTAGEER.G  
 0.999993 1 R.HLPNLQTHK[325.13]ENPVLDVVSNEQTAGEER.G  
 0.999993 0.9999 K.K[325.13]ADQKGVTIIGPATVGGIKPGC[160.03]FK.I  
 0.999993 1 R.GLDIPK[325.13]VQHVHIHYQVPR.T  
 0.999993 1 R.KQGLEQFINK[325.13]VAGHPLAQNER.C  
 0.999993 1 R.KQGLEQFINK[325.13]VAGHPLAQNER.C  
 0.999993 0.9963 R.ELPAQK[325.13]WWHTGALYR.I  
 0.999993 0.9999 R.FHK[325.13]LQNVQIALDYLR.H  
 0.999993 1 R.LEELMKPLK[325.13]VVDPDHPLAALVR.K  
 0.999993 1 R.DGVPIK[325.13]VANDNAPEHALRPGFLSTFALATDQGS  
 0.999993 1 R.DGVPIK[325.13]VANDNAPEHALRPGFLSTFALATDQGS  
 0.999993 0.9998 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V  
 0.999993 0.9999 R.RLAAVALINAAIQK[325.13]GVAEK.T  
 0.999993 1 K.HVTSEQEWDK[325.13]YC[160.03]HYVAGLVGIGLSR.L  
 0.999993 1 R.LDDLFLSFETDVK[325.13]PLKGDHLSR.A  
 0.999993 1 R.FVELHFDELPSSELETILHK[325.13]R.C  
 0.999993 0.9999 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTSGSFTS  
 0.999993 1 R.HLVSPALDLDLKD[325.13]LLR.Y  
 0.999993 0.9995 K.KTESHHK[325.13]AK.G  
 0.999993 1 K.K[325.13]TTLALHHLSSGHLK.W  
 0.999993 0.9993 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T  
 0.999993 1 R.LLHAK[325.13]NIIRPQLK.F  
 0.999993 1 R.LLHAK[325.13]NIIRPQLK.F  
 0.999993 1 R.HGQEHVEVYHAHYK[325.13]PLEFTVAGR.D  
 0.999993 1 R.HGQEHVEVYHAHYK[325.13]PLEFTVAGR.D  
 0.999993 0.9996 R.HWGGNVLGPK[325.13]SVAR.I  
 0.999993 1 R.SWVSQHC[160.03]K[325.13]SLAIPC[160.03]PAHYTPR.I  
 0.999993 1 R.SWVSQHC[160.03]K[325.13]SLAIPC[160.03]PAHYTPR.I

0.999993 1 R.YFQHLLGK[325.13]QADNPHVALYQAR.F  
0.999993 1 R.YFQHLLGK[325.13]QADNPHVALYQAR.F  
0.999993 1 R.NK[325.13]LHFPMDIHTLHPQR.Q  
0.999993 1 R.GVAGAHGLLC[160.03]LLSDHVDK[325.13]R.I  
0.999993 1 R.NK[325.13]DHPAFAPLYFPMELHR.K  
0.999993 1 R.LFFK[325.13]NVTGHIYISPFHDIPLK.V  
0.999993 1 R.LFFK[325.13]NVTGHIYISPFHDIPLK.V  
0.999993 1 R.GQLK[325.13]QWLDLHLHQEIPSTLLILSR.A  
0.999993 1 R.GQLK[325.13]QWLDLHLHQEIPSTLLILSR.A  
0.999993 1 R.TVALK[325.13]GPVTNAAILLAPVSMMLSSDFRPSLPLPHFNK  
0.999993 1 R.ATAGAYIASQTVK[325.13]K.V  
0.999993 1 K.VDK[325.13]GVVPLAGTDGETTTQGLDGLSER.C  
0.999993 1 R.GYDQSAYDGK[325.13]DYIALNEDLR.S  
0.999993 1 K.VDK[325.13]GVVPLAGTDGETTTQGLDGLSER.C  
0.999993 0.9955 K.EITALAPSTMKIK[325.13]IIAPPER.K  
0.999993 1 R.AFPNPYADYNK[325.13]SLAEGYFDAAGR.L  
0.999993 0.9999 K.ALELTGLK[325.13]VFGNEIK.L  
0.999993 0.9972 R.K[325.13]LFIGGLSFETTEESLR.N  
0.999993 0.9943 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G  
0.999993 1 K.DSQAALPK[325.13]YVLINWVGEDVPDAR.K  
0.999993 0.9993 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]LEPSANM  
0.999993 0.9994 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSANM  
0.999993 0.8811 R.YISPDQLADLYK[325.13]SFIK.D  
0.999993 0.9401 R.ADIK[325.13]EMGLSLQWLYSAR.G  
0.999993 1 R.K[325.13]GEQC[160.03]VHTASGPR.C  
0.999993 1 K.KTEAPAAPAAQETK[325.13]SDGAPASDSKPGSSEAAPSSK  
0.999993 1 K.KTEAPAAPAAQETK[325.13]SDGAPASDSKPGSSEAAPSSK  
0.999993 1 K.TSSFSC[160.03]EAHNAK[325.13]GVTTSR.T  
0.999993 1 K.TSSFSC[160.03]EAHNAK[325.13]GVTTSR.T  
0.999993 1 K.TSSFSC[160.03]EAHNAK[325.13]GVTTSR.T  
0.999993 1 R.LQDQGSPSWASGDSSNNHK[325.13]PR.E  
0.999993 0.9844 R.HQGVMMGM[147.04]GQK[325.13]DSYVGDEAQSK.R  
0.999993 1 R.TQK[325.13]TPPGLQHEYAAPADYFR.I  
0.999993 1 R.IEGLAPK[325.13]LDPEEMKR.K  
0.999993 1 R.MTVVQAYINEK[325.13]HYK.K  
0.999993 1 R.VFIK[325.13]SYSEDDIHR.S  
0.999993 1 R.VFIK[325.13]SYSEDDIHR.S  
0.999993 0.9999 R.LLFNDVQTLK[325.13]DGR.H  
0.999993 1 K.GSK[325.13]FYGPAGPYGIFAGR.D  
0.999993 1 R.ADGVTVTC[160.03]K[325.13]VEHESFEERALIPVTLVSR.Y  
0.999993 1 R.ADGVTVTC[160.03]K[325.13]VEHESFEERALIPVTLVSR.Y  
0.999993 1 R.LK[325.13]YSIIGQVPPSPTLFSMHPTTGVTITSSQLDR.E  
0.999993 1 R.LK[325.13]YSIIGQVPPSPTLFSMHPTTGVTITSSQLDR.E  
0.999993 1 R.LK[325.13]YSIIGQVPPSPTLFSMHPTTGVTITSSQLDR.E  
0.999993 0.9999 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L  
0.999993 0.9999 R.NPDDITQEEYGEFYK[325.13]SLTNDWEDHLAVK.H  
0.999993 1 R.NDVAHK[325.13]QLSAFGEYVAEILPK.Y

0.999993 0.9999 K.K[325.13]VGYTPDWIFLLR.N  
0.999993 0.9996 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E  
0.999993 1 R.SK[325.13]FALITWIGENVSLQR.A  
0.999993 1 K.VPLK[325.13]C[160.03]LAQEVNIPDWIVDLR.H  
0.999993 1 R.DQASQLLAGTEATLGHAK[325.13]TLAAIR.A  
0.999993 0.9996 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T  
0.999993 1 R.DYVLDC[160.03]NILPPLLQLFSK[325.13]QNR.L  
0.999993 1 R.DYVLDC[160.03]NILPPLLQLFSK[325.13]QNR.L  
0.999993 1 R.DAYTHPQFVTDVMK[325.13]PLQIENIIDQEVQTLSSGELC  
0.999993 1 R.DAYTHPQFVTDVMK[325.13]PLQIENIIDQEVQTLSSGELC  
0.999993 0.9998 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S  
0.999993 1 R.ITSPLMEPSSIEK[325.13]IVEIDAHIGC[160.03]AMSGLIAC  
0.999993 1 R.ITSPLMEPSSIEK[325.13]IVEIDAHIGC[160.03]AMSGLIAC  
0.999993 1 R.ALK[325.13]LPNLVDMAAQVAAGMAYIER.M  
0.999993 1 K.YLK[325.13]LPQLVDMAAQIADGMAYIER.M  
0.999993 1 R.K[325.13]GEQC[160.03]VHTASGPR.C  
0.999993 1 R.APGAAPSAAAK[325.13]SHR.C  
0.999993 1 R.IVAAHNK[325.13]C[160.03]PR.D  
0.999993 1 K.RGFEGSC[160.03]SQK[325.13]ESEEGNPVR.G  
0.999993 1 R.IQC[160.03]VPK[325.13]EPHSFQSR.L  
0.999993 1 K.HSK[325.13]LFEEDPSNR.S  
0.999993 0.8388 R.HQGVMMVGMGQKDSYVGDEAQSK[325.13]R.G  
0.999993 1 K.K[325.13]NYVHFAATQVQNR.I  
0.999993 1 K.K[325.13]SIAAC[160.03]HNVGLLAHDGQVNEDGQPDLG  
0.999993 1 K.K[325.13]SIAAC[160.03]HNVGLLAHDGQVNEDGQPDLG  
0.999993 1 R.EQPWHK[325.13]EC[160.03]FVC[160.03]TAC[160.03]R  
0.999993 1 R.EQPWHK[325.13]EC[160.03]FVC[160.03]TAC[160.03]R  
0.999993 1 K.DVGLHIK[325.13]AVR.S  
0.999993 1 K.IK[325.13]LGHYATQLQNTYDR.C  
0.999993 1 R.KQDFPLVK[325.13]AAVQK.A  
0.999993 1 R.FK[325.13]SQLPDLSGPHSYSPGR.N  
0.999993 1 R.KQDFPLVK[325.13]AAVQK.A  
0.999993 1 R.K[325.13]QVMGLITHTDSPYIR.A  
0.999993 1 R.K[325.13]PPARPSAAAAIAVAAAEER.R  
0.999993 0.9925 R.LLLPGELAK[325.13]HAVSEGK.A  
0.999993 1 R.VK[325.13]AIFSHAAGDNSTLLSFK.E  
0.999993 1 R.KVDATDASYPSVNTC[160.03]VHYLK[325.13]LPEYSSEEIN  
0.999993 1 R.VK[325.13]AIFSHAAGDNSTLLSFK.E  
0.999993 1 R.KVDATDASYPSVNTC[160.03]VHYLK[325.13]LPEYSSEEIN  
0.999993 1 R.GPGGSSLLIEALSNSHK[325.13]C[160.03]QADIR.H  
0.999993 1 R.TALLESDEHTC[160.03]PTC[160.03]HQNDVSPDALIANK[  
0.999993 1 K.LKDPANFQYPAESVLAYK[325.13]EGHLSPDIVAEQK.K  
0.999993 1 R.SAK[325.13]IAVYHLQELASAEK.E  
0.999993 0.9993 K.K[325.13]HSQFIGYPITLYLEK.E  
0.999993 0.9999 K.VTVLFAGQHIK[325.13]SPFEVYVDK.S  
0.999993 1 K.ADPSHFELLK[325.13]VLGQGSFGK.V  
0.999993 1 K.ALPLIVGAQLIHADK[325.13]LGEK.V

0.999993 1 K.AINQIAAALFTIHK[325.13]GSIEDR.L  
 0.999993 1 K.TGPFAEHSNQLWNISAVPSWSK[325.13]VNQGLIR.M  
 0.999993 1 K.K[325.13]SLDLTGPLLLGGVPNLPEDFPVHNR.Q  
 0.999993 1 K.K[325.13]SLDLTGPLLLGGVPNLPEDFPVHNR.Q  
 0.999993 1 K.TYTSQSIHQAVIAEQLAK[325.13]LAQGISQLDR.E  
 0.999993 1 R.DIAK[325.13]HLPDGC[160.03]PAMLVLPYASLPYAQQLF  
 0.999993 1 R.EPFVAQFSLPSNVLPSTLVPLHTTPK[325.13]AVEK.E  
 0.999993 1 K.SEDPLFVLEHSLPIDTQYYLEQQLAK[325.13]PLLR.I  
 0.999993 1 R.K[325.13]AENKYAGGNPVC[160.03]VRPTPK.W  
 0.999993 1 R.GQHEPSKPPPAGETVTGGFGAK[325.13]K.R  
 0.999993 0.9995 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L  
 0.999993 1 R.FDSK[325.13]PAPSAQPAPPPHPPSR.L  
 0.999993 1 R.YQVSWSLDHK[325.13]SAHAGTYEVR.F  
 0.999993 1 R.HEVAK[325.13]FIGSPPGYVGHEEGQLTK.K  
 0.999993 1 R.LKEQGQAPITPQQGQALAK[325.13]QIHAVR.Y  
 0.999993 1 R.LKEQGQAPITPQQGQALAK[325.13]QIHAVR.Y  
 0.999993 1 K.TK[325.13]FGYHIIMVEGR.K  
 0.999993 1 K.FFK[325.13]SKPELPPGLSPEATAPVTPSRPEGGEPLSK.T  
 0.999993 0.993 R.LLLPGELAK[325.13]HAVSEGTK.A  
 0.999993 1 K.FDPYEHEALFHTPVEGK[325.13]EPGTVALVSK.V  
 0.999993 0.9232 R.LLLPGELAK[325.13]HAVSEGTK.A  
 0.999993 1 K.FDPYEHEALFHTPVEGK[325.13]EPGTVALVSK.V  
 0.999993 0.8063 R.LK[325.13]LEPHEGLLLR.F  
 0.999993 1 R.K[325.13]TLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR.R  
 0.999993 0.9999 K.HSQFIGYPITLFVEK[325.13]ER.D  
 0.999993 1 K.TGPFAEHSNQLWNISAVPSWSK[325.13]VNQGLIR.M  
 0.999993 0.9999 R.LPLQDVYK[325.13]IGGIGTVPVGRVETGVLKPGMVVTFAF  
 0.999993 1 K.ELHAPLTVVADGLFSK[325.13]FR.K  
 0.999993 0.9999 R.TGGMAFHSYFMEAIAPELLQELK[325.13]K.V  
 0.999993 1 R.LNTHVK[325.13]PLIWIESVIEK.H  
 0.999993 1 R.LNTHVK[325.13]PLIWIESVIEK.H  
 0.999993 1 K.LLSAGATK[325.13]VYAILTHGIFSGPAISR.I  
 0.999992 0.9993 K.KPVGAAK[325.13]KPK.K  
 0.999992 1 R.K[325.13]VVHIEQGGGLVKPER.D  
 0.999992 1 R.K[325.13]AGHQFGVTWR.A  
 0.999992 1 R.TSVIQGIHTDHNTLK[325.13]LVPR.K  
 0.999992 0.9786 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
 0.999992 1 R.LHTK[325.13]PSQAPAVEVAPAGASYNPSFEDHQTLLSAAH  
 0.999992 1 R.LHVLGPDLDK[325.13]SVQSLATGPAGDPGC[160.03]QTC[  
 0.999992 0.9957 R.ELPAQK[325.13]WWHTGALYR.I  
 0.999992 1 K.SLSGGASYVDFLC[160.03]HMHK[325.13]EIR.Q  
 0.999992 1 R.VENSPQVDGSPGLEGLGGIGEK[325.13]GVHRPAPR.N  
 0.999992 1 R.VVLQLK[325.13]GHVSELEADLAEQQHLR.Q  
 0.999992 1 K.IHGAYSSEK[325.13]LSYFEHNLETWR.Q  
 0.999992 1 R.K[325.13]AAHVTLTSLVEGEAVHLAR.D  
 0.999992 1 R.VLNFLK[325.13]DHFLMDGQVR.S  
 0.999992 1 R.GFGVTFADPASVDK[325.13]VLGQPHHELSK.T

0.999992 1 R.HISPTAPDTLGC[160.03]YPFYK[325.13]TDPFIFPEC[160.03]  
0.999992 0.9996 R.DWSHYFK[325.13]IIEDLR.A  
0.999992 1 R.EKRPEAAQLLEDVQAALK[325.13]PFSVK.L  
0.999992 1 R.GSSLHLHVSK[325.13]PPR.E  
0.999992 1 K.FIHVSHLNANIK[325.13]SSSR.Y  
0.999992 1 R.K[325.13]SGVSDHWALDDHHLHLTR.K  
0.999992 1 K.VAGNFHITVGK[325.13]AIPHPR.G  
0.999992 1 R.LERPYTFFK[325.13]DFVLHPR.S  
0.999992 1 R.RGDFIHVMDNSDPNWWK[325.13]GAC[160.03]HGQTG  
0.999992 1 -.MLSEVLLVSAPGK[325.13]VILHGEHAVVHGK.V  
0.999992 0.9983 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR  
0.999992 1 K.IHNFLK[325.13]GNPGFSGNLNIPILSSLGSSAPSESHPSDFI  
0.999992 1 K.HYLDQLNHILGILGSPSQEDLNC[160.03]IINMK[325.13]AI  
0.999992 1 K.DHVFPVNDGFQALQGIIHSILK[325.13]K.S  
0.999992 1 K.DHVFPVNDGFQALQGIIHSILK[325.13]K.S  
0.999992 1 K.VVSSGAPHAILLK[325.13]FLPLPVVQLLDR.C  
0.999992 0.9993 R.GENSWFSTQVDTVATK[325.13]VK.D  
0.999992 0.9996 R.VETGVLK[325.13]PGM[147.04]VVTFAFVNVTTTEVK.S  
0.999992 0.9999 K.MPILGLGTWK[325.13]SPPGQVTEAVK.V  
0.999992 0.9992 K.TVTAMDVVYALK[325.13]R.Q  
0.999992 0.9929 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G  
0.999992 0.9982 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S  
0.999992 1 K.VSK[325.13]ASADLMSYC[160.03]EEHAR.S  
0.999992 0.9993 R.QTVAVGVK[325.13]AVDKK.A  
0.999992 1 K.VVYPSK[325.13]ADLATAPPHVTVVR.-  
0.999992 0.9991 R.APQC[160.03]LGK[325.13]FIEIAAR.K  
0.999992 1 R.NLGIVSVTSTDISSLYAK[325.13]AQHVAR.R  
0.999992 0.9921 K.VK[325.13]DALEFWLQAGVDGFQVR.D  
0.999992 1 R.IETALAGSPC[160.03]LGHNK[325.13]LSR.E  
0.999992 0.9998 R.FVPQEMGVHTVSVK[325.13]YR.G  
0.999992 0.9998 R.LDHK[325.13]FDLMYAK.R  
0.999992 0.9996 K.TEWLDGK[325.13]HVVFGK.V  
0.999992 1 R.GVLHTFSPSPK[325.13]LQNSASATALVSR.T  
0.999992 1 R.AYC[160.03]HILLGNYC[160.03]VAVADAK[325.13]K.S  
0.999992 1 R.LSQPFESYITAPPGTAAAPAK[325.13]PAPPATPGAPTSPAE  
0.999992 0.9992 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C  
0.999992 1 K.IKDLSTVEALQNLK[325.13]NLK.S  
0.999992 1 R.DEILLHQAAAK[325.13]VASER.D  
0.999992 1 R.HSTLDFMLGAK[325.13]ADGETILK.G  
0.999992 1 K.IAELLENVTLIHK[325.13]PVSLQPR.G  
0.999992 1 R.GQLSWHQK[325.13]TYAFSENPLPTVEIAIR.N  
0.999992 1 R.HDVVILDSLNYIK[325.13]GFR.Y  
0.999992 1 R.K[325.13]QEWTAIPNSQLIVIPYPHNVPR.S  
0.999992 0.9995 R.K[325.13]PLVIIAEDVDGEALSTLVLR.L  
0.999992 1 R.FFLNMK[325.13]PEIQPSDTSYLWHIPLSYVTEGR.N  
0.999992 1 K.DLQEVIELTK[325.13]DLLSTQPSETLASSDSFASTQPTHSW  
0.999992 1 R.TK[325.13]ASVHTLSGHTNAVATVR.C

0.999992 1 K.AYHNSPAYLAYINAK[325.13]SR.A  
0.999992 1 R.DLK[325.13]HSLPSGLGLSETQITSHGFDNTK.E  
0.999992 1 K.INNAHTIGC[160.03]NAVSWAPAVVPGSLIDHPSGQK[325  
0.999992 1 K.HSGIDFK[325.13]QLNFLT.K  
0.999992 1 R.FAK[325.13]VHILYVGSMP.LK.N  
0.999992 1 K.NIHPIYNIK[325.13]SLMIK.R  
0.999992 0.9999 R.LQALDTGWNELHK[325.13]MWENR.Q  
0.999992 1 R.GFGHPSLVK[325.13]ALSYLEK.L  
0.999992 1 K.VFGPTIVAHAVPNPDPVTMLQDIK[325.13]R.Q  
0.999992 1 R.SIGRPELK[325.13]NLDPFLLFDEFK.G  
0.999992 1 R.FAPYRPPDISLK[325.13]PLLFEVPSITTESVFVGR.D  
0.999992 1 R.FAPYKPDILLK[325.13]PLLFEVPSITTDVSVFVGR.D  
0.999992 0.7742 R.LK[325.13]LEPHEGLLLR.F  
0.999992 1 K.LQQQLPMPPIPGELLTLIGATGISYGMGLK[325.13]HR.F  
0.999992 1 R.LHAGPEPQALPAFSDLEALSSTLYSLQK[325.13]QLR.A  
0.999991 0.9993 R.GALQNIIPASTGAAK[325.13]AVGK.V  
0.999991 0.9999 R.TM[147.04]PVEQVFAK[325.13]NFR.V  
0.999991 0.994 K.EITALAPSTMKIK[325.13]IIAPPER.K  
0.999991 0.926 R.ADIK[325.13]EMGLSLQWLYSAR.G  
0.999991 0.9999 R.EVTVPVFYPTTEK[325.13]VWLEVEPVGM[147.04]LK.E  
0.999991 0.9816 R.HQGVMMVGM[147.04]GQK[325.13]DSYVGDEAQSK.R  
0.999991 0.9998 R.K[325.13]MC[160.03]LFAGFQR.K  
0.999991 0.9995 K.IILDILIESPIK[325.13]GR.A  
0.999991 0.9999 R.EMAGDNK[325.13]LLGQFTLIGIPPAPR.G  
0.999991 0.9991 K.K[325.13]HSQFIGYPITLYLEK.E  
0.999991 0.9998 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I  
0.999991 0.9996 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
0.999991 0.9989 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  
0.999991 0.9993 R.VSGPYFPTLLGLSLQVLEPPQHGAALQK[325.13]EDGPQAR.  
0.999991 0.0803 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L  
0.999991 0.991 R.LLLPGELAK[325.13]HAVSEGK.A  
0.99999 0.9992 K.SVHELEKSK[325.13]R.A  
0.99999 0.9821 R.LK[325.13]LEPHEGLLLR.F  
0.99999 0.9972 R.GHYTIGK[325.13]EIIDLVLDR.I  
0.99999 0.9957 R.RFDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V  
0.99999 0.9993 R.TLLIK[325.13]TVETR.D  
0.99999 0.9991 R.GENSWFSTQVDTVATK[325.13]VK.D  
0.99999 0.9999 R.AIIPC[160.03]IK[325.13]GYDVIAQAQSGTGK.T  
0.99999 0.9999 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V  
0.99999 0.9995 R.VETGV.LK[325.13]PGM[147.04]VVTFAFVNVTTTEVK.S  
0.99999 0.9999 K.MPILGLGTWK[325.13]SPPGQVTEAVK.V  
0.99999 0.9978 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S  
0.99999 0.9979 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S  
0.99999 0.9992 K.K[325.13]EDLYLKPIQR.T  
0.99999 0.9998 R.AWTSK[325.13]GSGPLSPSIQSR.T  
0.99999 0.9985 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R  
0.99999 0.997 R.GVLK[325.13]VFLENVIR.D

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| 0.99999  | 0.9998 R.DPYSGSTISLFQAMQK[325.13]GLVLR.Q             |
| 0.99999  | 0.9996 R.GTK[325.13]VILHLK.E                         |
| 0.99999  | 0.9999 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A          |
| 0.99999  | 0.9996 R.VSFELFADKVPK[325.13]TAENFR.A                |
| 0.99999  | 0.9961 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R   |
| 0.99999  | 0.9996 R.LLIHQSLAGGIIGVK[325.13]GAK.I                |
| 0.99999  | 0.9984 R.ELPAQK[325.13]WWHTGALYR.I                   |
| 0.99999  | 0.9951 R.DALSDLALHFLNK[325.13]MK.I                   |
| 0.99999  | 0.9985 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y         |
| 0.999989 | 0.998 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKF |
| 0.999989 | 0.9999 R.FHILFK[325.13]ALGEEK.G                      |
| 0.999989 | 0.994 K.SVVLMSHLGRPDGVPMPDK[325.13]YSLEPVAVELK.S     |
| 0.999989 | 0.9996 R.ISVYYNEATGGK[325.13]YVPR.A                  |
| 0.999989 | 0.9999 K.IYK[325.13]IGQGYLIK.D                       |
| 0.999989 | 0.999 K.AVELAANTK[325.13]GIC[160.03]FIR.T            |
| 0.999989 | 0.9978 R.LQSTLK[325.13]TLSFSFPNTVTGSER.V             |
| 0.999989 | 0.9908 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G         |
| 0.999989 | 0.9932 R.HQGVMMGM[147.04]GQK[325.13]DSYVGDEAQSK.R    |
| 0.999989 | 0.9706 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN |
| 0.999989 | 0.9991 R.NLQNLLILTAIK[325.13]ADR.T                   |
| 0.999989 | 0.9996 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVL.R       |
| 0.999989 | 0.9984 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y         |
| 0.999989 | 0.999 K.LHIEVGTPTGNQPFVK[325.13]K.A                  |
| 0.999989 | 0.9999 K.LDK[325.13]AQIHDVLVLVGGSTR.I                |
| 0.999989 | 0.9996 R.VSFELFADKVPK[325.13]TAENFR.A                |
| 0.999989 | 0.7169 R.DALSDLALHFLNK[325.13]M[147.04]K.I           |
| 0.999988 | 0.999 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V        |
| 0.999988 | 0.9994 R.SGPFQIFRPDNFVFGQSGAGNNWAK[325.13]GHYTEGA    |
| 0.999988 | 0.9997 K.EITALAPSTMK[325.13]IK.I                     |
| 0.999988 | 0.9992 R.TLLIK[325.13]TVETR.D                        |
| 0.999988 | 0.9998 K.SK[325.13]GIAYIEFK.T                        |
| 0.999988 | 0.9994 R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTEVK.S  |
| 0.999988 | 0.9995 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T            |
| 0.999988 | 0.9996 R.SIQLDGLVWGASK[325.13]LVPVGYGIR.K            |
| 0.999988 | 0.9974 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S     |
| 0.999988 | 0.9998 K.WSLLQQQK[325.13]TAR.S                       |
| 0.999988 | 0.999 K.ILLAELEQLK[325.13]GQGK.S                     |
| 0.999988 | 0.9993 K.IILDISESPIK[325.13]GR.A                     |
| 0.999988 | 0.999 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L          |
| 0.999988 | 0.9998 R.YAIC[160.03]SALAASALPALVMSK[325.13]GHR.I    |
| 0.999988 | 0.9997 R.DALSDLALHFLNK[325.13]M[147.04]K.I           |
| 0.999988 | 0.9997 R.DALSDLALHFLNK[325.13]M[147.04]K.I           |
| 0.999988 | 0.7588 R.EHALLAYTLGVK[325.13]QLIVGVNK.M              |
| 0.999988 | 0.9998 K.LGLVGVNLTLDGVK[325.13]SWLKPR.L              |
| 0.999987 | 0.9996 R.HK[325.13]NMSVHLSPC[160.03]FR.D             |
| 0.999987 | 0.997 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR   |
| 0.999987 | 0.9991 R.TLLIK[325.13]TVETR.D                        |

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| 0.999987 | 0.9998 R.YLAEK[325.13]YEWDAEAR.K                        |
| 0.999987 | 0.9996 K.M[147.04]LETK[325.13]WSLLQQQK.T                |
| 0.999987 | 0.992 K.EITALAPSTMKIK[325.13]IIPPER.K                   |
| 0.999987 | 0.9977 K.LDSTDFTGTIK[325.13]LLNENSYPVPR.E               |
| 0.999987 | 0.9991 R.TLLIK[325.13]TVETR.D                           |
| 0.999987 | 0.9997 R.AK[325.13]VTLNGVPAQPLGPR.A                     |
| 0.999987 | 0.998 R.DLTDYLM[147.04]K[325.13]ILTER.G                 |
| 0.999987 | 0.9994 R.FSGWYDADLSPAGHEEAK[325.13]R.G                  |
| 0.999987 | 0.9999 R.VRGEVAPDAK[325.13]SFVLNLGK.D                   |
| 0.999987 | 0.9713 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999987 | 0.9997 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I       |
| 0.999987 | 0.9992 R.LAHYNK[325.13]R.S                              |
| 0.999987 | 0.9993 R.ITLSK[325.13]HQNVLPR.E                         |
| 0.999987 | 0.9535 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I           |
| 0.999987 | 0.9998 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ     |
| 0.999986 | 0.9999 R.HKNPK[325.13]TGIYEK.H                          |
| 0.999986 | 0.9982 K.VK[325.13]GLVLGPIHK.N                          |
| 0.999986 | 0.9995 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V          |
| 0.999986 | 0.9968 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M               |
| 0.999986 | 0.9998 K.ALELTGLK[325.13]VFGNEIK.L                      |
| 0.999986 | 0.9883 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G            |
| 0.999986 | 0.9998 R.GELAIKDANAK[325.13]LSELEAALQR.A                |
| 0.999986 | 0.9999 K.DLAPYLPSVTPGLK[325.13]ASLLDPVPEVR.T            |
| 0.999986 | 0.8883 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999986 | 0.9941 R.HQGVLM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA   |
| 0.999986 | 0.9981 K.LAQMFSDMVLK[325.13]DGFQPSR.S                   |
| 0.999986 | 0.9918 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV    |
| 0.999986 | 0.9978 R.DLTDYLM[147.04]K[325.13]ILTER.G                |
| 0.999986 | 0.9998 K.LDSEDK[325.13]DKEGKPLLK.A                      |
| 0.999986 | 0.9999 R.GLK[325.13]GFVPSPTSQPGGHESLVDR.W               |
| 0.999986 | 0.9999 K.IQQLVK[325.13]EFFNGKEPSR.G                     |
| 0.999986 | 0.996 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999986 | 0.9991 R.LAHYNK[325.13]R.S                              |
| 0.999986 | 0.9998 K.KGGSWIQEINVAEK[325.13]NWYPR.Q                  |
| 0.999985 | 0.9999 K.SAPATGGVK[325.13]KPHR.Y                        |
| 0.999985 | 0.9998 K.DKGEYTLVVK[325.13]WGDEHIPGSPYR.V               |
| 0.999985 | 0.9991 K.TKPVTGNLRPEEALQALTIYEGK[325.13]FGR.L           |
| 0.999985 | 0.9998 K.VEAK[325.13]FINYVK.N                           |
| 0.999985 | 0.999 R.TLLIK[325.13]TVETR.D                            |
| 0.999985 | 0.9998 R.YLAEK[325.13]YEWDAEAR.K                        |
| 0.999985 | 0.9993 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                 |
| 0.999985 | 0.9999 K.TVDNFVALATGEK[325.13]GFGYK.N                   |
| 0.999985 | 0.9984 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE     |
| 0.999985 | 0.9998 R.LSVEEAVAAGVVGGEIQEK[325.13]LLSAER.A            |
| 0.999985 | 0.9998 K.STAISLFYELSENDLNFIK[325.13]QSK.D               |
| 0.999985 | 0.9997 R.FANYIDK[325.13]VR.F                            |
| 0.999985 | 0.9999 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V |



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| 0.999985 | 0.9995 R.SIQLDGLVWGASK[325.13]LVPVGYGIR.K               |
| 0.999985 | 0.9998 K.KAASGEAKPK[325.13]AK.K                         |
| 0.999985 | 0.9999 K.EGVHGGLINK[325.13]K.C                          |
| 0.999985 | 0.9999 K.TIGGGDDSFSTFFFC[160.03]ETGAGK[325.13]HVPR.A    |
| 0.999985 | 0.9999 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I              |
| 0.999985 | 0.9999 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D       |
| 0.999985 | 0.9995 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E           |
| 0.999985 | 0.9998 K.NMAEQIIQEISQIQSK[325.13]KK.I                   |
| 0.999985 | 0.9982 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |
| 0.999985 | 0.9448 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I           |
| 0.999985 | 0.9997 R.RYQK[325.13]STELLIR.K                          |
| 0.999985 | 0.9999 K.K[325.13]SAEFLHMLK.N                           |
| 0.999984 | 0.9999 R.RGEEGHDPK[325.13]EPEQLR.K                      |
| 0.999984 | 0.9977 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                |
| 0.999984 | 0.9999 R.VSFELFADK[325.13]VPK.T                         |
| 0.999984 | 0.9998 R.GIFPVLC[160.03]K[325.13]DPVQEAWAEDVDLR.V       |
| 0.999984 | 0.8714 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999984 | 0.9908 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R       |
| 0.999984 | 0.9668 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEAQSK.R       |
| 0.999984 | 0.9902 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV    |
| 0.999984 | 0.9936 K.WGDAGA EYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R     |
| 0.999984 | 0.9999 R.LLLNNGAK[325.13]MPIGLGTWK.S                    |
| 0.999984 | 0.9999 K.LC[160.03]YVALDFEQEMATAASSSSLEK[325.13]SYELPD  |
| 0.999984 | 0.4157 R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R               |
| 0.999984 | 0.9999 R.K[325.13]SNFAEALAAHK.Y                         |
| 0.999984 | 0.9998 R.LEK[325.13]HELIEFR.R                           |
| 0.999984 | 0.984 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999984 | 0.9993 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |
| 0.999984 | 0.9999 R.DAVTYTEHAK[325.13]RK.T                         |
| 0.999984 | 0.9988 R.LEKPAK[325.13]YDDIKK.V                         |
| 0.999984 | 0.9998 K.IGHPAPNFK[325.13]ATAVMPDGQFK.D                 |
| 0.999984 | 0.9556 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                |
| 0.999984 | 0.6097 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.999983 | 0.9994 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V          |
| 0.999983 | 0.9484 R.K[325.13]DGNASGTTLEALDC[160.03]ILPPTRPDKPLR.   |
| 0.999983 | 0.9948 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S           |
| 0.999983 | 0.9996 R.AK[325.13]VTLNGVPAQPLGPR.A                     |
| 0.999983 | 0.9999 R.GFPTIYFSPANK[325.13]K.L                        |
| 0.999983 | 0.9999 R.VTLNGVPC[160.03]KVTK[325.13]FGAQLQC[160.03]VTC |
| 0.999983 | 0.9993 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T               |
| 0.999983 | 0.9997 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK. |
| 0.999983 | 0.998 R.ETNLDLPLVDTHSK[325.13]R.T                       |
| 0.999983 | 0.9997 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H               |
| 0.999983 | 0.9523 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN    |
| 0.999983 | 0.9998 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E        |
| 0.999983 | 0.9999 R.GGNRFEPYANPTK[325.13]R.Y                       |
| 0.999983 | 0.9994 K.HGEAQVK[325.13]IWR.R                           |

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| 0.999983 | 0.9997 R.EAPHVK[325.13]NNAIISLR.K                       |
| 0.999983 | 0.9999 R.TVVTGIEM[147.04]FHK[325.13]SLER.A              |
| 0.999983 | 0.9999 R.TFSWASVTSK[325.13]NLPPSGAVPVTGIPPHVVK.V        |
| 0.999983 | 0.9996 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I       |
| 0.999983 | 0.9999 K.MKDAAIAK[325.13]LANQAADYFGDAFK.Q               |
| 0.999983 | 0.9986 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A          |
| 0.999983 | 0.9996 K.GFGYK[325.13]GSC[160.03]FHR.I                  |
| 0.999983 | 0.9955 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.999983 | 0.9957 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.999983 | 0.9998 K.HQILEQAVEDYAETVHQLSK[325.13]TSR.A              |
| 0.999983 | 0.9997 K.K[325.13]GDVVIVLTGWRPGSGFTNTMR.V               |
| 0.999982 | 0.9999 K.AHLGTALK[325.13]ANPFGGASHAK.G                  |
| 0.999982 | 0.996 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR      |
| 0.999982 | 0.9987 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V          |
| 0.999982 | 0.9991 K.NVTLPVFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999982 | 0.9999 K.AVLFC[160.03]LSEDK[325.13]K.N                  |
| 0.999982 | 0.9997 K.VGINYQPPTVVPGGDLAK[325.13]VQR.A                |
| 0.999982 | 0.9959 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M               |
| 0.999982 | 0.8554 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999982 | 0.9998 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK. |
| 0.999982 | 0.9999 K.AETAALK[325.13]HGEAQVK.I                       |
| 0.999982 | 0.9998 R.K[325.13]LFIGGLSFETDESRL.S                     |
| 0.999982 | 0.9996 R.VK[325.13]GGGHVAQIYAIR.Q                       |
| 0.999982 | 0.9992 K.TVDLKPDPWGK[325.13]GYSR.K                      |
| 0.999982 | 0.8113 R.LLLPGELAK[325.13]HAVSEGTK.A                    |
| 0.999982 | 0.9994 R.LREK[325.13]LQEEMLQR.E                         |
| 0.999981 | 0.9985 K.SPAKPK[325.13]AVKPK.A                          |
| 0.999981 | 0.9999 R.HRPELIEYDK[325.13]LR.K                         |
| 0.999981 | 0.9999 R.VLAEK[325.13]LAAIGEATR.L                       |
| 0.999981 | 0.9998 K.ESYSVYVYK[325.13]VLK.Q                         |
| 0.999981 | 0.9903 K.EITALAPSTMKIK[325.13]IIAPPER.K                 |
| 0.999981 | 0.9993 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVLRL          |
| 0.999981 | 0.9999 K.DELHIVEAEAMNYEGSPIK[325.13]VTLATLK.M           |
| 0.999981 | 0.999 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                   |
| 0.999981 | 0.999 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                   |
| 0.999981 | 0.9809 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.999981 | 0.9996 K.KLEDGPK[325.13]FLK.S                           |
| 0.999981 | 0.9987 R.DALSDLALHFLNK[325.13]MK.I                      |
| 0.99998  | 0.9991 R.HWGGNVLGPK[325.13]SVAR.I                       |
| 0.99998  | 0.9942 R.M[147.04]VNHFAIEFK[325.13]R.K                  |
| 0.99998  | 0.9948 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.99998  | 0.999 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                |
| 0.99998  | 0.9999 K.DVNAAIATIK[325.13]TK.R                         |
| 0.99998  | 0.9999 R.MK[325.13]LNTQEIFDDWAR.K                       |
| 0.99998  | 0.9999 K.SLADELALVDVLEDK[325.13]LK.G                    |
| 0.99998  | 0.9919 R.HQGVMM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA   |
| 0.99998  | 0.9999 R.VSQEHPVVLTK[325.13]FVEGAR.E                    |

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| 0.99998  | 0.9995 | R.ILGLLDAYLK[325.13]TR.T                        |
| 0.99998  | 0.9877 | K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV  |
| 0.99998  | 0.9999 | K.YMNSGPVVAMVWEGLNVVK[325.13]TGR.V              |
| 0.99998  | 0.9998 | K.SVK[325.13]LLQALAQYQNLQEQPR.K                 |
| 0.99998  | 0.9991 | R.LKDLEALLNSK[325.13]EAALSTALSEK.R              |
| 0.99998  | 0.9992 | R.IFAPNHVVAK[325.13]SR.F                        |
| 0.99998  | 0.944  | R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L               |
| 0.99998  | 0.9998 | K.KQGGLGPMNIPLVSDPK[325.13]R.T                  |
| 0.999979 | 0.9996 | R.AK[325.13]HHAISAK.L                           |
| 0.999979 | 0.9971 | R.MVNHFIAEFK[325.13]R.K                         |
| 0.999979 | 0.9945 | R.LK[325.13]LEPHEGLLLR.F                        |
| 0.999979 | 0.9997 | K.THINIVVIGHVDSGK[325.13]STTTGHLYK.C            |
| 0.999979 | 0.9998 | R.FLEGK[325.13]IKPHLMSQELPEDWDKQPVK.V           |
| 0.999979 | 0.9993 | R.HNGTGGK[325.13]SIYGEK.F                       |
| 0.999979 | 0.9997 | K.FAAK[325.13]GEGQLGPAER.A                      |
| 0.999979 | 0.9976 | R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M      |
| 0.999979 | 0.999  | R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTEVK.S    |
| 0.999979 | 0.9997 | R.LLDPEDVDVPQPDEK[325.13]SIITYVSSLYDAMPR.V      |
| 0.999979 | 0.9996 | R.DQHFKV[325.13]IQVK.D                          |
| 0.999979 | 0.9997 | R.LPMNK[325.13]EWPSNLDLR.K                      |
| 0.999979 | 0.9997 | R.K[325.13]YQPNIDVQESIHFLESEFSR.G               |
| 0.999979 | 0.9966 | R.DLTDYLM[147.04]K[325.13]ILTER.G               |
| 0.999979 | 0.9995 | K.IAPSFIVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S |
| 0.999979 | 0.9993 | K.AGAHLQGGAK[325.13]R.V                         |
| 0.999979 | 0.9998 | K.K[325.13]ISSIQSIVPALEIANHR.K                  |
| 0.999979 | 0.9998 | K.K[325.13]ISSIQSIVPALEIANHR.K                  |
| 0.999979 | 0.9993 | R.VFITDDFHDMMMPK[325.13]YLNFKV.G                |
| 0.999979 | 0.9993 | R.DLLDDLKSELTGK[325.13]FEK.L                    |
| 0.999979 | 0.9257 | K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I          |
| 0.999979 | 0.9996 | R.RYQK[325.13]STELLIR.K                         |
| 0.999979 | 0.9992 | R.GPVLQLHDLK[325.13]R.E                         |
| 0.999979 | 0.998  | K.LHIIEVGPPTGNQPFPPK[325.13]K.A                 |
| 0.999978 | 0.9999 | R.GLVMVK[325.13]PGSIKPHQK.V                     |
| 0.999978 | 0.9887 | R.K[325.13]DGNASGTTLEALDC[160.03]ILPPTRPDKPLR.  |
| 0.999978 | 0.9997 | R.GAVGALLVYDIK[325.13]HLTYENVER.W               |
| 0.999978 | 0.9985 | K.KTESHHK[325.13]AK.G                           |
| 0.999978 | 0.9997 | R.RGNVAGDSK[325.13]NDPPMEAAGFTAQVILNHPGQISA     |
| 0.999978 | 0.9998 | R.VTQKSYK[325.13]VSTSGPR.A                      |
| 0.999978 | 0.9949 | R.K[325.13]DLYANTVLSGGTTMYPGIADR.M              |
| 0.999978 | 0.9991 | R.LLQDSVDFSLADAINTEFK[325.13]NTR.T              |
| 0.999978 | 0.9955 | R.YISPDQLADLYK[325.13]SFIK.D                    |
| 0.999978 | 0.6761 | R.YISPDQLADLYK[325.13]SFIK.D                    |
| 0.999978 | 0.9996 | R.K[325.13]VSQPIEGHAASFAQFK.M                   |
| 0.999978 | 0.9996 | R.K[325.13]VSQPIEGHAASFAQFK.M                   |
| 0.999978 | 0.9995 | K.TM[147.04]QNVK[325.13]HPVTGQFLYQDSNWASK.V     |
| 0.999978 | 0.9996 | R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V             |
| 0.999978 | 0.9992 | R.ETAQAIK[325.13]GMHIR.K                        |

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| 0.999978 | 0.9999 K.VHAPGLNLSGVGGK[325.13]MQVGGDGVK.V               |
| 0.999978 | 0.9999 R.DYQGPKL[325.13]EHEVTIFVR.R                      |
| 0.999978 | 0.9999 K.LTSLALDQK[325.13]NVNAGGHK.L                     |
| 0.999978 | 0.9999 K.AGK[325.13]LDPHLVLDQLR.C                        |
| 0.999978 | 0.9986 R.LAHYNK[325.13]R.S                               |
| 0.999977 | 0.999 R.HWGGNVLGPK[325.13]SVAR.I                         |
| 0.999977 | 0.9993 R.HK[325.13]NMSVHLSPC[160.03]FR.D                 |
| 0.999977 | 0.9996 R.FDASFFGVHPK[325.13]QAHTMDPQLR.L                 |
| 0.999977 | 0.9998 K.IYK[325.13]IGQGYLIK.D                           |
| 0.999977 | 0.9999 R.DVFTK[325.13]GYGFGLIK.L                         |
| 0.999977 | 0.9974 R.APQC[160.03]LGK[325.13]FIEIAAR.K                |
| 0.999977 | 0.9996 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.  |
| 0.999977 | 0.9999 K.TLK[325.13]GLNSESMTETLKR.A                      |
| 0.999977 | 0.9994 K.VVLAYEPVWAIGTGK[325.13]TATPQQAQEVHEK.L          |
| 0.999977 | 0.9985 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R   |
| 0.999977 | 0.6112 R.HQGVMMVGMGQKDSYVGDEAQSK[325.13]R.G              |
| 0.999977 | 0.9973 K.GLVLGPIHK[325.13]NQK.D                          |
| 0.999976 | 0.9991 R.KPAGAAK[325.13]KPK.K                            |
| 0.999976 | 0.9932 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                 |
| 0.999976 | 0.9996 K.VGINYQPPTVVPGGDLAK[325.13]VQR.A                 |
| 0.999976 | 0.9998 R.MATEVAADALGEEWK[325.13]GYVVR.I                  |
| 0.999976 | 0.9999 R.ENEVLEAWK[325.13]SLLDAC[160.03]ESR.R            |
| 0.999976 | 0.9995 R.K[325.13]MC[160.03]LFAGFQR.K                    |
| 0.999976 | 0.9958 R.FLEQQNK[325.13]ILLAELEQLK.G                     |
| 0.999976 | 0.9992 R.LDSQK[325.13]HIDFSLR.S                          |
| 0.999976 | 0.9999 K.FVIHC[160.03]NSPVWGADK[325.13]C[160.03]EELLEK.T |
| 0.999976 | 0.9999 R.VYLFTIK[325.13]KGILGQHQFLEGPEGIENTR.F           |
| 0.999976 | 0.9999 K.LDVGK[325.13]VLQASVLDDWFPLQGGQGQVHLR.L          |
| 0.999976 | 0.9995 K.GATYGK[325.13]PVHHGVNQLK.F                      |
| 0.999976 | 0.9997 R.TPHVQAVQGPLGSPPK[325.13]R.G                     |
| 0.999976 | 0.9995 K.KLEDGPK[325.13]FLK.S                            |
| 0.999976 | 0.9984 R.LVNHFVEEFK[325.13]R.K                           |
| 0.999976 | 0.9999 K.LDVGK[325.13]VLQASVLDDWFPLQGGQGQVHLR.L          |
| 0.999975 | 0.9996 R.LQAEIEGLK[325.13]GQR.A                          |
| 0.999975 | 0.9992 R.TMPVEQVFAK[325.13]NFR.V                         |
| 0.999975 | 0.9998 K.NK[325.13]GLWVPEGQR.A                           |
| 0.999975 | 0.9993 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V               |
| 0.999975 | 0.9999 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y              |
| 0.999975 | 0.9995 R.K[325.13]LAVNMVPFPR.L                           |
| 0.999975 | 0.9999 R.TATESFASDPILYRPVAVALDTK[325.13]GPEIR.T          |
| 0.999975 | 0.9962 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R       |
| 0.999975 | 0.9992 K.AGAHLQGGAK[325.13]R.V                           |
| 0.999975 | 0.9991 R.ETAQAIK[325.13]GMHIR.K                          |
| 0.999975 | 0.9991 R.ETAQAIK[325.13]GMHIR.K                          |
| 0.999975 | 0.999 K.TAWLDGK[325.13]HVVFGK.V                          |
| 0.999975 | 0.9455 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E        |
| 0.999975 | 0.9995 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                |

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| 0.999975 | 0.9996 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I       |
| 0.999975 | 0.9928 K.ADKDYHFK[325.13]VDNDENEHQSLR.T                 |
| 0.999975 | 0.9984 R.SVPHLQK[325.13]VFDR.Y                          |
| 0.999975 | 0.9936 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.999975 | 0.9935 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.999975 | 0.9998 R.K[325.13]LTWVNEGLVDGWDDPRFPTVR.G               |
| 0.999974 | 0.9996 R.RLEEQAQHK[325.13]ADIEER.L                      |
| 0.999974 | 0.9999 K.FVIHC[160.03]NSPVWGADKC[160.03]EELLEK[325.13]T |
| 0.999974 | 0.9985 K.NVTLPVFK[325.13]APIRPDIVNFVHTNLR.K             |
| 0.999974 | 0.9997 K.SYK[325.13]VSTSGPR.A                           |
| 0.999974 | 0.9995 K.EITALAPSTM[147.04]K[325.13]IK.I                |
| 0.999974 | 0.9996 R.YLAEK[325.13]YEWDAEAR.K                        |
| 0.999974 | 0.997 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M        |
| 0.999974 | 0.997 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M        |
| 0.999974 | 0.998 K.NQK[325.13]DDVAQTDLLQIDPNFGSK.E                 |
| 0.999974 | 0.9999 R.EASLGEASK[325.13]LQQFLR.D                      |
| 0.999974 | 0.9999 R.TLQYK[325.13]LLEPVLLLGK.E                      |
| 0.999974 | 0.9983 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R  |
| 0.999974 | 0.9996 K.MPK[325.13]FSMPGFK.A                           |
| 0.999974 | 0.9981 R.ALMLQGVDLLADAVATMGPK[325.13]GR.T               |
| 0.999974 | 0.9996 K.RGEIIAK[325.13]QGGGGGGGSPGIER.M                |
| 0.999974 | 0.9996 R.TAPDLLPHK[325.13]PLPASAYIEDGR.F                |
| 0.999974 | 0.9996 K.APK[325.13]ISMPDVLHLK.G                        |
| 0.999974 | 0.9999 R.VLSGEFQIVNPHLLK[325.13]DLTER.G                 |
| 0.999974 | 0.9997 K.FEDENFILK[325.13]HTGPGILSMANAGPNTNGSQFFIC[16   |
| 0.999974 | 0.9995 R.RYQK[325.13]STELLIR.K                          |
| 0.999974 | 0.9996 R.GTK[325.13]VILHLKEDQTEYLEER.R                  |
| 0.999973 | 0.9992 R.KVDWLTEK[325.13]MHAR.D                         |
| 0.999973 | 0.9994 K.M[147.04]LETK[325.13]WSLLQQQK.T                |
| 0.999973 | 0.9994 R.VETGVLK[325.13]PGMVVTFAPVNVTTTEVK.S            |
| 0.999973 | 0.9999 K.VVLSK[325.13]LPIGDVATQYFADR.D                  |
| 0.999973 | 0.9996 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V               |
| 0.999973 | 0.9998 K.LYEEK[325.13]TGNAWHSK.N                        |
| 0.999973 | 0.9996 R.VLEALLPLK[325.13]GLEER.V                       |
| 0.999973 | 0.9996 R.C[160.03]QK[325.13]IC[160.03]DQWDALGSLTHSR.R   |
| 0.999973 | 0.9996 R.K[325.13]HGLEVIYMIEPIDEYC[160.03]VQQLK.E       |
| 0.999973 | 0.9994 R.NLGSIAK[325.13]MLQHAASNK.M                     |
| 0.999973 | 0.9893 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R      |
| 0.999972 | 0.9956 R.VIHLNLPHSGYSDSAVLK[325.13]LAEPYGK.I            |
| 0.999972 | 0.979 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPPSGK.L     |
| 0.999972 | 0.9997 K.DSYVGDEAQSK[325.13]R.G                         |
| 0.999972 | 0.9998 K.NK[325.13]ITITNDQNR.L                          |
| 0.999972 | 0.9813 K.EITALAPSTMKIK[325.13]IIAPPER.K                 |
| 0.999972 | 0.977 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G             |
| 0.999972 | 0.6097 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999972 | 0.9995 K.VLK[325.13]QVHPDTGISSK.A                       |
| 0.999972 | 0.9996 R.KATGPPVSELITK[325.13]AVAASK.E                  |

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| 0.999972 | 0.9999 | R.LAAIVAK[325.13]QVLLGR.K                        |
| 0.999972 | 0.9996 | R.SIVDYK[325.13]PNLDLLEQQHQLIQEALIFDNK.H         |
| 0.999972 | 0.9832 | K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV    |
| 0.999972 | 0.9995 | K.VLK[325.13]QVHPDTGISSK.A                       |
| 0.999972 | 0.9999 | R.LAHEVGWK[325.13]YQAVTATLEEK.R                  |
| 0.999972 | 0.9993 | R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.999972 | 0.9993 | K.KAKK[325.13]PAAAAGAK.K                         |
| 0.999972 | 0.9996 | K.KAEGGGGGGRPGAPAAAGDGK[325.13]TEQK.G            |
| 0.999972 | 0.9991 | K.AGAHLQGGAK[325.13]R.V                          |
| 0.999972 | 0.9996 | R.IC[160.03]SKPVVLPK[325.13]GPESESEDHR.A         |
| 0.999972 | 0.9991 | R.LREK[325.13]LQEEMLQR.E                         |
| 0.999972 | 0.9996 | K.KGGSWIQEINVAEK[325.13]NWYPR.Q                  |
| 0.999971 | 0.9992 | R.GFGFTYATVEEVDAAMNARPHK[325.13]VDGR.V           |
| 0.999971 | 0.9996 | R.SGK[325.13]YDLDFK.S                            |
| 0.999971 | 0.9991 | K.FIIPNVVK[325.13]YSPNC[160.03]K.L               |
| 0.999971 | 0.9999 | R.IIAQK[325.13]IYGADDIELLPEAQHK.A                |
| 0.999971 | 0.9996 | R.DGSIDLVINLPNNNTK[325.13]FVHDNYVIR.R            |
| 0.999971 | 0.9996 | R.K[325.13]MFTLLDVVNR.K                          |
| 0.999971 | 0.9978 | K.GLVLGPIHK[325.13]NQK.D                         |
| 0.999971 | 0.9998 | R.FLEQQNK[325.13]ILLAELEQLKGQ GK.S               |
| 0.999971 | 0.9996 | K.AAKPK[325.13]VVKPK.K                           |
| 0.999971 | 0.9993 | K.GFGYK[325.13]GSC[160.03]FHR.I                  |
| 0.999971 | 0.9997 | K.MKETAENYLGHTAK[325.13]NAVITVPAYFNDSQR.Q        |
| 0.99997  | 0.9999 | K.KNPIAK[325.13]IHSDLAER.G                       |
| 0.99997  | 0.9995 | R.WLPAGDALLQM[147.04]ITIHLPSVTAQK[325.13]YR.C    |
| 0.99997  | 0.9969 | R.K[325.13]EVKGDLEN AFLNLVQC[160.03]IQNKPLYFADR. |
| 0.99997  | 0.9981 | K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V  |
| 0.99997  | 0.9983 | R.GAEVHLPWNHDFTK[325.13]MEYDGILIAGGPGNPALAI      |
| 0.99997  | 0.999  | R.HNGTGGK[325.13]SIYGEK.F                        |
| 0.99997  | 0.9802 | K.EITALAPSTMKIK[325.13]IIAPPER.K                 |
| 0.99997  | 0.9996 | K.MPILGLGTWK[325.13]SPPGQVTEAVK.V                |
| 0.99997  | 0.9988 | R.LK[325.13]VPPAINQFTQALDR.Q                     |
| 0.99997  | 0.9996 | R.SHAQK[325.13]NENAR.Q                           |
| 0.99997  | 0.9999 | K.GRPC[160.03]K[325.13]IVEMSTSK.T                |
| 0.99997  | 0.9964 | K.GLVLGPIHK[325.13]NQK.D                         |
| 0.999969 | 0.9996 | R.LVSNHSLHETSSVFVDSLTK[325.13]ATC[160.03]APQHGA  |
| 0.999969 | 0.9994 | R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H             |
| 0.999969 | 0.9994 | R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H             |
| 0.999969 | 0.9998 | K.HKSDFGK[325.13]FVLSSGK.F                       |
| 0.999969 | 0.9998 | R.IGPYQPNVPVGIDYVIPK[325.13]TGFYC[160.03]K.L     |
| 0.999969 | 0.9996 | R.LLLEAQAATGFLDPVK[325.13]GER.L                  |
| 0.999969 | 0.9972 | K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI   |
| 0.999969 | 0.9995 | R.LGQSDPAPLQHQM DIYQK[325.13]R.C                 |
| 0.999969 | 0.9993 | R.K[325.13]MC[160.03]LFAGFQR.K                   |
| 0.999969 | 0.9996 | R.LEK[325.13]HELIEFR.R                           |
| 0.999969 | 0.9976 | R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E           |
| 0.999969 | 0.9963 | K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |

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| 0.999969 | 0.999 K.AGAHLQGGAK[325.13]R.V                            |
| 0.999969 | 0.9988 R.GPVLQLHDLK[325.13]R.E                           |
| 0.999969 | 0.9999 K.YGIIC[160.03]MEDLIHEIYTVGK[325.13]R.F           |
| 0.999968 | 0.9978 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L       |
| 0.999968 | 0.9994 K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK[325.13]YHH      |
| 0.999968 | 0.9996 K.SK[325.13]FADLSEAANR.N                          |
| 0.999968 | 0.999 R.TMPVEQVFAK[325.13]NFR.V                          |
| 0.999968 | 0.9973 R.APQC[160.03]LGK[325.13]FIEIAAR.K                |
| 0.999968 | 0.9996 R.GLFIIDDK[325.13]GILR.Q                          |
| 0.999968 | 0.9996 R.RPISADSAIMNPASK[325.13]VIALK.A                  |
| 0.999968 | 0.9992 K.KAK[325.13]KPAAAAGAK.K                          |
| 0.999968 | 0.9998 K.KPLPDHVSIVEPK[325.13]DEILPTTPISEQK.G            |
| 0.999968 | 0.9999 R.RGPFELEAFYSDPQGVPEAK[325.13]IGR.F               |
| 0.999967 | 0.9992 K.GFGYK[325.13]GSC[160.03]FHR.I                   |
| 0.999967 | 0.999 K.M[147.04]LETK[325.13]WSLLQQQK.T                  |
| 0.999967 | 0.9989 K.SIYGEK[325.13]FEDENFILK.H                       |
| 0.999967 | 0.9992 K.GFGYK[325.13]GSC[160.03]FHR.I                   |
| 0.999967 | 0.9818 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999966 | 0.9996 K.VDIDAPDVDVHGPDWHLK[325.13]MPK.M                 |
| 0.999966 | 0.9995 R.LK[325.13]STC[160.03]IYGGAPK.G                  |
| 0.999966 | 0.9998 R.VINEPTAAALAYGLDK[325.13]SEDK.V                  |
| 0.999966 | 0.9996 R.TM[147.04]PVEQVFAK[325.13]NFR.V                 |
| 0.999966 | 0.9927 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S         |
| 0.999966 | 0.9997 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D          |
| 0.999966 | 0.9995 R.YAIC[160.03]SALAASALPALVM[147.04]SK[325.13]GHR. |
| 0.999966 | 0.9995 R.YAIC[160.03]SALAASALPALVMSK[325.13]GHR.I        |
| 0.999965 | 0.9909 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999965 | 0.9945 R.VIHLSNLP HSGYSDSAVLK[325.13]LAEPYGK.I           |
| 0.999965 | 0.9999 K.FHHK[325.13]MVDNR.G                             |
| 0.999965 | 0.9993 R.HIADLAGNSEVILPVPFNVINGGSHAGNK[325.13]LAM[1      |
| 0.999965 | 0.9995 K.FYEAFSK[325.13]NLK.L                            |
| 0.999965 | 0.9996 R.K[325.13]LFIGGLSFETTDESLR.S                     |
| 0.999965 | 0.9993 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V                |
| 0.999965 | 0.9705 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G             |
| 0.999965 | 0.9995 R.DVTPGELLK[325.13]AEIIDQDLYER.L                  |
| 0.999965 | 0.9996 R.EVTVPVFYPTTEK[325.13]VWLEVEPVGM[147.04]LK.E     |
| 0.999965 | 0.9998 R.DPQFQK[325.13]LQQWYR.E                          |
| 0.999965 | 0.9996 R.K[325.13]LFIGGLSFETTDESLR.S                     |
| 0.999965 | 0.9996 R.K[325.13]LFIGGLSFETTDESLR.S                     |
| 0.999965 | 0.9998 R.VHGPGIQSGTTNK[325.13]PNK.F                      |
| 0.999965 | 0.9996 R.LPSGNHMK[325.13]ESR.E                           |
| 0.999965 | 0.9998 K.IAILTC[160.03]PFEPKPK[325.13]TK.H               |
| 0.999965 | 0.9998 R.SSGPGAGLC[160.03]LFPLDK[325.13]VHAK.M           |
| 0.999964 | 0.6507 R.LLLPGELAK[325.13]HAVSEGK.A                      |
| 0.999964 | 0.9999 K.ITK[325.13]FENAFLSHVVSQHQALLGTIR.A              |
| 0.999964 | 0.9994 R.K[325.13]FGYVDFESAEDLEK.A                       |
| 0.999964 | 0.9999 K.AMQDAEVSK[325.13]SDIGEVLVGGMTR.M                |

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| 0.999964 | 0.9994 R.VFSGLVSTGLK[325.13]VR.I                          |
| 0.999964 | 0.9969 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L              |
| 0.999964 | 0.9994 K.SK[325.13]DDQVTVIGAGVTLHEALAAELLK.K              |
| 0.999964 | 0.9994 R.VLFPATGYLSIVWK[325.13]TLAR.A                     |
| 0.999964 | 0.9983 K.IK[325.13]GEHPGLSIGDVAK.K                        |
| 0.999964 | 0.9967 R.LEKPAK[325.13]YDDIKK.V                           |
| 0.999964 | 0.9906 R.LK[325.13]LEPHEGLLLR.F                           |
| 0.999964 | 0.9974 K.GLVLGPIHKNQK[325.13]DDVAQTDLLQIDPNFGSK.E         |
| 0.999963 | 0.9998 K.TVIGELPPASSGSALAANVC[160.03]K[325.13]K.I         |
| 0.999963 | 0.9999 K.WPK[325.13]ETVKPVEVEEGESVVLPC[160.03]NPPPSAEI    |
| 0.999963 | 0.9991 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.999963 | 0.9999 K.AASLK[325.13]SNYNLPMHK.M                         |
| 0.999963 | 0.9994 R.VTYK[325.13]NVPNWHR.D                            |
| 0.999963 | 0.9999 K.GHQK[325.13]SNGEFWDPGR.V                         |
| 0.999963 | 0.9995 K.VSYFPTVPGVYIVSTK[325.13]FADEHVPGSPFTVK.I         |
| 0.999963 | 0.9998 R.TSSAQVEGGVHSLHSYEK[325.13]R.L                    |
| 0.999963 | 0.9984 R.GLDISNVK[325.13]HVINFDLPSDIEEYVHR.I              |
| 0.999963 | 0.9996 K.HNQLPLVIEFTEQTAPK[325.13]IFGGEIK.T               |
| 0.999962 | 0.9976 K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V    |
| 0.999962 | 0.9995 R.SFPFVSK[325.13]TLGVDFIDVATK.V                    |
| 0.999962 | 0.9998 R.TPC[160.03]EEILVK[325.13]HVGSR.L                 |
| 0.999962 | 0.9991 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S    |
| 0.999962 | 0.9998 R.VYLFTIKK[325.13]GILGQHGFLEGPEGIENTR.F            |
| 0.999962 | 0.963 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I              |
| 0.999962 | 0.9972 K.K[325.13]AKKPAAATVTK.K                           |
| 0.999962 | 0.9998 K.VHLDK[325.13]AQQNNVEHK.V                         |
| 0.999962 | 0.9987 K.TAWLDGK[325.13]HVVFGK.V                          |
| 0.999962 | 0.9975 R.LLIHQSLAGGIIGVK[325.13]GAK.I                     |
| 0.999961 | 0.9994 R.YLAEK[325.13]YEWDAEAR.K                          |
| 0.999961 | 0.9996 K.ESYSVYVYK[325.13]VLK.Q                           |
| 0.999961 | 0.9986 K.TFVNITPAEVGVLVGK[325.13]DR.S                     |
| 0.999961 | 0.9993 R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V                |
| 0.999961 | 0.9993 R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V                |
| 0.999961 | 0.9992 R.K[325.13]LAVNMVPFPR.L                            |
| 0.999961 | 0.9995 R.LEK[325.13]HELIEFR.R                             |
| 0.999961 | 0.9962 R.KVESLQEEIAFLK[325.13]K.L                         |
| 0.999961 | 0.9991 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I         |
| 0.999961 | 0.998 R.K[325.13]PLVIAEDVDGEALSTLVLR.L                    |
| 0.999961 | 0.9967 K.VK[325.13]GLVLGPIHK.N                            |
| 0.99996  | 0.9996 R.AIIPC[160.03]IK[325.13]GYDVIAQAQSGTGK.T          |
| 0.99996  | 0.9996 R.K[325.13]LAQQYYLVYQEPIPTAQLVQR.V                 |
| 0.99996  | 0.9999 R.HESGASIK[325.13]IDEPLEGSEDR.I                    |
| 0.99996  | 0.9994 K.TVDGPSGK[325.13]LWR.D                            |
| 0.99996  | 0.9973 R.TLLIK[325.13]TVETR.D                             |
| 0.99996  | 0.9992 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                 |
| 0.99996  | 0.9845 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R        |
| 0.99996  | 0.9939 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y              |



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| 0.99996  | 0.9987 K.AGAHLQGGAK[325.13]R.V                          |
| 0.99996  | 0.9999 K.YGK[325.13]AGEVFIHK.D                          |
| 0.99996  | 0.9999 K.EAGELKPEEEITVGPVQK[325.13]LVTEMGTATQSALSSSF    |
| 0.99996  | 0.9975 R.LAHYNK[325.13]R.S                              |
| 0.99996  | 0.9998 K.K[325.13]QLLC[160.03]GAAIGTHEDDKYR.L           |
| 0.999959 | 0.9999 K.VLDFEHFLPMLQTVAK[325.13]NK.D                   |
| 0.999959 | 0.9904 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR     |
| 0.999959 | 0.9999 K.AQAYQTGK[325.13]DISTNYYASQK.K                  |
| 0.999959 | 0.9997 R.DIM[147.04]LATGK[325.13]LSPDAIPGK.W            |
| 0.999959 | 0.9984 R.SEGVVAVLLTK[325.13]K.S                         |
| 0.999959 | 0.9992 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T               |
| 0.999959 | 0.9984 R.SLDLDGIIAEVK[325.13]AQYEEMAK.C                 |
| 0.999959 | 0.9999 K.LMELHGEGSSSGK[325.13]ATGDETGAK.V               |
| 0.999959 | 0.9995 R.VLADPSDDTK[325.13]GFFDPNTHENLTYSR.Q            |
| 0.999959 | 0.9999 R.NLLSVAYK[325.13]NVIGAR.R                       |
| 0.999959 | 0.96 K.VK[325.13]DALEFWLQAGVDGFQVR.D                    |
| 0.999959 | 0.9997 R.VHK[325.13]ISNVNK.A                            |
| 0.999959 | 0.9998 K.ISMPDFDLHLK[325.13]GPK.V                       |
| 0.999959 | 0.9998 K.ISMPDFDLHLK[325.13]GPK.V                       |
| 0.999959 | 0.9994 K.APK[325.13]ISMPDFDLHLK.G                       |
| 0.999959 | 0.9916 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                 |
| 0.999958 | 0.9972 R.LVNHFVEEFK[325.13]R.K                          |
| 0.999958 | 0.9998 K.RC[160.03]EAFGWHAIIVDGHSEELC[160.03]K[325.13]. |
| 0.999958 | 0.9994 R.TAPDLLPHK[325.13]PLPASAYIEDGRFDLSMPHVQDPSLV    |
| 0.999958 | 0.9993 K.SK[325.13]GIAYIEFK.T                           |
| 0.999958 | 0.9994 K.GLVQALQTK[325.13]VTQQGLK.M                     |
| 0.999958 | 0.9985 K.TFVNITPAEVGVLVGK[325.13]DR.S                   |
| 0.999958 | 0.9994 K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q          |
| 0.999958 | 0.9983 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T               |
| 0.999958 | 0.9994 R.GVLK[325.13]EYGVKVLGTSVESIMATEDR.Q             |
| 0.999958 | 0.9915 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999958 | 0.9995 R.WQLK[325.13]ANEALR.L                           |
| 0.999958 | 0.9943 K.LAQMFSDMVLK[325.13]DGFQPSR.S                   |
| 0.999958 | 0.999 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S   |
| 0.999958 | 0.9994 K.NQTAEKEEFEHQK[325.13]ELEK.V                    |
| 0.999958 | 0.9993 K.EGKPLLK[325.13]AVMR.R                          |
| 0.999958 | 0.9995 K.VDWLTEK[325.13]MHAR.D                          |
| 0.999958 | 0.9994 K.KAEGGGGGGRPGAPAAAGDGK[325.13]TEQK.G            |
| 0.999958 | 0.9998 K.AC[160.03]VK[325.13]TYHYHC[160.03]GVQDK.A      |
| 0.999958 | 0.9994 K.KGGSWIQEINVAEK[325.13]NWYPR.Q                  |
| 0.999957 | 0.9996 R.MAQEVLTHLK[325.13]EHPDAWTR.V                   |
| 0.999957 | 0.9999 R.IESLSSQLSNLQK[325.13]ESR.A                     |
| 0.999957 | 0.9991 K.KLEDGPK[325.13]FLK.S                           |
| 0.999957 | 0.9994 K.KQGGGLGPM[147.04]NIPLVSDPK[325.13]R.T          |
| 0.999957 | 0.9995 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H               |
| 0.999957 | 0.9997 R.LAAFGQLHK[325.13]VLGMDPLPSK.M                  |
| 0.999956 | 0.9875 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                |

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| 0.999956 | 0.9994 K.K[325.13]HLEINPDHSIIETLR.Q                       |
| 0.999956 | 0.9994 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                 |
| 0.999956 | 0.9993 R.LQAEIEGLK[325.13]GQR.A                           |
| 0.999956 | 0.9998 R.GC[160.03]ITIIGGGDTATC[160.03]C[160.03]AK[325.13 |
| 0.999956 | 0.9992 R.K[325.13]VSQPIEGHAASFAQFK.M                      |
| 0.999956 | 0.9991 R.K[325.13]LAVNMVFPFR.L                            |
| 0.999956 | 0.9998 K.GLHVVEVTYDDVPIPNPSPFK[325.13]VAVTEGC[160.03]QI   |
| 0.999956 | 0.9998 K.ILES DRK[325.13]EPLFGISTGNLITGLAAGAK.T           |
| 0.999956 | 0.9999 R.RAAATQPD AK[325.13]DTPDEPWAFPAR.E                |
| 0.999956 | 0.9996 K.ARPFPDGLAEDIDK[325.13]GEVSAR.Q                   |
| 0.999956 | 0.9994 R.C[160.03]QK[325.13]IC[160.03]DQWDALGSLTHSR.R     |
| 0.999956 | 0.9982 R.VSFELFADKVPK[325.13]TAENFR.A                     |
| 0.999956 | 0.9997 R.YFPTQALNFAFKDK[325.13]YK.Q                       |
| 0.999956 | 0.9761 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                   |
| 0.999956 | 0.969 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                    |
| 0.999956 | 0.9995 R.LPSGNHMK[325.13]ESR.E                            |
| 0.999956 | 0.9994 R.HDK[325.13]VEDALNLKEEFDR.L                       |
| 0.999955 | 0.9993 R.RLEEQAQHK[325.13]ADIEER.L                        |
| 0.999955 | 0.9996 R.VTQKSYK[325.13]VSTSGPR.A                         |
| 0.999955 | 0.9995 R.LK[325.13]VGLQVAVK.A                             |
| 0.999955 | 0.9943 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M                 |
| 0.999955 | 0.9995 K.INQVFHGSC[160.03]ITEGNETLK[325.13]TLIK.L         |
| 0.999955 | 0.9992 R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V                |
| 0.999955 | 0.9992 K.NAQK[325.13]SNQNGKDSKPSSTPR.S                    |
| 0.999955 | 0.9996 K.KPAEK[325.13]KPTTEEK.K                           |
| 0.999955 | 0.9993 R.FHVEEEGK[325.13]GK.D                             |
| 0.999955 | 0.9993 R.FHVEEEGK[325.13]GK.D                             |
| 0.999955 | 0.9999 R.LEHAAK[325.13]QAAASATQTIAAAQHAAS TP.K.A          |
| 0.999955 | 0.9998 K.C[160.03]NEIINWLDK[325.13]NQTAEEKEFEHQK.E        |
| 0.999955 | 0.9993 K.LLLQGEADQSLTFIDK[325.13]AMHGELQK.A               |
| 0.999955 | 0.9999 R.IEPHTGLLLSVQK[325.13]R.S                         |
| 0.999954 | 0.9981 R.IFAPNHVVAK[325.13]SR.F                           |
| 0.999954 | 0.9993 R.FTLTGLK[325.13]PD TTYDIK.V                       |
| 0.999954 | 0.9996 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG    |
| 0.999954 | 0.9696 K.EITALAPSTMKIK[325.13]IIAPPER.K                   |
| 0.999954 | 0.6638 R.ADIK[325.13]EMGLSLQWLYSAR.G                      |
| 0.999954 | 0.9999 R.VK[325.13]ATPMP SRPSTTPFIDK.K                    |
| 0.999954 | 0.9995 K.SAFLC[160.03]GVMK[325.13]TYR.Q                   |
| 0.999954 | 0.9999 K.HVPGGGNVQIQNK[325.13]K.V                         |
| 0.999954 | 0.9991 R.VTYK[325.13]NVPNWHR.D                            |
| 0.999954 | 0.9991 R.VTYK[325.13]NVPNWHR.D                            |
| 0.999954 | 0.9999 R.LK[325.13]HGDVITIIDR.S                           |
| 0.999954 | 0.9993 K.HSQFIGYPITLYLEK[325.13]ER.E                      |
| 0.999954 | 0.9941 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPMDQK.    |
| 0.999954 | 0.999 K.YEELQSLAGK[325.13]HGDDLRR.T                       |
| 0.999954 | 0.9863 R.GVLK[325.13]VFLENVIR.D                           |
| 0.999953 | 0.9999 R.TSTQK[325.13]HTHLAVSFGR.S                        |

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| 0.999953 | 0.9997 R.GNVAGDSK[325.13]NDPPM[147.04]EAAGFTAQVIILNHI   |
| 0.999953 | 0.9999 R.DHC[160.03]VAHK[325.13]LFNNLK.-                |
| 0.999953 | 0.9993 R.GELAIK[325.13]DANAK.L                          |
| 0.999953 | 0.9998 K.LTFDSSFSPNTGK[325.13]K.N                       |
| 0.999953 | 0.9993 R.GELAIKDANAK[325.13]LSELEAALQR.A                |
| 0.999953 | 0.9994 K.K[325.13]GWLYYEAGQR.F                          |
| 0.999953 | 0.9998 R.C[160.03]VLLSNLSSTSHVPEVDPGSAELQK[325.13]VLQG  |
| 0.999953 | 0.9992 R.LK[325.13]LLLPWLEAR.I                          |
| 0.999953 | 0.9997 K.GGHGAASPSEK[325.13]GAHPSGGADDVAK.K             |
| 0.999953 | 0.9999 R.RWDQTADQTPGATPK[325.13]K.L                     |
| 0.999953 | 0.9999 K.TGNAWHSK[325.13]NFTK.Y                         |
| 0.999953 | 0.9983 K.HGEAQVK[325.13]IWR.R                           |
| 0.999953 | 0.999 R.QLFHPEQLITGK[325.13]EDAANNYAR.G                 |
| 0.999953 | 0.8973 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999953 | 0.9957 K.ALESPERPFLAILGGAK[325.13]VADK.I                |
| 0.999953 | 0.9964 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I               |
| 0.999952 | 0.9998 K.FLK[325.13]HWDHLTQVK.K                         |
| 0.999952 | 0.9996 R.GITGVDLFGTTDAVVK[325.13]HVLEGHDR.G             |
| 0.999952 | 0.9999 K.GVFTK[325.13]ELPSGK.K                          |
| 0.999952 | 0.9992 R.GIYAYGF EK[325.13]PSAIQQR.A                    |
| 0.999952 | 0.9999 K.VELEAK[325.13]VDALNDEINFLR.T                   |
| 0.999952 | 0.9999 K.LLLQVQHASK[325.13]QITADK.Q                     |
| 0.999952 | 0.9996 R.YM[147.04]AQGK[325.13]HIGK.V                   |
| 0.999952 | 0.9993 K.KAEVEGK[325.13]DLPEHAVLK.M                     |
| 0.999952 | 0.9999 K.DHFTK[325.13]LAVEAVLR.L                        |
| 0.999951 | 0.9993 K.SLVSK[325.13]GTLVQTK.G                         |
| 0.999951 | 0.9947 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE     |
| 0.999951 | 0.9992 R.IAAYLFK[325.13]GNNR.W                          |
| 0.999951 | 0.9984 R.K[325.13]LDYGQHV VAGTPGR.V                     |
| 0.999951 | 0.9999 K.LK[325.13]DYAFIHFDER.D                         |
| 0.999951 | 0.9991 R.EHSSWDLVGLEK[325.13]WTEYR.V                    |
| 0.999951 | 0.9995 K.SVK[325.13]LLQALAQYQNLQEQPR.K                  |
| 0.999951 | 0.9856 R.GVLK[325.13]VFLENVIR.D                         |
| 0.999951 | 0.9941 K.GLVLGPIHK[325.13]NQK.D                         |
| 0.999951 | 0.9873 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.999951 | 0.9999 K.KPGSK[325.13]NFQNI FPPSATLHLSNIPPSVSEEDLK.V    |
| 0.999951 | 0.9991 K.K[325.13]HSQFIGYPITLFVEK.K                     |
| 0.99995  | 0.9999 R.VTAQK[325.13]QVLLSLKGSQTLTV C[160.03]PGSVQPLSS |
| 0.99995  | 0.9998 R.DFLLK[325.13]PELLR.A                           |
| 0.99995  | 0.9952 R.NLQNLLILTAIK[325.13]ADR.T                      |
| 0.99995  | 0.9953 K.LHIIEVGTPPTGNQPF PK[325.13]K.A                 |
| 0.99995  | 0.9992 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I       |
| 0.99995  | 0.9994 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E        |
| 0.999949 | 0.9996 R.HAK[325.13]WFQAR.A                             |
| 0.999949 | 0.9993 K.VEAK[325.13]FINYVK.N                           |
| 0.999949 | 0.994 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M        |
| 0.999949 | 0.9994 R.TM[147.04]PVEQVFAK[325.13]NFR.V                |

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| 0.999949 | 0.9882 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M                |
| 0.999949 | 0.9982 K.ANEVISK[325.13]LYAVHQEGNK.N                     |
| 0.999949 | 0.9993 K.KGATLK[325.13]ITLDNAYMEK.C                      |
| 0.999949 | 0.9999 R.AK[325.13]ELLGQGLLLR.S                          |
| 0.999949 | 0.9993 K.KAASGEAKPK[325.13]AK.K                          |
| 0.999949 | 0.999 K.FHGTVK[325.13]AENGK.L                            |
| 0.999949 | 0.9995 K.ADK[325.13]DYHFK.V                              |
| 0.999949 | 0.9979 R.VSFELFADKVPK[325.13]TAENFR.A                    |
| 0.999948 | 0.9992 R.RLEEQAQHK[325.13]ADIEER.L                       |
| 0.999948 | 0.9992 R.HLYTK[325.13]DIDIHEVR.I                         |
| 0.999948 | 0.9939 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M        |
| 0.999948 | 0.9966 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R.L |
| 0.999948 | 0.6307 R.ADIK[325.13]EMGLSLQWLYSAR.G                     |
| 0.999948 | 0.9953 R.SIFSAVLDELK[325.13]VAQAPWK.A                    |
| 0.999948 | 0.9999 R.YTLHYK[325.13]TDAPLNIR.S                        |
| 0.999948 | 0.9992 K.LLLQGEADQSLLTFIDK[325.13]AMHGELQK.A             |
| 0.999948 | 0.9987 K.KAKK[325.13]PAAAAGAK.K                          |
| 0.999947 | 0.9996 K.GIVEFSGK[325.13]PAAR.K                          |
| 0.999947 | 0.9996 K.GIVEFSGK[325.13]PAAR.K                          |
| 0.999947 | 0.9991 K.VGINYQPPTVVPGGDLAK[325.13]VQR.A                 |
| 0.999947 | 0.995 R.GENSWFSTQVDTVATK[325.13]VK.D                     |
| 0.999947 | 0.9975 R.SEGVVAVLLTK[325.13]K.S                          |
| 0.999947 | 0.9992 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V                |
| 0.999947 | 0.9993 R.SGVSLAALKK[325.13]ALAAAGYDVEK.N                 |
| 0.999947 | 0.9999 R.EATK[325.13]GFYDKDSSGWSSSK.D                    |
| 0.999947 | 0.9996 R.K[325.13]QVVNIPSFIVR.L                          |
| 0.999947 | 0.9993 R.AFITNIPFDVK[325.13]WQSLK.D                      |
| 0.999947 | 0.9993 K.ITLPVDFVTADKFDENAK[325.13]TGQATVASGIPAGWMC      |
| 0.999947 | 0.9993 R.SHAQK[325.13]NENAR.Q                            |
| 0.999947 | 0.9996 R.K[325.13]IEEIKDFLLTAR.R                         |
| 0.999947 | 0.9995 R.HGK[325.13]YM[147.04]AC[160.03]C[160.03]LLYR.G  |
| 0.999947 | 0.9934 K.VK[325.13]GLVLGPIHK.N                           |
| 0.999946 | 0.9994 K.K[325.13]C[160.03]GHTNNLRPK.K                   |
| 0.999946 | 0.9996 K.NTHC[160.03]SSLPHYQK[325.13]LK.K                |
| 0.999946 | 0.9927 R.MVNHFIAEFK[325.13]R.K                           |
| 0.999946 | 0.9994 K.HQILEQAVEDYAETVHQLSK[325.13]TSR.A               |
| 0.999946 | 0.9973 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                |
| 0.999946 | 0.955 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G              |
| 0.999946 | 0.9994 K.INQVFHGSC[160.03]ITEGNETK[325.13]TLIK.L         |
| 0.999946 | 0.9999 K.MFIGGLSWDTTK[325.13]K.D                         |
| 0.999946 | 0.9991 K.LDSEDKDKEGK[325.13]PLLK.A                       |
| 0.999946 | 0.9991 K.EGKPLK[325.13]AVMR.R                            |
| 0.999946 | 0.9996 R.YFPTQALNFAFKDK[325.13]YK.Q                      |
| 0.999946 | 0.9999 R.GEGYAKPNEGAIVEVALEGYYKDK[325.13]LFDQR.E         |
| 0.999946 | 0.9841 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999946 | 0.9955 K.VK[325.13]GLVLGPIHK.N                           |
| 0.999945 | 0.9996 K.NK[325.13]ITITNDQNR.L                           |

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| 0.999945 | 0.9788 R.K[325.13]LFIGGLSFETTEESLR.N                    |
| 0.999945 | 0.6143 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999945 | 0.9957 R.ALEHFTDLYDIK[325.13]R.A                        |
| 0.999945 | 0.9986 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.999945 | 0.9925 R.MVNHFIAEFK[325.13]R.K                          |
| 0.999945 | 0.9838 R.GVLK[325.13]VFLENVIR.D                         |
| 0.999944 | 0.9874 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR     |
| 0.999944 | 0.9992 K.GLVQALQTK[325.13]VTQQGLK.M                     |
| 0.999944 | 0.9999 K.GPGSAVSPYPTFNPSSDVAALHK[325.13]AIMVK.G         |
| 0.999944 | 0.9998 R.LSHYLQK[325.13]GC[160.03]R.L                   |
| 0.999944 | 0.9998 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q               |
| 0.999944 | 0.9999 K.VLLPEYGGTK[325.13]VVLDDKDYFLFR.D               |
| 0.999944 | 0.9992 R.K[325.13]YQPNIDVQESIHFLESEFSR.G                |
| 0.999944 | 0.9933 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |
| 0.999944 | 0.9954 R.LEK[325.13]PAKYDDIKK.V                         |
| 0.999944 | 0.9718 R.KDGNASGTTLLEALDC[160.03]ILPPTRPDTK[325.13]PLR. |
| 0.999944 | 0.9992 R.QHFPATPLLDYALEVEK[325.13]ITTSK.K               |
| 0.999943 | 0.9972 R.DWSHYFK[325.13]IIEDLR.A                        |
| 0.999943 | 0.9997 R.K[325.13]YAYSAASGGR.R                          |
| 0.999943 | 0.9951 R.GALQNIIPASTGAAK[325.13]AVGK.V                  |
| 0.999943 | 0.9993 K.TVTAM[147.04]DVVYALK[325.13]R.Q                |
| 0.999943 | 0.9996 K.DLAPYLPSVTPGLK[325.13]ASLLDPVPEVR.T            |
| 0.999943 | 0.8049 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I           |
| 0.999943 | 0.9999 K.LLTK[325.13]GLSWQPPPYTPTPR.F                   |
| 0.999943 | 0.9989 R.DQHFKV[325.13]IQVK.D                           |
| 0.999943 | 0.9429 R.LLLPGELAK[325.13]HAVSEGK.A                     |
| 0.999943 | 0.9964 R.LAHYNK[325.13]R.S                              |
| 0.999943 | 0.9996 K.K[325.13]IKDPDASKPEDWDER.A                     |
| 0.999942 | 0.9996 R.WYHPGC[160.03]FVK[325.13]NR.E                  |
| 0.999942 | 0.9992 K.VEAK[325.13]FINYVK.N                           |
| 0.999942 | 0.9992 K.TLNNK[325.13]FASFIDK.V                         |
| 0.999942 | 0.9972 R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTTEVK.S    |
| 0.999942 | 0.9972 R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTTEVK.S    |
| 0.999942 | 0.9518 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G            |
| 0.999942 | 0.5986 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999942 | 0.9903 R.YISPDQLADLYK[325.13]SFIK.D                     |
| 0.999942 | 0.9991 K.SLGQWLQEEK[325.13]VPAIYGVDTR.M                 |
| 0.999942 | 0.9992 R.K[325.13]MFTLLDVVNR.K                          |
| 0.999942 | 0.9991 R.VISGVLQLGNIVFK[325.13]K.E                      |
| 0.999942 | 0.9976 R.GTK[325.13]VILHLK.E                            |
| 0.999942 | 0.9999 K.EYGFC[160.03]IMDNHK[325.13]ER.I                |
| 0.999942 | 0.9996 R.GFC[160.03]FLEYEDHK[325.13]TAAQAR.R            |
| 0.999942 | 0.9996 K.IQQLVK[325.13]EFFNGKEPSR.G                     |
| 0.999942 | 0.9994 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A             |
| 0.999942 | 0.9999 K.LEHEYIQNFK[325.13]ILQAGFK.R                    |
| 0.999942 | 0.9993 R.K[325.13]FVHLLDQSDQDFQEELDMK.M                 |
| 0.999942 | 0.9998 R.EKIK[325.13]SDHPGISITDLSK.K                    |

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| 0.999942 | 0.9999 K.KQEGLLK[325.13]NIQVSHQEFSK.M                      |
| 0.999942 | 0.9999 K.HLQDLMEGLTAK[325.13]VFR.T                         |
| 0.999941 | 0.9991 R.AALQEELQLC[160.03]K[325.13]GLVQALQTK.V            |
| 0.999941 | 0.9874 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S           |
| 0.999941 | 0.9992 R.TAVDSGIPLLTNFQVTK[325.13]LFAEAVQK.S               |
| 0.999941 | 0.5917 R.ADIK[325.13]EMGLSLQWLYSAR.G                       |
| 0.999941 | 0.9991 K.FINYVK[325.13]NC[160.03]FR.M                      |
| 0.999941 | 0.9996 K.K[325.13]LSSWDQAETPGHTPSLR.W                      |
| 0.999941 | 0.9999 K.EIVVIHQDPEALKDIK[325.13]SLEK.Y                    |
| 0.999941 | 0.9996 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D          |
| 0.999941 | 0.9991 K.LGLVGVNLTLDGVK[325.13]SWLKPR.L                    |
| 0.99994  | 0.9987 R.FHK[325.13]LQNVQIALDYLR.H                         |
| 0.99994  | 0.9937 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.99994  | 0.999 R.GYFEYIEENK[325.13]YSR.A                            |
| 0.99994  | 0.9956 R.GALQNIIPASTGAAK[325.13]AVGK.V                     |
| 0.99994  | 0.9992 R.LDYLSSLK[325.13]VK.G                              |
| 0.99994  | 0.9956 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K            |
| 0.99994  | 0.9995 R.MATEVAADALGEEWK[325.13]GYVVR.I                    |
| 0.99994  | 0.9897 K.LDSTDFTGTIK[325.13]LLNENSYPVR.E                   |
| 0.99994  | 0.9991 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V                  |
| 0.99994  | 0.9991 K.SK[325.13]DDQVTVIGAGVTLHEALAAEELLK.K              |
| 0.99994  | 0.9983 K.VVLAYEPVWAIGTGK[325.13]TATPQQAQEVHEK.L            |
| 0.99994  | 0.9999 R.EHAMLAK[325.13]TAGVK.H                            |
| 0.99994  | 0.9937 K.AFGQAK[325.13]HQPTAIIAK.T                         |
| 0.99994  | 0.9997 K.HFVALSTNTTK[325.13]VK.E                           |
| 0.99994  | 0.999 K.EGKPLLK[325.13]AVMR.R                              |
| 0.99994  | 0.995 K.GLVLGPIHK[325.13]NQK.D                             |
| 0.99994  | 0.87 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E            |
| 0.999939 | 0.9991 K.AVGK[325.13]VIPELNGK.L                            |
| 0.999939 | 0.9601 K.EITALAPSTMKIK[325.13]IIAPPER.K                    |
| 0.999939 | 0.9996 R.RLEDGEDFNLGDALDSSNSMQTIQK[325.13]TTTR.R           |
| 0.999939 | 0.9383 R.LLLPGELAK[325.13]HAVSEGTK.A                       |
| 0.999939 | 0.9992 K.VHSFPTLK[325.13]FFPASADR.T                        |
| 0.999938 | 0.9991 K.GLGLSK[325.13]AYVGQK.S                            |
| 0.999938 | 0.9994 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                   |
| 0.999938 | 0.9992 R.SGVSLAALK[325.13]KALAAAGYDVEK.N                   |
| 0.999938 | 0.9934 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]LK.E |
| 0.999938 | 0.9993 R.EVTVPVFYPTTEK[325.13]VWLEVEPVGM[147.04]LK.E       |
| 0.999938 | 0.9996 K.NFGIGQDIQPK[325.13]R.D                            |
| 0.999938 | 0.9994 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V    |
| 0.999938 | 0.9996 R.YFPTQALNFAFK[325.13]DK.Y                          |
| 0.999938 | 0.9992 K.AVKPK[325.13]AAKPK.A                              |
| 0.999938 | 0.9961 R.LAHYNK[325.13]R.S                                 |
| 0.999937 | 0.9996 R.ADHPPEVTSHAASGAK[325.13]ADQEEQIHPR.S              |
| 0.999937 | 0.9999 R.NSQGK[325.13]GAHRPEHASGR.R                        |
| 0.999937 | 0.9999 K.QHYIDLK[325.13]DRPFPGLVK.Y                        |
| 0.999937 | 0.9758 R.K[325.13]LFIGGLSFETTEESLR.N                       |

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| 0.999937 | 0.9991 K.LGLK[325.13]SLVSK.G                             |
| 0.999937 | 0.9991 K.LGLK[325.13]SLVSK.G                             |
| 0.999937 | 0.9992 R.GLFIIDDK[325.13]GILR.Q                          |
| 0.999937 | 0.9995 K.FETLQAQAGK[325.13]HGDDL.R.N                     |
| 0.999937 | 0.9814 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999936 | 0.9991 R.FHILFK[325.13]ALGEEK.G                          |
| 0.999936 | 0.8613 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E        |
| 0.999936 | 0.9991 K.TIAPALVSK[325.13]K.L                            |
| 0.999936 | 0.999 K.SLGQWLQEEK[325.13]VPAIYGVDR.M                    |
| 0.999936 | 0.9958 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R.L |
| 0.999936 | 0.9999 K.EEQHQLAVTAYLK[325.13]NSR.K                      |
| 0.999936 | 0.999 K.RGEIIAK[325.13]QGGGGGGGSPGIER.M                  |
| 0.999936 | 0.9996 R.KIEEIK[325.13]DFLLTAR.R                         |
| 0.999936 | 0.8277 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN     |
| 0.999936 | 0.9953 R.SVPHLQK[325.13]VFDR.Y                           |
| 0.999936 | 0.9999 K.YAQVKPDGTYVKPLSNK[325.13]LTYGTMVFVR.S           |
| 0.999935 | 0.9999 R.NLHHYK[325.13]LHGVNINVEASK.N                    |
| 0.999935 | 0.9999 R.LFVGNLPADITEDEFK[325.13]R.L                     |
| 0.999935 | 0.9991 R.K[325.13]MFTLLDVVNR.K                           |
| 0.999935 | 0.9997 R.TLQYK[325.13]LLEPVLLLGK.E                       |
| 0.999935 | 0.9992 K.KPAAAGVK[325.13]K.V                             |
| 0.999935 | 0.9996 K.K[325.13]VHVIFNYK.G                             |
| 0.999935 | 0.9996 R.DAVTYTEHAK[325.13]RK.T                          |
| 0.999935 | 0.9996 K.TFSFAIPLIEK[325.13]LHGELQDR.K                   |
| 0.999934 | 0.9999 R.DKEC[160.03]GQLLISENQK[325.13]VAAHHK.C          |
| 0.999934 | 0.9997 K.YGGPPPDVSVYSGVQPGIGTEVFVGK[325.13]IPR.D         |
| 0.999934 | 0.9997 R.WC[160.03]NEHLK[325.13]C[160.03]VSK.R           |
| 0.999934 | 0.9997 K.MSPYK[325.13]DILETHLR.E                         |
| 0.999934 | 0.9995 R.VSEK[325.13]VSHVLAALQAGNR.G                     |
| 0.999934 | 0.9964 K.RVTIMPK[325.13]DIQLAR.R                         |
| 0.999934 | 0.9986 R.QLFHPEQLITGK[325.13]EDAANNYAR.G                 |
| 0.999933 | 0.9995 R.KAHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D    |
| 0.999933 | 0.9884 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR      |
| 0.999933 | 0.9991 R.LDYLSSLK[325.13]VK.G                            |
| 0.999933 | 0.9973 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                |
| 0.999933 | 0.9991 R.LSVEEAVAAGVVGGEIQEK[325.13]LLSAER.A             |
| 0.999933 | 0.9995 R.VNFAMNVGK[325.13]AR.G                           |
| 0.999933 | 0.9989 R.IAAYLFK[325.13]GNNR.W                           |
| 0.999933 | 0.9991 R.VLDPFTIK[325.13]PLDR.K                          |
| 0.999933 | 0.9966 R.FGFPEGSVELYAEK[325.13]VATR.G                    |
| 0.999933 | 0.9998 K.QFLQAAEAIDDIPFGITSNSDVFSK[325.13]YQLDKDGVVLF    |
| 0.999933 | 0.9989 R.VTYK[325.13]NVPNWHR.D                           |
| 0.999933 | 0.9994 R.ELAILLGMLDPAEKDEK[325.13]GMPVTAR.V              |
| 0.999933 | 0.9979 R.DLLDDLKSELTKGK[325.13]FEK.L                     |
| 0.999933 | 0.9991 K.GLGILSLK[325.13]QQEMMAALTDAIQDKK.N              |
| 0.999933 | 0.9954 R.DALSDLALHFLNK[325.13]MK.I                       |
| 0.999933 | 0.9992 R.K[325.13]VAC[160.03]IGAWHPAR.V                  |

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| 0.999933 | 0.998 R.GLDISNVK[325.13]HVINFDLPSDIEEYVHR.I             |
| 0.999932 | 0.9995 K.NTHC[160.03]SSLPHYQK[325.13]LK.K               |
| 0.999932 | 0.9987 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y       |
| 0.999932 | 0.9996 R.INLAQK[325.13]AFC[160.03]GFEDPR.T              |
| 0.999932 | 0.999 R.GIFPVLC[160.03]K[325.13]DPVQEAWAEDVDLR.V        |
| 0.999932 | 0.9988 R.LPMNK[325.13]EWPSNLDLR.K                       |
| 0.999932 | 0.9998 R.TFK[325.13]TVFAEHISDEC[160.03]K.R              |
| 0.999932 | 0.9528 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                 |
| 0.999931 | 0.999 K.TIAPALVSK[325.13]K.L                            |
| 0.999931 | 0.9999 K.FSAYIK[325.13]NSNPALNDNLEK.G                   |
| 0.999931 | 0.9999 -.MK[325.13]VELC[160.03]SFSGYK.I                 |
| 0.999931 | 0.9994 R.DAVTYTEHAK[325.13]R.K                          |
| 0.999931 | 0.9991 K.MPILGLGTWK[325.13]SPPGQVTEAVK.V                |
| 0.999931 | 0.9996 R.VHGPGIQSGTTNK[325.13]PNK.F                     |
| 0.999931 | 0.9996 R.TANDAVELHIK[325.13]NVQPSDQGHYK.C               |
| 0.999931 | 0.9996 R.EAILAIHK[325.13]EAQR.I                         |
| 0.999931 | 0.999 K.FADEHVPGSPFTVK[325.13]ISGEGR.V                  |
| 0.999931 | 0.999 R.YAIC[160.03]SALAASALPALVM[147.04]SK[325.13]GHR. |
| 0.99993  | 0.999 K.ESWHGKPLPK[325.13]NMAEQIIQEISQIQSK.K            |
| 0.99993  | 0.9993 R.VSFELFADK[325.13]VPK.T                         |
| 0.99993  | 0.9997 K.ATGPPVSELITK[325.13]AVAASK.E                   |
| 0.99993  | 0.9417 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G            |
| 0.99993  | 0.9999 R.NQSFC[160.03]PTVNLDK[325.13]LWTLVSEQTR.V       |
| 0.99993  | 0.9993 R.MFAPTK[325.13]TWR.R                            |
| 0.99993  | 0.9996 K.HFVALSTNTTK[325.13]VK.E                        |
| 0.99993  | 0.9986 R.VAAAVDLIHK[325.13]SHQGLDR.Q                    |
| 0.99993  | 0.9998 R.FQSSAVMALQEAC[160.03]EAYLVGLFEDTNLC[160.03]A   |
| 0.99993  | 0.8181 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                |
| 0.99993  | 0.9937 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L         |
| 0.999929 | 0.9946 K.SVHELEK[325.13]SKR.A                           |
| 0.999929 | 0.9994 K.IVSGK[325.13]DYNVTANSK.L                       |
| 0.999929 | 0.9996 R.FQLQATTK[325.13]EGPGEAIVR.E                    |
| 0.999929 | 0.9992 R.LK[325.13]VGLQVVAVK.A                          |
| 0.999929 | 0.9968 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                 |
| 0.999929 | 0.9995 R.AEAESM[147.04]YQIK[325.13]YEELQSLAGK.H         |
| 0.999929 | 0.9982 K.SGDAAIVDM[147.04]VPGK[325.13]PMC[160.03]VESFS  |
| 0.999929 | 0.9993 K.NSSYFVEWIPNNVK[325.13]TAVC[160.03]DIPPR.G      |
| 0.999929 | 0.9966 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV    |
| 0.999929 | 0.999 K.NGVK[325.13]ITLPVDFVTADKFDENAK.T                |
| 0.999929 | 0.9998 R.K[325.13]LTWVNEGLVDGWDDPR.F                    |
| 0.999929 | 0.9995 R.K[325.13]IPNPDDFFEDLEPFR.M                     |
| 0.999929 | 0.9995 K.DLPEHAVLK[325.13]M[147.04]K.G                  |
| 0.999929 | 0.9994 K.IGHAPAPNFK[325.13]ATAVM[147.04]PDGQFK.D        |
| 0.999929 | 0.9995 K.ILGSGISSSVLHGMVFK[325.13]K.E                   |
| 0.999929 | 0.9982 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.999929 | 0.9969 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |
| 0.999928 | 0.9973 R.KPAGAAK[325.13]KPK.K                           |



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| 0.999928 | 0.9983 K.SVVLMSHLGRPDGVPM[147.04]PDK[325.13]YSLEPVAVI    |
| 0.999928 | 0.999 K.LK[325.13]LEAELGNMQGLVEDFK.N                     |
| 0.999928 | 0.999 R.ALM[147.04]LQGVDLLADAVAVTMGPK[325.13]GR.T        |
| 0.999928 | 0.9991 K.IGHAPPNFK[325.13]ATAVMPDGQFK.D                  |
| 0.999928 | 0.9996 K.DIHTLAQLISAYSLVDPEK[325.13]AK.A                 |
| 0.999928 | 0.9992 R.LQLETEIEALKEELFMK[325.13]K.N                    |
| 0.999927 | 0.9984 K.YEELQSLAGK[325.13]HGDDLRR.T                     |
| 0.999927 | 0.9958 R.LLLPGELAKHAVSEGK[325.13]AVTK.Y                  |
| 0.999927 | 0.9996 K.LIK[325.13]GVIVDKDFSHPQMPK.K                    |
| 0.999927 | 0.999 K.VGINYQPPTVVPGGDLAK[325.13]VQR.A                  |
| 0.999927 | 0.9989 K.TVDGPSGK[325.13]LWR.D                           |
| 0.999927 | 0.9993 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTD.R.V |
| 0.999927 | 0.9948 K.IAK[325.13]AFAISGPFNVQFLVK.G                    |
| 0.999927 | 0.9965 R.LVNHFVEEFK[325.13]R.K                           |
| 0.999926 | 0.999 K.LKNK[325.13]HEAMITDLEER.L                        |
| 0.999926 | 0.9913 R.MVNHFAIEFK[325.13]R.K                           |
| 0.999926 | 0.9996 R.K[325.13]LFIGGLSFETDDSLREHF.K.W                 |
| 0.999926 | 0.9994 K.NK[325.13]GLWVPEGQR.A                           |
| 0.999926 | 0.9957 K.IILDLISEPIK[325.13]GR.A                         |
| 0.999926 | 0.9993 K.FEDENFILK[325.13]HTGPGILSMANAGPNTNGSQFFIC[16    |
| 0.999926 | 0.9942 R.VSGPYFPTLLGLSLQVLEPPQHGAALQK[325.13]EDGPQAR.    |
| 0.999925 | 0.9995 R.TKLQNK[325.13]EHVIEALR.R                        |
| 0.999925 | 0.9992 K.DSYVGDEAQSK[325.13]R.G                          |
| 0.999925 | 0.9989 K.FYEAFSK[325.13]NLK.L                            |
| 0.999925 | 0.9995 R.TFIAIK[325.13]PDGVQR.G                          |
| 0.999925 | 0.9996 R.DISEASVFDAYVLPK[325.13]LYVK.L                   |
| 0.999925 | 0.9988 R.LGQSDPAPLQHQMIDIYQK[325.13]R.C                  |
| 0.999925 | 0.999 R.VVDLMAHMASK[325.13]E.-                           |
| 0.999925 | 0.9995 R.LIDFLEC[160.03]GK[325.13]TNLR.R                 |
| 0.999925 | 0.9999 K.LYDIDVAK[325.13]VNTLIRPDGEK.K                   |
| 0.999925 | 0.9995 K.HGK[325.13]APILIATDVASR.G                       |
| 0.999925 | 0.9996 K.VHLDK[325.13]AQQNNVEHK.V                        |
| 0.999925 | 0.9945 R.SVPHLQK[325.13]VFDR.Y                           |
| 0.999925 | 0.9973 R.GPVLQLHDLK[325.13]R.E                           |
| 0.999925 | 0.9996 R.LSNIFVIGK[325.13]GNKPWISLPR.G                   |
| 0.999924 | 0.9996 R.KSHLAK[325.13]EGLYQYK.N                         |
| 0.999924 | 0.9935 R.GALQNIIPASTGAAK[325.13]AVGK.V                   |
| 0.999924 | 0.9971 R.K[325.13]LPIDVTEGEVISLGLPFGK.V                  |
| 0.999924 | 0.9986 R.K[325.13]VSQPIEGHAASFAQFK.M                     |
| 0.999924 | 0.9991 R.WQLK[325.13]ANEALR.L                            |
| 0.999924 | 0.9996 R.NLLSVAYK[325.13]NVVGAR.R                        |
| 0.999924 | 0.9995 K.EILVGDVGQTVDDPYATFVK[325.13]MLPDKDC[160.03]F    |
| 0.999924 | 0.9994 R.KPNEGADGQWK[325.13]K.G                          |
| 0.999924 | 0.9996 R.RK[325.13]QEELQQLEQQR.R                         |
| 0.999924 | 0.9994 R.RPDQQLQGEGK[325.13]IIDR.R                       |
| 0.999924 | 0.9924 R.TNIQVTVTGPPSPSPVK[325.13]FLIDTHNR.L             |
| 0.999924 | 0.9967 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I    |

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| 0.999923 | 0.9991 R.TM[147.04]PVEQVFAK[325.13]NFR.V               |
| 0.999923 | 0.9991 R.TM[147.04]PVEQVFAK[325.13]NFR.V               |
| 0.999923 | 0.9994 K.AEDKEWMPVTK[325.13]LGR.L                      |
| 0.999923 | 0.9996 K.DK[325.13]GFGFIR.L                            |
| 0.999923 | 0.9994 K.K[325.13]HGVYNPNK.I                           |
| 0.999923 | 0.9995 R.HIVK[325.13]EFK.R                             |
| 0.999923 | 0.9993 R.M[147.04]KENQK[325.13]HIYYITGETK.D            |
| 0.999923 | 0.9992 K.WK[325.13]PPMIDNPSYQGIWKPR.K                  |
| 0.999922 | 0.9944 K.KPVGAAK[325.13]KPK.K                          |
| 0.999922 | 0.9995 R.SSFHYSGLK[325.13]HEDK.R                       |
| 0.999922 | 0.9947 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L     |
| 0.999922 | 0.9994 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T           |
| 0.999922 | 0.9995 R.TVVTGIEMFHK[325.13]SLER.A                     |
| 0.999922 | 0.9993 K.DIEK[325.13]AC[160.03]QSIYPLHDVFVR.K          |
| 0.999922 | 0.9966 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I  |
| 0.999921 | 0.9994 R.ILK[325.13]HGINC[160.03]FINR.Q                |
| 0.999921 | 0.9987 R.WLPAGDALLQM[147.04]ITIHLSPVTAQK[325.13]YR.C   |
| 0.999921 | 0.9889 R.WLPAGDALLQMITIHLSPVTAQK[325.13]YR.C           |
| 0.999921 | 0.9989 K.FYEQFSK[325.13]NIK.L                          |
| 0.999921 | 0.9994 R.K[325.13]QVVNIPSFIVR.L                        |
| 0.999921 | 0.9991 R.K[325.13]LFIGGLSFETTDESLR.S                   |
| 0.999921 | 0.9994 R.YK[325.13]LLGGLAVR.R                          |
| 0.999921 | 0.9993 K.KPAEK[325.13]KPTTEEK.K                        |
| 0.999921 | 0.9974 R.K[325.13]LDYQGHVVAGTPGR.V                     |
| 0.99992  | 0.9995 R.VDFNVPMK[325.13]NNQITNNQR.I                   |
| 0.99992  | 0.9995 -.MQIFVK[325.13]TLTGK.T                         |
| 0.99992  | 0.9968 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T              |
| 0.99992  | 0.9976 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S |
| 0.99992  | 0.9962 K.IK[325.13]GEHPGLSIGDVAK.K                     |
| 0.99992  | 0.9994 R.FVPQEM[147.04]GVHTVSVK[325.13]YR.G            |
| 0.99992  | 0.9992 R.KTVTAMDVVYALK[325.13]R.Q                      |
| 0.99992  | 0.9992 K.LHQAMK[325.13]GVGTR.H                         |
| 0.99992  | 0.9995 K.FK[325.13]MPEMHFK.T                           |
| 0.999919 | 0.9991 K.K[325.13]C[160.03]GHTNNLRPK.K                 |
| 0.999919 | 0.9988 R.LK[325.13]STC[160.03]IYGGAPK.G                |
| 0.999919 | 0.9995 R.MIAGQVLDINLAAEPK[325.13]VNR.G                 |
| 0.999919 | 0.9994 R.VNFAMNVGK[325.13]AR.G                         |
| 0.999919 | 0.9996 R.INEILSNALK[325.13]R.G                         |
| 0.999919 | 0.9995 R.FFTVK[325.13]LPVALDPGAK.I                     |
| 0.999919 | 0.9995 K.K[325.13]VHVIFNYK.G                           |
| 0.999919 | 0.9996 R.EHPFLVK[325.13]GGEDLR.Q                       |
| 0.999919 | 0.9996 R.FTLTGLKPDTTYDIK[325.13]VR.A                   |
| 0.999919 | 0.9989 K.GFGYK[325.13]GSC[160.03]FHR.I                 |
| 0.999918 | 0.9998 K.RPDADLK[325.13]TYFTDKK.T                      |
| 0.999918 | 0.9989 K.LDSGK[325.13]ELHINLIPNKQDR.T                  |
| 0.999918 | 0.9996 R.NQLTAMSSVLAK[325.13]ALEVIKPAHILQEK.E          |
| 0.999918 | 0.9998 K.AQAYQTGK[325.13]DISTNYASQK.K                  |

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| 0.999918 | 0.9998 K.AQAYQTGK[325.13]DISTNYYASQK.K                  |
| 0.999918 | 0.9924 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF      |
| 0.999918 | 0.9992 K.IK[325.13]IIAPPERK.Y                           |
| 0.999918 | 0.9993 K.IGHAPPNFK[325.13]ATAVM[147.04]PDGQFK.D         |
| 0.999918 | 0.9975 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R            |
| 0.999918 | 0.9949 R.LLLPGELAK[325.13]HAVSEGTKAVTK.Y                |
| 0.999918 | 0.9997 R.K[325.13]LAKTQGNVFATDAILATLMSC[160.03]TR.S     |
| 0.999918 | 0.9968 K.TAWLDGK[325.13]HVVFGK.V                        |
| 0.999918 | 0.9999 R.FKAK[325.13]FVGDPALVLNDIHK.K                   |
| 0.999917 | 0.9949 R.HWGGNVLGPK[325.13]SVAR.I                       |
| 0.999917 | 0.9993 K.IVSGK[325.13]DYNVTANSK.L                       |
| 0.999917 | 0.9991 R.K[325.13]AVVVC[160.03]PK.D                     |
| 0.999917 | 0.9988 K.GLGLSK[325.13]AYVGQK.S                         |
| 0.999917 | 0.9996 R.SNQQLENDLNLMEDIK[325.13]IGLLVK.N               |
| 0.999917 | 0.9996 K.IPVQLVFK[325.13]NK.I                           |
| 0.999917 | 0.9999 R.GQGNWGPPGGEMTFSIPTHK[325.13]C[160.03]GLVIGR    |
| 0.999917 | 0.9992 K.KPAPEK[325.13]KPAEK.K                          |
| 0.999916 | 0.9995 K.IGKPHTVPC[160.03]K[325.13]VTGR.C               |
| 0.999916 | 0.9988 K.THINIVVIGHVDSGK[325.13]STTTGHLIYK.C            |
| 0.999916 | 0.9971 K.ITPENLPQILLQLK[325.13]R.R                      |
| 0.999916 | 0.9996 K.NSSNKPAVTTK[325.13]SPAVKPAAAPK.Q               |
| 0.999916 | 0.99 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I     |
| 0.999916 | 0.9989 K.VHSFPTLK[325.13]FFPASADR.T                     |
| 0.999916 | 0.9999 R.HPAENGK[325.13]SNFLNC[160.03]YVSGFHPSDIEVDLLK  |
| 0.999916 | 0.9916 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L         |
| 0.999915 | 0.9984 K.EITALAPSTM[147.04]K[325.13]IK.I                |
| 0.999915 | 0.9987 K.MPK[325.13]FSMPGFK.A                           |
| 0.999915 | 0.9993 R.IPK[325.13]EQGVLSFWR.G                         |
| 0.999915 | 0.9996 R.AK[325.13]AVVQLKPR.H                           |
| 0.999914 | 0.9993 R.MHAPGK[325.13]GLSQSALPYR.R                     |
| 0.999914 | 0.9916 R.DWSHYFK[325.13]IIEDLR.A                        |
| 0.999914 | 0.1769 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.999914 | 0.9995 R.GGNRFEPYANPTK[325.13]R.Y                       |
| 0.999913 | 0.9994 K.NK[325.13]ITITNDQNR.L                          |
| 0.999913 | 0.9996 K.YIEIYVQK[325.13]VNPSR.L                        |
| 0.999913 | 0.9996 K.VTFDPTSSYTLEDLK[325.13]PDTLYR.F                |
| 0.999913 | 0.9996 K.EGIPALDNFLDK[325.13]L.-                        |
| 0.999913 | 0.9996 K.K[325.13]AEGGGGGGRPGAPAAGDGK.T                 |
| 0.999913 | 0.9998 R.K[325.13]GVAINMVTEEDKR.T                       |
| 0.999913 | 0.9996 K.ITLQDVVSHSK[325.13]K.L                         |
| 0.999913 | 0.9996 K.WNTEDK[325.13]VSHVSTGGGASLELLEGK.I             |
| 0.999913 | 0.9479 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAV   |
| 0.999913 | 0.9996 R.SPNLWLK[325.13]DVLK.E                          |
| 0.999913 | 0.9991 K.EAESC[160.03]DC[160.03]LQGFQLTHSLGGGTGSGMGTI   |
| 0.999913 | 0.9943 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVLR.L |
| 0.999913 | 0.9909 K.AFGQAK[325.13]HQPTAIIAK.T                      |
| 0.999913 | 0.9996 R.TIEKFEK[325.13]EAAEMGK.G                       |

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| 0.999913 | 0.9999 R.K[325.13]HIMGQNVADYMR.Y                         |
| 0.999913 | 0.3878 R.LLLPGELAK[325.13]HAVSEGTK.A                     |
| 0.999913 | 0.9996 R.YK[325.13]ATGLHFR.H                             |
| 0.999913 | 0.9996 R.RK[325.13]DPELWGSVLLESNPYR.R                    |
| 0.999912 | 0.9998 K.FLSPVVPNYDNPVHPNYHK[325.13]EPFLQQLK.V           |
| 0.999912 | 0.9995 R.HMYHSLYLK[325.13]VK.G                           |
| 0.999912 | 0.999 R.K[325.13]LFIGGLSFETTDESLR.S                      |
| 0.999912 | 0.9996 R.IDKPILK[325.13]AGR.A                            |
| 0.999912 | 0.9996 K.YNDK[325.13]HIPGSPFTAK.I                        |
| 0.999912 | 0.9996 K.AKFENLC[160.03]K[325.13]LMK.E                   |
| 0.999912 | 0.9986 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I        |
| 0.999912 | 0.9997 K.ILVDISNNLK[325.13]INQYPESNAEYLAHLVPGAHVVK.A     |
| 0.999911 | 0.999 R.LK[325.13]VGLQVVAVK.A                            |
| 0.999911 | 0.9566 K.EITALAPSTMKIK[325.13]IIAPPER.K                  |
| 0.999911 | 0.9994 K.GMTLVTPQLLLFASK[325.13]K.V                      |
| 0.999911 | 0.9749 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                 |
| 0.999911 | 0.9737 R.GVLK[325.13]VFLENVIR.D                          |
| 0.99991  | 0.9993 R.HAK[325.13]WFQAR.A                              |
| 0.99991  | 0.9993 R.HAK[325.13]WFQAR.A                              |
| 0.99991  | 0.9999 R.AHMESDKHLEALC[160.03]LFK[325.13]AEHWNR.C        |
| 0.99991  | 0.9996 K.GFK[325.13]EQIYDVYR.Y                           |
| 0.99991  | 0.9996 K.GFK[325.13]EQIYDVYR.Y                           |
| 0.99991  | 0.711 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I             |
| 0.99991  | 0.9986 K.NQSQGYNQWQQGQFWGQK[325.13]PWSQHYHQGGY.-         |
| 0.99991  | 0.997 R.ETAQAIK[325.13]GMHIR.K                           |
| 0.999909 | 0.9996 R.DMFC[160.03]K[325.13]ILHGFK.N                   |
| 0.999909 | 0.9995 R.GDGTGGK[325.13]SIYGER.F                         |
| 0.999909 | 0.9959 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                  |
| 0.999909 | 0.9959 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                  |
| 0.999909 | 0.9996 R.K[325.13]ASDVHEVR.K                             |
| 0.999909 | 0.9935 K.ILLAELEQLK[325.13]GQGK.S                        |
| 0.999909 | 0.999 K.LTPK[325.13]IGFPWSEIR.N                          |
| 0.999909 | 0.9996 R.K[325.13]ASDVHEVR.K                             |
| 0.999909 | 0.9982 R.VAAAVDLIK[325.13]SHQGLDR.Q                      |
| 0.999908 | 0.9996 R.GREEYEGPNKK[325.13]PR.F                         |
| 0.999908 | 0.9978 K.GFGYK[325.13]GSC[160.03]FHR.I                   |
| 0.999908 | 0.9995 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S      |
| 0.999908 | 0.9999 K.TIAEC[160.03]LADELINAAC[325.13]GSSNSYAIK.K      |
| 0.999908 | 0.9977 R.AK[325.13]LTPGC[160.03]EAEAETEAIC[160.03]FFVQQF |
| 0.999908 | 0.9942 R.LAHYNK[325.13]R.S                               |
| 0.999908 | 0.9995 R.MK[325.13]VAC[160.03]ITEQVLTLVNKR.I             |
| 0.999907 | 0.9996 K.GPK[325.13]VDIDAPDVDVHGPDWHLK.M                 |
| 0.999907 | 0.9987 K.FYEQFSK[325.13]NIK.L                            |
| 0.999907 | 0.9996 R.AEMEVLLASK[325.13]AR.A                          |
| 0.999907 | 0.9946 K.IILDISESPIK[325.13]GR.A                         |
| 0.999907 | 0.9996 R.MPSGK[325.13]VAQPTITDNKDGTVTVR.Y                |
| 0.999907 | 0.9996 R.TGVELGK[325.13]PTHFTVNAK.A                      |

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| 0.999907 | 0.9996 K.DK[325.13]ADFC[160.03]IIHYAGK.V              |
| 0.999907 | 0.9996 K.AMKEENVK[325.13]TVLMNPNIASVQTNEVGLK.Q        |
| 0.999907 | 0.9996 K.QLFDQVVK[325.13]TIGLR.E                      |
| 0.999907 | 0.9994 R.ASNGDAWVEAHGK[325.13]LYSPSQIGAFVLMK.M        |
| 0.999907 | 0.9991 K.IK[325.13]IIAPPERK.Y                         |
| 0.999907 | 0.9996 R.KEPLFGISTGNLITGLAAGAK[325.13]TYK.M           |
| 0.999907 | 0.9994 K.HGEVC[160.03]PAGWKPGSDTIK[325.13]PDVQK.S     |
| 0.999907 | 0.9996 K.RTLLIK[325.13]TVETR.D                        |
| 0.999906 | 0.9994 R.GLK[325.13]YELISETGGSHDKR.F                  |
| 0.999906 | 0.9995 K.VK[325.13]LEAEIATYR.R                        |
| 0.999906 | 0.9837 R.FLEQQNK[325.13]ILLAELEQLK.G                  |
| 0.999906 | 0.9992 K.K[325.13]HPDASVNFSEFSK.K                     |
| 0.999906 | 0.9998 K.K[325.13]PLPDHVSIVEPK.D                      |
| 0.999906 | 0.9994 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R   |
| 0.999906 | 0.9994 R.K[325.13]FLVYVANFDEKDPR.T                    |
| 0.999906 | 0.9928 R.K[325.13]TFTAWC[160.03]NSHLR.K               |
| 0.999905 | 0.9994 K.IGPK[325.13]KPLPDHVSIVEPK.D                  |
| 0.999905 | 0.9996 K.AVK[325.13]EEGFPIRPHYFWPLLVR.R               |
| 0.999905 | 0.9915 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI |
| 0.999905 | 0.9983 K.NAQK[325.13]SNQNGKDSKPSSTPR.S                |
| 0.999904 | 0.9999 K.NISFTVWDVGGQDK[325.13]IRPLWR.H               |
| 0.999904 | 0.9929 R.GNPTVEVDLFTSK[325.13]GLFR.A                  |
| 0.999904 | 0.9998 K.LLLQVQHASK[325.13]QITADK.Q                   |
| 0.999904 | 0.9995 R.LIFAGK[325.13]QLEDGR.T                       |
| 0.999904 | 0.9999 R.IIGLK[325.13]PEGVPR.I                        |
| 0.999904 | 0.9995 R.LIFAGK[325.13]QLEDGR.T                       |
| 0.999904 | 0.9995 K.VFQFLNAK[325.13]C[160.03]ESAFLSK.R           |
| 0.999904 | 0.9994 K.VK[325.13]EFGIDPQNMFEFWDWVGGR.Y              |
| 0.999904 | 0.9994 R.KQLATK[325.13]AAR.K                          |
| 0.999904 | 0.9994 R.LRENELTYYC[160.03]C[160.03]K[325.13]K.D      |
| 0.999904 | 0.9998 K.YK[325.13]DAIHFYNK.S                         |
| 0.999904 | 0.9341 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F               |
| 0.999904 | 0.9996 R.LNHQEFK[325.13]SC[160.03]LR.S                |
| 0.999904 | 0.992 K.VK[325.13]GLVLGPIHK.N                         |
| 0.999904 | 0.9999 R.FLQPVHK[325.13]IDMNLTDLLGELQR.D              |
| 0.999903 | 0.9993 K.SAPATGGVK[325.13]KPHR.Y                      |
| 0.999903 | 0.9999 R.KGDYLGK[325.13]TVQVPHITDAIQEWVMR.Q           |
| 0.999903 | 0.9986 K.IVTTTGAVPGRPTMMISTTAMNTALLQWHPPK[325.13]EI   |
| 0.999903 | 0.9998 K.K[325.13]AC[160.03]GNFGIPC[160.03]ELR.V      |
| 0.999903 | 0.9989 K.FEDENFILK[325.13]HTGPGILSMANAGPNTNGSQFFIC[16 |
| 0.999902 | 0.9997 R.INVYYNEATGGK[325.13]YVPR.A                   |
| 0.999902 | 0.9994 R.K[325.13]SQVLFSVTR.G                         |
| 0.999902 | 0.9994 R.K[325.13]SQVLFSVTR.G                         |
| 0.999902 | 0.9977 K.VVLAYEPVWAIGTGK[325.13]TATPQQAQEVHEK.L       |
| 0.999902 | 0.9943 K.IILDLIESPICK[325.13]GR.A                     |
| 0.999902 | 0.9998 K.GGAAVDPDSGLEHSAHVLEK[325.13]GGK.V            |
| 0.999902 | 0.9996 K.AK[325.13]FVGDPALVLNDIHK.K                   |

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| 0.999902 | 0.9999 K.TSFVNFTDIC[160.03]K[325.13]LLHR.Q              |
| 0.999901 | 0.9996 R.DLEK[325.13]PFLLPVEAVYSVPGR.G                  |
| 0.999901 | 0.9994 R.GC[160.03]ALQC[160.03]AILSPAFAK[325.13]VR.E    |
| 0.999901 | 0.9992 K.LTLHGLQQYYVK[325.13]LK.D                       |
| 0.999901 | 0.9994 K.MKDAILAK[325.13]LANQAADYFGDAFK.Q               |
| 0.999901 | 0.9997 K.RVTIM[147.04]PK[325.13]DIQLAR.R                |
| 0.9999   | 0.9995 R.GGEPNQRPELK[325.13]NHIDR.V                     |
| 0.9999   | 0.9998 K.RFGFPEGSVELYAEK[325.13]VATR.G                  |
| 0.9999   | 0.9993 K.AIADTGANVVVTGGK[325.13]VADMALHYANK.Y           |
| 0.9999   | 0.9993 K.AIADTGANVVVTGGK[325.13]VADMALHYANK.Y           |
| 0.9999   | 0.9998 R.AISAK[325.13]GMTLVTPQLQLLFASK.K                |
| 0.9999   | 0.3499 R.LLLPGELAK[325.13]HAVSEGTK.A                    |
| 0.9999   | 0.9996 R.NDLMEYAK[325.13]QHGIPIPVTPK.N                  |
| 0.9999   | 0.9988 K.VLVLSQDYGK[325.13]HLLGVEDLLQK.H                |
| 0.9999   | 0.9999 K.LFKPGQEAVK[325.13]YQGPR.D                      |
| 0.999899 | 0.9958 K.DFLAGGVAAAISK[325.13]TAVAPIER.V                |
| 0.999899 | 0.9993 R.ALTVPILTQQVFDK[325.13]NMMAAC[160.03]DPR.H      |
| 0.999899 | 0.9997 R.VTFLPTGITFK[325.13]SVTR.E                      |
| 0.999899 | 0.9992 K.HVVFGK[325.13]VK.E                             |
| 0.999899 | 0.9998 K.LWC[160.03]TYHEK[325.13]GLVK.G                 |
| 0.999898 | 0.9995 R.K[325.13]TAPYKNVNVQNFHISWK.D                   |
| 0.999898 | 0.9991 K.IYK[325.13]IGQGYLIK.D                          |
| 0.999898 | 0.9994 K.MKDAILAK[325.13]LANQAADYFGDAFK.Q               |
| 0.999898 | 0.9999 R.K[325.13]REDC[160.03]SPADKPYIDEAR.R            |
| 0.999898 | 0.9995 R.K[325.13]GLVGPELHDR.L                          |
| 0.999897 | 0.9998 R.HGVSHK[325.13]VDDSSGSIGR.R                     |
| 0.999897 | 0.9984 K.K[325.13]HLEINPDHPIVETLR.Q                     |
| 0.999897 | 0.9994 R.TVPQYK[325.13]YAAGVR.N                         |
| 0.999897 | 0.9969 K.M[147.04]LETK[325.13]WSLLQQQK.T                |
| 0.999897 | 0.9993 K.TVDNFVALATGEK[325.13]GFGYK.N                   |
| 0.999897 | 0.9998 R.EALLSSAVDHGSDEVK[325.13]FR.Q                   |
| 0.999897 | 0.998 R.RYQK[325.13]STELLIR.K                           |
| 0.999896 | 0.9993 R.HKNPK[325.13]TGIYEK.H                          |
| 0.999896 | 0.9999 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L        |
| 0.999896 | 0.9994 K.TVIGELPPASSGSALAANVC[160.03]K[325.13]K.I       |
| 0.999896 | 0.9994 R.VTIMPK[325.13]DIQLAR.R                         |
| 0.999896 | 0.9879 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M       |
| 0.999896 | 0.9982 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK. |
| 0.999896 | 0.9994 R.DPQFQK[325.13]LQQWYR.E                         |
| 0.999896 | 0.9998 K.ITSC[160.03]IFQLQEAGIK[325.13]TAFTR.K          |
| 0.999896 | 0.9986 R.DIK[325.13]EKLC[160.03]YVALDFEQEMATAASSSSLEK.S |
| 0.999896 | 0.9935 R.LAHYNK[325.13]R.S                              |
| 0.999896 | 0.9992 R.GHNC[160.03]PK[325.13]PVLNFYEANFPANVMDVIAR.C   |
| 0.999896 | 0.9998 R.K[325.13]GSEHQAIVQHLEK.S                       |
| 0.999895 | 0.9998 K.RAFDSAVAK[325.13]ALEHHR.S                      |
| 0.999895 | 0.9995 K.YGGPPPDVYSGVQPGIGTEVFVGK[325.13]IPR.D          |
| 0.999895 | 0.9988 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK. |

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| 0.999895 | 0.9993 K.YK[325.13]PAVNQIEC[160.03]HPYLTQEK.L            |
| 0.999895 | 0.9992 R.K[325.13]QVVNIPSFIVR.L                          |
| 0.999895 | 0.9998 R.VHPVSTMIK[325.13]GLYGIK.D                       |
| 0.999895 | 0.9984 R.LDYLSSLKVK[325.13]GLVLGPIHK.N                   |
| 0.999894 | 0.9988 R.K[325.13]LFIGGLSFETTDESLR.S                     |
| 0.999894 | 0.4109 R.ADIK[325.13]EMGLSLQWLYSAR.G                     |
| 0.999894 | 0.9993 R.GHYTIGK[325.13]EIDPVLDR.I                       |
| 0.999894 | 0.9993 K.LTLHGLQQYYVK[325.13]LK.D                        |
| 0.999894 | 0.9999 K.LAENNINLIFAVTK[325.13]NHYMLYK.N                 |
| 0.999894 | 0.999 R.HGK[325.13]YM[147.04]AC[160.03]C[160.03]LLYR.G   |
| 0.999893 | 0.9993 K.TAITVEHLAIK[325.13]C[160.03]HWTQR.A             |
| 0.999893 | 0.9998 K.TLVLLMGK[325.13]EGVHGGLINKK.C                   |
| 0.999893 | 0.9311 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTRPDKPLR.   |
| 0.999893 | 0.9995 K.FWHK[325.13]AC[160.03]FHC[160.03]ETC[160.03]K.M |
| 0.999893 | 0.9971 R.HK[325.13]NMSVHLSPC[160.03]FR.D                 |
| 0.999893 | 0.9993 K.LAQMFSDM[147.04]VLK[325.13]DGFQPSR.S            |
| 0.999893 | 0.9575 R.HQGVM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA     |
| 0.999893 | 0.9994 R.IAESNHIK[325.13]LSGSNPYTTVTPQIINSK.W            |
| 0.999893 | 0.7237 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN     |
| 0.999893 | 0.9972 K.DLPEHAVLK[325.13]MK.G                           |
| 0.999893 | 0.9917 R.K[325.13]TFTAWC[160.03]NSHLR.K                  |
| 0.999892 | 0.9993 K.HKPGGGDVK[325.13]IESQK.L                        |
| 0.999892 | 0.9997 K.ITK[325.13]FENAFLSHVVSQHQALLGTIR.A              |
| 0.999892 | 0.9964 R.HNGTGGK[325.13]SIYGEK.F                         |
| 0.999892 | 0.9994 K.VTQQGLK[325.13]MVVPGLDGAQIPR.D                  |
| 0.999892 | 0.9991 R.MATEVAADALGEEWK[325.13]GYVVR.I                  |
| 0.999892 | 0.9997 R.KTC[160.03]TTVAFTQVNSEDK[325.13]GALAK.L         |
| 0.999892 | 0.9913 R.QTVAVGVK[325.13]AVDKK.A                         |
| 0.999892 | 0.9991 R.YM[147.04]AQGK[325.13]HIGK.V                    |
| 0.999892 | 0.9012 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.999892 | 0.9995 K.K[325.13]WTTLNSLQLHGLQLR.I                      |
| 0.999892 | 0.9998 R.DPVWK[325.13]YLQTVQYGVHGNFPR.L                  |
| 0.999891 | 0.9993 R.LYKEELEQTYHAK[325.13]LENAR.L                    |
| 0.999891 | 0.9891 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K          |
| 0.999891 | 0.9995 R.LDSSAVLDTGK[325.13]YVGLVR.V                     |
| 0.999891 | 0.9995 K.IK[325.13]WGDAGAEYVVESTGVFTTMEK.A               |
| 0.999891 | 0.9995 R.EVTLGQVAK[325.13]LLEAETQR.Q                     |
| 0.999891 | 0.999 R.SRK[325.13]ESYSVYVK.V                            |
| 0.999891 | 0.9995 K.FLSAIVSSVDK[325.13]IPYGM.R.F                    |
| 0.999891 | 0.9995 R.APGSGLALLPLK[325.13]ITFR.S                      |
| 0.999891 | 0.9999 K.LDSPAGTALSPSGHTK[325.13]LLPR.S                  |
| 0.999891 | 0.9991 K.SAEAFGK[325.13]IVAERP GTNSTGPAPMAPPR.A          |
| 0.999891 | 0.9995 R.LAQFVEHWK[325.13]ELK.Q                          |
| 0.999891 | 0.9998 R.LPSGLGC[160.03]STVLSPEGSAQFAAQIFGLSNHLVWSK[3    |
| 0.99989  | 0.9999 R.FTAQGLPDLNHSQVYAVK[325.13]TVLQRPLSLIQGPPGTC     |
| 0.99989  | 0.9991 R.EIAQDFK[325.13]TDLR.F                           |
| 0.99989  | 0.9995 R.SGVSLAALK[325.13]K.A                            |

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| 0.99989  | 0.9998 K.K[325.13]YDAFLASESLIK.Q                       |
| 0.99989  | 0.991 R.LEK[325.13]PAKYDDIKK.V                         |
| 0.99989  | 0.9995 R.HGYIK[325.13]GIVK.D                           |
| 0.99989  | 0.9976 K.QVHPDTGISSK[325.13]AMGIM[147.04]NSFVNDIFER.I  |
| 0.99989  | 0.9991 R.MHAPGK[325.13]GLSQSALPYR.R                    |
| 0.99989  | 0.1946 R.DALSDLALHFLNK[325.13]M[147.04]K.I             |
| 0.999889 | 0.9996 R.ELLTEFGYK[325.13]GEETPVIVGSALC[160.03]ALEGR.D |
| 0.999889 | 0.9991 K.NK[325.13]GLWVPEGQR.A                         |
| 0.999889 | 0.9993 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D        |
| 0.999889 | 0.9999 R.VLPSITTEILK[325.13]SVVAR.F                    |
| 0.999889 | 0.9984 K.LDSEDK[325.13]DKEGKPLLK.A                     |
| 0.999889 | 0.9991 R.LDHK[325.13]FDLM[147.04]YAK.R                 |
| 0.999889 | 0.9941 R.LM[147.04]AEGAPK[325.13]WPKETVKPVEVEEGESVVL   |
| 0.999889 | 0.6583 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I          |
| 0.999889 | 0.9964 R.LREK[325.13]LQEEMLQR.E                        |
| 0.999889 | 0.9883 R.VEYHFLSPYVSPK[325.13]ESPFR.H                  |
| 0.999889 | 0.9877 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I              |
| 0.999888 | 0.9992 K.NTHC[160.03]SSLPHYQK[325.13]LK.K              |
| 0.999888 | 0.9973 K.EITALAPSTMK[325.13]JK.I                       |
| 0.999888 | 0.9991 R.SSFYVNGTLGGQK[325.13]C[160.03]SVIR.D          |
| 0.999888 | 0.9998 K.IVTVK[325.13]TQAYQDQKPGTSGLR.K                |
| 0.999888 | 0.9991 R.MPK[325.13]VQQTVDLFR.A                        |
| 0.999888 | 0.9993 R.KQLATK[325.13]AAR.K                           |
| 0.999888 | 0.9999 R.SEFYK[325.13]HIVLSGGSTMYPGLPSR.L              |
| 0.999888 | 0.9999 K.QDLPNAMNAEITDK[325.13]LGLHSLR.H               |
| 0.999888 | 0.9733 R.HQGVMM[147.04]VGMGQK[325.13]DSYVGDEAQSKR.G    |
| 0.999888 | 0.9999 K.KIEISQHAK[325.13]YTC[160.03]SFC[160.03]GK.T   |
| 0.999887 | 0.9993 K.IGKPHTVPC[160.03]K[325.13]VTGR.C              |
| 0.999887 | 0.9965 R.TLSDYNIQK[325.13]ESTLHLVLR.L                  |
| 0.999887 | 0.9999 K.HALIYDDLSK[325.13]QAVAYR.Q                    |
| 0.999887 | 0.9999 R.YVWLVEQDRPLK[325.13]C[160.03]DEPILSNR.S       |
| 0.999886 | 0.9981 R.ASFNHFDK[325.13]DHGGALGPEEFK.A                |
| 0.999886 | 0.9993 R.M[147.04]IAGQVLDINLAAEPK[325.13]VNR.G         |
| 0.999886 | 0.9971 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S       |
| 0.999886 | 0.9994 R.REEAAVDAQQK[325.13]R.S                        |
| 0.999886 | 0.9999 K.LLGPHVEGLK[325.13]AEER.H                      |
| 0.999885 | 0.9994 R.KSHLAK[325.13]EGLYQYK.N                       |
| 0.999885 | 0.9992 R.TADGIVSHLK[325.13]K.Q                         |
| 0.999885 | 0.9992 R.TADGIVSHLK[325.13]K.Q                         |
| 0.999885 | 0.9976 K.KLEDGPK[325.13]FLK.S                          |
| 0.999885 | 0.9994 R.TPC[160.03]EEILVK[325.13]HVGSR.L              |
| 0.999885 | 0.997 K.DLPEHAVLK[325.13]MK.G                          |
| 0.999885 | 0.9989 K.K[325.13]ISSIQSIVPALEIANHR.K                  |
| 0.999885 | 0.9991 K.K[325.13]HGVYNPNK.I                           |
| 0.999884 | 0.931 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV    |
| 0.999884 | 0.9965 R.FSGWYDADLSPAGHEEAK[325.13]R.G                 |
| 0.999884 | 0.9977 K.TPSSDVLVFDYTK[325.13]HPAKPDPSGEC[160.03]NPDLF |



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| 0.999884 | 0.9979 K.HPVTGQFLYQDSNWASK[325.13]VEK.L                |
| 0.999884 | 0.9999 K.NVPNLHVMK[325.13]AMQSLK.S                     |
| 0.999884 | 0.9998 R.DFKPGDLIFAK[325.13]MK.G                       |
| 0.999884 | 0.9995 R.VSVADHSLHLSK[325.13]AK.I                      |
| 0.999884 | 0.9988 K.FSGK[325.13]HVVFIAQR.R                        |
| 0.999884 | 0.9208 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                |
| 0.999883 | 0.9996 K.IVIQK[325.13]YHTVNGHNC[160.03]EVR.K           |
| 0.999883 | 0.9996 K.IVIQK[325.13]YHTVNGHNC[160.03]EVR.K           |
| 0.999883 | 0.9995 R.HLGVILPAVMLALK[325.13]EK.L                    |
| 0.999883 | 0.9995 K.VVAK[325.13]GLGLSK.A                          |
| 0.999883 | 0.9995 K.GC[160.03]GVVK[325.13]FESPEVAER.A             |
| 0.999883 | 0.9996 R.SYSK[325.13]LLC[160.03]GLLAER.L               |
| 0.999883 | 0.9995 K.DPYSKG[325.13]LISLFQAMK.K                     |
| 0.999883 | 0.9997 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T       |
| 0.999883 | 0.9995 R.VSAPEVSVGHK[325.13]GGKPGLTIQAPQLEVSVPSANIEG   |
| 0.999883 | 0.9995 R.LKPYVAAQLDVLPEFTLGDK[325.13]K.N               |
| 0.999882 | 0.9665 R.M[147.04]VNHFAIEFK[325.13]R.K                 |
| 0.999882 | 0.9993 R.DLYEDELVPLFEK[325.13]AGPIWDLR.L               |
| 0.999882 | 0.9944 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                 |
| 0.999882 | 0.999 K.IGHAPNFK[325.13]ATAVM[147.04]PDGQFK.D          |
| 0.999882 | 0.987 R.VEYHFLSPYVSPK[325.13]ESPFR.H                   |
| 0.999881 | 0.9991 R.ILK[325.13]HGINC[160.03]FINR.Q                |
| 0.999881 | 0.9984 K.GLVQALQTK[325.13]VTQQGLK.M                    |
| 0.999881 | 0.9993 R.INLAQK[325.13]AFC[160.03]GFEDPR.T             |
| 0.999881 | 0.9959 K.TFVNITPAEVLVVGK[325.13]DR.S                   |
| 0.999881 | 0.9961 R.K[325.13]LDYGQHVVGTPGR.V                      |
| 0.999881 | 0.9876 K.AFGQAK[325.13]HQPTAIIAK.T                     |
| 0.999881 | 0.9935 K.RVTIMPK[325.13]DIQLAR.R                       |
| 0.999881 | 0.9696 R.LK[325.13]LEPHEGLLLR.F                        |
| 0.99988  | 0.9998 R.GWLK[325.13]SNVSDAVAQSTR.I                    |
| 0.99988  | 0.9971 K.EITALAPSTMK[325.13]IK.I                       |
| 0.99988  | 0.9985 R.LGQSDPAPLQHQMIDIYQK[325.13]R.C                |
| 0.99988  | 0.9992 R.TFIAIK[325.13]PDGVQR.G                        |
| 0.99988  | 0.9996 R.FELSC[160.03]YSLAPQIK[325.13]VIAPWR.M         |
| 0.99988  | 0.999 R.SSSGLLEWESK[325.13]SDALETGLFLNHYQMK.N          |
| 0.99988  | 0.9913 K.KEDLYLK[325.13]PIQR.T                         |
| 0.99988  | 0.9996 K.YGIIC[160.03]MEDLIHEIYTVGK[325.13]R.F         |
| 0.999879 | 0.9977 R.AK[325.13]HHAISAK.L                           |
| 0.999879 | 0.9993 R.K[325.13]TSYAQHQQVR.Q                         |
| 0.999879 | 0.9997 R.LLM[147.04]HGK[325.13]EVGSIIQK.K              |
| 0.999879 | 0.9998 R.K[325.13]HGVVPLATYMR.I                        |
| 0.999878 | 0.9993 R.EDSQRPGAHLTVK[325.13]K.I                      |
| 0.999878 | 0.9992 K.KHPDASVNFSEFSK[325.13]K.C                     |
| 0.999878 | 0.9969 K.SGDAAIVDM[147.04]VPGK[325.13]PMC[160.03]VESFS |
| 0.999878 | 0.9995 R.ENEVLEAWK[325.13]SLLDAC[160.03]ESR.R          |
| 0.999878 | 0.9995 R.HEAFEK[325.13]SAATWDER.F                      |
| 0.999878 | 0.9994 K.ISMPDFDLHLK[325.13]GPK.V                      |

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| 0.999878 | 0.9992 K.TIGGGDDSF TTFFC[160.03]ETGAGK[325.13]HVPR.A     |
| 0.999878 | 0.9994 K.MPEMHFK[325.13]TPK.I                            |
| 0.999878 | 0.9904 R.VSGPYFPTLLGLSLQVLEPPQH GALQK[325.13]EDGPQAR.    |
| 0.999877 | 0.9984 K.VHSFPTLK[325.13]FFPASADR.T                      |
| 0.999877 | 0.9985 K.TVTAM[147.04]DVVYALK[325.13]R.Q                 |
| 0.999877 | 0.992 K.EK[325.13]LC[160.03]YVALDFENEMATAASSSSLEKSYELF   |
| 0.999877 | 0.9988 K.ADK[325.13]DYHFK.V                              |
| 0.999877 | 0.9991 R.YFPTQALNFAFKDK[325.13]YK.Q                      |
| 0.999877 | 0.9971 R.LDHK[325.13]FDLMYAK.R                           |
| 0.999877 | 0.9995 R.LK[325.13]ALGTLVSHVTLR.L                        |
| 0.999876 | 0.9993 R.FQLQATTK[325.13]EGPGEAIVR.E                     |
| 0.999876 | 0.9937 R.FGFPEGSVELYAEK[325.13]VATR.G                    |
| 0.999876 | 0.9988 K.IK[325.13]IIAPPERK.Y                            |
| 0.999876 | 0.9999 R.NIK[325.13]VGRPSNIGQAQPIIDQLAEER.A              |
| 0.999876 | 0.9995 R.KK[325.13]TATAVAHC[160.03]K.R                   |
| 0.999875 | 0.9991 K.SAPATGGVK[325.13]KPHR.Y                         |
| 0.999875 | 0.9978 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y        |
| 0.999875 | 0.9993 K.AVLFC[160.03]LSEDK[325.13]K.N                   |
| 0.999875 | 0.9914 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V                |
| 0.999875 | 0.9986 R.GVNASAQK[325.13]FATDGEGYKPC[160.03]DPQVIR.D     |
| 0.999875 | 0.9996 R.VNVPVIGGHAGK[325.13]TIIP LISQC[160.03]TPK.V     |
| 0.999875 | 0.9991 R.VIFGLFGK[325.13]TVPK.T                          |
| 0.999875 | 0.6818 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN     |
| 0.999874 | 0.9983 R.YLEGTSC[160.03]IAGVLVPAK[325.13]DQPGRQEK.M      |
| 0.999874 | 0.9995 K.SYENQKPPFDAK[325.13]NPFLAAVTTNR.K               |
| 0.999874 | 0.9996 R.LALQALTEK[325.13]LLR.S                          |
| 0.999874 | 0.9998 R.K[325.13]NNFSDTGNGFGIQEHIDLGK.Y                 |
| 0.999873 | 0.9992 K.LWNTLGVC[160.03]K[325.13]YTVQDESHSEWVSC[160.03] |
| 0.999873 | 0.9991 R.GLGK[325.13]GFVPSPTSQPGGHESLVDR.W               |
| 0.999873 | 0.9998 K.FHEAQLSEK[325.13]ISLQAIQQLVR.K                  |
| 0.999872 | 0.8954 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G             |
| 0.999871 | 0.9992 R.MIAGQVLDINLAAEPK[325.13]VNR.G                   |
| 0.999871 | 0.9994 K.VINTGIK[325.13]VWC[160.03]R.N                   |
| 0.999871 | 0.9995 R.VMK[325.13]FSVSPVVR.V                           |
| 0.999871 | 0.9977 K.NAQK[325.13]SNQNGKDSKPSSTPR.S                   |
| 0.999871 | 0.9994 R.GK[325.13]PLPEYHVR.I                            |
| 0.999871 | 0.9988 K.TRDENIK[325.13]VGSPFELVVSGNK.R                  |
| 0.999871 | 0.9993 R.TSSAQVEGGVHSLHSYEK[325.13]R.L                   |
| 0.99987  | 0.9996 K.K[325.13]EMQPTHPIR.L                            |
| 0.99987  | 0.9996 K.ILIANTGMDTDKIK[325.13]IFGSR.V                   |
| 0.99987  | 0.9991 R.TFSWASVTSK[325.13]NLPPSGAVPVTGIPPHVVK.V         |
| 0.99987  | 0.9984 K.LNILK[325.13]LAPGGHVGR.F                        |
| 0.99987  | 0.9993 K.K[325.13]SAEFLHMLK.N                            |
| 0.999869 | 0.9996 R.FK[325.13]EANNFLWPFK.L                          |
| 0.999869 | 0.9994 K.NLK[325.13]LGIHEDSTNR.R                         |
| 0.999869 | 0.9994 K.KFYEQFSK[325.13]NIK.L                           |
| 0.999869 | 0.9994 R.YK[325.13]ATGLHFR.H                             |

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| 0.999869 | 0.9993 K.K[325.13]KDQVTAQEIFQDNHEDGPTAK.K             |
| 0.999869 | 0.9994 R.K[325.13]IAKAFAISGPFNVQFLVK.G                |
| 0.999868 | 0.999 R.YALYDATYETK[325.13]ESK.K                      |
| 0.999868 | 0.9994 K.ANPFGGASHAK[325.13]GIVLEK.V                  |
| 0.999868 | 0.9994 K.WLK[325.13]EDKLEC[160.03]SEELGDLVK.S         |
| 0.999868 | 0.8738 K.VK[325.13]DALEFWLQAGVDGFQVR.D                |
| 0.999868 | 0.9994 R.VHFK[325.13]NTR.E                            |
| 0.999868 | 0.9662 R.LK[325.13]LEPHEGLLLR.F                       |
| 0.999868 | 0.9879 K.VMIGENVDEK[325.13]HLPTLDHPIIPADYVAIK.A       |
| 0.999867 | 0.9993 K.AENGK[325.13]LVINGNPITIFQER.D                |
| 0.999867 | 0.9994 R.GDLGIEIPA EK[325.13]VFLAQK.M                 |
| 0.999867 | 0.9981 K.VEGGVK[325.13]GGQIGLQAPGLSVSGPQGHLESGSGK.V   |
| 0.999867 | 0.9998 K.K[325.13]GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLS |
| 0.999867 | 0.9994 K.VDGHK[325.13]DIQMPDGIR.R                     |
| 0.999867 | 0.9936 K.TEWLDGK[325.13]HVVFGK.V                      |
| 0.999867 | 0.9099 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F               |
| 0.999866 | 0.9999 R.YTC[160.03]HVQHEGLPK[325.13]PLTLR.W          |
| 0.999866 | 0.9996 K.GVVEVTHDLQK[325.13]HLAGLGLTEAIDK.N           |
| 0.999866 | 0.9977 R.NDNDTFTVK[325.13]YTPR.G                      |
| 0.999866 | 0.9866 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K       |
| 0.999866 | 0.9993 R.MLQTLK[325.13]ELEAHSAEAR.A                   |
| 0.999866 | 0.9995 R.GSNTIASAAADKIPGLLGVFQK[325.13]LIASK.A        |
| 0.999866 | 0.9999 K.VGAVDADK[325.13]HHS LGGQYGVQGFPTIK.I         |
| 0.999866 | 0.9991 R.TLTAVHDAILEDLVFPSEIVGK[325.13]R.I            |
| 0.999865 | 0.9991 R.TKLQNK[325.13]EHVIEALR.R                     |
| 0.999865 | 0.9991 R.ALSTGEK[325.13]GFGYK.G                       |
| 0.999865 | 0.9996 R.VITEEEKNFK[325.13]AFASLR.M                   |
| 0.999865 | 0.9991 K.NQQFHK[325.13]ER.E                           |
| 0.999865 | 0.9999 K.VLTFALSEEVRPQDTVSVIGGVAGGSK[325.13]HGR.K     |
| 0.999865 | 0.9999 K.NKPK[325.13]WLLQGIFSTTVLC[160.03]QK.L        |
| 0.999864 | 0.9995 R.K[325.13]EGGLGPLNIPLLADVTR.R                 |
| 0.999864 | 0.9994 K.YGK[325.13]IVGC[160.03]SVHK.G                |
| 0.999863 | 0.9975 R.AWTSK[325.13]GSGPLSPSIQSR.T                  |
| 0.999863 | 0.9994 R.NVDSNNK[325.13]ELSIAR.G                      |
| 0.999863 | 0.9991 K.K[325.13]VNVTVDYIRPASPATETVPAFSER.T          |
| 0.999863 | 0.998 R.VLEALLPLK[325.13]GLEER.V                      |
| 0.999863 | 0.9998 R.DTLFC[160.03]YHK[325.13]ASEVFLQR.L           |
| 0.999863 | 0.9999 R.LWK[325.13]AIHTAPVATMAFDPTSTLLATGGC[160.03]D |
| 0.999863 | 0.9837 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I |
| 0.999862 | 0.8872 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G          |
| 0.999862 | 0.9877 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI |
| 0.999862 | 0.9991 K.NFGIGQDIQPK[325.13]R.D                       |
| 0.999862 | 0.9994 R.DIFNK[325.13]GFGFGLVK.L                      |
| 0.999862 | 0.9997 K.FTLK[325.13]AGQVVTIWAAGAGATHSPPTDLVWK.A      |
| 0.999862 | 0.9906 R.HGESGSM[147.04]AVFHQTQGSPSYSESK[325.13]R.L   |
| 0.999862 | 0.9993 R.QLLHNFPPDQLTSSGAPFWSGPK[325.13]R.C           |
| 0.999861 | 0.9997 R.TLDAHEDK[325.13]VWGLHC[160.03]SR.L           |

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| 0.999861 | 0.9984 | K.AVTK[325.13]YTSSK.-                              |
| 0.999861 | 0.9992 | R.VTIMPK[325.13]DIQLAR.R                           |
| 0.999861 | 0.9993 | R.VSQEHPVVLTK[325.13]FVEGAR.E                      |
| 0.999861 | 0.9977 | R.VFSGLVSTGLK[325.13]VR.I                          |
| 0.999861 | 0.9992 | R.K[325.13]TSYAQHQQVR.Q                            |
| 0.99986  | 0.9993 | R.GGEPNQRPELK[325.13]NHIDR.V                       |
| 0.99986  | 0.9994 | K.KAGGTKPKK[325.13]PVGAAK.K                        |
| 0.99986  | 0.9617 | R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S             |
| 0.99986  | 0.9911 | K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V    |
| 0.99986  | 0.9994 | R.K[325.13]VVPC[160.03]LVTPVTGR.E                  |
| 0.99986  | 0.9991 | R.GPIK[325.13]FNVWDTAGQEK.F                        |
| 0.99986  | 0.9994 | K.VTDFGDK[325.13]VEDPTFLNQLQSGVNR.W                |
| 0.99986  | 0.8859 | R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G              |
| 0.99986  | 0.9994 | K.HVQSK[325.13]AIEAR.H                             |
| 0.999859 | 0.9994 | K.AAEVLNK[325.13]HSLSGRPLK.V                       |
| 0.999859 | 0.9996 | R.AVLK[325.13]FAAATGATPIAGR.F                      |
| 0.999859 | 0.9992 | K.NLNTLC[160.03]WAIGSISGAMHEEDEK[325.13]R.F        |
| 0.999858 | 0.9992 | R.GAFGK[325.13]PQGTVAR.V                           |
| 0.999858 | 0.9978 | R.TLLAK[325.13]NLPYK.V                             |
| 0.999858 | 0.9978 | K.EDLYLK[325.13]PIQR.T                             |
| 0.999858 | 0.9996 | K.AM[147.04]K[325.13]GLGTDEESILTLLTSR.S            |
| 0.999858 | 0.9867 | K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]K.K |
| 0.999858 | 0.9991 | R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D           |
| 0.999858 | 0.9991 | R.DLFEDELVPLFEK[325.13]AGPIWDLR.L                  |
| 0.999857 | 0.9991 | R.YQK[325.13]STELLIR.K                             |
| 0.999856 | 0.9993 | R.GREEYEGPNK[325.13]KPR.F                          |
| 0.999856 | 0.9993 | R.LGQEATVGK[325.13]ATGFLK.N                        |
| 0.999856 | 0.9983 | K.LSPDAIPGK[325.13]WTSQDSELLGMEFSGR.D              |
| 0.999856 | 0.9997 | K.FYGDEEK[325.13]DKGLQTSQDAR.F                     |
| 0.999856 | 0.0544 | R.HQGVMVGMGQK[325.13]DSYVGDEAQSK.R                 |
| 0.999856 | 0.9991 | K.VK[325.13]EFGIDPQNMFEFWDWVGGR.Y                  |
| 0.999856 | 0.9988 | K.VGLQVVAVK[325.13]APGFGDNRK.N                     |
| 0.999856 | 0.9998 | K.NIK[325.13]HSGNITFDEIVNIAR.Q                     |
| 0.999856 | 0.9978 | R.LDYLSSLKVK[325.13]GLVLGPIHK.N                    |
| 0.999855 | 0.9993 | K.SDFGK[325.13]FVLSSGK.F                           |
| 0.999855 | 0.997  | R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTTEVK.S      |
| 0.999855 | 0.9992 | K.AETAAK[325.13]HGAEQVK.I                          |
| 0.999855 | 0.9996 | K.FQEHIIQAPK[325.13]PVEAIK.R                       |
| 0.999855 | 0.9995 | R.SPVFLYEDHTGK[325.13]PGPEDYPLFR.G                 |
| 0.999855 | 0.9994 | K.IVGC[160.03]SVHK[325.13]GFAFVQYVNER.N            |
| 0.999855 | 0.9996 | R.IYWMNSK[325.13]ILHIK.Q                           |
| 0.999854 | 0.9979 | R.GVLK[325.13]EYGVKVLGTSVESIMATEDR.Q               |
| 0.999854 | 0.9996 | K.DSPSVWAAVPGK[325.13]TFVNITPAEVGVLVGK.D           |
| 0.999854 | 0.9997 | K.K[325.13]TKPYIQVDIGGGQTK.T                       |
| 0.999854 | 0.9996 | K.VSPVSHK[325.13]VDLAVLAAVEIR.G                    |
| 0.999853 | 0.9998 | R.NGNPAPK[325.13]ITWYR.N                           |
| 0.999853 | 0.9996 | R.VLALSVETDYTFPLAEK[325.13]VK.A                    |

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| 0.999853 | 0.9997 K.GEVIK[325.13]AWDIAIATMK.V                      |
| 0.999853 | 0.9862 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]V |
| 0.999853 | 0.9998 K.HGEVC[160.03]PAGWK[325.13]PGSETIIPDPAGK.L      |
| 0.999853 | 0.9972 K.NMAEQIIQEIYSQIQSK[325.13]K.K                   |
| 0.999852 | 0.9996 K.LAHK[325.13]YRPETK.Q                           |
| 0.999852 | 0.9987 K.K[325.13]AASGEAKPK.A                           |
| 0.999852 | 0.9891 K.AFGQAK[325.13]HQPTAIIAK.T                      |
| 0.999852 | 0.9997 K.KQELLEALTK[325.13]HFQD.-                       |
| 0.999851 | 0.9969 K.EITALAPSTMK[325.13]JK.I                        |
| 0.999851 | 0.9928 R.VETGVLK[325.13]PGM[147.04]VVTFAFVNVTTTEVK.S    |
| 0.999851 | 0.9999 K.LEVAPISDIIAIK[325.13]SPDTFVR.T                 |
| 0.999851 | 0.9997 K.RPAEDMEEEQAFK[325.13]R.S                       |
| 0.999851 | 0.9998 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q                |
| 0.999851 | 0.9977 K.APK[325.13]ISMPDVDLHLK.G                       |
| 0.999851 | 0.1056 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.99985  | 0.9992 K.VK[325.13]LEAEIATYR.R                          |
| 0.99985  | 0.9978 R.SKGQESFK[325.13]K.Q                            |
| 0.99985  | 0.999 R.VIFGLFGK[325.13]TVPK.T                          |
| 0.99985  | 0.9995 R.FELSC[160.03]YSLAPQIK[325.13]VIAPWR.M          |
| 0.99985  | 0.9996 K.RPWITGDESIVGLMK[325.13]DIVGANER.E              |
| 0.999849 | 0.9993 K.LGLAK[325.13]SIHHAR.V                          |
| 0.999849 | 0.9989 R.DIM[147.04]LATGK[325.13]LSPDAIPGK.W            |
| 0.999849 | 0.999 R.LIDFLEC[160.03]GK[325.13]TNLR.R                 |
| 0.999848 | 0.9906 R.HAYYVTVEAAPYWLHK[325.13]PQSHLYGPGETAR.L        |
| 0.999848 | 0.9995 R.SPK[325.13]LFYADHPFIFLVR.D                     |
| 0.999848 | 0.9996 R.YPMAVGLNK[325.13]GHK.V                         |
| 0.999848 | 0.9993 K.VPPGYHPLDVEK[325.13]EWGK.L                     |
| 0.999847 | 0.9993 R.GQHVPGPSFQFTVGPLGEGGAHK[325.13]VR.A            |
| 0.999847 | 0.9984 K.TDK[325.13]TLVLLMGK.E                          |
| 0.999847 | 0.9993 K.SSFTVDC[160.03]SK[325.13]AGNNMMLLVGVHGPR.T     |
| 0.999847 | 0.9993 K.FAGGLHFSGPK[325.13]VEGGVK.G                    |
| 0.999847 | 0.6897 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.999846 | 0.9856 R.M[147.04]VNHFAIEFK[325.13]R.K                  |
| 0.999846 | 0.9976 R.TLLAK[325.13]NLPYK.V                           |
| 0.999846 | 0.9866 R.FLEQQNK[325.13]ILLAELEQLK.G                    |
| 0.999846 | 0.9991 R.FSK[325.13]SQLDIIHSLK.K                        |
| 0.999846 | 0.9993 K.FK[325.13]IPEMHLK.A                            |
| 0.999845 | 0.999 R.KNHLEGK[325.13]AAISNK.I                         |
| 0.999845 | 0.9995 R.MISK[325.13]QFHHQLR.V                          |
| 0.999845 | 0.9955 R.TAQSTPSAPPQK[325.13]VMC[160.03]VSMGSTTVR.V     |
| 0.999845 | 0.9999 K.TYNFLPEFLVSTQK[325.13]TYGADLASVDFQHASEDAR.K    |
| 0.999844 | 0.9996 K.VLDFEHFLPMLQTVAK[325.13]NK.D                   |
| 0.999844 | 0.9816 R.WLPAGDALLQMITIHLPSVTAQK[325.13]YR.C            |
| 0.999844 | 0.9991 R.DPQFQK[325.13]LQQWYR.E                         |
| 0.999844 | 0.9406 R.K[325.13]LFIGGLSFETTEESLR.N                    |
| 0.999844 | 0.3032 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999844 | 0.9999 R.LVFVPLLLLC[160.03]NIK[325.13]PR.R              |

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| 0.999844 | 0.9979 R.ALTQTGGPHVK[325.13]AR.V                       |
| 0.999844 | 0.9991 R.GGNRFEPYANPTK[325.13]R.Y                      |
| 0.999844 | 0.9997 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT |
| 0.999844 | 0.999 R.SSGPGAGLC[160.03]LFPLDK[325.13]VHAK.M          |
| 0.999843 | 0.9991 K.KAK[325.13]KPALVAK.S                          |
| 0.999843 | 0.9996 K.K[325.13]PGSKNFQNIFFSATLHLSNIPPSVSEEDLK.V     |
| 0.999843 | 0.9948 R.HNGTGGK[325.13]SIYGEK.F                       |
| 0.999843 | 0.9999 R.LPNFGSHVLTPEAEMEAFK[325.13]QR.H               |
| 0.999842 | 0.9968 R.FANYIDK[325.13]VR.F                           |
| 0.999842 | 0.9993 R.IAAYK[325.13]SILQER.V                         |
| 0.999842 | 0.9994 R.EASLGEASK[325.13]LQQFLR.D                     |
| 0.999842 | 0.9978 K.LK[325.13]LEAELGNMQGLVEDFK.N                  |
| 0.999842 | 0.9992 R.LNVLEK[325.13]SSPGHR.A                        |
| 0.999841 | 0.9971 R.TYTWLK[325.13]GHQK.S                          |
| 0.999841 | 0.999 K.LLQK[325.13]GIHPTIISSEFQK.A                    |
| 0.999841 | 0.9995 K.YLAIAPPIK[325.13]QSTIVC[160.03]HNR.V          |
| 0.999841 | 0.9992 K.SPNK[325.13]HNR.L                             |
| 0.99984  | 0.9977 K.TIAPALVSK[325.13]K.L                          |
| 0.99984  | 0.9977 K.K[325.13]VGYTPDWIFLLR.N                       |
| 0.99984  | 0.9952 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S |
| 0.99984  | 0.9868 K.VK[325.13]GLVLGPIHK.N                         |
| 0.999839 | 0.9992 K.QIFLGGVDK[325.13]HTQFWR.Y                     |
| 0.999839 | 0.9993 R.K[325.13]GNLQLQGTR.L                          |
| 0.999839 | 0.9991 K.VTQQGLK[325.13]MVVPGLDGAQIPR.D                |
| 0.999839 | 0.9985 R.IYDLNKPEAEPK[325.13]EISGHTSGIK.K              |
| 0.999839 | 0.9999 R.VVVSGLPPSGSWQDLK[325.13]DHMR.E                |
| 0.999839 | 0.9996 R.LLM[147.04]HGK[325.13]EVGSIIHK.K              |
| 0.999839 | 0.9999 K.IAGYVTHLMK[325.13]R.I                         |
| 0.999838 | 0.9996 R.LAK[325.13]AAFDDAIAELDTLSEESYK.D              |
| 0.999838 | 0.9966 K.GATYGK[325.13]PVHHGVNQLK.F                    |
| 0.999837 | 0.9981 R.TM[147.04]PVEQVFAK[325.13]NFR.V               |
| 0.999837 | 0.999 R.M[147.04]IAGQVLDINLAAEPK[325.13]VNR.G          |
| 0.999837 | 0.9979 R.AEAESMYQIK[325.13]YEELQSLAGK.H                |
| 0.999837 | 0.999 R.VVLIGGK[325.13]PDR.V                           |
| 0.999837 | 0.9971 R.EAPHVK[325.13]NNAIISLR.K                      |
| 0.999837 | 0.9999 R.DAVSGMGVIVHIEK[325.13]DK.I                    |
| 0.999837 | 0.9993 R.VSVADHSLHLSK[325.13]AK.I                      |
| 0.999837 | 0.9992 K.YGGPYHIGGSPFK[325.13]AK.V                     |
| 0.999836 | 0.9993 K.KVIQYLAYVASSHK[325.13]SK.K                    |
| 0.999836 | 0.9998 R.DILK[325.13]EMFPYEASTPTGISASC[160.03]R.R      |
| 0.999836 | 0.9993 K.K[325.13]AALSALLESFLK.Q                       |
| 0.999836 | 0.9993 R.ESPEVLLTDILK[325.13]HGK.R                     |
| 0.999836 | 0.9989 K.NQQFHK[325.13]ER.E                            |
| 0.999835 | 0.9984 K.ADK[325.13]DYHFK.V                            |
| 0.999835 | 0.9998 K.ENK[325.13]LFEHYQELK.I                        |
| 0.999834 | 0.9999 R.DVFLPK[325.13]PTWGNHTPIFR.D                   |
| 0.999834 | 0.978 R.GGMGSGGLATGIAGGLAGMGGIQNEK[325.13]ETMQSLI      |

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| 0.999834 | 0.9895 R.EVTVPVFYPTK[325.13]VWLEVEPVGMLK.E             |
| 0.999834 | 0.9991 R.EDSVKPGAHLTVK[325.13]K.I                      |
| 0.999833 | 0.9993 R.K[325.13]YAYSAASGGR.R                         |
| 0.999833 | 0.9961 R.AK[325.13]VTLNGVPAQPLGPR.A                    |
| 0.999833 | 0.9993 R.GFAFVTFESPADAK[325.13]DAAR.D                  |
| 0.999833 | 0.9995 R.LAATEK[325.13]LLEYLR.G                        |
| 0.999833 | 0.999 K.GSETPGATPGSK[325.13]IWDPTPSHTPAGAATPGR.G       |
| 0.999833 | 0.6664 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E      |
| 0.999832 | 0.9988 K.NTHC[160.03]SSLPHYQK[325.13]LK.K              |
| 0.999832 | 0.0938 R.LK[325.13]LEPHEGLLLR.F                        |
| 0.999832 | 0.9999 R.TGDGK[325.13]ILYSQC[160.03]GDVMR.A            |
| 0.999832 | 0.9995 R.GTNLNK[325.13]AM[147.04]TLQEAEAFVGAER.C       |
| 0.999832 | 0.9974 R.AALQEELQLC[160.03]K[325.13]GLVQALQTK.V        |
| 0.999832 | 0.9998 K.DK[325.13]MMNGGHHYTYSEN.R.V                   |
| 0.999832 | 0.9998 K.DK[325.13]MMNGGHHYTYSEN.R.V                   |
| 0.999832 | 0.9996 K.SEVQQPVHPK[325.13]PLSPDSR.A                   |
| 0.999832 | 0.9994 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q              |
| 0.999831 | 0.9976 K.SLVSK[325.13]GTLVQTK.G                        |
| 0.999831 | 0.9991 K.VK[325.13]LEAEIATYR.R                         |
| 0.999831 | 0.9991 R.MVQEAER[325.13]YKAEDEK.Q                      |
| 0.999831 | 0.9991 R.FK[325.13]IPGSPPEMGR.G                        |
| 0.999831 | 0.9997 R.ILQEHEQIK[325.13]K.K                          |
| 0.999831 | 0.9947 K.TVDLKPDPWGK[325.13]GYSR.K                     |
| 0.999831 | 0.9995 R.VITEEKNFK[325.13]AFASLR.M                     |
| 0.999831 | 0.9948 R.TLSDYNIQK[325.13]ESTLHLVLR.L                  |
| 0.99983  | 0.9968 R.TLLIK[325.13]TVETR.D                          |
| 0.99983  | 0.9996 K.TVMPYISTTPAK[325.13]LR.N                      |
| 0.99983  | 0.9995 K.SNNVEMDWVLK[325.13]HTGPNSPDTANDGFVR.L         |
| 0.99983  | 0.9991 R.K[325.13]YSNEDTLSVALPYFWEHFDK.D               |
| 0.99983  | 0.9996 R.K[325.13]NGGLGHMNIALLSDLTK.Q                  |
| 0.99983  | 0.9996 R.K[325.13]NGGLGHMNIALLSDLTK.Q                  |
| 0.99983  | 0.9991 R.LFTK[325.13]VKPLLQVSR.Q                       |
| 0.999829 | 0.998 R.K[325.13]EAESC[160.03]DC[160.03]LQGFQLTHSLGGGT |
| 0.999829 | 0.9345 K.WGDAGAEEYVVESTGVFTTMEK[325.13]AGAHLLQGGAK.R   |
| 0.999829 | 0.999 R.FVGHTK[325.13]DVLSVAFSSDN.R.Q                  |
| 0.999828 | 0.9991 R.K[325.13]YAYSAASGGR.R                         |
| 0.999828 | 0.9991 K.VFQFLNAK[325.13]C[160.03]ESAFLSK.R            |
| 0.999828 | 0.9997 R.ITK[325.13]VLNMKPPEILSMIEEAAGTR.M             |
| 0.999827 | 0.9993 K.DLAGSIIGK[325.13]GGQR.I                       |
| 0.999827 | 0.9727 R.DLTDYLM[147.04]K[325.13]ILTER.G               |
| 0.999827 | 0.999 R.RTK[325.13]TEISEMNR.N                          |
| 0.999827 | 0.9991 R.TPC[160.03]EEILVK[325.13]HVGSR.L              |
| 0.999826 | 0.9976 R.K[325.13]MFTLLDVVNR.K                         |
| 0.999826 | 0.9997 R.SYSK[325.13]LLC[160.03]GLLAER.L               |
| 0.999826 | 0.9976 R.K[325.13]MFTLLDVVNR.K                         |
| 0.999826 | 0.9992 K.WHDK[325.13]QYK.K                             |
| 0.999826 | 0.9997 R.KGPAPELQGEVALAPEEELDPMAMTQK[325.13]YEEHV      |

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| 0.999825 | 0.9992 K.YIEIYVQK[325.13]VNPSR.L                          |
| 0.999825 | 0.9992 K.YGK[325.13]DATNVGDEGGFAPNILENK.E                 |
| 0.999825 | 0.9934 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                   |
| 0.999825 | 0.9991 K.DANAK[325.13]LSELEAALQR.A                        |
| 0.999825 | 0.9992 R.TPEAVQK[325.13]LLEQGLR.H                         |
| 0.999825 | 0.9953 R.LDSQK[325.13]HIDFSLR.S                           |
| 0.999825 | 0.9992 R.IGAEVYHNLK[325.13]NVIK.E                         |
| 0.999825 | 0.9992 R.EIGTHK[325.13]PLPGITVGDIGPK.F                    |
| 0.999825 | 0.9999 K.K[325.13]IGSGGFGLIYLAFTNKPEK.D                   |
| 0.999825 | 0.9873 R.SVPHLQK[325.13]VFDR.Y                            |
| 0.999824 | 0.9989 R.VDFNVPMK[325.13]NNQITNNQR.I                      |
| 0.999824 | 0.9994 R.SYSK[325.13]LLC[160.03]GLLAER.L                  |
| 0.999824 | 0.9996 R.AAQAPSSFQLLYDLK[325.13]LPVEDK.I                  |
| 0.999824 | 0.9992 K.TVTPAK[325.13]AVTTPGKK.G                         |
| 0.999824 | 0.9973 K.FINYVK[325.13]NC[160.03]FR.M                     |
| 0.999824 | 0.9994 R.SYSK[325.13]LLC[160.03]GLLAER.L                  |
| 0.999824 | 0.9991 R.K[325.13]YSNEDTLSVALPYFWEHFDK.D                  |
| 0.999824 | 0.9995 R.DGVHFK[325.13]PK.E                               |
| 0.999824 | 0.9999 K.AVPLNASK[325.13]QDGPMPKPHSVSLNDTETR.K            |
| 0.999824 | 0.9991 R.IFHELTQTDK[325.13]ALFNR.L                        |
| 0.999824 | 0.9852 R.ALEHFTDLYDIK[325.13]R.A                          |
| 0.999823 | 0.9994 K.GRPC[160.03]K[325.13]IVEMSTSK.T                  |
| 0.999823 | 0.9993 K.SYENQKPPFDAK[325.13]NPFLAAVTTNR.K                |
| 0.999823 | 0.9975 R.NPDDITQEEYGEFYK[325.13]SLTNDWEDHLAVK.H           |
| 0.999823 | 0.9992 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y               |
| 0.999823 | 0.9996 R.K[325.13]VAHSDKPGSTSTASFR.D                      |
| 0.999822 | 0.9987 R.RLYWDDLK[325.13]R.K                              |
| 0.999822 | 0.9914 R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTEVK.S       |
| 0.999822 | 0.9999 K.STVTLWKPVQK[325.13]VEIGQK.R                      |
| 0.999822 | 0.9994 K.LLEPVLLLGK[325.13]ER.F                           |
| 0.999822 | 0.9996 K.IQGEYK[325.13]YTQVGPDHNR.S                       |
| 0.999822 | 0.9966 R.DQHFKV[325.13]IQVK.D                             |
| 0.999822 | 0.9955 R.DALSDLALHFLNK[325.13]M[147.04]K.I                |
| 0.999821 | 0.9902 K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V    |
| 0.999821 | 0.9973 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V                 |
| 0.999821 | 0.9964 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                 |
| 0.999821 | 0.985 R.LEK[325.13]PAKYDDIKK.V                            |
| 0.999821 | 0.9996 K.DLDFEK[325.13]AKPR.M                             |
| 0.999821 | 0.9996 R.GC[160.03]RPGK[325.13]IVQMTEAEVR.G               |
| 0.999821 | 0.9986 K.K[325.13]HGVYNPNK.I                              |
| 0.999821 | 0.999 R.FMQTFVLAPEGSVANK[325.13]FYVHNDIFR.Y               |
| 0.99982  | 0.9989 K.IKGEHPGLSIGDVAK[325.13]K.L                       |
| 0.99982  | 0.9996 K.TAK[325.13]LHVAVK.V                              |
| 0.99982  | 0.9992 K.GRLDYLSSLK[325.13]VK.G                           |
| 0.999819 | 0.9996 R.IHFPLATYAPVISA EK[325.13]AYHEQLTVAEITNAC[160.03] |
| 0.999819 | 0.9992 R.IAAYK[325.13]SILQER.V                            |
| 0.999819 | 0.987 K.ILLAELEQLK[325.13]GQGK.S                          |



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| 0.999819 | 0.9972 R.K[325.13]HGLEVIYMIIEPIDEYC[160.03]VQQLK.E      |
| 0.999819 | 0.9993 R.IVSQLLTMDGLK[325.13]QR.A                       |
| 0.999819 | 0.9992 R.K[325.13]ASDVHEVR.K                            |
| 0.999819 | 0.9991 K.LLLQVQHASK[325.13]QIAADK.Q                     |
| 0.999819 | 0.9996 R.LKPAQK[325.13]AFIGFEGVK.G                      |
| 0.999819 | 0.9995 R.IYWMNSK[325.13]ILHIK.Q                         |
| 0.999818 | 0.9999 R.AVLLGPPGAGK[325.13]GTQAPR.L                    |
| 0.999818 | 0.9996 K.FLAAGTHLGGTNLDFQMEQYIK[325.13]R.K              |
| 0.999818 | 0.9999 K.LILEYVK[325.13]ASEAGEVPFNHEILR.E               |
| 0.999818 | 0.9144 R.DALSDLALHFLNK[325.13]MK.I                      |
| 0.999818 | 0.9999 R.GHFK[325.13]VVDSR.M                            |
| 0.999818 | 0.9989 R.NRPPLPAGTNSK[325.13]GPPDFSSDEEREPTPVLGSGAAA    |
| 0.999817 | 0.9996 R.K[325.13]C[160.03]GETAFIAPQC[160.03]EMPIEWVC[1 |
| 0.999817 | 0.9991 K.LTLDKLDVK[325.13]GK.R                          |
| 0.999817 | 0.9991 K.LTLDKLDVK[325.13]GK.R                          |
| 0.999817 | 0.9925 R.GTK[325.13]VILHLK.E                            |
| 0.999817 | 0.9991 K.MPEMHFK[325.13]TPK.I                           |
| 0.999817 | 0.9991 K.MPEMHFK[325.13]TPK.I                           |
| 0.999817 | 0.999 R.IFHELTQTDK[325.13]ALFNR.L                       |
| 0.999817 | 0.9964 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I        |
| 0.999816 | 0.9993 K.FYHDAK[325.13]EIFGR.I                          |
| 0.999816 | 0.9993 R.GHQK[325.13]EGYGLSWNSNLSGHLLSASDDHTVC[160.0    |
| 0.999816 | 0.9995 R.LVVPATQC[160.03]GSLIGK[325.13]GGC[160.03]K.I   |
| 0.999816 | 0.9978 K.TLQLLK[325.13]VGEEDDGEYR.C                     |
| 0.999816 | 0.9978 K.TLQLLK[325.13]VGEEDDGEYR.C                     |
| 0.999816 | 0.9852 K.ILLAELEQLK[325.13]GQGK.S                       |
| 0.999816 | 0.986 K.IAK[325.13]AFAISGPFNVQFLVK.G                    |
| 0.999815 | 0.9997 K.IITPLNK[325.13]DHIPITDSPVVVQQHMLPPK.K          |
| 0.999815 | 0.9996 K.AAVVK[325.13]FHPIQGHR.V                        |
| 0.999815 | 0.9983 K.FIDTTSK[325.13]FGHGR.F                         |
| 0.999814 | 0.9963 R.K[325.13]HEAFESDLAAHQDR.V                      |
| 0.999814 | 0.9993 R.IFLC[160.03]QGK[325.13]RPR.S                   |
| 0.999814 | 0.9996 R.KEFSFGTITSK[325.13]VMMEGGR.S                   |
| 0.999814 | 0.9992 R.EESGKPGAHVTVK[325.13]K.L                       |
| 0.999813 | 0.9997 K.VANVSLALYK[325.13]GK.K                         |
| 0.999813 | 0.9996 K.SK[325.13]LPKPVDLIK.M                          |
| 0.999813 | 0.9992 K.K[325.13]LKSMEAEMIQLQEELAAAER.A                |
| 0.999813 | 0.9973 K.KAEGGGGGGRPGAPAAAGDGK[325.13]TEQK.G            |
| 0.999812 | 0.9999 R.THIFK[325.13]IHAR.S                            |
| 0.999812 | 0.9992 K.KVEK[325.13]VTISNR.L                           |
| 0.999812 | 0.9931 K.VTLATLK[325.13]MSVQPTVSLGGFEITPPVVL.R          |
| 0.999812 | 0.9956 R.LDHK[325.13]FDLMYAK.R                          |
| 0.999812 | 0.9995 R.KNPIEK[325.13]NLQMWEEMK.K                      |
| 0.99981  | 0.9996 R.EANQAINPK[325.13]LLQLVEDR.G                    |
| 0.99981  | 0.9992 R.YLYTLVITDKEK[325.13]AEK.L                      |
| 0.99981  | 0.9976 R.GLFIDDK[325.13]GILR.Q                          |
| 0.99981  | 0.7033 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSK.R       |

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| 0.99981  | 0.9996 R.HIYAK[325.13]VSGGPSLEQR.F                      |
| 0.999809 | 0.9996 R.NVESYTK[325.13]LGNPTR.S                        |
| 0.999809 | 0.9996 R.SGSK[325.13]FPVFNMSYNPAENAVLLC[160.03]TR.A     |
| 0.999809 | 0.9987 R.ENTQTTIK[325.13]LFQEC[160.03]C[160.03]PHSTDR.V |
| 0.999809 | 0.9995 K.IHK[325.13]NSSTYWEGK.A                         |
| 0.999809 | 0.947 R.MVNHFIAEFK[325.13]R.K                           |
| 0.999808 | 0.9996 K.DWYDVK[325.13]APAMFNIR.N                       |
| 0.999808 | 0.9992 R.ALDTM[147.04]NFDVIK[325.13]GKPVR.I             |
| 0.999808 | 0.9968 R.FHVEEEGKGK[325.13]DASGNK.V                     |
| 0.999807 | 0.9995 R.TDITYPAGFM[147.04]DVISIDK[325.13]TGENFR.L      |
| 0.999807 | 0.9996 K.EDLVFIFWAPESAPLK[325.13]SK.M                   |
| 0.999806 | 0.9988 K.DAIHFYNK[325.13]SLAEHR.T                       |
| 0.999806 | 0.9973 K.FYEQFSK[325.13]NIK.L                           |
| 0.999806 | 0.999 K.DANAK[325.13]LSELEAALQR.A                       |
| 0.999806 | 0.9995 K.VVNPLFEK[325.13]RPK.N                          |
| 0.999805 | 0.9798 K.ADKDYHFK[325.13]VDNDENEHQSLR.T                 |
| 0.999805 | 0.9996 K.K[325.13]AC[160.03]GNFGIPC[160.03]ELR.V        |
| 0.999805 | 0.9814 K.NQK[325.13]DDVAQTDLLQIDPNFGSK.E                |
| 0.999805 | 0.9996 K.GEVIK[325.13]AWDIAIATMK.V                      |
| 0.999805 | 0.9991 R.AQDGDIFFSK[325.13]EHTDTFNFR.I                  |
| 0.999805 | 0.9994 K.K[325.13]GLTPSQIGVILR.D                        |
| 0.999805 | 0.9998 R.YYVGHK[325.13]GK.F                             |
| 0.999805 | 0.9995 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T        |
| 0.999805 | 0.9995 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T        |
| 0.999805 | 0.9985 R.SLHDALC[160.03]VLAQTVK[325.13]DSR.T            |
| 0.999804 | 0.9994 K.NALESYAFNMK[325.13]SAVEDEGLK.G                 |
| 0.999804 | 0.9992 R.AGK[325.13]PVIC[160.03]ATQMLESNIK.K            |
| 0.999804 | 0.9991 R.TLQYK[325.13]LLEPVLLLGK.E                      |
| 0.999804 | 0.9991 R.TLQYK[325.13]LLEPVLLLGK.E                      |
| 0.999804 | 0.9991 K.WNTEDK[325.13]VSHVSTGGGASLELLEGK.I             |
| 0.999804 | 0.9996 R.LGGLTQAPGNPVLAVQINQDK[325.13]NFAFLEFR.S        |
| 0.999803 | 0.9996 R.TFNTSTGGLLLPSDTK[325.13]R.S                    |
| 0.999803 | 0.9996 K.GVALK[325.13]SVTAFFK.W                         |
| 0.999803 | 0.9997 K.K[325.13]PYC[160.03]NAHYPK.Q                   |
| 0.999803 | 0.9991 K.NLK[325.13]LGIHEDSTNR.R                        |
| 0.999803 | 0.9991 K.KFYEQFSK[325.13]NIK.L                          |
| 0.999803 | 0.9991 K.K[325.13]FVIKPIDK.K                            |
| 0.999803 | 0.9987 K.LTLHGLQQYYVK[325.13]LK.D                       |
| 0.999803 | 0.9998 K.TFK[325.13]EFLSLDDSVDETEAVKR.Y                 |
| 0.999803 | 0.9986 K.LTGIK[325.13]HELQANC[160.03]YEEVKDR.C          |
| 0.999802 | 0.9997 K.ALLNNSHYHMAHGK[325.13]DFASR.G                  |
| 0.999802 | 0.9992 K.DLAGSIIGK[325.13]GGQR.I                        |
| 0.999802 | 0.9992 K.YK[325.13]WC[160.03]EYGLTFTEK.W                |
| 0.999802 | 0.2465 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999802 | 0.999 R.VSQEHPVVLTK[325.13]FVEGAR.E                     |
| 0.999802 | 0.9991 R.VHFK[325.13]NTR.E                              |
| 0.999802 | 0.9967 K.LDSEDKDKEGK[325.13]PLLK.A                      |

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| 0.999802 | 0.9929 R.GPVLQLHDLK[325.13]R.E                          |
| 0.999801 | 0.9838 K.SVHELEKSK[325.13]R.A                           |
| 0.999801 | 0.9987 K.LSPDAIPGK[325.13]WTSQDSLLGM[147.04]EFSGR.D     |
| 0.999801 | 0.9985 K.AHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D    |
| 0.9998   | 0.9996 K.HDTK[325.13]LLILALER.L                         |
| 0.9998   | 0.9992 K.LTFDTTFSPNTGK[325.13]K.S                       |
| 0.999799 | 0.9999 R.LGAQALLGAAK[325.13]M[147.04]LLHSEQHPGQLK.D     |
| 0.999799 | 0.8393 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G            |
| 0.999799 | 0.9996 K.ALEAVFGK[325.13]YGR.I                          |
| 0.999799 | 0.9995 K.EK[325.13]THVADFAPEVAWVTR.S                    |
| 0.999799 | 0.9995 R.ETAQAIK[325.13]GM[147.04]HIR.K                 |
| 0.999799 | 0.9991 K.SPVTTLLEC[160.03]MHK[325.13]LGNSC[160.03]EFR.L |
| 0.999798 | 0.9925 R.KPAGAAK[325.13]KPK.K                           |
| 0.999798 | 0.9995 K.SFPKDDPSK[325.13]PVHLTAFLGYK.A                 |
| 0.999798 | 0.9945 R.SIQLDGLVWGASK[325.13]LVPVGYGIR.K               |
| 0.999798 | 0.9996 R.AALLK[325.13]SMLNFLK.K                         |
| 0.999798 | 0.9979 K.TIGGGDDSFNTFFSETGAGK[325.13]HVPR.A             |
| 0.999798 | 0.9999 K.GSQGPLPFHEK[325.13]VLLGSVSLAGGFVGT PADLVNVI    |
| 0.999797 | 0.9897 R.EVTVPVFYPTKEK[325.13]VWLEVEPVGMLK.E            |
| 0.999797 | 0.999 R.FTLTGLKPDTTYDIK[325.13]VR.A                     |
| 0.999797 | 0.9999 R.K[325.13]TLISSTDFLSHPFGIAVFEDK.V               |
| 0.999797 | 0.9991 K.MPEMHFK[325.13]APK.I                           |
| 0.999797 | 0.9996 K.RQELVTK[325.13]IDHILDAL.-                      |
| 0.999796 | 0.9998 R.HISVLVPC[160.03]FLT FPK[325.13]QC[160.03]R.M   |
| 0.999796 | 0.9871 K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V  |
| 0.999796 | 0.9998 K.LFKPGQEAVK[325.13]YQGPR.D                      |
| 0.999796 | 0.9977 K.MVINHLEK[325.13]LFVTNDAATILR.E                 |
| 0.999795 | 0.9971 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L           |
| 0.999795 | 0.996 K.VSASPLLYTLIEK[325.13]TMQNVK.H                   |
| 0.999795 | 0.9991 R.HC[160.03]IAK[325.13]SQER.V                    |
| 0.999794 | 0.9994 R.NFK[325.13]VSNTQDASVSIVDYEPR.R                 |
| 0.999794 | 0.9996 K.K[325.13]FDLGQDVIDFTGHALALYR.T                 |
| 0.999794 | 0.9986 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D       |
| 0.999793 | 0.9929 R.GFGVITYATVEEVDAAMNARPHK[325.13]VDGR.V          |
| 0.999793 | 0.9991 R.K[325.13]GNLQLQGTR.L                           |
| 0.999793 | 0.9988 R.TVPQYK[325.13]YAAGVR.N                         |
| 0.999793 | 0.9994 R.QTATQLLK[325.13]LAHK.Y                         |
| 0.999793 | 0.9999 R.SHDTTSNTLAQLLAK[325.13]AER.V                   |
| 0.999793 | 0.9996 R.AC[160.03]K[325.13]AVGHPFVIQLGR.I              |
| 0.999793 | 0.9955 R.NLGSIAK[325.13]MLQHAASNK.M                     |
| 0.999793 | 0.1867 R.LLLPGELAK[325.13]HAVSEGK.A                     |
| 0.999792 | 0.9996 R.VM[147.04]LGETNPADSK[325.13]PGTIR.G            |
| 0.999792 | 0.9998 R.ILNEK[325.13]VNTPTTTVYR.C                      |
| 0.999792 | 0.9991 R.AYILNLVK[325.13]QIK.K                          |
| 0.999792 | 0.9997 K.AFQYVETHGEVC[160.03]PANWTPDSPTIK[325.13]PSPA   |
| 0.999791 | 0.9996 K.K[325.13]YDAFLASESLIK.Q                        |
| 0.999791 | 0.999 R.ETLMDLSTK[325.13]AFAMTNQILVEK.S                 |

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| 0.999791 | 0.9998 K.GNDISSGTVLSDYVGSGPPK[325.13]GTGLHR.Y            |
| 0.99979  | 0.9996 K.LPNFGFVVFDDSEPVQK[325.13]VLSNRPIMFR.G           |
| 0.99979  | 0.9991 K.HLPTLDHPIIPADYVAIK[325.13]APMFSWPR.L            |
| 0.99979  | 0.9991 R.SPFEVK[325.13]VGTEC[160.03]GNQK.V               |
| 0.99979  | 0.9991 K.EVC[160.03]FAC[160.03]VDGK[325.13]EFR.L         |
| 0.99979  | 0.9996 R.VASATK[325.13]IALYETPTGWK.F                     |
| 0.99979  | 0.9991 K.IEFEGQPVDVDPNK[325.13]QNLIAEVSTK.D              |
| 0.99979  | 0.9995 K.SEVQQPVHPK[325.13]PLSPDSR.A                     |
| 0.99979  | 0.9991 K.AGQK[325.13]LIDVNHYAK.D                         |
| 0.99979  | 0.9991 K.NK[325.13]ITLQDVVSHSK.K                         |
| 0.99979  | 0.9991 K.ELHINLIPNK[325.13]QDR.T                         |
| 0.999789 | 0.9996 K.K[325.13]KEAGGGGVGGPGAK.S                       |
| 0.999789 | 0.9972 R.YAIC[160.03]SALAASALPALVM[147.04]SK[325.13]GHR. |
| 0.999788 | 0.9988 K.TYSAK[325.13]LDNAR.Q                            |
| 0.999788 | 0.9991 K.SK[325.13]FGANAILGVSLAVC[160.03]K.A             |
| 0.999788 | 0.9958 R.VAAAVDLIHK[325.13]SHQGLDR.Q                     |
| 0.999788 | 0.9995 R.K[325.13]NGGLGHMNIALSLDLTK.Q                    |
| 0.999788 | 0.9995 R.K[325.13]NGGLGHMNIALSLDLTK.Q                    |
| 0.999788 | 0.997 R.VIHSELQGGNK[325.13]SPVTLTAYIVTSLLGYR.K           |
| 0.999787 | 0.9995 K.KYHNVGLSK[325.13]C[160.03]EIK.V                 |
| 0.999787 | 0.958 R.YISPDQLADLYK[325.13]SFIK.D                       |
| 0.999787 | 0.9984 R.K[325.13]IEEIKDFLLTAR.R                         |
| 0.999786 | 0.997 K.DDQHFTVTGLHK[325.13]GTTYIFR.L                    |
| 0.999786 | 0.9996 K.K[325.13]EDLVFIFWAPESAPLK.S                     |
| 0.999785 | 0.9995 -.M[147.04]QIFVK[325.13]TLTGK.T                   |
| 0.999785 | 0.9998 R.EPVGTC[160.03]FLQDGTK[325.13]TVEYAPC[160.03]R.S |
| 0.999785 | 0.9996 K.MFIGGLSWDTTK[325.13]K.D                         |
| 0.999785 | 0.9967 K.NQSQGYNQWQQGQFWGQK[325.13]PWSQHYHQGY.-          |
| 0.999785 | 0.9971 K.APK[325.13]ISMPDVLHLK.G                         |
| 0.999785 | 0.9907 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I    |
| 0.999784 | 0.9971 K.VEGGVK[325.13]GGQIGLQAPGLSVSGPQGHLESQSGK.V      |
| 0.999784 | 0.9977 K.FASFIDK[325.13]VR.F                             |
| 0.999784 | 0.9971 R.VLDPFTIK[325.13]PLDR.K                          |
| 0.999784 | 0.9973 K.IGHPAPNFK[325.13]ATAVMPDGQFK.D                  |
| 0.999783 | 0.9995 K.AK[325.13]DPFAHLPK.S                            |
| 0.999783 | 0.9994 K.FQEHIIQAPK[325.13]PVEAIK.R                      |
| 0.999783 | 0.9988 K.DIHTLAQLISAYSLVDPEK[325.13]AK.A                 |
| 0.999783 | 0.9996 K.K[325.13]LKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFR.A    |
| 0.999782 | 0.9995 K.AQAK[325.13]VGSLDNVGHLPAGGAVK.T                 |
| 0.999782 | 0.9996 K.FTISDHPQPIDPLLK[325.13]NC[160.03]IGDFLK.T       |
| 0.999781 | 0.9958 R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H              |
| 0.999781 | 0.9992 K.VVLSK[325.13]LPIGDVATQYFADR.D                   |
| 0.999781 | 0.9908 R.LQLETEIEALK[325.13]EELLFM[147.04]K.K            |
| 0.999781 | 0.9955 K.DLPEHAVLK[325.13]MK.G                           |
| 0.999781 | 0.9995 R.RAAATQPDAK[325.13]DTPDEPWAFPAR.E                |
| 0.999781 | 0.9995 K.HK[325.13]FM[147.04]VQTIFAPPNTSDMEAVWK.E        |
| 0.999781 | 0.9995 K.HK[325.13]FM[147.04]VQTIFAPPNTSDMEAVWK.E        |

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| 0.99978  | 0.9977 | K.VDWLTEK[325.13]MHAR.D                         |
| 0.999779 | 0.9998 | R.VFTK[325.13]VKPLLQVTR.Q                       |
| 0.999778 | 0.9995 | R.IVATK[325.13]PLYVALAQR.K                      |
| 0.999778 | 0.9956 | R.DPYSGSTISLFQAMQK[325.13]GLVLR.Q               |
| 0.999778 | 0.9968 | K.KLEDGPK[325.13]FLK.S                          |
| 0.999778 | 0.9983 | R.GHNC[160.03]PK[325.13]PVLNFYEANFPANVMDVIAR.C  |
| 0.999777 | 0.9998 | R.DHAVVGVYRPPPK[325.13]VK.N                     |
| 0.999777 | 0.9928 | R.HPDSHQLFIGNLPHEVDK[325.13]SELKDFQSYGNVVELR    |
| 0.999777 | 0.9996 | R.TDGK[325.13]VFQFLNAK.C                        |
| 0.999777 | 0.9992 | R.GHYK[325.13]GQQIGK.V                          |
| 0.999777 | 0.9991 | R.KK[325.13]TATAVAHC[160.03]K.R                 |
| 0.999776 | 0.9847 | R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L     |
| 0.999776 | 0.9989 | R.ETGSSK[325.13]GFGFVDFNSEEDAK.A                |
| 0.999776 | 0.9948 | R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M      |
| 0.999776 | 0.9926 | R.VSFELFADK[325.13]VPKTAENFR.A                  |
| 0.999776 | 0.9996 | K.GIIWGEDTLMEYLENPK[325.13]K.Y                  |
| 0.999776 | 0.9997 | R.SNTTSK[325.13]PSHLVDAHTAEVNC[160.03]LSFNPYSEF |
| 0.999776 | 0.9991 | R.LK[325.13]GSGNLEAIHIK.K                       |
| 0.999776 | 0.9991 | R.LK[325.13]GSGNLEAIHIK.K                       |
| 0.999775 | 0.9995 | K.GTVLIK[325.13]TAEELMNFSK.G                    |
| 0.999775 | 0.81   | K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I          |
| 0.999775 | 0.9873 | R.TLSDYNIQK[325.13]ESTLHLVLR.L                  |
| 0.999775 | 0.9994 | R.KNPIEK[325.13]NLQMWEEMK.K                     |
| 0.999774 | 0.9987 | R.EDSQRPGAHLTVK[325.13]K.I                      |
| 0.999774 | 0.9786 | R.NLQNLILTAK[325.13]ADR.T                       |
| 0.999774 | 0.9992 | R.LSHYLQK[325.13]GC[160.03]R.L                  |
| 0.999774 | 0.9999 | R.SYHEEFNPPKEPMK[325.13]DDITGEPLIR.R            |
| 0.999774 | 0.999  | R.DMFC[160.03]K[325.13]ILHGFK.N                 |
| 0.999773 | 0.9957 | R.AK[325.13]HHAISAK.L                           |
| 0.999773 | 0.9999 | R.TK[325.13]TPGPGAQSALR.A                       |
| 0.999773 | 0.9994 | R.DGWPAMGIHGDK[325.13]SQQER.D                   |
| 0.999773 | 0.9992 | R.YIGIVK[325.13]QAGLER.M                        |
| 0.999773 | 0.9991 | K.SK[325.13]IAHLAGVK.D                          |
| 0.999773 | 0.9993 | R.HYPVFENPK[325.13]QGK.L                        |
| 0.999773 | 0.9968 | K.VILHLK[325.13]EDQTEYLEER.W                    |
| 0.999772 | 0.9492 | R.K[325.13]DLYANTVLSGGTTMYPGIADR.M              |
| 0.999772 | 0.999  | K.EGLELLK[325.13]TAIGK.A                        |
| 0.999772 | 0.999  | R.HC[160.03]IAK[325.13]SQER.V                   |
| 0.999772 | 0.9991 | K.KLYDIDVAK[325.13]VNTLIRPDGEK.K                |
| 0.999771 | 0.9995 | R.K[325.13]FAVSQMSALLDSAHLLASSTQR.N             |
| 0.999771 | 0.9942 | R.DALSDLALHFLNK[325.13]M[147.04]K.I             |
| 0.99977  | 0.955  | R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKI  |
| 0.99977  | 0.0862 | R.EHALLAYTLGVK[325.13]QLIVGVNK.M                |
| 0.999769 | 0.9851 | K.KAK[325.13]VAKPK.K                            |
| 0.999769 | 0.9891 | R.SEGVVAVLLTK[325.13]K.S                        |
| 0.999768 | 0.9995 | R.KVK[325.13]FTQQNYHDR.L                        |
| 0.999768 | 0.999  | R.DLQQYQSQAK[325.13]QLFR.K                      |

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| 0.999768 | 0.9916 R.FGFPEGSVELYAEK[325.13]VATR.G                 |
| 0.999768 | 0.9997 R.GINLSDGK[325.13]WHR.I                        |
| 0.999767 | 0.9996 K.SLK[325.13]FATEAAITILR.I                     |
| 0.999767 | 0.9954 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y          |
| 0.999767 | 0.9981 R.RAPFDLFENK[325.13]K.K                        |
| 0.999766 | 0.9995 K.TLGDFAAEYAK[325.13]SNR.S                     |
| 0.999766 | 0.9961 R.K[325.13]FGYVDFESAEDLEK.A                    |
| 0.999766 | 0.9984 R.TLK[325.13]IPAMTIK.N                         |
| 0.999766 | 0.9992 R.SYSK[325.13]LLC[160.03]GLLAER.L              |
| 0.999766 | 0.999 K.AHVVP[160.03]FDASK[325.13]VK.C                |
| 0.999766 | 0.9996 R.LNTGILNK[325.13]HLQDLMEGLTAK.V               |
| 0.999765 | 0.9967 R.LK[325.13]STC[160.03]IYGGAPK.G               |
| 0.999765 | 0.9991 K.C[160.03]C[160.03]SGAIVLTK[325.13]SGR.S      |
| 0.999765 | 0.9999 R.MYGK[325.13]SLYHDISGDTSGDYR.K                |
| 0.999764 | 0.9999 R.HLSDSINQK[325.13]HFEQAIER.V                  |
| 0.999764 | 0.9896 R.FSGWYDADLSPAGHEEAK[325.13]R.G                |
| 0.999763 | 0.9999 R.AFGFSHLEALLDDSK[325.13]ELQR.F                |
| 0.999763 | 0.9985 R.TIAQDYGVLK[325.13]ADEGISFR.G                 |
| 0.999763 | 0.9994 K.SC[160.03]GK[325.13]DGFHIR.V                 |
| 0.999763 | 0.9991 K.FYHDAK[325.13]EIFGR.I                        |
| 0.999762 | 0.9966 K.EDLYLK[325.13]PIQR.T                         |
| 0.999762 | 0.9593 R.FLEQQNK[325.13]ILLAELEQLK.G                  |
| 0.999762 | 0.8664 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI |
| 0.999762 | 0.9995 K.TGTAYTFFTPNNIK[325.13]QVSDLISVLR.E           |
| 0.999762 | 0.9992 R.K[325.13]LPAIALDLLR.L                        |
| 0.999761 | 0.9996 K.K[325.13]GKPHC[160.03]SR.N                   |
| 0.999761 | 0.9797 R.GALQNIIPASTGAAK[325.13]AVGK.V                |
| 0.999761 | 0.999 R.GFAFVTFESPADAK[325.13]DAAR.D                  |
| 0.999761 | 0.9994 R.YGK[325.13]SPYLYPLYGLGELPQGFAR.L             |
| 0.999761 | 0.9992 R.FGLPAAAPC[160.03]PK[325.13]GSFGTAVR.H        |
| 0.999761 | 0.9995 K.GIVK[325.13]DIIHDPGR.G                       |
| 0.99976  | 0.996 K.LDSGK[325.13]ELHINLIPNKQDR.T                  |
| 0.99976  | 0.9989 K.YGK[325.13]DATNVGDEGGFAPNILENK.E             |
| 0.99976  | 0.9989 R.IK[325.13]VFGPGIEGK.D                        |
| 0.99976  | 0.9995 R.K[325.13]YDEVLMVR.N                          |
| 0.99976  | 0.999 R.ALDTM[147.04]NFDVIK[325.13]GKPVR.I            |
| 0.99976  | 0.996 K.LLLQGEADQSLTFIDK[325.13]AMHGELQK.A            |
| 0.999759 | 0.9785 R.ISVYYNEATGGK[325.13]YVPR.A                   |
| 0.999759 | 0.9984 R.FLQDYFDGNLK[325.13]R.Y                       |
| 0.999759 | 0.9996 K.NLKPIK[325.13]PMQFLGDEETVR.K                 |
| 0.999759 | 0.9993 K.K[325.13]TTHFVEGGDAGNREDQINR.L               |
| 0.999758 | 0.9994 K.AAVVK[325.13]FHPIQGHR.V                      |
| 0.999758 | 0.984 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T      |
| 0.999757 | 0.9913 R.GPVLQLHDLK[325.13]R.E                        |
| 0.999757 | 0.9999 R.K[325.13]ASPPSGLWSPAYASH.-                   |
| 0.999757 | 0.9992 R.GTNLNK[325.13]AMTLQEAEAFVGAER.C              |
| 0.999757 | 0.9996 K.IK[325.13]SDHPGISITDLSK.K                    |

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| 0.999757 | 0.9913 R.ALK[325.13]MIVDPVEPHGEMK.F                       |
| 0.999757 | 0.9956 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                 |
| 0.999757 | 0.9995 R.DMHSAKY[325.13]HADGK.K                           |
| 0.999756 | 0.9997 R.K[325.13]VADLYELVQYAGNIIPR.L                     |
| 0.999755 | 0.9978 K.AVTK[325.13]YTSAK.-                              |
| 0.999755 | 0.9996 R.GTK[325.13]LMC[160.03]SLC[160.03]HC[160.03]PGAT  |
| 0.999754 | 0.9963 K.NVK[325.13]LTVSNVLK.E                            |
| 0.999754 | 0.9965 K.VK[325.13]VLPTHDASK.V                            |
| 0.999754 | 0.9995 K.THISK[325.13]GTLGK.F                             |
| 0.999754 | 0.9995 K.DVK[325.13]GSYVSIHSSGFR.D                        |
| 0.999753 | 0.9997 R.DDGYSTK[325.13]DSYSSR.D                          |
| 0.999753 | 0.9992 K.EVDEQMLNVQNK[325.13]NSSYFVEWIPNNVK.T             |
| 0.999753 | 0.9958 R.LK[325.13]LLLPWLEAR.I                            |
| 0.999752 | 0.9449 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M                 |
| 0.999752 | 0.9995 R.DKPLK[325.13]DVIIADC[160.03]GK.I                 |
| 0.999752 | 0.9998 R.NIK[325.13]VGRPSNIGQAQPIIDQLAEEAR.A              |
| 0.999751 | 0.9986 R.GAFGK[325.13]PQGTVAR.V                           |
| 0.999751 | 0.9953 K.EITALAPSTM[147.04]K[325.13]IK.I                  |
| 0.999751 | 0.9939 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.999751 | 0.9982 R.SSIAGLLLK[325.13]ATNEK.L                         |
| 0.999751 | 0.9984 R.SSGPGAGLC[160.03]LFPLDK[325.13]VHAK.M            |
| 0.999751 | 0.999 R.NDLMEYAK[325.13]QHGIPIVTPK.N                      |
| 0.999751 | 0.9978 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D           |
| 0.99975  | 0.9995 K.HDTK[325.13]LLILALER.L                           |
| 0.99975  | 0.8834 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLR.     |
| 0.99975  | 0.9992 R.VNVPVIGGHAGK[325.13]TIIP LISQC[160.03]TPK.V      |
| 0.99975  | 0.9991 R.FAK[325.13]NFLPILFNLYGQPVAAGDTPAPR.R             |
| 0.999749 | 0.9984 R.RPDQQLQGEGK[325.13]IIDR.R                        |
| 0.999749 | 0.9991 R.VLSGEFQIVNPHLLK[325.13]DLTER.G                   |
| 0.999748 | 0.9965 R.TIC[160.03]SHVQNM IK[325.13]GVT LGFR.Y           |
| 0.999748 | 0.9988 R.HGEK[325.13]VEEC[160.03]QR.F                     |
| 0.999748 | 0.9994 K.SEVQQPVHPK[325.13]PLSPDSR.A                      |
| 0.999748 | 0.9932 R.KYGGPPPD SVYSGVQPGIGTEVFVGK[325.13]IPR.D         |
| 0.999748 | 0.9995 R.DKTIIMWK[325.13]LTR.D                            |
| 0.999747 | 0.9991 R.NDSFTTC[160.03]IELGK[325.13]SLLAR.K              |
| 0.999747 | 0.9989 R.SLLVIPNTLAVNAAQDSTD LVAK[325.13]LR.A             |
| 0.999747 | 0.9996 K.ALAPLLAFVTK[325.13]PNSALESC[160.03]SFAR.H        |
| 0.999747 | 0.9999 R.KPGVIDK[325.13]FTSDTKPIINK.V                     |
| 0.999746 | 0.9999 K.IINEVSK[325.13]PLAHHIPVEK.I                      |
| 0.999746 | 0.9995 K.K[325.13]LIYFQLHR.A                              |
| 0.999746 | 0.9991 R.LSHYLQK[325.13]GC[160.03]R.L                     |
| 0.999746 | 0.9951 R.VTYK[325.13]NVPNWHR.D                            |
| 0.999744 | 0.998 K.K[325.13]HGVYNPNK.I                               |
| 0.999743 | 0.9254 R.VSDGLQASPPATLK[325.13]VVAIRPAIQIHR.S             |
| 0.999743 | 0.9703 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M         |
| 0.999743 | 0.9935 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S          |
| 0.999743 | 0.9983 R.NLK[325.13]ASLENSLR.E                            |

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| 0.999743 | 0.9912 K.TAWLDGK[325.13]HVVFGK.V                         |
| 0.999743 | 0.9995 K.FELGK[325.13]LMELHGEHSSSGK.A                    |
| 0.999742 | 0.9963 R.KVDSK[325.13]SLFHYR.Q                           |
| 0.999742 | 0.9984 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV |
| 0.999742 | 0.9984 K.SLETEHK[325.13]ALTSEIALLQSR.L                   |
| 0.999742 | 0.0619 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999741 | 0.9658 R.MVNHFAIEFK[325.13]R.K                           |
| 0.999741 | 0.9985 K.TVIGELPPASSGSALAANVC[160.03]K[325.13]K.I        |
| 0.999741 | 0.9996 R.VLELVSITANK[325.13]NTC[160.03]PGDR.S            |
| 0.999741 | 0.9994 R.LIK[325.13]VHLDK.A                              |
| 0.999741 | 0.9995 K.YK[325.13]QIFLGGVDKR.T                          |
| 0.999741 | 0.9995 K.RK[325.13]TVTAMDVVYALK.R                        |
| 0.99974  | 0.9978 K.K[325.13]HPDASVNFSEFSK.K                        |
| 0.999739 | 0.9979 R.SSFYVNGLTGGQK[325.13]C[160.03]SVIR.D            |
| 0.999739 | 0.1919 R.ADIK[325.13]EMGLSLQWLYSAR.G                     |
| 0.999739 | 0.9982 R.TVSLGAGAK[325.13]DELHIVEAEAM[147.04]NYEGSPIK.'  |
| 0.999739 | 0.9989 K.K[325.13]EKEHASGSGAQSEAAGR.T                    |
| 0.999739 | 0.9992 K.IHK[325.13]NSSTYWEGK.A                          |
| 0.999739 | 0.9985 R.EDSQRPGAHLTVK[325.13]K.I                        |
| 0.999739 | 0.9994 K.AK[325.13]DPFAHLPK.S                            |
| 0.999738 | 0.9978 K.KQGGGLGPMNIPLVSDPK[325.13]R.T                   |
| 0.999737 | 0.9921 R.IM[147.04]GPNYTPGKK[325.13]EDLYLKPIQR.T         |
| 0.999737 | 0.999 K.DWHRPC[160.03]LK[325.13]C[160.03]EK.C            |
| 0.999737 | 0.9989 R.NLHVFTMNPSSEGLK[325.13]DR.A                     |
| 0.999737 | 0.9992 R.RGEFC[160.03]IAK[325.13]FVDGEWYR.A              |
| 0.999737 | 0.9992 R.RGEFC[160.03]IAK[325.13]FVDGEWYR.A              |
| 0.999736 | 0.9977 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L            |
| 0.999736 | 0.9957 R.VTYK[325.13]NVPNWHR.D                           |
| 0.999736 | 0.9962 K.KLEDGPK[325.13]FLK.S                            |
| 0.999735 | 0.9975 R.K[325.13]ESYSVYVYK.V                            |
| 0.999735 | 0.9995 K.DTNGSQFFITTVK[325.13]TAWLDGK.H                  |
| 0.999735 | 0.9991 R.K[325.13]AHLTNQYM[147.04]QR.V                   |
| 0.999734 | 0.9995 R.NINITK[325.13]DLLDLLVEAK.Q                      |
| 0.999734 | 0.998 R.K[325.13]IEEIKDFLLTAR.R                          |
| 0.999733 | 0.9987 R.LGQEATVGK[325.13]ATGFLK.N                       |
| 0.999733 | 0.9996 K.GSAITGPVAK[325.13]EC[160.03]ADLWPR.I            |
| 0.999733 | 0.9995 K.MVVESAYEVIK[325.13]LK.G                         |
| 0.999733 | 0.8759 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI    |
| 0.999733 | 0.9992 R.ALK[325.13]MIVDPVEPHGEM[147.04]K.F              |
| 0.999733 | 0.982 R.TLLIK[325.13]TVETR.D                             |
| 0.999733 | 0.9996 R.VLPSITTEILK[325.13]SVVAR.F                      |
| 0.999732 | 0.9992 R.VFIGNLNTLVVK[325.13]K.S                         |
| 0.999732 | 0.9998 R.EASIDILHSIVK[325.13]R.D                         |
| 0.99973  | 0.9995 R.K[325.13]YEMFAQTLQQSR.G                         |
| 0.99973  | 0.9993 K.EVPNYK[325.13]LITPAVVSER.L                      |
| 0.99973  | 0.9996 R.GMGSLDAMDK[325.13]HLSSQNR.Y                     |
| 0.99973  | 0.9994 R.THQK[325.13]FVIATSTK.I                          |



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| 0.99973  | 0.9996 K.IVSLFAEHNDLQYAAPGGLIGVGTK[325.13]IDPTLC[160.0 |
| 0.99973  | 0.9914 K.GILADEDSSRPVWLK[325.13]AINC[160.03]ATSGVVGLV  |
| 0.999729 | 0.898 R.K[325.13]LFIGGLSFETTEESLR.N                    |
| 0.999729 | 0.9991 R.STGEAFVQFASQEIAEK[325.13]ALK.K                |
| 0.999729 | 0.9994 R.DGWPAMC[160.03]IHGDK[325.13]SQPER.D           |
| 0.999729 | 0.9992 K.SNNVEMDWVLK[325.13]HTGPNSPDTANDGFVR.L         |
| 0.999729 | 0.9972 K.EAESC[160.03]DC[160.03]LQGFQLTHSLGGGTGSGMGTI  |
| 0.999729 | 0.9946 K.LLGK[325.13]VTIAQGGVLPNIQAVLLPK.K             |
| 0.999729 | 0.9999 R.AVGNIVTGTDEQTQVVLNC[160.03]DVLSHFNPILLSHPK[3  |
| 0.999728 | 0.9987 K.LTFDSSFSPNTGK[325.13]K.N                      |
| 0.999728 | 0.9995 K.VAC[160.03]ITEQVLTVLNK[325.13]R.I             |
| 0.999728 | 0.9995 R.EDSVK[325.13]PGAHLTVK.K                       |
| 0.999728 | 0.9996 K.EAEIHSK[325.13]PVFITVK.M                      |
| 0.999727 | 0.9995 R.LYDAYELK[325.13]HALK.G                        |
| 0.999726 | 0.9995 R.VIIK[325.13]YYTR.L                            |
| 0.999726 | 0.9993 K.TC[160.03]TTVAFTQVNSEDK[325.13]GALAK.L        |
| 0.999726 | 0.9996 K.AGLQVYNK[325.13]C[160.03]WK.F                 |
| 0.999726 | 0.9828 R.EVTPVPFYPTK[325.13]VWLEVEPVGMLK.E             |
| 0.999726 | 0.9999 R.VMTIAPGLFGTPLTSLPEK[325.13]VC[160.03]NFLASQVI |
| 0.999726 | 0.996 R.RQQEGFK[325.13]GTFPDAR.E                       |
| 0.999725 | 0.9994 K.LIVLVPPSK[325.13]PTVNIPSSATIGNR.A             |
| 0.999725 | 0.9995 R.ISEVLQK[325.13]LQNEILK.D                      |
| 0.999725 | 0.9999 K.LSSDVLTLIK[325.13]QYC[160.03]R.E              |
| 0.999725 | 0.9983 R.SIPAYLAETLYYAMK[325.13]GAGTDDHTLIR.V          |
| 0.999724 | 0.9993 R.RNPDTQWITK[325.13]PVHK.H                      |
| 0.999724 | 0.9954 R.FHVEEEGKGK[325.13]DASGNK.V                    |
| 0.999723 | 0.9979 R.ILK[325.13]HGINC[160.03]FINR.Q                |
| 0.999723 | 0.9984 K.MQASIEK[325.13]GGSLPK.V                       |
| 0.999723 | 0.9954 K.WK[325.13]PPM[147.04]IDNPSYQGIWKPR.K          |
| 0.999722 | 0.999 R.DVQIGDIVTVGEC[160.03]RPLSK[325.13]TVR.F        |
| 0.999722 | 0.9998 R.GLEAIC[160.03]AK[325.13]FTHEsqR.Q             |
| 0.999721 | 0.9994 K.DQLIYNLLK[325.13]EEQTPQNK.I                   |
| 0.999721 | 0.9994 K.NQALFPAC[160.03]VLK[325.13]NAELK.F            |
| 0.999721 | 0.9966 K.TVTAM[147.04]DVVYALK[325.13]R.Q               |
| 0.999721 | 0.9964 K.AEQPDGLILGMGGQTALNC[160.03]GVELFK[325.13]R.G  |
| 0.999721 | 0.9993 R.DQSAVVVQGLPEGVAFK[325.13]HPENYDLATLK.W        |
| 0.999721 | 0.9816 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T      |
| 0.999721 | 0.9999 K.ELGITALHIK[325.13]LR.A                        |
| 0.99972  | 0.9982 R.ASNGDAWVEAHGK[325.13]LYSPSQIGAFVLMK.M         |
| 0.99972  | 0.9981 R.FDDPGLMLMGFK[325.13]PLVLLK.K                  |
| 0.99972  | 0.9992 K.RPK[325.13]NFGIGQDIQPK.R                      |
| 0.999719 | 0.9996 R.HVFGESDELIGQK[325.13]VAHALAEGLGVIAC[160.03]IG |
| 0.999719 | 0.9998 R.VAAGLQIK[325.13]NSLTSKDPDIK.A                 |
| 0.999719 | 0.9994 R.RWDQTADQTPGATPK[325.13]K.L                    |
| 0.999719 | 0.9994 K.SK[325.13]LPKPVQDLIK.M                        |
| 0.999718 | 0.9998 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L       |
| 0.999718 | 0.9997 R.AALQELLSK[325.13]GLIK.L                       |

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| 0.999718 | 0.9938 R.VK[325.13]GGGHVAQIYAIR.Q                        |
| 0.999718 | 0.9997 K.AMK[325.13]GLGTDEDTIIDITHR.S                    |
| 0.999717 | 0.9993 K.AAVVK[325.13]FHPIQGHR.V                         |
| 0.999715 | 0.9987 R.LTTDFGNAEK[325.13]TDR.F                         |
| 0.999715 | 0.9975 K.INEAVEC[160.03]LLSLK[325.13]AQYK.E              |
| 0.999715 | 0.1769 R.ADIK[325.13]EMGLSLQWLYSAR.G                     |
| 0.999715 | 0.9998 R.YLEVQYK[325.13]PQVHIQMTYPLQGLTR.E               |
| 0.999715 | 0.9973 K.K[325.13]ISSIQSIVPALEIANAHK.R                   |
| 0.999714 | 0.9999 K.HQPHK[325.13]VTQYK.K                            |
| 0.999714 | 0.9706 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                 |
| 0.999714 | 0.995 K.GATLK[325.13]ITLDNAYMEK.C                        |
| 0.999714 | 0.7767 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G             |
| 0.999714 | 0.9996 K.K[325.13]IHTEPQLSAALEYVR.S                      |
| 0.999713 | 0.9998 R.AELRDDPIISTHLAK[325.13]LYDNLLEQNLIR.V           |
| 0.999713 | 0.8453 K.EITALAPSTMKIK[325.13]IIAPPER.K                  |
| 0.999713 | 0.9993 R.YTLHYK[325.13]TDAPLNIR.S                        |
| 0.999713 | 0.9999 R.ELHGQNPVVTPC[160.03]NK[325.13]QFLSQFEMQSR.K     |
| 0.999713 | 0.9995 R.RPFTK[325.13]NLGLEELGIELDPR.G                   |
| 0.999712 | 0.9991 K.NLYIISVK[325.13]GIK.G                           |
| 0.999712 | 0.9995 K.LPDGYEFK[325.13]FPNR.L                          |
| 0.999712 | 0.9982 R.FVGHTK[325.13]DVLSVAFSSDNR.Q                    |
| 0.999711 | 0.9901 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                |
| 0.999711 | 0.9992 R.KTC[160.03]TTVAFTQVNSEDK[325.13]GALAK.L         |
| 0.999711 | 0.9991 K.ALDVMVSTFHK[325.13]YSGK.E                       |
| 0.99971  | 0.9995 R.FSNISAAK[325.13]AVADAIR.T                       |
| 0.99971  | 0.9674 R.APQC[160.03]LGK[325.13]FIEIAAR.K                |
| 0.99971  | 0.998 R.TVSLGAGAK[325.13]DELHIVEAEAM[147.04]NYEGSPIK.'   |
| 0.99971  | 0.9939 R.QLFHPEQLITGK[325.13]EDAANNYAR.G                 |
| 0.99971  | 0.9765 R.LEKPAK[325.13]YDDIKK.V                          |
| 0.999709 | 0.9955 R.GILTLK[325.13]YPIEHGIVTNWDDMEK.I                |
| 0.999708 | 0.9943 K.FHGTVK[325.13]AENGK.L                           |
| 0.999708 | 0.9977 K.HVVFGK[325.13]VK.E                              |
| 0.999708 | 0.999 R.NLFNVVDC[160.03]K[325.13]LHWQK.N                 |
| 0.999708 | 0.9907 K.GILADESSRPVWLK[325.13]AINC[160.03]ATSGVVGLV'    |
| 0.999706 | 0.9985 R.KITIGQAPTEK[325.13]GHTR.T                       |
| 0.999706 | 0.9711 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K          |
| 0.999706 | 0.9952 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.999706 | 0.9986 K.NSSNKPAVTTK[325.13]SPAVKPAAAPK.Q                |
| 0.999706 | 0.9913 K.HGEAQVK[325.13]IWR.R                            |
| 0.999705 | 0.9995 K.YYIEK[325.13]LFER.Y                             |
| 0.999705 | 0.9992 K.GHQK[325.13]SNGEFWDPR.V                         |
| 0.999704 | 0.9996 K.K[325.13]LETAVNLAWTAGNSNTR.F                    |
| 0.999703 | 0.9997 R.ASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGG        |
| 0.999703 | 0.9942 K.FHGTVK[325.13]AENGK.L                           |
| 0.999703 | 0.9991 R.KTVTAM[147.04]DVVYALK[325.13]R.Q                |
| 0.999703 | 0.9991 K.RVTIM[147.04]PK[325.13]DIQLAR.R                 |
| 0.999702 | 0.9994 R.KVK[325.13]FTQQNYHDR.L                          |

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| 0.999702 | 0.9981 R.AFDSAVAK[325.13]ALEHHR.S                         |
| 0.999702 | 0.9991 K.VC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M       |
| 0.999702 | 0.9998 K.IC[160.03]QFK[325.13]LVLLGESAVGK.S               |
| 0.999702 | 0.9941 R.AK[325.13]QIVWNGPVGVFWEAFAR.G                    |
| 0.999702 | 0.9985 K.SPNK[325.13]HNR.L                                |
| 0.999701 | 0.9992 R.KVESTK[325.13]TDSR.D                             |
| 0.999701 | 0.9957 K.FAAK[325.13]GEGQLGPAER.A                         |
| 0.999701 | 0.9979 R.LGGHGPSFPLK[325.13]GITEQQK.E                     |
| 0.999701 | 0.9997 K.LFKPGQEAVK[325.13]YQGPR.D                        |
| 0.9997   | 0.9998 R.ALGNPTNAEVLK[325.13]VLGNPK.S                     |
| 0.9997   | 0.999 K.HQIK[325.13]QAVK.K                                |
| 0.9997   | 0.999 K.HQIK[325.13]QAVK.K                                |
| 0.9997   | 0.9983 R.FMQTFVLAPEGSVANK[325.13]FYVHNDIFR.Y              |
| 0.999699 | 0.9995 K.IVADFSASVK[325.13]KPHTLLQR.V                     |
| 0.999699 | 0.9993 R.IESLSSQLSNLQK[325.13]ESR.A                       |
| 0.999699 | 0.9955 K.SK[325.13]GIAYIEFK.T                             |
| 0.999698 | 0.9957 K.FINYVK[325.13]NC[160.03]FR.M                     |
| 0.999698 | 0.9992 K.FVADGIFK[325.13]AELNEFLTR.E                      |
| 0.999697 | 0.9981 R.YQK[325.13]STELLIR.K                             |
| 0.999697 | 0.9993 R.LK[325.13]LAQQQAALLMQQEER.A                      |
| 0.999697 | 0.9702 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K           |
| 0.999697 | 0.994 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V                  |
| 0.999697 | 0.9977 R.K[325.13]QVVNIPSFIVR.L                           |
| 0.999697 | 0.9991 R.VTFLPTGITFK[325.13]SVTR.E                        |
| 0.999697 | 0.9994 R.K[325.13]DKFSFDLGK.G                             |
| 0.999697 | 0.9995 R.WSK[325.13]QTDVGITHFR.S                          |
| 0.999696 | 0.9929 R.TMPVEQVFAK[325.13]NFR.V                          |
| 0.999696 | 0.9968 R.EGQEDQGLTK[325.13]DYGNSPLHR.F                    |
| 0.999696 | 0.9955 R.TAPDLLPHK[325.13]PLPASAYIEDGR.F                  |
| 0.999696 | 0.9986 R.AQDGDFIFSK[325.13]EHTDTFNFR.I                    |
| 0.999696 | 0.9995 K.VTLEYRPVIDK[325.13]TLNEADC[160.03]ATVPPAIR.S     |
| 0.999696 | 0.9992 R.YPMAVGLNK[325.13]GHK.V                           |
| 0.999695 | 0.999 K.KNPIAK[325.13]IHSDLAEEER.G                        |
| 0.999695 | 0.9994 K.K[325.13]LIYFQLHR.A                              |
| 0.999695 | 0.9984 R.DIENLK[325.13]DASSFLAEWQNITK.G                   |
| 0.999695 | 0.9966 K.KPAAATVTK[325.13]K.V                             |
| 0.999695 | 0.9985 R.K[325.13]GLVGPELHDR.L                            |
| 0.999695 | 0.9959 R.NLGSIAK[325.13]MLQHAASNK.M                       |
| 0.999694 | 0.9342 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKf     |
| 0.999694 | 0.9974 K.IGHPAPNFK[325.13]ATAVM[147.04]PDGQFK.D           |
| 0.999694 | 0.994 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I           |
| 0.999693 | 0.9579 R.WLPAGDALLQMITIHLSPVTAQK[325.13]YR.C              |
| 0.999693 | 0.9993 R.AAATQPDAK[325.13]DTPDEPWAFPAR.E                  |
| 0.999693 | 0.9996 R.SAK[325.13]AGVIFPVGR.M                           |
| 0.999693 | 0.9992 K.LIC[160.03]C[160.03]DILDVLDK[325.13]HLIPAANTGESK |
| 0.999693 | 0.9987 R.K[325.13]PVTVHSR.A                               |
| 0.999693 | 0.993 R.FVPQEMGVHTVSVK[325.13]YR.G                        |

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| 0.999693 | 0.9992 K.HLK[325.13]ALTSELANAR.D                          |
| 0.999692 | 0.9976 K.KAAATK[325.13]KPAPEK.K                           |
| 0.999692 | 0.9992 K.KIYK[325.13]IGQGYLIK.D                           |
| 0.999691 | 0.9998 R.MHC[160.03]C[160.03]DEVQPK[325.13]HVK.E          |
| 0.999691 | 0.9983 R.GDGTGGK[325.13]SIYGER.F                          |
| 0.999691 | 0.9956 K.AVGK[325.13]VIPELNGK.L                           |
| 0.99969  | 0.9936 R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTEVK.S        |
| 0.99969  | 0.9995 R.IALSVHK[325.13]K.N                               |
| 0.99969  | 0.4744 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E         |
| 0.999689 | 0.9826 R.LQLETEIEALK[325.13]EELLFM[147.04]K.K             |
| 0.999689 | 0.9987 K.LFEC[160.03]DRDQMYYNLLK[325.13]LYK.I             |
| 0.999688 | 0.9994 K.AAYLQETGK[325.13]PLDETLKK.A                      |
| 0.999688 | 0.9988 R.FAK[325.13]NFLPILFNLYGQPVAAGDTPAPR.R             |
| 0.999687 | 0.9997 R.AGK[325.13]IVVNLTGR.L                            |
| 0.999687 | 0.9955 R.RLQEDK[325.13]EQMAQQLAEETQGFQR.T                 |
| 0.999687 | 0.9955 R.TGVELGKPTHFTVNAK[325.13]AAGK.G                   |
| 0.999687 | 0.999 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E    |
| 0.999686 | 0.9982 K.KAK[325.13]KPALVAK.S                             |
| 0.999686 | 0.9983 R.KIEEIK[325.13]DFLLTAR.R                          |
| 0.999685 | 0.9956 K.MPK[325.13]FSMPGFK.A                             |
| 0.999685 | 0.9985 R.HGEK[325.13]VEEC[160.03]QR.F                     |
| 0.999685 | 0.9953 R.LDYLSSLKVK[325.13]GLVLGPIHK.N                    |
| 0.999684 | 0.9989 K.ITK[325.13]FENAFLSHVVSQHQALLGTIR.A               |
| 0.999684 | 0.9998 K.NSTIVFPLPIDMLQGII GAK[325.13]HSHLG.-             |
| 0.999682 | 0.9929 R.YVEPIEDVPC[160.03]GNIVGLVGVDQFLVK[325.13]TGTI    |
| 0.999682 | 0.9991 R.AVLK[325.13]FAAATGATPIAGR.F                      |
| 0.999682 | 0.9987 K.ESWHGK[325.13]PLPK.N                             |
| 0.999682 | 0.9984 R.ALPFWN EIVPQIK[325.13]EGKR.V                     |
| 0.999681 | 0.994 R.TLLIK[325.13]TVETR.D                              |
| 0.999681 | 0.9944 R.LPMNK[325.13]EWPSNLDLR.K                         |
| 0.999681 | 0.9991 K.AM[147.04]K[325.13]GLGTDEESILTLLTSR.S            |
| 0.999681 | 0.9975 R.KPNEGADGQWK[325.13]K.G                           |
| 0.999681 | 0.9998 R.VFQSLPHENK[325.13]PLTLSNYQTNK.A                  |
| 0.999681 | 0.999 K.SMTEAEQQQLIDDHFLFDK[325.13]PVSPLLLASGMAR.D        |
| 0.99968  | 0.9957 K.STAISLFYELSENDLNFIK[325.13]QSK.D                 |
| 0.99968  | 0.9872 R.ITLSK[325.13]HQNVQLPR.E                          |
| 0.99968  | 0.9954 K.HSQFIGYPITLFVEK[325.13]ER.D                      |
| 0.999679 | 0.9953 R.K[325.13]HGLEVIYMI EPIDEYC[160.03]VQQLK.E        |
| 0.999679 | 0.3287 R.HQGVMMVGMGQK[325.13]DSYVGDEAQSK.R                |
| 0.999679 | 0.9997 R.RPYAPINANA IAK[325.13]AEC[160.03]SIR.L           |
| 0.999678 | 0.9978 R.HMYHSLYLK[325.13]VK.G                            |
| 0.999678 | 0.978 R.QTVAVGV I K[325.13]AVDKK.A                        |
| 0.999678 | 0.9993 K.TFNLEK[325.13]QNHTPR.K                           |
| 0.999678 | 0.9998 R.EHTALLK[325.13]IEGVYAR.D                         |
| 0.999677 | 0.9995 R.LFVG NLPADITEDEFK[325.13]R.L                     |
| 0.999677 | 0.9893 R.HNGTGGK[325.13]SIYGEK.F                          |
| 0.999677 | 0.9999 R.LTTINC[160.03]EEGDKLK[325.13]LTC[160.03]FELAPK.S |

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| 0.999677 | 0.9994 R.VAAPK[325.13]HWMLDK.L                         |
| 0.999677 | 0.9994 R.YGDGPRPPK[325.13]MAR.Y                        |
| 0.999676 | 0.9922 R.K[325.13]LAVNMVFPFR.L                         |
| 0.999676 | 0.9995 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT |
| 0.999675 | 0.999 K.K[325.13]GLTPSQIGVILR.D                        |
| 0.999675 | 0.9993 K.FLYQLHETEK[325.13]EDLIR.E                     |
| 0.999674 | 0.9944 K.K[325.13]GIIRPGTAFELLEQAATGYVIDPIK.G          |
| 0.999674 | 0.9994 K.FTFIEK[325.13]C[160.03]NNPR.S                 |
| 0.999674 | 0.9991 K.ANIK[325.13]HKPGGGDVK.I                       |
| 0.999674 | 0.9996 K.LMDALK[325.13]HASNMLGELR.T                    |
| 0.999674 | 0.9994 K.GVLFGVPGAFTPGC[160.03]SK[325.13]THLPGFVEQAEA  |
| 0.999673 | 0.9953 K.IPQK[325.13]GILIGIQSFRPR.F                    |
| 0.999673 | 0.999 R.INVYYNEATGGK[325.13]YVPR.A                     |
| 0.999673 | 0.9308 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S       |
| 0.999672 | 0.9994 K.GIVVTAYSPLGSPDRPWAK[325.13]PEDPSLLEDPR.I      |
| 0.999672 | 0.9985 R.SPNLWLK[325.13]DVLK.E                         |
| 0.999672 | 0.9992 R.K[325.13]AHLTNQYMQR.V                         |
| 0.999672 | 0.9994 R.DQK[325.13]LPHLER.I                           |
| 0.999672 | 0.9985 R.HK[325.13]PLLIDMNK.V                          |
| 0.999672 | 0.9985 R.LYSLALHPNAFK[325.13]R.L                       |
| 0.999671 | 0.9996 R.DDGYSTK[325.13]DSYSSR.D                       |
| 0.999671 | 0.9956 R.SKGQESFK[325.13]K.Q                           |
| 0.999671 | 0.9993 R.MEELHNQEVQK[325.13]R.K                        |
| 0.999671 | 0.9999 K.IITYKDPDNPEYLEFLK[325.13]QLK.H                |
| 0.999671 | 0.9946 K.AGAHLQGGAK[325.13]R.V                         |
| 0.999671 | 0.9913 R.K[325.13]GHAVGDIPGVR.F                        |
| 0.999671 | 0.9994 R.AHQLVLPPC[160.03]DVVIK[325.13]AVADYVR.N       |
| 0.99967  | 0.9109 R.MVNHFAIEFK[325.13]R.K                         |
| 0.99967  | 0.9945 R.GYFEYIEENK[325.13]YSR.A                       |
| 0.99967  | 0.9733 R.LEK[325.13]PAKYDDIKK.V                        |
| 0.999669 | 0.9992 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V           |
| 0.999669 | 0.9983 K.DANAK[325.13]LSELEAALQR.A                     |
| 0.999669 | 0.9992 K.LMELHGEGSSSGK[325.13]ATGDETGAK.V              |
| 0.999669 | 0.9992 K.LMELHGEGSSSGK[325.13]ATGDETGAK.V              |
| 0.999669 | 0.9998 R.TC[160.03]LITFK[325.13]PGAFIGAPVQPVVLR.Y      |
| 0.999668 | 0.9991 R.LVVPATQC[160.03]GSLIGK[325.13]GGC[160.03]K.I  |
| 0.999668 | 0.9992 R.KESYSIYVYK[325.13]VLK.Q                       |
| 0.999668 | 0.9997 R.ETELPAAAEPGAENALTQGLK[325.13]PDTAYDLQVR.A     |
| 0.999668 | 0.9933 R.FANYIDK[325.13]VR.F                           |
| 0.999668 | 0.9951 R.QLFHPEQLITGK[325.13]EDAANNYAR.G               |
| 0.999668 | 0.9981 R.VPELQGLVTEHVFLDK[325.13]C[160.03]LR.E         |
| 0.999667 | 0.9992 K.TLTGK[325.13]TITLEVEPSDTIENVK.A               |
| 0.999667 | 0.9985 K.EGK[325.13]LIMGIGHR.V                         |
| 0.999667 | 0.999 K.KGVLGK[325.13]SPLSALAR.K                       |
| 0.999666 | 0.9988 R.ALANSLAC[160.03]QGK[325.13]YTPSGQAGAAASESLFV! |
| 0.999666 | 0.9999 R.GHVTQDAPIPGSPLYTIK[325.13]AFIPAIDSFGFETDLR.T  |
| 0.999665 | 0.9988 R.LK[325.13]GYLISGSSYAR.S                       |

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| 0.999664 | 0.9993 R.AK[325.13]LEAAIAEAEER.G                        |
| 0.999664 | 0.9991 R.GLTSVINQK[325.13]LKDDEVAQLK.K                  |
| 0.999664 | 0.9951 R.VLEALLPLK[325.13]GLEER.V                       |
| 0.999664 | 0.9999 R.NIILGK[325.13]SHYVLYGLVAAMQPR.M                |
| 0.999663 | 0.9993 R.LLELGPK[325.13]PEVAQQTR.K                      |
| 0.999663 | 0.8053 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPPVTDWAW   |
| 0.999663 | 0.9994 R.EHAMLAK[325.13]TAGVK.H                         |
| 0.999663 | 0.9995 K.KVK[325.13]TDTVLILC[160.03]R.K                 |
| 0.999662 | 0.9943 K.VGINYQPPTVVPGGDLAK[325.13]VQR.A                |
| 0.999662 | 0.9997 R.DDHTLK[325.13]IR.K                             |
| 0.999661 | 0.9955 R.LSAEAEK[325.13]VLALPEPSPAAPT.LR.S              |
| 0.99966  | 0.9982 R.RK[325.13]QEELQQLEQQR.R                        |
| 0.99966  | 0.9068 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E                |
| 0.99966  | 0.9996 R.RYIGIVK[325.13]QAGLER.M                        |
| 0.99966  | 0.9961 R.RQFASQANVVGWPWIQTK[325.13]MEEIGR.I             |
| 0.999659 | 0.9978 R.KNHLEGK[325.13]AAISNK.I                        |
| 0.999659 | 0.9992 K.GHK[325.13]FHHTIGGS.R                          |
| 0.999659 | 0.999 R.SNQFFSLDPVTGAVTTAEELDRETK[325.13]STHVFR.V       |
| 0.999658 | 0.9954 K.AKKPAGAAK[325.13]KPK.K                         |
| 0.999658 | 0.999 K.LTSLNVK[325.13]YNNDK.S                          |
| 0.999658 | 0.9996 K.VDVFREDLC[160.03]TK[325.13]TENLLGSYFPK.K       |
| 0.999657 | 0.9954 K.IK[325.13]IIAPPER.K                            |
| 0.999657 | 0.9998 K.K[325.13]GLMYPYIFHVLTK.G                       |
| 0.999656 | 0.9998 K.SAHLTNPWNEHKPVK[325.13]IGR.D                   |
| 0.999656 | 0.996 R.TM[147.04]PVEQVFAK[325.13]NFR.V                 |
| 0.999655 | 0.992 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M        |
| 0.999655 | 0.9953 K.KAASGEAKPK[325.13]AK.K                         |
| 0.999655 | 0.9992 R.FC[160.03]SINSGLSYMEMPLEC[160.03]ILTEK[325.13] |
| 0.999655 | 0.9992 R.DLANDIMTLMSHTK[325.13]PYIR.K                   |
| 0.999654 | 0.9993 K.LK[325.13]DYAFIHFDER.D                         |
| 0.999653 | 0.9978 R.IGPYQPNVPVGIDYVIPK[325.13]TGFYC[160.03]K.L     |
| 0.999653 | 0.9996 K.AGLQVYNK[325.13]C[160.03]WKFEHC[160.03]NFNDVT  |
| 0.999652 | 0.9993 R.NQSFC[160.03]PTVNLDK[325.13]LWTLVSEQTR.V       |
| 0.999652 | 0.996 K.FDLMYAK[325.13]R.A                              |
| 0.999652 | 0.995 K.NFINNPLAQADWAAK[325.13]K.L                      |
| 0.999652 | 0.9992 K.AK[325.13]DPFAHLPK.S                           |
| 0.999652 | 0.9953 K.AAKPK[325.13]AAKPK.A                           |
| 0.999652 | 0.9972 K.KPAPEK[325.13]KPAEK.K                          |
| 0.999652 | 0.9993 R.YHVLVNLGK[325.13]K.I                           |
| 0.999651 | 0.9996 R.YK[325.13]QIVLTGILEQVVNC[160.03]R.D            |
| 0.999651 | 0.9991 K.MVEAAK[325.13]GAAAHPDSEEQQQR.L                 |
| 0.999651 | 0.9991 K.MVEAAK[325.13]GAAAHPDSEEQQQR.L                 |
| 0.999651 | 0.9991 K.MVEAAK[325.13]GAAAHPDSEEQQQR.L                 |
| 0.999651 | 0.9994 K.SGVK[325.13]IHVSDQELQSANASVDDSRLEELK.A         |
| 0.99965  | 0.9984 K.VTVLFAGQHISK[325.13]SPFEVSVDK.A                |
| 0.99965  | 0.998 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L              |
| 0.99965  | 0.9996 K.LKPQYLEELPGQLK[325.13]QFSMFLGK.F               |

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| 0.999649 | 0.9972 R.TFK[325.13]TVFAEHISDEC[160.03]KR.R            |
| 0.999649 | 0.9996 K.VEAQVYILSK[325.13]EEGGR.H                     |
| 0.999649 | 0.995 K.NVK[325.13]LTVSNVLK.E                          |
| 0.999649 | 0.9994 K.GFVVINQK[325.13]GIDPFSLDALSK.E                |
| 0.999649 | 0.9925 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L            |
| 0.999648 | 0.9995 R.LNYGIPAIVK[325.13]LLNQPNQWPLVK.A              |
| 0.999648 | 0.9983 R.GVQDIVVGEGTHFLIPWVQK[325.13]PIIFDC[160.03]R.S |
| 0.999647 | 0.9996 K.VK[325.13]ADRDESSPYAAMLAAQDVAQR.C             |
| 0.999647 | 0.9993 R.KDDPLTNLNTAFDVAEK[325.13]YLDIPK.M             |
| 0.999646 | 0.9994 K.YYIEK[325.13]LFER.Y                           |
| 0.999646 | 0.9991 R.ELTGLK[325.13]ALYETELADAR.R                   |
| 0.999646 | 0.995 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L           |
| 0.999646 | 0.9993 K.AGISFIIK[325.13]RPFLEPK.K                     |
| 0.999645 | 0.9914 R.ILGLLDAYLK[325.13]TR.T                        |
| 0.999645 | 0.9971 R.IYDLNKPEAEPK[325.13]EISGHTSGIK.K              |
| 0.999645 | 0.9994 R.TEM[147.04]DWVLK[325.13]HSGPNSADSANDGFVR.L    |
| 0.999645 | 0.9982 R.LLEAQIATGGIIDPEESHRLPVEVAYK[325.13]R.G        |
| 0.999645 | 0.9974 R.ASVPDGFELSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ   |
| 0.999644 | 0.9982 R.K[325.13]VIDDTNITR.L                          |
| 0.999644 | 0.9991 R.HESGASIK[325.13]IDEPLEGSEDR.I                 |
| 0.999644 | 0.9991 K.YGK[325.13]AGEVFIHK.D                         |
| 0.999644 | 0.9497 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T               |
| 0.999643 | 0.9978 R.FFTVK[325.13]LPVALDPGAK.I                     |
| 0.999643 | 0.9952 R.IC[160.03]SKPVVLPK[325.13]GPESESEDHR.A        |
| 0.999641 | 0.9994 R.DELTLEGIK[325.13]QFFVAVER.E                   |
| 0.999641 | 0.9973 K.AHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D   |
| 0.999641 | 0.9993 K.KDWYDVK[325.13]APAMFNIR.N                     |
| 0.99964  | 0.9681 R.ISVYYNEATGGK[325.13]YVPR.A                    |
| 0.99964  | 0.9982 K.VK[325.13]AFGPGLQGSAGSPAR.F                   |
| 0.99964  | 0.9899 K.HGEAQVK[325.13]IWR.R                          |
| 0.999639 | 0.9979 K.LIK[325.13]GVIVDKDFSHPQMPK.K                  |
| 0.999639 | 0.9994 R.GWLK[325.13]SNVSDAVAQSTR.I                    |
| 0.999639 | 0.999 R.KTC[160.03]TTVAFTQVNSEDK[325.13]GALAK.L        |
| 0.999639 | 0.9976 K.YK[325.13]PAVNQIEC[160.03]HPYLTQEK.L          |
| 0.999639 | 0.9913 R.K[325.13]LAVNMVPFPR.L                         |
| 0.999639 | 0.7924 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV   |
| 0.999638 | 0.9994 K.LVPVLSAK[325.13]AAQASDLEK.I                   |
| 0.999637 | 0.999 K.MK[325.13]GYPHWPAR.V                           |
| 0.999637 | 0.9995 K.YTEGVQSLNWTk[325.13]IMK.T                     |
| 0.999637 | 0.9993 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT |
| 0.999637 | 0.9993 K.RK[325.13]TVTAMDVVYALK.R                      |
| 0.999636 | 0.9807 K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V |
| 0.999636 | 0.9996 K.VAGHSLGYGFVNYVTAK[325.13]DAER.A               |
| 0.999635 | 0.7972 K.EITALAPSTMKIK[325.13]IIAPPER.K                |
| 0.999635 | 0.9968 K.INEAVEC[160.03]LLSLK[325.13]AQYK.E            |
| 0.999635 | 0.9982 R.EAATQAQQTGSGTIDK[325.13]ATGILLYGLASR.L        |
| 0.999635 | 0.9996 R.YTIYSPK[325.13]DGQPC[160.03]MDHDR.Q           |

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| 0.999635 | 0.9996 K.EK[325.13]LDQLKQEFEFWYPVDLR.V                  |
| 0.999635 | 0.9938 R.LK[325.13]LLLPWLEAR.I                          |
| 0.999634 | 0.9954 K.FYWGHK[325.13]EILIPVFK.N                       |
| 0.999633 | 0.7739 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPPSGK.L    |
| 0.999632 | 0.3876 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                |
| 0.999631 | 0.9902 R.VK[325.13]GGGHVAQIYAIR.Q                       |
| 0.99963  | 0.9993 R.HLIGK[325.13]SGANINR.I                         |
| 0.99963  | 0.9985 K.YDYNNGEELSYK[325.13]GHFGPIHC[160.03]VR.F       |
| 0.99963  | 0.9997 R.LLDHMQNTPGFMKY[325.13]NLQC[160.03]LVIDEADR.I   |
| 0.99963  | 0.9979 R.FMQTFVLAPEGSVANK[325.13]FYVHNDIFR.Y            |
| 0.999629 | 0.9998 K.VVAC[160.03]TSAFLLWDPTK[325.13]VPPR.L          |
| 0.999629 | 0.9934 R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V              |
| 0.999629 | 0.9769 R.LAHYNK[325.13]R.S                              |
| 0.999628 | 0.9925 R.FANYIDK[325.13]VR.F                            |
| 0.999628 | 0.9994 R.TWQK[325.13]IHEPIMLK.Y                         |
| 0.999628 | 0.9988 R.YGLLK[325.13]HSR.E                             |
| 0.999628 | 0.997 K.LTLHGLQQYYVK[325.13]LK.D                        |
| 0.999627 | 0.9991 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V            |
| 0.999627 | 0.9995 R.AGMFVSK[325.13]FFGGYVPEMVLTPDDQR.L             |
| 0.999626 | 0.9998 R.NIHSSDWPKE[325.13]FFEK.Y                       |
| 0.999625 | 0.9998 R.THIFK[325.13]IHAR.S                            |
| 0.999625 | 0.9974 R.DAVTYTEHAK[325.13]R.K                          |
| 0.999624 | 0.9999 K.TSVQFQNFSPVTVHPGDLQTLAVQTK[325.13]R.V          |
| 0.999623 | 0.9999 R.LC[160.03]C[160.03]LEK[325.13]GPNGYGFHLHGEK.G  |
| 0.999623 | 0.973 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K          |
| 0.999623 | 0.9996 K.HELLQPFNVLYEK[325.13]EGEFVAQFK.F               |
| 0.999622 | 0.9976 K.LK[325.13]HYGPGWVSMANAGK.D                     |
| 0.999621 | 0.9965 R.MAQEVLTHLK[325.13]EHPDAWTR.V                   |
| 0.999621 | 0.1352 R.ADIK[325.13]EMGLSLQWLYSAR.G                    |
| 0.999621 | 0.9999 R.LWAHVYAGAPVSSPEYTK[325.13]K.I                  |
| 0.999621 | 0.9837 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |
| 0.999621 | 0.9996 R.K[325.13]VGITLFTVSHR.K                         |
| 0.99962  | 0.9981 R.GGEPNQRPELK[325.13]NHIDR.V                     |
| 0.99962  | 0.9994 R.DK[325.13]ELTGALIASLINC[160.03]YIR.D           |
| 0.99962  | 0.9272 R.LPLQDVYK[325.13]IGGIGTVPVGR.V                  |
| 0.99962  | 0.9925 R.AK[325.13]QIVWNGPVGVEWEAFAR.G                  |
| 0.999619 | 0.9947 R.TIC[160.03]SHVQNMILK[325.13]GVTLGFR.Y          |
| 0.999619 | 0.9996 R.EGGWDSVQDWMDVLSGGEK[325.13]QR.M                |
| 0.999618 | 0.9996 R.DGIIVLK[325.13]YVDGDLG[160.03]PDGIR.K          |
| 0.999618 | 0.9934 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK. |
| 0.999618 | 0.9996 R.IIGLK[325.13]PEGVPR.I                          |
| 0.999618 | 0.9921 R.K[325.13]MC[160.03]LFAGFQR.K                   |
| 0.999617 | 0.9938 K.VEAK[325.13]FINYVK.N                           |
| 0.999617 | 0.9993 R.DQK[325.13]LPHLER.I                            |
| 0.999617 | 0.9957 K.MVINHLEK[325.13]LFVTNDAATILR.E                 |
| 0.999615 | 0.9992 K.IK[325.13]DPDASKPEDWDER.A                      |
| 0.999615 | 0.9923 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H               |



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| 0.999614 | 0.966 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V                                               |
| 0.999614 | 0.997 R.GEIIAK[325.13]QGGGGGGGSPGIER.M                                                      |
| 0.999614 | 0.9645 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]HGEVC[160.03]PAGWKPGSDTIKF            |
| 0.999613 | 0.918 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIKF                                        |
| 0.999613 | 0.9996 R.KGDYLGK[325.13]TVQVPHITDAIQEWVMR.Q                                                 |
| 0.999613 | 0.9743 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGPGGFG                                       |
| 0.999612 | 0.9994 K.SFLK[325.13]DSETSQR.L                                                              |
| 0.999612 | 0.9943 K.AVGK[325.13]VIPELNGK.L                                                             |
| 0.999612 | 0.999 R.YYK[325.13]NIGLGFK.T                                                                |
| 0.999612 | 0.9967 K.IGHAPNFK[325.13]ATAVM[147.04]PDGQFK.D                                              |
| 0.999612 | 0.9996 K.GISVHISNAEPK[325.13]HNSNR.Q                                                        |
| 0.999611 | 0.7861 K.EITALAPSTMKIK[325.13]IIAPPER.K                                                     |
| 0.999611 | 0.9936 R.GFEVVMTEPIDEYC[160.03]VQQLK[325.13]EFDGK.S                                         |
| 0.999611 | 0.8906 R.SLDMDSIIAEVK[325.13]AQYEDIANR.S                                                    |
| 0.99961  | 0.9944 R.IWDTLQK[325.13]LGAVYDVSHYNALLK.V                                                   |
| 0.999609 | 0.9996 K.K[325.13]TGQPMINLYTDR.E                                                            |
| 0.999609 | 0.9996 K.K[325.13]TGQPMINLYTDR.E                                                            |
| 0.999609 | 0.9991 R.NLLSVAYK[325.13]NVIGAR.R                                                           |
| 0.999609 | 0.9995 K.GFGFGLVK[325.13]LDVK.T                                                             |
| 0.999609 | 0.9995 R.NHAAPFSK[325.13]VLTFLR.R                                                           |
| 0.999608 | 0.9905 R.ILGLLDAYLK[325.13]TR.T                                                             |
| 0.999608 | 0.9993 R.ELAVQIQK[325.13]GLLALGDYMNVC[160.03]HAC[160.03]SHLGNVHDQDN.-                       |
| 0.999608 | 0.9997 R.NIK[325.13]SHLGNVHDQDN.-                                                           |
| 0.999608 | 0.9909 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPM[147.04]PGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V |
| 0.999608 | 0.999 K.K[325.13]PGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V                                          |
| 0.999607 | 0.9548 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M                                           |
| 0.999607 | 0.9982 K.ASGPPVSELITK[325.13]AVAASK.E                                                       |
| 0.999607 | 0.9952 R.K[325.13]MFTLLDVVNR.K                                                              |
| 0.999607 | 0.9982 R.IHDVLC[160.03]K[325.13]LVEK.G                                                      |
| 0.999607 | 0.9998 R.EIPSHVLSK[325.13]VC[160.03]MYFTYK.V                                                |
| 0.999606 | 0.9947 R.GITGVEDKESWHGKPLPK[325.13]NMAEQIIQEISQIQSK.                                        |
| 0.999606 | 0.9997 K.DGVVEITGK[325.13]HEER.Q                                                            |
| 0.999606 | 0.9993 R.GLGHQVATDALVAMEK[325.13]AMK.R                                                      |
| 0.999605 | 0.9981 K.ETGEHLVHVK[325.13]K.N                                                              |
| 0.999605 | 0.9919 R.VETGVLK[325.13]PGMVVTFAPVNVTTTEVK.S                                                |
| 0.999605 | 0.997 K.K[325.13]LRPLYDIPYMFAR.E                                                            |
| 0.999604 | 0.9996 R.GPVGLEGLLTTK[325.13]WLLR.G                                                         |
| 0.999604 | 0.9996 R.IHVLEAQDLIAK[325.13]DR.F                                                           |
| 0.999603 | 0.7516 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK                                          |
| 0.999603 | 0.9967 R.YM[147.04]AQGK[325.13]HIGK.V                                                       |
| 0.999602 | 0.9892 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V                                              |
| 0.999601 | 0.9982 R.K[325.13]LIADLQPNTEYSFVLMNR.G                                                      |
| 0.999601 | 0.9913 R.LREK[325.13]LQEEMLQR.E                                                             |
| 0.9996   | 0.9976 K.GFVLHK[325.13]SK.S                                                                 |
| 0.9996   | 0.9996 K.TPLK[325.13]IHPLVR.L                                                               |
| 0.999599 | 0.9824 R.FSGWYDADLSPAGHEEAK[325.13]R.G                                                      |
| 0.999599 | 0.9997 R.NIK[325.13]VGRPSNIGQAQPIIDQLAEER.A                                                 |

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| 0.999599 | 0.9994 R.RK[325.13]DGVFLYFEDNAGVIVNNK.G                |
| 0.999599 | 0.9991 K.FLDAGHK[325.13]LNFAVASR.K                     |
| 0.999598 | 0.9935 K.VEAK[325.13]FINYVK.N                          |
| 0.999598 | 0.9912 K.M[147.04]LETK[325.13]WSLLQQQK.T               |
| 0.999598 | 0.9957 K.HAVSEGTK[325.13]AVTKYTSSK.-                   |
| 0.999598 | 0.9979 K.VQK[325.13]HQAFAELSANQSR.I                    |
| 0.999597 | 0.9749 R.SVPHLQK[325.13]VFDR.Y                         |
| 0.999596 | 0.9013 K.K[325.13]YVATLGVEVHPLVFHTNR.G                 |
| 0.999596 | 0.9641 R.LVYLVENPGGYVAYSK[325.13]AATVTGK.L             |
| 0.999596 | 0.9996 K.LFIGGLNTETNEK[325.13]ALEAVFGK.Y               |
| 0.999596 | 0.9991 K.AK[325.13]QFLPFLQR.A                          |
| 0.999595 | 0.9931 R.NDNDTFTVK[325.13]YTPR.G                       |
| 0.999595 | 0.996 R.LVVFPTDDISLK[325.13]C[160.03]EASGKPEVQFR.W     |
| 0.999594 | 0.9995 K.YVSHGATGK[325.13]GNDQVR.F                     |
| 0.999594 | 0.9965 R.KESYSVYVYK[325.13]VLK.Q                       |
| 0.999594 | 0.9994 K.ALAPLLAFVTK[325.13]PNSALESC[160.03]SFAR.H     |
| 0.999594 | 0.9987 R.LALK[325.13]EDKFPR.F                          |
| 0.999593 | 0.9992 R.TWNDPSVQQDIK[325.13]FLPFK.V                   |
| 0.999593 | 0.9991 R.DGWPAMC[160.03]IHGDK[325.13]SQPER.D           |
| 0.999592 | 0.9999 K.HC[160.03]VDPTSFLKPIAK[325.13]LFSVIK.N        |
| 0.999592 | 0.998 R.LLAAGK[325.13]VPQR.A                           |
| 0.999592 | 0.9991 R.SK[325.13]LILFPR.K                            |
| 0.999592 | 0.9937 R.GITGVEDK[325.13]ESWHGKPLPK.N                  |
| 0.999592 | 0.9993 K.HLQDLMEGLTAK[325.13]VFR.T                     |
| 0.999591 | 0.9951 K.HAVSEGTK[325.13]AVTKYTSK.-                    |
| 0.999591 | 0.9943 R.DGSIDLVINLPNNNTK[325.13]FVHDNYVIR.R           |
| 0.999591 | 0.9954 R.ISIEMNGTLEDQLSHLK[325.13]QYER.S               |
| 0.999591 | 0.9974 R.NVNVFK[325.13]FIIPQIVK.Y                      |
| 0.99959  | 0.9942 R.K[325.13]YQPNIDVQESIHFLESEFSR.G               |
| 0.99959  | 0.9949 K.K[325.13]LLEAQSHFR.K                          |
| 0.999589 | 0.9733 K.KTESHHK[325.13]AK.G                           |
| 0.999589 | 0.9996 R.NEK[325.13]APVDFGYVGIDSILEQMR.R               |
| 0.999588 | 0.9992 K.K[325.13]RTELFIAAEGIHTGQFVYC[160.03]GK.K      |
| 0.999588 | 0.9992 R.LLDSVPPTAISHFK[325.13]QSAEK.L                 |
| 0.999588 | 0.9976 R.WK[325.13]AGLYGLPR.R                          |
| 0.999588 | 0.9995 R.NEMQK[325.13]LQAEAPHIVVGTGPR.V                |
| 0.999587 | 0.9999 R.VLYAYGYTGEPK[325.13]R.S                       |
| 0.999587 | 0.9996 K.HYEVEILDAK[325.13]TR.E                        |
| 0.999587 | 0.9988 R.SNQFFSLDPVTGAVTTAEELDRETK[325.13]STHVFR.V     |
| 0.999586 | 0.9664 K.KPVGAAGK[325.13]KPK.K                         |
| 0.999586 | 0.9992 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V           |
| 0.999586 | 0.9995 K.K[325.13]IGQQPQQPGAPPQQDYTK.A                 |
| 0.999586 | 0.9972 K.KVSYSHIQSK[325.13]C[160.03]GSK.D              |
| 0.999585 | 0.9735 K.KAK[325.13]VAKPK.K                            |
| 0.999585 | 0.9962 R.SRK[325.13]ESYSVYVYK.V                        |
| 0.999585 | 0.9992 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT |
| 0.999585 | 0.9992 K.RK[325.13]TVTAMDVVYALK.R                      |

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| 0.999585 | 0.9981 R.K[325.13]IAKAFAISGPFNVQFLVK.G                    |
| 0.999584 | 0.9996 R.ILNEK[325.13]VNTPTTTTVYR.C                       |
| 0.999583 | 0.9993 R.AAMK[325.13]GLGTDEDTLIEILASR.T                   |
| 0.999583 | 0.995 K.HAVSEGTK[325.13]AVTKYTSAK.-                       |
| 0.999582 | 0.9985 R.AAPGAEFAPNK[325.13]R.R                           |
| 0.999582 | 0.9974 R.LDHLAEK[325.13]FR.Q                              |
| 0.999581 | 0.9996 K.VEYQIK[325.13]TFSGQTHGFVHR.K                     |
| 0.999581 | 0.9976 K.SK[325.13]GYAFIEFASFEDAK.E                       |
| 0.999581 | 0.9994 R.NK[325.13]LDHYAIK.F                              |
| 0.999581 | 0.9995 K.NVIHK[325.13]IFSK.F                              |
| 0.99958  | 0.9999 R.VC[160.03]K[325.13]SHLLNC[160.03]C[160.03]PHDVLS |
| 0.99958  | 0.9991 R.EDLQLDKPASGVK[325.13]EEWYAR.I                    |
| 0.999579 | 0.9982 K.K[325.13]HQALQAEIAGHEPR.I                        |
| 0.999578 | 0.9992 K.K[325.13]EVAGAKPHITAAEGK.L                       |
| 0.999577 | 0.9981 R.GLQQQNSDWYLK[325.13]QLLSDK.Q                     |
| 0.999577 | 0.9967 K.AEDKEWMPVTK[325.13]LGR.L                         |
| 0.999577 | 0.9898 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I   |
| 0.999576 | 0.9991 K.K[325.13]GYEVIYLTEPVDEYC[160.03]IQALPEFDGK.R     |
| 0.999575 | 0.9939 K.IPQK[325.13]GILIGIQSFRPR.F                       |
| 0.999575 | 0.9974 R.M[147.04]IAGQVLDINLAAEPK[325.13]VNR.G            |
| 0.999575 | 0.9999 K.K[325.13]LAPPLVTLISGEPEVQYVALR.N                 |
| 0.999574 | 0.9989 K.KVVNPLFEK[325.13]RPK.N                           |
| 0.999574 | 0.9969 K.LYEEK[325.13]TGNAWHSK.N                          |
| 0.999574 | 0.9991 R.VK[325.13]LLLQVQHASK.Q                           |
| 0.999573 | 0.9998 K.AK[325.13]DQTKAQAAAPASVPAQAPK.R                  |
| 0.999573 | 0.9979 R.FTLTGLKPDTTYDIK[325.13]VR.A                      |
| 0.999573 | 0.9553 K.LAQMFSDMVLK[325.13]DGFQPSR.S                     |
| 0.999573 | 0.9979 R.K[325.13]GLVGPELHDR.L                            |
| 0.999572 | 0.9993 K.LSEGVVISYK[325.13]SYC[160.03]K.N                 |
| 0.999572 | 0.9995 R.GFGGK[325.13]FGVQMDR.V                           |
| 0.999571 | 0.9957 R.GVLK[325.13]VFLENVIR.D                           |
| 0.999571 | 0.9945 R.LQALDTGWNEHLK[325.13]MWENR.Q                     |
| 0.99957  | 0.9996 R.ISRPHPSTAESK[325.13]APTPK.F                      |
| 0.99957  | 0.9976 K.SNQNGK[325.13]DSKPSSTPR.S                        |
| 0.99957  | 0.996 R.VQAQGPGLK[325.13]EAFTNKPNVFTVVTR.G                |
| 0.99957  | 0.9982 R.QLSQSLLPAIVELAEDAK[325.13]WR.V                   |
| 0.99957  | 0.9989 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T          |
| 0.999569 | 0.9963 R.DAK[325.13]LDKAQIHDLVLVGGSTR.I                   |
| 0.999569 | 0.9993 R.QIYGAK[325.13]GFSLSQVPAEISGEHLR.I                |
| 0.999568 | 0.9995 K.AGLQVYNK[325.13]C[160.03]WKFEHC[160.03]NFNDVT    |
| 0.999568 | 0.999 R.LK[325.13]LAQQQAALLMQQEER.A                       |
| 0.999568 | 0.9969 R.VIFGLFGK[325.13]TVPK.T                           |
| 0.999568 | 0.9991 K.DWYDVK[325.13]APAMFNIR.N                         |
| 0.999568 | 0.9328 R.DLTDYLM[147.04]K[325.13]ILTER.G                  |
| 0.999568 | 0.9977 R.FSK[325.13]SQLDIIHSLK.K                          |
| 0.999567 | 0.9991 K.DC[160.03]EEC[160.03]IQLEPTFIK[325.13]GYTR.K     |
| 0.999567 | 0.9997 K.DGPLNM[147.04]ILDDGGDLTNLIHTK[325.13]YPQLLPGI    |

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| 0.999566 | 0.9899 R.AK[325.13]VTLNGVPAQPLGPR.A                     |
| 0.999566 | 0.9992 K.FTFIEK[325.13]C[160.03]NNPR.S                  |
| 0.999566 | 0.996 R.KESYSVYVYK[325.13]VLK.Q                         |
| 0.999566 | 0.7545 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV    |
| 0.999566 | 0.9999 R.K[325.13]LEELIQGAQC[160.03]VHSPR.F             |
| 0.999565 | 0.9915 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T               |
| 0.999564 | 0.9754 R.VHIQSSQTVESSGLYTLQSILK[325.13]AQLVK.E          |
| 0.999564 | 0.989 R.DALSDLALHFLNK[325.13]M[147.04]K.I               |
| 0.999563 | 0.9999 R.IEC[160.03]K[325.13]AYGENIGYSEK.D              |
| 0.999563 | 0.9993 K.YKSEK[325.13]C[160.03]FSVLGFC[160.03]K.S       |
| 0.999563 | 0.9998 R.TVLEHYALEDPLAAFK[325.13]QR.Q                   |
| 0.999563 | 0.999 R.KFVADGIFK[325.13]AELNEFLTR.E                    |
| 0.999562 | 0.9966 R.HAK[325.13]WFQAR.A                             |
| 0.999562 | 0.9868 R.VFITDDFHDMMPK[325.13]YLNFKV.G                  |
| 0.999561 | 0.998 K.FWHK[325.13]AC[160.03]FHC[160.03]ETC[160.03]K.M |
| 0.999561 | 0.9999 K.HLNEIDLFHC[160.03]IDPNDSKHK[325.13]R.T         |
| 0.999561 | 0.9991 K.RPDADLK[325.13]TYFTDK.K                        |
| 0.999561 | 0.999 K.VESPAK[325.13]IHVFYIDYGNR.E                     |
| 0.999561 | 0.9991 R.DDPIISTHLAK[325.13]LYDNLLEQNLR.V               |
| 0.999559 | 0.9985 K.GVVEVTHDLQK[325.13]HLAGLGLTEAIDK.N             |
| 0.999559 | 0.9997 R.FPLEK[325.13]ALEAFETFK.K                       |
| 0.999557 | 0.9943 K.STHDHWK[325.13]ALVTK.K                         |
| 0.999557 | 0.6748 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G            |
| 0.999557 | 0.9995 K.FLVQNIHTLAELK[325.13]MTGNC[160.03]LK.G         |
| 0.999556 | 0.9991 R.SK[325.13]VDEAVAVLQAHQAK.E                     |
| 0.999556 | 0.9933 R.VFSGLVSTGLK[325.13]VR.I                        |
| 0.999556 | 0.9007 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSKR.G      |
| 0.999555 | 0.9967 R.FK[325.13]KPGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V   |
| 0.999555 | 0.9984 R.DLEK[325.13]PFLPVEAVYSVPGR.G                   |
| 0.999555 | 0.9969 K.HGEVC[160.03]PAGWK[325.13]PGSDTIKPDVQK.S       |
| 0.999554 | 0.9936 R.LTVNEAVK[325.13]EGVVGPELHHK.L                  |
| 0.999553 | 0.9695 K.KAK[325.13]VAKPK.K                             |
| 0.999553 | 0.8347 R.K[325.13]LFIGGLSFETTEESLR.N                    |
| 0.999552 | 0.9605 R.ISVYYNEATGGK[325.13]YVPR.A                     |
| 0.999551 | 0.9946 K.KGATLK[325.13]ITLDNAYMEK.C                     |
| 0.99955  | 0.9976 K.LSDVDRDGMMLDDEEFALASHLIEAK[325.13]LEGHGLPANL   |
| 0.99955  | 0.9992 R.DNIQGITK[325.13]PAIR.R                         |
| 0.99955  | 0.9953 K.TDK[325.13]TLVLLMGK.E                          |
| 0.99955  | 0.9991 K.KPEAK[325.13]FFTPSK.S                          |
| 0.99955  | 0.999 R.VGK[325.13]VEHGSVALPAIMR.S                      |
| 0.99955  | 0.9991 R.ILVK[325.13]KEELTLEGIR.Q                       |
| 0.999549 | 0.6699 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G            |
| 0.999549 | 0.9992 K.K[325.13]C[160.03]TPPIEASQC[160.03]HEAEMTDNVNC |
| 0.999549 | 0.9991 R.AISAK[325.13]GMTLVTPQLLLFASK.K                 |
| 0.999549 | 0.9611 K.ALESPERPFLAILGGAK[325.13]VADK.I                |
| 0.999548 | 0.9994 R.AGGK[325.13]ILTFDQLALDSPK.G                    |
| 0.999548 | 0.9991 K.TVSPDRLELEAAQK[325.13]FLER.A                   |

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| 0.999547 | 0.9366 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                  |
| 0.999547 | 0.9996 R.MELLAHLLGEK[325.13]WMGPIPPAVNAR.L                |
| 0.999547 | 0.9995 K.HIVK[325.13]TVDFTQDSNYLLTGGQDK.L                 |
| 0.999546 | 0.9991 K.LNISFPATGC[160.03]QK[325.13]LIEVDDER.K           |
| 0.999546 | 0.9998 R.VLFLIPK[325.13]NNPPTLVGDFTK.S                    |
| 0.999546 | 0.9991 K.LWC[160.03]TYHEK[325.13]GLVK.G                   |
| 0.999545 | 0.9995 R.HSHALVSLSFLK[325.13]NLR.L                        |
| 0.999545 | 0.9679 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T     |
| 0.999544 | 0.9991 R.K[325.13]LFIGGLSFETDDSLR.E                       |
| 0.999543 | 0.9849 R.HNGTGGK[325.13]SIYGEK.F                          |
| 0.999543 | 0.9922 R.VTYTPMAPGSYLISIK[325.13]YGGPYHIGGSPFK.A          |
| 0.999542 | 0.9932 R.TK[325.13]TEISEMNR.N                             |
| 0.999542 | 0.9976 R.DIENLK[325.13]DASSFLAEWQNITK.G                   |
| 0.999542 | 0.9988 K.SAEAFGK[325.13]IVAERPNTNSTGPAPM[147.04]APPR./    |
| 0.999541 | 0.0659 R.HQGVMMVGMGQKDSYVGDEAQS[325.13]R.G                |
| 0.999541 | 0.9995 R.HK[325.13]PAFTEEDVLNIFPVVK.H                     |
| 0.999541 | 0.9599 R.SIFSAVLDELK[325.13]VAQAPWK.A                     |
| 0.99954  | 0.9947 K.AVTK[325.13]YTSSK.-                              |
| 0.99954  | 0.9893 R.AK[325.13]VTLNGVPAQPLGPR.A                       |
| 0.99954  | 0.9996 R.LLVPTQFVGAIIGK[325.13]EGATIR.N                   |
| 0.99954  | 0.8385 R.KDGNASGTTLLEALDC[160.03]ILPPTRPDK[325.13]PLR.    |
| 0.999539 | 0.999 R.EAGLSWK[325.13]EFLPEGQDIGAFVAEQK.V                |
| 0.999539 | 0.9992 R.LVQLLVK[325.13]AHQDAQR.H                         |
| 0.999539 | 0.9995 K.VSNLQYLHSYLYIK[325.13]LSTAIK.R                   |
| 0.999538 | 0.9999 R.VVPDSC[160.03]C[160.03]K[325.13]TVVALC[160.03]GC |
| 0.999537 | 0.9991 K.SDEMNVK[325.13]VLDFEHFLPMLQTVAK.N                |
| 0.999537 | 0.9991 K.SDEMNVK[325.13]VLDFEHFLPMLQTVAK.N                |
| 0.999537 | 0.9979 R.VLEQHK[325.13]LNK.D                              |
| 0.999537 | 0.9998 R.LLM[147.04]TEVAWTK[325.13]DELKEALDDVTLPR.L       |
| 0.999536 | 0.9987 K.KQKK[325.13]PLVGK.K                              |
| 0.999536 | 0.9986 R.GHLDNISNLLIGAINIENGK[325.13]ANSVR.N              |
| 0.999535 | 0.9992 K.SLK[325.13]FATEAAITILR.I                         |
| 0.999534 | 0.9988 K.MVEAAK[325.13]GAAAHDPDSEEQQQR.L                  |
| 0.999534 | 0.9991 K.YK[325.13]QIFLGVDKR.T                            |
| 0.999533 | 0.9992 K.MAILQIMK[325.13]ELNK.R                           |
| 0.999532 | 0.998 K.IALGIPLPEIK[325.13]NVVSGK.T                       |
| 0.999532 | 0.9992 R.DLLDDLK[325.13]SELTGK.F                          |
| 0.999532 | 0.9957 R.SRK[325.13]ESYSVYVK.V                            |
| 0.999532 | 0.9993 R.VLPSITTEILK[325.13]SVVAR.F                       |
| 0.999531 | 0.9979 K.ELLYK[325.13]FIC[160.03]TTSIQNR.F                |
| 0.999531 | 0.9958 K.DIEK[325.13]AC[160.03]QSIYPLHDVFVR.K             |
| 0.999531 | 0.9993 K.VLQHMK[325.13]AVQADQER.E                         |
| 0.999531 | 0.9995 R.TLAGLLPHNYDPDK[325.13]R.S                        |
| 0.999531 | 0.989 R.MKENQK[325.13]HIYYITGETK.D                        |
| 0.999531 | 0.9996 K.K[325.13]LPIQEFHLSR.I                            |
| 0.99953  | 0.999 K.AQNLIWNIK[325.13]DELKK.V                          |
| 0.999529 | 0.9976 R.KITIGQAPTEK[325.13]GHTR.T                        |

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| 0.999529 | 0.968 R.HGESGSM[147.04]AVFHQTQGPPSYSESK[325.13]R.L         |
| 0.999529 | 0.9998 R.LVVPASQC[160.03]GSLIGK[325.13]GGC[160.03]K.I      |
| 0.999529 | 0.1097 R.ADIK[325.13]EMGLSLQWLYSAR.G                       |
| 0.999529 | 0.9993 R.LGNDFHTNK[325.13]R.V                              |
| 0.999528 | 0.9932 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK.  |
| 0.999528 | 0.9951 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                  |
| 0.999527 | 0.9983 R.AAPGAEFAPNK[325.13]R.R                            |
| 0.999527 | 0.9956 R.VQAQGPGLK[325.13]EAFTNKPNVFTVVTR.G                |
| 0.999525 | 0.9971 R.GVTFLFPIQAK[325.13]TFHHVYSGK.D                    |
| 0.999525 | 0.9884 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK.  |
| 0.999525 | 0.9996 R.TTDFSDFLSIVGC[160.03]TK[325.13]GR.H               |
| 0.999525 | 0.9968 K.GMTLVTPQLLLFASK[325.13]K.V                        |
| 0.999525 | 0.9864 R.LDSQK[325.13]HIDFSLR.S                            |
| 0.999525 | 0.9991 R.HLIGK[325.13]SGANINR.I                            |
| 0.999524 | 0.9995 R.ITELMQVLK[325.13]DLNHGK.Y                         |
| 0.999523 | 0.9995 K.GAVDGGSLIPHSTK[325.13]R.F                         |
| 0.999522 | 0.9989 R.TLDAHEDK[325.13]VWGLHC[160.03]SR.L                |
| 0.999522 | 0.8744 R.MVNHFIAEFK[325.13]R.K                             |
| 0.999522 | 0.9989 K.AK[325.13]DPFAHLPK.S                              |
| 0.999521 | 0.9972 R.IGSSM[147.04]K[325.13]SVGEVMAIGR.T                |
| 0.999521 | 0.9994 K.ISK[325.13]PAPYWEGTAVIDGEFK.E                     |
| 0.99952  | 0.999 R.AHWK[325.13]FLK.T                                  |
| 0.99952  | 0.9998 K.TLVMNK[325.13]HVGHLR.T                            |
| 0.99952  | 0.9991 R.NINITK[325.13]DLLDLLVEAK.Q                        |
| 0.99952  | 0.9993 R.HQK[325.13]PAGAPATK.K                             |
| 0.999519 | 0.9701 R.EVTVPVFYPTK[325.13]VWLEVEPVGMLK.E                 |
| 0.999519 | 0.9978 K.VDVGKDQEFTVK[325.13]SK.G                          |
| 0.999519 | 0.9996 K.ELNPSLNFK[325.13]EVTYELDHPGFQIR.D                 |
| 0.999517 | 0.9671 K.KAK[325.13]VAKPK.K                                |
| 0.999517 | 0.9969 K.AYAALAALEK[325.13]LFPDTPLALDANK.K                 |
| 0.999517 | 0.9999 R.LEK[325.13]HLDALLR.Q                              |
| 0.999517 | 0.9961 R.RGPC[160.03]IYNEDNGIHK[325.13]AFR.N               |
| 0.999515 | 0.9972 R.K[325.13]PYIWEYSR.L                               |
| 0.999515 | 0.9999 R.FLQPVQK[325.13]IDMNLTDLLGELQR.D                   |
| 0.999515 | 0.9949 K.HAVSEGK[325.13]AVTKYTSK.-                         |
| 0.999513 | 0.9996 R.IC[160.03]HGK[325.13]PVTQVTWHGR.G                 |
| 0.999513 | 0.9991 R.K[325.13]YEMFAQTLQQSR.G                           |
| 0.999513 | 0.9839 R.HNGTGGK[325.13]SIYGEK.F                           |
| 0.999512 | 0.993 K.VK[325.13]PIVAKLIAALSTPSQQVQESVASC[160.03]LPPL     |
| 0.999512 | 0.999 R.GQK[325.13]VLDSGAPIKIPVGPETLGR.I                   |
| 0.999512 | 0.9869 R.KYGGPPPSVYSGVQPGIGTEVFVGK[325.13]IPR.D            |
| 0.999511 | 0.9976 K.KAK[325.13]KPAAAGVK.K                             |
| 0.999511 | 0.9983 K.AYHEQLSVAEITNAC[160.03]FEPANQMVK[325.13]C[160.03] |
| 0.999511 | 0.9991 K.GVLFGVPGAFTPGC[160.03]SK[325.13]THLPGFVEQAEA      |
| 0.999509 | 0.9979 K.NLQEAEEWYK[325.13]SK.F                            |
| 0.999509 | 0.9978 R.GAGIGGLGITVEGPSESK[325.13]INC[160.03]R.D          |
| 0.999509 | 0.9973 R.GAPLAK[325.13]VVFR.D                              |

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| 0.999508 | 0.9936 K.DDQHFTVTGLHK[325.13]GTTYIFR.L                  |
| 0.999508 | 0.9934 K.DKGEYTLVVK[325.13]WGDEHIPGSPYR.V               |
| 0.999508 | 0.9963 R.FVPQEM[147.04]GVHTVSVK[325.13]YR.G             |
| 0.999508 | 0.9996 R.EHTALLK[325.13]IEGVYAR.D                       |
| 0.999507 | 0.9995 R.AYGGSMLC[160.03]AK[325.13]C[160.03]VR.D        |
| 0.999507 | 0.9992 K.NKEEAAEYAK[325.13]LLAK.R                       |
| 0.999505 | 0.9929 R.LTVNEAVK[325.13]EGVVGPELHHK.L                  |
| 0.999505 | 0.9993 R.RNK[325.13]LDHYAIK.F                           |
| 0.999505 | 0.9951 R.VSFELFADK[325.13]VPK.T                         |
| 0.999505 | 0.9877 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG   |
| 0.999505 | 0.9932 R.K[325.13]MFTLLDVNR.K                           |
| 0.999505 | 0.9991 K.LK[325.13]DYAFVHFEDR.G                         |
| 0.999504 | 0.9996 K.FFEVILIDPFHK[325.13]AIR.R                      |
| 0.999504 | 0.9991 K.VDLGVLGK[325.13]QQFDLENK.F                     |
| 0.999504 | 0.9974 R.K[325.13]HPEVDVLINFASLR.S                      |
| 0.999503 | 0.9875 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S        |
| 0.999503 | 0.999 K.DAIIAK[325.13]LANQAADYFGDAFK.Q                  |
| 0.999503 | 0.9997 R.TC[160.03]LITFK[325.13]PGAFIPGAPVQPVVLR.Y      |
| 0.999503 | 0.9936 R.DAK[325.13]LDKSQIHDIVLVGGSTR.I                 |
| 0.999502 | 0.9857 R.TAQSTPSAPPQK[325.13]VMC[160.03]VSMGSTTVR.V     |
| 0.999502 | 0.9994 R.EGAPIEPDPPVSHWK[325.13]PEAVQYYEDGAR.I          |
| 0.999501 | 0.2378 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I           |
| 0.999501 | 0.995 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999501 | 0.9973 K.HQPTAIIAK[325.13]TFK.G                         |
| 0.999501 | 0.991 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                |
| 0.9995   | 0.9994 K.LTSLALVDGK[325.13]SINAGGHK.V                   |
| 0.999499 | 0.9949 R.K[325.13]ESYSVYVYK.V                           |
| 0.999499 | 0.9972 K.SNQNGK[325.13]DSKPSSTPR.S                      |
| 0.999498 | 0.9969 K.IGKPHTVPC[160.03]K[325.13]VTGR.C               |
| 0.999498 | 0.9994 K.NVIHK[325.13]IFSK.F                            |
| 0.999497 | 0.9977 K.VTVLFAGQHISK[325.13]SPFEVSVDK.A                |
| 0.999497 | 0.9995 R.FAIGSQVSEHSIIK[325.13]DFTK.Q                   |
| 0.999497 | 0.9414 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |
| 0.999497 | 0.9977 R.LAK[325.13]SDPMVQC[160.03]IIEESGEHIIAGAGELHLEI |
| 0.999496 | 0.995 K.K[325.13]C[160.03]GHTNNLRPK.K                   |
| 0.999496 | 0.999 K.EDK[325.13]DAQFYC[160.03]ELNYR.L                |
| 0.999496 | 0.9975 K.SAAK[325.13]AVKPK.A                            |
| 0.999495 | 0.9907 R.LLFNDVQTLK[325.13]DGRHPQGEQMYR.R               |
| 0.999495 | 0.9994 K.GVTIPYRPK[325.13]PSSSPVIFAGGQDR.Y              |
| 0.999493 | 0.9991 K.LNPK[325.13]TGLIDYNQLALTAR.L                   |
| 0.999493 | 0.9998 K.FEQLTLDGHNLPVLC[160.03]VITGK[325.13]GPLR.E     |
| 0.999492 | 0.995 K.ESYSVYVYK[325.13]VLK.Q                          |
| 0.999492 | 0.6434 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I           |
| 0.999492 | 0.9999 K.VHK[325.13]ISNPWQSPSGTLPALR.T                  |
| 0.99949  | 0.998 R.ENVIMSQLPC[160.03]IK[325.13]ELVSDANQHVK.S       |
| 0.99949  | 0.9966 R.TEMDWVLK[325.13]HSGPNSADSANDGFVR.L             |
| 0.99949  | 0.9974 R.IFHELTQTDK[325.13]ALFNR.L                      |

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| 0.999489 | 0.9975 K.SAPSTGGVK[325.13]KPHR.Y                         |
| 0.999489 | 0.9973 K.EAMEDGEIDGNKVTLDWAK[325.13]PK.G                 |
| 0.999489 | 0.9996 R.HIITVDGK[325.13]PPTWSEFPK.G                     |
| 0.999488 | 0.9966 K.FLK[325.13]SGDAAIVDMVPGKPM[147.04]C[160.03]VE   |
| 0.999488 | 0.999 K.K[325.13]FKDPNAPK.R                              |
| 0.999487 | 0.999 K.EQGYDVIAYLANIGQK[325.13]EDFEEAR.K                |
| 0.999487 | 0.9949 R.EVTVPVFYPTTEK[325.13]VWLEVEPVGM[147.04]LK.E     |
| 0.999487 | 0.9968 K.AVPYQK[325.13]FEAHPNDLYVEGLPENIPFR.S            |
| 0.999487 | 0.9983 R.AHQVVEDGYEFFAK[325.13]R.Q                       |
| 0.999486 | 0.7339 K.EITALAPSTMKIK[325.13]IIAPPER.K                  |
| 0.999486 | 0.9978 R.K[325.13]EPLFGISTGNLITGLAAGAK.T                 |
| 0.999486 | 0.9978 R.MK[325.13]QVEELYHSLLELGEK.R                     |
| 0.999486 | 0.9993 K.K[325.13]VKTDTVLILC[160.03]R.K                  |
| 0.999486 | 0.9978 K.HDVGAYMLMYK[325.13]GANR.T                       |
| 0.999485 | 0.9996 R.AK[325.13]LNWLSVDFNNWK.D                        |
| 0.999485 | 0.9996 R.AK[325.13]LNWLSVDFNNWK.D                        |
| 0.999484 | 0.9926 R.SLQAVPGAK[325.13]DGTSLWDLSSC[160.03]HFTEEQR     |
| 0.999484 | 0.9971 K.TLVLLMGK[325.13]EGVHGGLINK.K                    |
| 0.999483 | 0.9988 R.IESLSSQLSNLQK[325.13]ESR.A                      |
| 0.999483 | 0.9974 K.SPNK[325.13]HNR.L                               |
| 0.999482 | 0.95 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K            |
| 0.999482 | 0.9996 R.VNSK[325.13]FDTIYQILLK.K                        |
| 0.999482 | 0.9995 R.HGK[325.13]QVLDGNSNPYDIFLK.D                    |
| 0.999482 | 0.9995 K.AAIDWFDGK[325.13]EFHGNIK.V                      |
| 0.999481 | 0.9968 K.IGKPHTVPC[160.03]K[325.13]VTGR.C                |
| 0.999481 | 0.9952 R.EMAGDNK[325.13]LLGQFTLIGIPPAPR.G                |
| 0.999481 | 0.9991 R.LVQLLVK[325.13]AHQDAQR.H                        |
| 0.999481 | 0.9995 K.FYAPWC[160.03]GHC[160.03]K[325.13]TLAPTWEELSK.  |
| 0.99948  | 0.9927 K.VK[325.13]VLPHTDASK.V                           |
| 0.999479 | 0.9946 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                |
| 0.999479 | 0.9992 R.SLGEISALTSK[325.13]LADLRR.Q                     |
| 0.999478 | 0.6296 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G             |
| 0.999478 | 0.9915 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.999478 | 0.9995 K.QDLPNAMNAAEITDK[325.13]LGLHSLR.H                |
| 0.999478 | 0.9991 K.IDIDYQK[325.13]LHDAFFK.W                        |
| 0.999477 | 0.9987 K.AALLNQHYQVNFK[325.13]GK.L                       |
| 0.999477 | 0.9996 R.DKLNNLVLFDK[325.13]ATYDK.L                      |
| 0.999476 | 0.9996 R.LQVK[325.13]EHQHEEIQNVR.N                       |
| 0.999476 | 0.9991 K.YRPLFDYFLK[325.13]C[160.03]K.E                  |
| 0.999476 | 0.9969 R.GFIYVHK[325.13]PPVHIR.F                         |
| 0.999476 | 0.997 K.SK[325.13]GYAFIEFASFEDAK.E                       |
| 0.999476 | 0.9991 R.LTTVK[325.13]ALTLIAGSPLK.I                      |
| 0.999475 | 0.9991 R.LQEK[325.13]LSPPYSSPQEFAQDVGR.M                 |
| 0.999475 | 0.9936 R.K[325.13]MFTLLDVVNR.K                           |
| 0.999475 | 0.9976 R.IHDVLC[160.03]K[325.13]LVEK.G                   |
| 0.999475 | 0.9597 R.VSGPYFPTLLGLSLQVLEPPQHGAQK[325.13]EDGPQAR.      |
| 0.999474 | 0.9984 R.K[325.13]M[147.04]FTLLDVVNR.K                   |



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| 0.999474 | 0.9993 K.NFLEK[325.13]FVQGLDIGPTK.T                      |
| 0.999474 | 0.9996 K.LPGIPIK[325.13]IVMEAIQQASVAK.K                  |
| 0.999474 | 0.9972 R.LGGHGPSFPLK[325.13]GITEQQK.E                    |
| 0.999473 | 0.9996 K.AVVK[325.13]TDIQIALPSGC[160.03]YGR.V            |
| 0.999473 | 0.9992 K.K[325.13]PYC[160.03]NAHYPK.Q                    |
| 0.999472 | 0.9924 K.FYEAFSK[325.13]NLK.L                            |
| 0.999472 | 0.9974 R.INEILSNALK[325.13]R.G                           |
| 0.99947  | 0.9975 K.WEK[325.13]VQQLVPK.R                            |
| 0.99947  | 0.9993 K.K[325.13]VWLDPNETNEIANANSR.Q                    |
| 0.99947  | 0.9985 R.AVLK[325.13]FAAATGATPIAGR.F                     |
| 0.99947  | 0.9984 R.VKLPSGSK[325.13]K.V                             |
| 0.999468 | 0.9949 R.DAK[325.13]LDKAQIHDLVLVGGSTR.I                  |
| 0.999467 | 0.9993 K.AVLK[325.13]GVHSHK.K                            |
| 0.999467 | 0.9994 K.VK[325.13]TDTVLILC[160.03]R.K                   |
| 0.999467 | 0.9989 K.K[325.13]QGGLGPMNIPLVSDPK.R                     |
| 0.999466 | 0.999 K.DLSDGIHVVK[325.13]DAR.E                          |
| 0.999466 | 0.9901 R.ALTQTGGPHVK[325.13]AR.V                         |
| 0.999466 | 0.9965 R.GLKPSC[160.03]TIPLM[147.04]K[325.13]K.D         |
| 0.999465 | 0.9989 K.AGLQVYNK[325.13]C[160.03]WK.F                   |
| 0.999465 | 0.9859 K.VTIAQGGVLPNIQAVLLPK[325.13]K.T                  |
| 0.999465 | 0.9985 R.IDAM[147.04]HGVVGPYVK[325.13]K.I                |
| 0.999464 | 0.9995 K.TFNQVEIK[325.13]PEMIGHYLGFEFSITYKPVK.H          |
| 0.999462 | 0.9963 K.K[325.13]SAEFLHMLK.N                            |
| 0.999462 | 0.9923 K.VVLKSK[325.13]DDQVTVIGAGVTLHEALAAEELLK.K        |
| 0.999462 | 0.9977 R.SISLYYTGEK[325.13]GQNQDYR.G                     |
| 0.999462 | 0.9924 R.LSAEAEK[325.13]VLALPEPSAAPT.LR.S                |
| 0.999462 | 0.9977 R.LIALLEVLSQK[325.13]R.M                          |
| 0.999462 | 0.9992 R.K[325.13]TLGHNLLVSELYNQLK.F                     |
| 0.999462 | 0.9992 R.LGNDFHTNK[325.13]R.V                            |
| 0.999461 | 0.999 R.C[160.03]LADGNPPPHFSISK[325.13]QNPSTR.E          |
| 0.99946  | 0.8846 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR      |
| 0.99946  | 0.9925 K.THINIVVIGHVDSGK[325.13]STTTGHLIYK.C             |
| 0.999458 | 0.99 R.GC[160.03]GPEK[325.13]DHVYLQLHHLPEQLATR.L         |
| 0.999458 | 0.9964 R.VIFGLFGK[325.13]TVPK.T                          |
| 0.999458 | 0.9819 R.LDSQK[325.13]HIDFS.LR.S                         |
| 0.999457 | 0.9972 R.HRPELIEYDK[325.13]LR.K                          |
| 0.999457 | 0.9995 R.TDEAAFQK[325.13]LMSNLDSNR.D                     |
| 0.999457 | 0.999 K.FTFIEK[325.13]C[160.03]NNPR.S                    |
| 0.999457 | 0.2841 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                 |
| 0.999457 | 0.9944 K.FSGK[325.13]HVVFAQR.R                           |
| 0.999457 | 0.9994 K.EK[325.13]ISMFC[160.03]HVEPEQVIC[160.03]VHDVSSI |
| 0.999456 | 0.9927 K.HQGLK[325.13]LATTILQHWK.K                       |
| 0.999456 | 0.9935 K.AVTK[325.13]YTSSK.-                             |
| 0.999454 | 0.9988 R.LK[325.13]HGDVITI.DR.S                          |
| 0.999453 | 0.9996 R.GGAGVGSM.TK[325.13]IYGGR.Q                      |
| 0.999453 | 0.9975 K.K[325.13]FVIKPIDK.K                             |
| 0.999452 | 0.9994 R.K[325.13]GVAINFVTEEDKR.I                        |

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| 0.999451 | 0.9949 R.RMEELHNQEVQK[325.13]R.K                         |
| 0.999451 | 0.9962 R.DAVTYTEHAK[325.13]R.K                           |
| 0.999447 | 0.9996 R.HSDENDGGQPHK[325.13]R.R                         |
| 0.999447 | 0.9979 K.DWHRPC[160.03]LK[325.13]C[160.03]EK.C           |
| 0.999447 | 0.991 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13]  |
| 0.999447 | 0.9926 R.IMK[325.13]AQALR.D                              |
| 0.999447 | 0.9971 R.ASEEHLK[325.13]QHYIDLK.D                        |
| 0.999446 | 0.9945 R.EVTVPVFYPTTEK[325.13]VWLEVEPVGM[147.04]LK.E     |
| 0.999445 | 0.999 K.IFQISK[325.13]TIEEYAVC[160.03]PDLK.V             |
| 0.999444 | 0.9871 R.AK[325.13]VTLNGVPAQPLGPR.A                      |
| 0.999443 | 0.9842 K.MLETK[325.13]WSLLQQQK.T                         |
| 0.999443 | 0.9996 K.MIK[325.13]PFFHSLSEK.Y                          |
| 0.999442 | 0.9996 R.VKPAPDETSFSEALLK[325.13]R.N                     |
| 0.999442 | 0.9571 R.LESGMQNMSIHTK[325.13]TTSYGAGGLSSAYGGLTSPGLS     |
| 0.999442 | 0.9995 R.SEFYK[325.13]HIVLSGGSTMYPGLPSR.L                |
| 0.999441 | 0.999 R.HAQGEK[325.13]TAGINVR.K                          |
| 0.99944  | 0.9593 K.KPVGAAK[325.13]KPK.K                            |
| 0.99944  | 0.9977 R.SYDVPPPPMEPDHPFYSNISK[325.13]DR.R               |
| 0.99944  | 0.9987 R.FC[160.03]SINSGLHXYMEMPLEC[160.03]ILTEK[325.13] |
| 0.999439 | 0.9999 R.HGLQSLGK[325.13]VGISR.R                         |
| 0.999437 | 0.9953 K.K[325.13]NLVEQHIQDIVVHYTFNK.V                   |
| 0.999437 | 0.9947 K.LDK[325.13]AQIHDLVLVGGSTR.I                     |
| 0.999435 | 0.9556 R.GALQNIIPASTGAAK[325.13]AVGK.V                   |
| 0.999435 | 0.9964 R.FPGAYLK[325.13]GK.K                             |
| 0.999434 | 0.9996 K.YPASTVQILGAEK[325.13]ALFR.A                     |
| 0.999434 | 0.9968 R.HEMLPEFYK[325.13]TVSPALISR.F                    |
| 0.999433 | 0.9993 R.ILMEHIHK[325.13]LK.A                            |
| 0.999433 | 0.9421 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]   |
| 0.999433 | 0.9966 K.DSEDNPQTLLFSATC[160.03]PHWVFNVAK[325.13]K.Y     |
| 0.999432 | 0.9991 R.ELNITAAK[325.13]EIEVGGGRK.A                     |
| 0.999432 | 0.997 R.VYLFTIKK[325.13]GILGQHGFLEGPEGIENTR.F            |
| 0.999431 | 0.9498 K.AVELAANTK[325.13]GIC[160.03]FIR.T               |
| 0.99943  | 0.9996 K.NFSEIHPGMLLIGFVK[325.13]SIK.D                   |
| 0.99943  | 0.999 K.DSSGWSSSK[325.13]DKDAYSSFGSR.S                   |
| 0.999429 | 0.9994 K.ADDGRPFQVIK[325.13]SK.G                         |
| 0.999429 | 0.985 R.VIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I            |
| 0.999429 | 0.9996 R.NALQQENHIIDGVK[325.13]VQVHTR.R                  |
| 0.999429 | 0.9117 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999428 | 0.9982 R.VGPAVELALAQVK[325.13]ARPDLLPGWTVR.T             |
| 0.999428 | 0.9994 R.EGGWDSVQDWMDVLSGGEK[325.13]QR.M                 |
| 0.999428 | 0.9996 R.VANILHDDC[160.03]AFLSAFGDVSK[325.13]PER.Y       |
| 0.999427 | 0.8631 R.LK[325.13]LEPHEGLLLR.F                          |
| 0.999427 | 0.9912 R.ASLSK[325.13]LGDVYVNDAFGTAHR.A                  |
| 0.999426 | 0.9974 K.SIDNK[325.13]ALYDTFSAFGNILSC[160.03]K.V         |
| 0.999425 | 0.997 K.VQK[325.13]HQAFAELSANQSR.I                       |
| 0.999424 | 0.9922 K.VGINYQPPTVVPGGDLAK[325.13]VQR.A                 |
| 0.999424 | 0.9989 K.K[325.13]QLLHLAEEK.Q                            |

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| 0.999423 | 0.9985 R.TVIEQSWGSPK[325.13]VTK.D                         |
| 0.999423 | 0.999 R.LVQLLVK[325.13]AHQDAQR.H                          |
| 0.999423 | 0.9887 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I          |
| 0.999422 | 0.9988 R.ANQAIQMAC[160.03]QSLGEPGC[160.03]TQAQVLSAAT      |
| 0.999422 | 0.9999 R.FFLIK[325.13]SNNHENVSLAK.A                       |
| 0.999421 | 0.9996 K.TIK[325.13]LQIWDTAGQER.F                         |
| 0.999421 | 0.9978 R.GENSC[160.03]K[325.13]ATGQVC[160.03]HALC[160.03] |
| 0.999421 | 0.9993 K.K[325.13]VTSVVFHPSQDLVFSASPDATIR.I               |
| 0.999421 | 0.9996 R.THFGGGK[325.13]TTGFGM[147.04]IYDSL DYAK.K        |
| 0.99942  | 0.9999 R.I LHENTQTDK[325.13]ALYNR.L                       |
| 0.99942  | 0.9981 K.IAVMELFRPK[325.13]GESK.D                         |
| 0.99942  | 0.999 K.LLVHLK[325.13]ATR.N                               |
| 0.99942  | 0.9946 K.VHSFPTLK[325.13]FFPASADR.T                       |
| 0.999419 | 0.9996 K.K[325.13]AEAGAGSATEFQFR.G                        |
| 0.999419 | 0.9914 K.GVSK[325.13]AVEHINK.T                            |
| 0.999419 | 0.9996 R.VQIEHISSLIK[325.13]LSK.A                         |
| 0.999418 | 0.9995 K.SVVAK[325.13]FNASQLITQR.A                        |
| 0.999417 | 0.999 R.LFLLPHK[325.13]DQR.Q                              |
| 0.999416 | 0.9988 K.AGLQVYNK[325.13]C[160.03]WK.F                    |
| 0.999416 | 0.9991 R.AGVK[325.13]MVMIQDGPQNTGADKPLR.I                 |
| 0.999416 | 0.9976 K.NLLIFENLIDLK[325.13]R.R                          |
| 0.999416 | 0.9674 R.TLSDYNIQK[325.13]ESTLHLVLR.L                     |
| 0.999414 | 0.998 R.SYSK[325.13]LLC[160.03]GLLAER.L                   |
| 0.999414 | 0.9996 K.EHIK[325.13]NPDWR.Y                              |
| 0.999414 | 0.9956 K.AHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D      |
| 0.999414 | 0.999 K.HTGAVLK[325.13]GPFSR.Y                            |
| 0.999413 | 0.9968 R.TVVTGIEM[147.04]FHK[325.13]SLER.A                |
| 0.999413 | 0.9994 R.NVK[325.13]LIALSIDSVEDHLAWSK.D                   |
| 0.999413 | 0.9999 K.QEK[325.13]RPLFLAPDFDR.W                         |
| 0.999412 | 0.9965 R.FDDAVVQSDMK[325.13]HWPFFMVVNDAGRPK.V             |
| 0.999412 | 0.9964 K.LIPDSIGK[325.13]DIEKAC[160.03]QSIYPLHDVFVR.K     |
| 0.999412 | 0.9993 K.DK[325.13]MMNGGGHYTYSEN.R.V                      |
| 0.999412 | 0.9996 R.FPLEK[325.13]ALEAFETFK.K                         |
| 0.999412 | 0.9954 K.ERQEAEAK[325.13]EALLQASR.D                       |
| 0.999411 | 0.9496 R.AGLLHNILPSQSTDHLHHSVGTLLSLVYK[325.13]GIAPGDE     |
| 0.999411 | 0.996 K.KVSYSHIQSK[325.13]C[160.03]GSK.D                  |
| 0.99941  | 0.9916 K.SLVSK[325.13]GTLVQTK.G                           |
| 0.99941  | 0.9966 R.K[325.13]TSYAQHQQVR.Q                            |
| 0.99941  | 0.9973 R.C[160.03]PPGVVPAC[160.03]HNSK[325.13]DTVTISGPO   |
| 0.999409 | 0.9976 R.EDSQRPGAHLTVK[325.13]K.I                         |
| 0.999409 | 0.9921 R.IAAYLFK[325.13]GNNR.W                            |
| 0.999409 | 0.9973 K.LDSGK[325.13]ELHINLIPNK.Q                        |
| 0.999408 | 0.9966 R.EDSQRPGAHLTVK[325.13]K.I                         |
| 0.999408 | 0.9912 K.WSLLQQQK[325.13]TAR.S                            |
| 0.999408 | 0.9885 K.VSASPLLYTLIEK[325.13]TMQNVK.H                    |
| 0.999408 | 0.9976 R.ARAEEAEQK[325.13]R.Q                             |
| 0.999407 | 0.9601 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V                 |

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| 0.999407 | 0.9992 K.AQTK[325.13]APPKPAR.A                          |
| 0.999407 | 0.9972 R.VAYVSFGPHAGK[325.13]LVAIVDVIDQNR.A             |
| 0.999405 | 0.9975 R.LPPK[325.13]VESLESlyFTPIPAR.S                  |
| 0.999403 | 0.9922 K.FYEQFSK[325.13]NIK.L                           |
| 0.999403 | 0.9971 K.APLK[325.13]IFAQDGEGQR.I                       |
| 0.999403 | 0.992 R.LEVNLQAMK[325.13]AQFER.D                        |
| 0.999403 | 0.999 K.EISLWFK[325.13]PEELVDYK.S                       |
| 0.999403 | 0.9884 K.VSASPLLYTLIEK[325.13]TMQNVK.H                  |
| 0.999403 | 0.9944 R.HGK[325.13]YM[147.04]AC[160.03]C[160.03]LLYR.G |
| 0.999402 | 0.9916 K.LGLK[325.13]SLVSK.G                            |
| 0.999401 | 0.9996 R.K[325.13]LDPELHLDIK.V                          |
| 0.999399 | 0.9575 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K         |
| 0.999399 | 0.999 K.ALAGC[160.03]DFLTISPK[325.13]LLGELLQDNAK.L      |
| 0.999399 | 0.9459 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF        |
| 0.999398 | 0.9991 R.VLPSITTEILK[325.13]SVVAR.F                     |
| 0.999397 | 0.907 R.DLTDYLM[147.04]K[325.13]ILTER.G                 |
| 0.999397 | 0.9756 R.GTK[325.13]VILHLK.E                            |
| 0.999397 | 0.9996 K.K[325.13]VLC[160.03]LAVAVGHVK.M                |
| 0.999397 | 0.997 R.LSNIFVIGKGNK[325.13]PWISLPR.G                   |
| 0.999396 | 0.997 R.AK[325.13]FEELNMDLFR.S                          |
| 0.999396 | 0.9996 R.VFDHK[325.13]QGTYYGGYFR.D                      |
| 0.999396 | 0.9548 R.K[325.13]TFTAWC[160.03]NSHLR.K                 |
| 0.999395 | 0.9987 K.NQALFPAC[160.03]VLK[325.13]NAELK.F             |
| 0.999395 | 0.9995 R.DNGK[325.13]HALIYYDDLK.Q                       |
| 0.999395 | 0.9996 R.DVFLPK[325.13]PTWGNHTPIFR.D                    |
| 0.999394 | 0.9982 K.AMK[325.13]GLGTDEESILTLLTSR.S                  |
| 0.999394 | 0.9455 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF        |
| 0.999393 | 0.9912 R.GELAIK[325.13]DANAK.L                          |
| 0.999393 | 0.9994 K.YGVK[325.13]VGLTNYAAAYC[160.03]TGLLLAR.R       |
| 0.999393 | 0.9993 K.AGLQVYNK[325.13]C[160.03]WKFEHC[160.03]NFNDVT  |
| 0.999393 | 0.9995 R.KISSPTGSK[325.13]DLQMVNISLR.V                  |
| 0.999392 | 0.9914 K.VK[325.13]VLPHTDASK.V                          |
| 0.999392 | 0.9974 K.K[325.13]QELEEIC[160.03]HDLEAR.V               |
| 0.999391 | 0.9928 R.MVTSESKNVK[325.13]LTVSNVLK.E                   |
| 0.999391 | 0.9941 K.GSFK[325.13]TLTLPSLPLNSADEIYELR.V              |
| 0.999391 | 0.9994 K.YQAVTATLEEK[325.13]RK.E                        |
| 0.999391 | 0.9991 K.ISK[325.13]SPDGAHLTWEPPSVTSGK.I                |
| 0.999391 | 0.9987 R.IC[160.03]FELLELLK[325.13]AHK.K                |
| 0.99939  | 0.9993 K.K[325.13]TGQPM[147.04]INLYTDR.E                |
| 0.99939  | 0.9993 K.K[325.13]TGQPM[147.04]INLYTDR.E                |
| 0.999389 | 0.9996 R.GFGGITHGPPEK[325.13]K.M                        |
| 0.999389 | 0.998 K.IAVMELFRPK[325.13]GESK.D                        |
| 0.999388 | 0.8547 R.LK[325.13]LEPHEGLLLR.F                         |
| 0.999388 | 0.9972 K.VTFDPTSSYTLEDLK[325.13]PDTLYR.F                |
| 0.999388 | 0.9918 R.DQHfVK[325.13]IQVK.D                           |
| 0.999388 | 0.9991 K.IAHLAGVK[325.13]DQLTK.E                        |
| 0.999387 | 0.9567 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K         |

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| 0.999386 | 0.962 R.LAHYNK[325.13]R.S                                |
| 0.999385 | 0.9995 K.GKTPALK[325.13]YQQLFEDIR.G                      |
| 0.999384 | 0.9998 K.IGSLIDVNQSK[325.13]DPEGLR.V                     |
| 0.999384 | 0.9973 R.HC[160.03]IAK[325.13]SQER.V                     |
| 0.999383 | 0.9966 R.GFIYVHK[325.13]PPVHIR.F                         |
| 0.999383 | 0.9995 R.FLTAVNLEHPEMLEK[325.13]ASR.E                    |
| 0.999382 | 0.9999 K.K[325.13]SLTPAVPVESKPDKPSGK.S                   |
| 0.999381 | 0.0842 R.ADIK[325.13]EMGLSLQWLYSAR.G                     |
| 0.999381 | 0.9966 K.IWFDKFK[325.13]YDDAER.R                         |
| 0.99938  | 0.9991 R.SPEAQPK[325.13]TLPLTGSTFHDQIAMLHR.C             |
| 0.99938  | 0.9428 K.NQK[325.13]DDVAQTDLLQIDPNFGSK.E                 |
| 0.99938  | 0.998 R.YGLLK[325.13]HSR.E                               |
| 0.999379 | 0.9994 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L         |
| 0.999378 | 0.9695 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                |
| 0.999378 | 0.9996 R.LVFVPLLLC[160.03]NIK[325.13]PR.R                |
| 0.999378 | 0.9994 K.AAIDWFDGK[325.13]EFHGNIK.V                      |
| 0.999378 | 0.9971 R.VVVLMGSTSDLGHC[160.03]EK[325.13]IKK.A           |
| 0.999377 | 0.9772 R.KPAGAAK[325.13]KPK.K                            |
| 0.999375 | 0.9961 K.EVAGAKPHITAAEGK[325.13]LHNMIVDLDNVVK.K          |
| 0.999375 | 0.9981 R.ALQASALK[325.13]AWGGK.K                         |
| 0.999375 | 0.9924 K.TVTAM[147.04]DVVYALK[325.13]R.Q                 |
| 0.999375 | 0.9729 R.LKDLEALLNSK[325.13]EAALSTALSEK.R                |
| 0.999374 | 0.998 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E   |
| 0.999373 | 0.999 K.EWFLQAAK[325.13]DPSAVAK.H                        |
| 0.999373 | 0.9383 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C        |
| 0.999372 | 0.996 R.RPDQQLQGEGK[325.13]IIDR.R                        |
| 0.999371 | 0.9932 R.SAPGGGSK[325.13]VPQK.K                          |
| 0.99937  | 0.9915 K.AAKPK[325.13]VVKPK.K                            |
| 0.999369 | 0.999 R.VWYVSNIDGTHIAK[325.13]TLAQLNPESLFIASK.T          |
| 0.999368 | 0.9958 R.TFIAIK[325.13]PDGVQR.G                          |
| 0.999368 | 0.9973 R.K[325.13]IWC[160.03]FGPDGTGPNILTDITK.G          |
| 0.999367 | 0.9965 R.HLGYTLC[160.03]K[325.13]QIGTLAELR.E             |
| 0.999366 | 0.9981 R.ALK[325.13]MIVDPVEPHGEM[147.04]K.F              |
| 0.999366 | 0.9359 R.VEYHFLSPYVSPK[325.13]ESPFR.H                    |
| 0.999365 | 0.9996 R.SNDPK[325.13]SQNHPPGWLMR.G                      |
| 0.999364 | 0.9993 R.EALAAVLTYAK[325.13]PDEFSALC[160.03]DLLGTR.L     |
| 0.999364 | 0.9909 R.TGVELGKPTHFTVNAK[325.13]AAGK.G                  |
| 0.999363 | 0.949 K.LDSTDFTGTIK[325.13]LLNENSYPVR.E                  |
| 0.999362 | 0.9996 R.VFQSLPHENK[325.13]PLTLSNYQTNK.A                 |
| 0.999362 | 0.9575 R.TLLIK[325.13]TVETR.D                            |
| 0.999362 | 0.9966 K.NFATSLYSMIK[325.13]GDTSGDYKK.A                  |
| 0.999361 | 0.9955 K.LLETK[325.13]WTLLQEQK.S                         |
| 0.999361 | 0.9919 R.LQALDTGWNELHK[325.13]MWENR.Q                    |
| 0.99936  | 0.9896 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.99936  | 0.9989 K.SLK[325.13]FATEAAITILR.I                        |
| 0.999359 | 0.9994 K.IGEHMEEHGIK[325.13]FIR.Q                        |
| 0.999359 | 0.9991 K.K[325.13]KVLDPNETNEIANANSR.Q                    |

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| 0.999359 | 0.9902 K.APK[325.13]ISM P D V D L H L K . G                                |
| 0.999358 | 0.9878 R.RFDDAVVQSDMK[325.13]HWP F M [147.04]V V N D A G R P               |
| 0.999357 | 0.9991 K.SAILGLPQPLLELNDSPVFK[325.13]T V L E R . M                         |
| 0.999356 | 0.9994 R.AFTELFQVAC[160.03]A K [325.13]P P P L G L C [160.03]D Y P         |
| 0.999356 | 0.9974 K.KFYEA F S K [325.13]N L K . L                                     |
| 0.999355 | 0.9981 R.GETTLWNPGC[160.03]D H A G I A T Q V V V E K [325.13]K . L         |
| 0.999355 | 0.9999 R.DAK[325.13]H T N F V E F R . N                                    |
| 0.999354 | 0.9977 K.FGDPVVQSDMK[325.13]H W P F Q V I N D G D K P K . V                |
| 0.999354 | 0.9965 K.RFDDPGLMLMGFK[325.13]P L V L L K . K                              |
| 0.999354 | 0.9971 R.GDLGIEIPA EK [325.13]V F L A Q K . M                              |
| 0.999354 | 0.9939 R.RGPC[160.03]I I Y N E D N G I I K [325.13]A F R . N               |
| 0.999351 | 0.9487 K.SVHELEKSK[325.13]R . A                                            |
| 0.999351 | 0.9934 R.K[325.13]E S Y S V Y V Y K . V                                    |
| 0.999349 | 0.9992 R.YHPDK[325.13]N K E P G A E E K . F                                |
| 0.999349 | 0.9956 K.HVVFGK[325.13]V K . E                                             |
| 0.999348 | 0.9999 R.TQK[325.13]T P P G L Q H E Y A A P A D Y F R . I                  |
| 0.999347 | 0.9995 R.NDEELNK[325.13]L L G R . V                                        |
| 0.999347 | 0.9988 K.FTISDHPQPIDPLLK[325.13]N C [160.03]I G D F L K . T                |
| 0.999346 | 0.996 R.M[147.04]I A G Q V L D I N L A A E P K [325.13]V N R . G           |
| 0.999346 | 0.9792 R.SIQLDGLVWGASK[325.13]L V P V G Y G I R . K                        |
| 0.999346 | 0.9995 K.VRDK[325.13]L N N L V L F D K . A                                 |
| 0.999344 | 0.0796 R.ADIK[325.13]E M G L S L Q W L Y S A R . G                         |
| 0.999344 | 0.9986 K.K[325.13]P L P D H V S I V E P K . D                              |
| 0.999343 | 0.9995 K.DGVVEITGK[325.13]H E E R . Q                                      |
| 0.999343 | 0.9996 R.LTGVSISQVNHK[325.13]P L R . T                                     |
| 0.999343 | 0.9913 R.YAIC[160.03]S A L A A S A L P A L V M [147.04]S K [325.13]G H R . |
| 0.999342 | 0.9972 K.AK[325.13]L K P G A P L K P K . L                                 |
| 0.999341 | 0.9996 R.K[325.13]T G Q A P G Y S Y T A A N K . N                          |
| 0.999341 | 0.9972 K.VIADNVK[325.13]D W S K . V                                        |
| 0.999341 | 0.999 R.LDQELK[325.13]L I G E Y G L R . N                                  |
| 0.999341 | 0.9991 R.LDQLIYIPLDEK[325.13]S R . V                                       |
| 0.99934  | 0.9986 K.NLGTIAK[325.13]S G T S E F L N K . M                              |
| 0.99934  | 0.9939 R.EMAGDNK[325.13]L L G Q F T L I G I P P A P R . G                  |
| 0.99934  | 0.9968 R.GQKPTLWALLNSEYVTEEK[325.13]K . L                                  |
| 0.99934  | 0.9999 R.LIEPGSK[325.13]N P H L I T N W G P A A F T E A E L E E R . E      |
| 0.999339 | 0.9992 K.K[325.13]V T S V V F H P S Q D L V F S A S P D A T I R . I        |
| 0.999337 | 0.9999 R.AHAWPSPYK[325.13]D Y E V K . K                                    |
| 0.999336 | 0.9967 R.KVLRDNIQGITK[325.13]P A I R . R                                   |
| 0.999335 | 0.9977 K.VK[325.13]L I V L V P P S K P T V N I P S S A T I G N R . A       |
| 0.999335 | 0.9629 R.LLLPGELAKHAVSEGK[325.13]A V T K . Y                               |
| 0.999335 | 0.9999 R.YQVSWSLDHK[325.13]S A H A G T Y E V R . F                         |
| 0.999334 | 0.9913 K.FYEQFSK[325.13]N I K . L                                          |
| 0.999334 | 0.9993 K.ADDGRFPQVIK[325.13]S K . G                                        |
| 0.999332 | 0.9993 R.GYK[325.13]H P V L L L H P L G G W T K . D                        |
| 0.999332 | 0.9897 R.FANYIDK[325.13]V R . F                                            |
| 0.999331 | 0.9418 R.ISVYYNEATGGK[325.13]Y V P R . A                                   |
| 0.999329 | 0.9956 R.IPK[325.13]E Q G V L S F W R . G                                  |

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| 0.999329 | 0.9995 K.K[325.13]ALIEVLQPLIAEHQAR.R                     |
| 0.999328 | 0.9991 K.LYDIDVAK[325.13]VNTLIRPDGEK.K                   |
| 0.999328 | 0.9845 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPM[147.  |
| 0.999326 | 0.978 R.ETAQAIK[325.13]GMHIR.K                           |
| 0.999325 | 0.9943 R.K[325.13]LLEGEESR.I                             |
| 0.999325 | 0.9502 K.IAK[325.13]AFAISGPFNVQFLVK.G                    |
| 0.999325 | 0.9998 K.SK[325.13]THAVLVALK.R                           |
| 0.999324 | 0.9963 K.VIPSPFK[325.13]HADIVTTTTHK.T                    |
| 0.999324 | 0.999 K.ISK[325.13]SPDGAHLTWEPPSVTSGK.I                  |
| 0.999324 | 0.9904 R.MSHLK[325.13]VGSAADIPINISSETDLSLLTATVVPPSGR.E   |
| 0.999322 | 0.9971 K.STC[160.03]IYGGAPK[325.13]GPQIR.D               |
| 0.999322 | 0.9999 R.ITSPLMEPSSIEK[325.13]IVEIDAHIGC[160.03]AMSGLIAC |
| 0.999321 | 0.9988 K.GFQQILAGEYDHLPEQAFYMGVPIEEAVAK[325.13]ADK.L     |
| 0.999321 | 0.9999 R.RPSAAPASQQLSLESK[325.13]LTSVR.F                 |
| 0.999321 | 0.9964 R.LFTK[325.13]VKPLLQVSR.Q                         |
| 0.99932  | 0.9995 R.IVQK[325.13]HPHTGDTKEEK.D                       |
| 0.99932  | 0.9932 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999319 | 0.9878 K.HPVTGQFLYQDSNWASK[325.13]VEK.L                  |
| 0.999317 | 0.9909 K.SFIK[325.13]DYPVVSIEDPFDQDDWGAWQK.F             |
| 0.999317 | 0.9994 K.ALLGSVK[325.13]DSIVQGFQWGTR.E                   |
| 0.999316 | 0.9563 K.TKPVGTGNLRPEEALQALTIYEGK[325.13]FGR.L           |
| 0.999316 | 0.999 R.DTLFC[160.03]YHK[325.13]ASEVFLQR.L               |
| 0.999315 | 0.999 K.VVK[325.13]VANVSLLALYK.G                         |
| 0.999313 | 0.9238 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPMGTAN     |
| 0.999313 | 0.9998 R.K[325.13]PAAGLSAAPVPTAPAAGAPLMDFGNDFFVPPAPF     |
| 0.999312 | 0.9956 R.GFK[325.13]DQIYDIFQK.L                          |
| 0.999311 | 0.9969 K.AAKPKK[325.13]APK.S                             |
| 0.99931  | 0.9908 R.VLDPFTIK[325.13]PLDR.K                          |
| 0.99931  | 0.9998 K.GFTAAGVLAHK[325.13]IMASSPDMDLATVSALR.K          |
| 0.99931  | 0.9993 K.TFK[325.13]EFLLSLDDSVDETEAVKR.Y                 |
| 0.999309 | 0.9971 K.VVLK[325.13]HLK.K                               |
| 0.999309 | 0.9912 K.EKYIDQEELNKTk[325.13]PIWTR.N                    |
| 0.999307 | 0.9984 K.KYHNVGLSK[325.13]C[160.03]EIK.V                 |
| 0.999307 | 0.9843 R.FVPQEMGVHTSVK[325.13]YR.G                       |
| 0.999307 | 0.9997 K.K[325.13]HVNPVQALSEFK.A                         |
| 0.999307 | 0.9994 R.HISPSAK[325.13]PFENGQYLDIYGITR.D                |
| 0.999307 | 0.9966 K.KAK[325.13]KPAAAGVK.K                           |
| 0.999306 | 0.892 R.YISPDQLADLYK[325.13]SFIK.D                       |
| 0.999305 | 0.9936 R.K[325.13]TVTAMDVVYALK.R                         |
| 0.999305 | 0.9959 R.DLYEDELVPLFEK[325.13]AGPIWDLR.L                 |
| 0.999304 | 0.9995 K.MIK[325.13]PFFHSLSEK.Y                          |
| 0.999303 | 0.9992 K.IPVDTYNNILTVLK[325.13]LK.H                      |
| 0.999303 | 0.9995 R.VKPAPDETSFSEALLK[325.13]R.N                     |
| 0.999303 | 0.9999 R.K[325.13]IIIPPFLAYGEK.G                         |
| 0.999303 | 0.9975 R.GHYK[325.13]GQQIGK.V                            |
| 0.999303 | 0.9953 K.NLQYYDISAK[325.13]SNYNFEKPFLWLAR.K              |
| 0.999303 | 0.9949 K.NTHC[160.03]SSLPHYQK[325.13]LK.K                |

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| 0.999303 | 0.9991 R.GINLSDGK[325.13]WHR.I                                 |
| 0.999303 | 0.9991 R.GINLSDGK[325.13]WHR.I                                 |
| 0.999302 | 0.9793 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S         |
| 0.999302 | 0.9992 R.K[325.13]HIMGQNVADYMR.Y                               |
| 0.999302 | 0.9992 R.K[325.13]HIMGQNVADYMR.Y                               |
| 0.999302 | 0.9995 R.ALETLTGALFQRPPLIAAVK[325.13]R.Q                       |
| 0.999301 | 0.987 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I                  |
| 0.999301 | 0.99 K.STLTDSLVC[160.03]K[325.13]AGIIASAR.A                    |
| 0.999301 | 0.9888 K.NAQK[325.13]SNQNGKDSKPSSTPR.S                         |
| 0.999301 | 0.9996 K.DGPVGFADFVYK[325.13]HIVPAC[160.03]FLAPLK.Q            |
| 0.999299 | 0.9975 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q                      |
| 0.999298 | 0.9995 R.VAAGLQIK[325.13]NSLTSKDPDIK.A                         |
| 0.999298 | 0.2272 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                       |
| 0.999298 | 0.994 K.VM[147.04]IGENVDEK[325.13]HLPDLDHPIIPADYVAIK.A         |
| 0.999297 | 0.9987 K.IVSWLEYESSFSNEEAQK[325.13]AQALR.L                     |
| 0.999296 | 0.9996 K.AVPLNASK[325.13]QDGPMPKPHSVSLNDTETR.K                 |
| 0.999295 | 0.9944 R.K[325.13]LTWVNEGLVDGWDDPRFPTVR.G                      |
| 0.999294 | 0.9995 R.IC[160.03]HGK[325.13]PVTQVTHGR.G                      |
| 0.999294 | 0.9993 R.HQVK[325.13]YLGLENLR.V                                |
| 0.999293 | 0.9996 R.SPAHYAGYWK[325.13]AVQELWLR.L                          |
| 0.999293 | 0.993 K.LHQAMK[325.13]GVGTR.H                                  |
| 0.999292 | 0.9996 K.K[325.13]HEEEEEAKAER.E                                |
| 0.999291 | 0.9969 R.QLLHNFPPDQLTSSGAPFWSGPK[325.13]R.C                    |
| 0.999291 | 0.9996 K.IGEGTYGVVYK[325.13]GR.H                               |
| 0.999291 | 0.9996 R.IFGSNK[325.13]WTTEQQQR.F                              |
| 0.999291 | 0.9873 K.VLK[325.13]QVHPDTGISSK.A                              |
| 0.99929  | 0.996 R.FQLQATTK[325.13]EGPGEAIVR.E                            |
| 0.999289 | 0.6223 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK             |
| 0.999289 | 0.9995 R.KIIK[325.13]DGEQHEDLNEVAK.L                           |
| 0.999288 | 0.9539 K.KAK[325.13]VAKPK.K                                    |
| 0.999288 | 0.9947 R.KAHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D          |
| 0.999288 | 0.9905 K.IK[325.13]IIAPPER.K                                   |
| 0.999287 | 0.9909 K.LFVGGIK[325.13]EDTEEHHLR.D                            |
| 0.999287 | 0.9433 R.AGLLHNILPSQSTDHLHHSVGTLLSLVYK[325.13]GIAPGDE          |
| 0.999287 | 0.9996 R.K[325.13]VAQVPLGPEC[160.03]SR.A                       |
| 0.999286 | 0.9911 K.K[325.13]ALAAAGYDVEK.N                                |
| 0.999285 | 0.9867 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I                 |
| 0.999285 | 0.9996 K.TTWAIK[325.13]HAASNPSK.K                              |
| 0.999285 | 0.9946 R.YK[325.13]LLGGLAVR.R                                  |
| 0.999284 | 0.997 R.K[325.13]YAYSASGGR.R                                   |
| 0.999284 | 0.9983 R.LQAEIDNIK[325.13]NQR.A                                |
| 0.999284 | 0.9965 R.IAEDDGKPRPAFSNALEPDFK[325.13]ATSITVTGSGSC[160.03]IR.S |
| 0.999282 | 0.9996 R.YTC[160.03]HVQHEGLPK[325.13]PLTLR.W                   |
| 0.99928  | 0.6191 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK             |
| 0.99928  | 0.9956 R.GFGFVTFDDHDPVVK[325.13]IVLQK.Y                        |
| 0.999279 | 0.9953 K.HKSDFGK[325.13]FVLSSGK.F                              |
| 0.999278 | 0.9967 R.LQAEK[325.13]AHAFVQVK.E                               |



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| 0.999278 | 0.9897 K.AGGTKPK[325.13]KPVGAAG.K                       |
| 0.999277 | 0.9998 R.K[325.13]GSLESPATDVFGSTEEGEKR.W                |
| 0.999277 | 0.9993 K.SM[147.04]TEAEQQQLIDHFLFDK[325.13]PVSPLLLASC   |
| 0.999276 | 0.9995 R.THFGGGK[325.13]TTGFGM[147.04]IYDSL DYAK.K      |
| 0.999275 | 0.9941 R.MHAPGK[325.13]GLSQSALPYR.R                     |
| 0.999275 | 0.9969 K.DIYALISDQK[325.13]HMR.K                        |
| 0.999275 | 0.9969 K.LLSSLGGFK[325.13]LAHGLLEELK.T                  |
| 0.999274 | 0.9995 K.K[325.13]AEAGAGSATEFQFR.G                      |
| 0.999274 | 0.9947 R.YFPTQALNFAFK[325.13]DK.Y                       |
| 0.999274 | 0.9974 R.LAHEVGWK[325.13]YQAVTATLEEK.R                  |
| 0.999273 | 0.9993 R.YESHPVC[160.03]ADLQAK[325.13]ILQC[160.03]YR.E  |
| 0.999273 | 0.9993 K.FYAPWC[160.03]GHC[160.03]K[325.13]TLAPTWEELSK. |
| 0.999272 | 0.9956 R.GRPSGKGIVEFSGK[325.13]PAAR.K                   |
| 0.999271 | 0.9783 K.M[147.04]LETK[325.13]WSLLQQQK.T                |
| 0.999271 | 0.9963 R.LTLYDIAHTPGVAADLSHIETK[325.13]AAVK.G           |
| 0.99927  | 0.9986 R.SIFDFSALK[325.13]ELLSGPNR.L                    |
| 0.99927  | 0.9958 R.TANDAVELHIK[325.13]NVQPSDQGHYK.C               |
| 0.999268 | 0.9979 K.SNYNLPMHK[325.13]MINTDLSR.I                    |
| 0.999266 | 0.9996 R.APSHSESALNNDISK[325.13]TC[160.03]NTNPHLNALSTD: |
| 0.999265 | 0.9952 R.KAHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D   |
| 0.999263 | 0.9995 K.K[325.13]AAVHYDR.S                             |
| 0.999262 | 0.9757 R.HNGTGGK[325.13]SIYGEK.F                        |
| 0.99926  | 0.9989 R.LGNDFHTNK[325.13]R.V                           |
| 0.99926  | 0.9901 K.HSQFIGYPITLYLEK[325.13]ER.E                    |
| 0.999259 | 0.9949 R.HKNPK[325.13]TGIYEEK.H                         |
| 0.999259 | 0.9777 K.IGYNPDTVAFPVISGWNGDNMLEPSANMPWFK[325.13]C      |
| 0.999259 | 0.9998 K.TTFDEAMADLHTLSEDSYK[325.13]DSTLIMQLLR.D        |
| 0.999257 | 0.9984 R.KVK[325.13]FTQQNYHDR.L                         |
| 0.999256 | 0.999 K.VNNSSLIGLGYTQTLK[325.13]PGIK.L                  |
| 0.999256 | 0.9504 R.LQSTLK[325.13]TLSFSFPNTVTGSER.V                |
| 0.999256 | 0.973 K.LLSK[325.13]TPELNLDQFHDK.T                      |
| 0.999255 | 0.9998 K.YSNSALGHVNC[160.03]TIK[325.13]ELR.R            |
| 0.999254 | 0.9999 R.DC[160.03]HYLK[325.13]MSIAQC[160.03]TSSHPIIR.Q |
| 0.999254 | 0.9999 R.TVALK[325.13]GPVTNAAILLAPVSMSSDFRPSLPLPHFNK    |
| 0.999254 | 0.9999 K.AELSK[325.13]LVIVAK.A                          |
| 0.999254 | 0.9999 K.GQYFGELALVTNK[325.13]PR.A                      |
| 0.999254 | 0.9999 R.IEGLAPK[325.13]LDPEEMKR.K                      |
| 0.999253 | 0.9986 K.MVVESAYEVIK[325.13]LK.G                        |
| 0.999252 | 0.9796 K.IAPSFIVESIEDALK[325.13]AADTIGYPVMIR.S          |
| 0.999251 | 0.9853 R.FDASFFGVHPK[325.13]QAHTMDPQLR.L                |
| 0.999251 | 0.9968 R.DGK[325.13]LVSESSDVLPK.-                       |
| 0.999251 | 0.9968 K.VIQC[160.03]FAETGQVQK[325.13]IVLYAK.K          |
| 0.999251 | 0.9957 R.EDSQRPGAHLTVK[325.13]K.I                       |
| 0.99925  | 0.974 R.ISVYYNEATGGK[325.13]YVPR.A                      |
| 0.999249 | 0.995 R.LYKEELEQTYHAK[325.13]LENAR.L                    |
| 0.999249 | 0.9945 R.AIMKDPDDHTVC[160.03]HLLFANQTEK[325.13]DILLRPE  |
| 0.999249 | 0.9996 K.YKETDLLILFK[325.13]DDYFAK.K                    |

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| 0.999248 | 0.9996 R.TGLK[325.13]ITSLTEVVVC[160.03]GLDLC[160.03]NQGN  |
| 0.999248 | 0.9973 R.GHYK[325.13]GQQIGK.V                             |
| 0.999247 | 0.9877 R.GFEVVYMTPEIDEC[160.03]VQQLK[325.13]EFDGK.S       |
| 0.999247 | 0.9964 R.ALIPLAK[325.13]AEELVNTAPLTGVPQHVPVR.L            |
| 0.999246 | 0.9992 R.KADVIK[325.13]AAHLC[160.03]AEAALR.L              |
| 0.999246 | 0.9989 K.AGLQVYNK[325.13]C[160.03]WK.F                    |
| 0.999246 | 0.9955 R.HIVK[325.13]EFK.R                                |
| 0.999246 | 0.9944 K.GHLSGLAK[325.13]R.A                              |
| 0.999245 | 0.9992 R.IFSAYIK[325.13]EVEERPAPTPWGSK.M                  |
| 0.999244 | 0.9995 K.GLTDL SAC[160.03]K[325.13]AQLGLGHSYSR.A          |
| 0.999243 | 0.9954 K.K[325.13]HGVYNPNK.I                              |
| 0.999242 | 0.9953 K.SLETEHK[325.13]ALTSEIALLQSR.L                    |
| 0.999242 | 0.9622 R.LVNH FVEEFK[325.13]R.K                           |
| 0.999241 | 0.9762 K.FIIPNVVK[325.13]YSPNC[160.03]K.L                 |
| 0.999241 | 0.9894 K.NGVK[325.13]ITLPVDFVTADKFDENAK.T                 |
| 0.999241 | 0.9993 K.ILTFDQLALDSPK[325.13]GC[160.03]GTVLLSGPR.K       |
| 0.99924  | 0.9996 K.RPAC[160.03]TLK[325.13]PEC[160.03]VQQLVC[160.03] |
| 0.999238 | 0.9978 K.K[325.13]EM[147.04]QPTHPIR.L                     |
| 0.999237 | 0.9993 K.NPTLFIFAENDVVIPLK[325.13]DVSLTQK.L               |
| 0.999237 | 0.9045 R.MVNH FIAEFK[325.13]R.K                           |
| 0.999235 | 0.9338 R.LVYLVENPGGYVAYSK[325.13]AATVTGK.L                |
| 0.999235 | 0.9992 R.DLLVQQASQC[160.03]LSK[325.13]LVQIASR.T           |
| 0.999234 | 0.9964 K.K[325.13]FVIKPIDKK.A                             |
| 0.999234 | 0.9907 K.TVTAM[147.04]DVVYALK[325.13]R.Q                  |
| 0.999234 | 0.9994 R.GFK[325.13]LPDTPQGGLGEAR.M                       |
| 0.999233 | 0.9947 K.NK[325.13]ITITNDQNR.L                            |
| 0.999232 | 0.9995 K.EQSILELGSLAK[325.13]TGQAAELGGLK.Y                |
| 0.999232 | 0.9999 R.MQQEAQHVLFLSK[325.13]NQAIR.Q                     |
| 0.999231 | 0.8423 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR       |
| 0.99923  | 0.9897 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLRL     |
| 0.99923  | 0.8823 R.DLTDYLM[147.04]K[325.13]ILTER.G                  |
| 0.999228 | 0.9939 R.RPDQQLQGEGK[325.13]IIDR.R                        |
| 0.999227 | 0.9999 K.YRPVK[325.13]LNEIVGNEDTVSR.L                     |
| 0.999226 | 0.994 R.HAK[325.13]WFAQAR.A                               |
| 0.999226 | 0.9994 K.VTLPDGK[325.13]QVDAESWK.T                        |
| 0.999226 | 0.9929 R.SRK[325.13]ESYSVYVK.V                            |
| 0.999226 | 0.9865 R.LPMNK[325.13]EWPSNLDLR.K                         |
| 0.999226 | 0.985 K.VSASPLLYTLIEK[325.13]TMQNVK.H                     |
| 0.999225 | 0.998 K.KVVNPLFEK[325.13]RPK.N                            |
| 0.999224 | 0.9992 K.GISVHISNAEPK[325.13]HNSNR.Q                      |
| 0.999224 | 0.9955 R.ASVPDGFSEL TQQLAQATGK[325.13]PPQYIAVHVVPDQ       |
| 0.999223 | 0.9344 R.AGLLHNILPSQSTDLHHSVGTLLSLVYK[325.13]GIAPGDE      |
| 0.999223 | 0.9994 K.IC[160.03]QFK[325.13]LVLLGESAVGK.S               |
| 0.999223 | 0.9951 K.SNYNFEK[325.13]PFLWLAR.K                         |
| 0.999223 | 0.9981 R.EVK[325.13]EWHGC[160.03]R.A                      |
| 0.999223 | 0.9814 R.FVPQEMGVHTVSVK[325.13]YR.G                       |
| 0.999222 | 0.9993 R.HNSEKPPPEVKPEVK[325.13]TTEK.K                    |

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| 0.99922  | 0.9923 R.AK[325.13]VTLNGVPAQPLGPR.A                   |
| 0.99922  | 0.9998 R.IWQYVYSK[325.13]DQLQTFSEEHPVLLTEAPLNPR.K     |
| 0.99922  | 0.9943 R.VHK[325.13]ISNVNK.A                          |
| 0.999217 | 0.9862 R.LLFNDVQTLK[325.13]DGRHPQGEQMYR.R             |
| 0.999215 | 0.9996 R.K[325.13]ALHSDRPPSASQPR.G                    |
| 0.999215 | 0.9992 K.GNDISSGTVLSDYVGSPPK[325.13]GTGLHR.Y          |
| 0.999215 | 0.9966 R.DIFNK[325.13]GFGFGLVK.L                      |
| 0.999215 | 0.9991 R.K[325.13]HIMGQNVADYMR.Y                      |
| 0.999214 | 0.9965 K.AASGEAKPK[325.13]AK.K                        |
| 0.999214 | 0.9961 K.GYEK[325.13]KPYC[160.03]NAHYPK.Q             |
| 0.999214 | 0.9997 R.TRPWLQELSMGSPGVTNK[325.13]ATK.I              |
| 0.999212 | 0.9964 K.EGIPALDNFLDK[325.13]L.-                      |
| 0.999211 | 0.9964 K.GYAFIEFASFEDAK[325.13]EALNSC[160.03]NKR.E    |
| 0.99921  | 0.9964 K.VK[325.13]C[160.03]SGPGLSPGMVR.A             |
| 0.999209 | 0.9994 K.AVVK[325.13]TDIQIALPSGC[160.03]YGR.V         |
| 0.999209 | 0.9921 R.GVLK[325.13]VFLENVIR.D                       |
| 0.999205 | 0.9999 R.IVLHPDTEHSK[325.13]GC[160.03]AFAQFMTQEAAQK.C |
| 0.999205 | 0.9942 R.YFPTQALNFAFK[325.13]DK.Y                     |
| 0.999204 | 0.9947 R.RGEEGHDPK[325.13]EPEQLR.K                    |
| 0.999204 | 0.9985 R.KYGGPPPDVSVSGQQPSVGTEIFVGK[325.13]IPR.D      |
| 0.999204 | 0.9993 K.ALLGSVK[325.13]DSIVQGFWGTR.E                 |
| 0.999203 | 0.9996 R.AAK[325.13]VLEQLTGQTPVFSK.A                  |
| 0.999202 | 0.9999 R.LFPHEVADVEPVLDLVTIQNPK[325.13]DHEAWETR.Y     |
| 0.999202 | 0.9999 R.IK[325.13]SGETVINTANYHDTSPYR.W               |
| 0.999202 | 0.9999 R.LLAQHATSEC[160.03]PK[325.13]R.T              |
| 0.999202 | 0.9999 R.K[325.13]AAVSHWQQQSYLDSGIHSGATTTAPSLSGK.G    |
| 0.999202 | 0.9888 R.GQAGGK[325.13]LHIIEVGTPPTGNQPFPK.K           |
| 0.999202 | 0.9999 R.VTQPNTFGLFLYK[325.13]EQGYHR.L                |
| 0.999201 | 0.9891 R.GELAIKDANAK[325.13]LSELEAALQR.A              |
| 0.9992   | 0.9991 R.VSVGIHK[325.13]EDIDAAIETYNLLSER.W            |
| 0.999199 | 0.9949 K.IGYNPDTVAFPVPIGWNGDNMLEPSANM[147.04]PWFK[    |
| 0.999198 | 0.9995 K.IAGYVTHLMK[325.13]R.I                        |
| 0.999197 | 0.9963 R.LQDEIQNMK[325.13]EEMAR.H                     |
| 0.999197 | 0.9964 K.GFGFVDFNSEEDAK[325.13]AAK.E                  |
| 0.999197 | 0.999 R.YNLEELYQAVENLC[160.03]SHK[325.13]VSPMLYK.Q    |
| 0.999194 | 0.9954 K.ELNYFAK[325.13]ALESPERPFLAILGGAK.V           |
| 0.999193 | 0.9858 K.GATLK[325.13]ITLDNAYMEK.C                    |
| 0.999193 | 0.9994 R.YHQIGSGK[325.13]C[160.03]EIK.V               |
| 0.999193 | 0.9986 R.KLFNLSK[325.13]EDDVR.Q                       |
| 0.999193 | 0.9992 R.HQVK[325.13]YLGLLENLR.V                      |
| 0.999192 | 0.9982 R.LHFHNLVK[325.13]GLTDLSAC[160.03]K.A          |
| 0.999191 | 0.9998 K.AMTAK[325.13]GGDISVC[160.03]EWYQR.V          |
| 0.999191 | 0.9994 R.SSSILK[325.13]GMELSVLDSLNR.M                 |
| 0.999189 | 0.9985 R.MEK[325.13]GEHSIVYLKPSYAFGSVGK.E             |
| 0.999188 | 0.9877 R.ASVPDGFLSELTQQLAQATGK[325.13]PPQYIAVHVVPDQ   |
| 0.999187 | 0.9996 R.HSTC[160.03]K[325.13]DSGHAGAR.D              |
| 0.999187 | 0.9965 K.ITGEAFVQFASQELA EK[325.13]ALGK.H             |

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| 0.999186 | 0.9961 K.SLLGK[325.13]DVLFLK.D                        |
| 0.999186 | 0.9948 R.K[325.13]SNFAEALAAHK.Y                       |
| 0.999186 | 0.9954 R.VTGNFK[325.13]HASPILPITEFSDIPR.R             |
| 0.999184 | 0.9925 R.K[325.13]TVTAMDVVYALK.R                      |
| 0.999184 | 0.9884 K.VEGGVK[325.13]GGQIGLQAPGLSVSGPQGHLESGSGK.V   |
| 0.999183 | 0.9934 K.RGILTLK[325.13]YPIEHGIITNWDDMEK.I            |
| 0.999183 | 0.9246 K.TVTAMDVVYALK[325.13]R.Q                      |
| 0.999183 | 0.9985 R.GRDPVNPEK[325.13]LLVITVATAETEGYLR.F          |
| 0.999182 | 0.9919 K.K[325.13]C[160.03]GHTNNLRPK.K                |
| 0.999182 | 0.99 K.LNILK[325.13]LAPGGHVGR.F                       |
| 0.999182 | 0.9459 K.KTESHHK[325.13]AK.G                          |
| 0.999181 | 0.9965 R.SLETC[160.03]MYDHK[325.13]TFSEILNR.V         |
| 0.999179 | 0.9962 R.TTEEDRGNYC[160.03]VVSATWK[325.13]QR.N        |
| 0.999179 | 0.9983 R.FLNEQK[325.13]NLHSEISGK.R                    |
| 0.999178 | 0.9984 R.HGVSHK[325.13]VDDSSGSIGR.R                   |
| 0.999178 | 0.9976 K.LTSLNVK[325.13]YNNDK.S                       |
| 0.999178 | 0.9998 R.NPQQQESLK[325.13]HATR.I                      |
| 0.999177 | 0.9942 R.SSGPYGGGGQYFAK[325.13]PR.N                   |
| 0.999174 | 0.9967 K.ESPLLK[325.13]FR.A                           |
| 0.999174 | 0.993 K.IGHAPNFK[325.13]ATAVM[147.04]PDGQFK.D         |
| 0.999174 | 0.9995 K.AQPVPHYGVFPK[325.13]PQIPEAR.T                |
| 0.999173 | 0.9993 R.HLVYESDK[325.13]NKDEK.L                      |
| 0.999172 | 0.9969 K.ASMK[325.13]GLGTDEDSLIEIC[160.03]SR.T        |
| 0.999172 | 0.9995 R.IALYC[160.03]HQLNIC[160.03]SK[325.13]VK.A    |
| 0.99917  | 0.9991 R.FFSDC[160.03]K[325.13]IQNGAQGIR.F            |
| 0.99917  | 0.9991 R.FFSDC[160.03]K[325.13]IQNGAQGIR.F            |
| 0.99917  | 0.9991 R.FFSDC[160.03]K[325.13]IQNGAQGIR.F            |
| 0.999168 | 0.9721 K.ITPENLPQILLQLK[325.13]R.R                    |
| 0.999166 | 0.9964 R.EQSHK[325.13]VYVQHLLK.Q                      |
| 0.999166 | 0.9464 K.TKPVGTGNLRPEEALQALTIYEGK[325.13]FGR.L        |
| 0.999166 | 0.9991 K.VADWTGATYQDK[325.13]R.Y                      |
| 0.999164 | 0.9993 R.LVC[160.03]YNNK[325.13]ITASYEDR.V            |
| 0.999163 | 0.9996 K.NAK[325.13]FYPVTR.E                          |
| 0.999162 | 0.7894 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T              |
| 0.999162 | 0.9888 R.GQAGGK[325.13]LHIEVGTPTGNQPFPK.K             |
| 0.99916  | 0.9942 K.IGYNPDTVAFPISGWNGDNM[147.04]LEPSANMPWFK[     |
| 0.99916  | 0.9929 K.K[325.13]HPDASVNFSEFSK.K                     |
| 0.99916  | 0.999 R.K[325.13]C[160.03]C[160.03]NHPYLFDGAEPGPYTTDN |
| 0.999158 | 0.9723 R.HNGTGGK[325.13]SIYGEK.F                      |
| 0.999158 | 0.9972 R.STGEAFVQFASQEIAEK[325.13]ALK.K               |
| 0.999156 | 0.9991 K.KFHTVSGSK[325.13]C[160.03]EIK.V              |
| 0.999155 | 0.9831 R.FANYIDK[325.13]VR.F                          |
| 0.999155 | 0.9959 R.YQHLLK[325.13]GK.N                           |
| 0.999153 | 0.9979 R.FHMYEGYPLWK[325.13]VTFPVR.V                  |
| 0.999153 | 0.9804 R.AK[325.13]VTLNGVPAQPLGPR.A                   |
| 0.999153 | 0.9985 R.EANFTVSSMHGDMPQK[325.13]ER.E                 |
| 0.999152 | 0.9974 K.HTGPILSM[147.04]ANAGPNTNGSQFFIC[160.03]TAK[  |

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| 0.99915  | 0.9951 R.GGNRFEPYANPTK[325.13]R.Y                            |
| 0.999149 | 0.9986 R.KHTLSYVDVGTGK[325.13]VTLEYRVIDK.T                   |
| 0.999147 | 0.9995 R.DLISHDEMFSDIYK[325.13]IR.E                          |
| 0.999147 | 0.9953 R.VEAVNMAEGIIHDTETK[325.13]MEEFKDQLPADEC[160.03]IR.H  |
| 0.999147 | 0.9991 R.K[325.13]VGITLFTVSHR.K                              |
| 0.999145 | 0.9887 R.YAIC[160.03]SALAASALPALVM[147.04]SK[325.13]GHR.     |
| 0.999144 | 0.9994 R.NALQQENHIIDGVK[325.13]VQVHTR.R                      |
| 0.999144 | 0.9996 R.MYQK[325.13]GQETSTNPIASIFAWTR.G                     |
| 0.999144 | 0.93 R.ETNLDLPLVDTHSK[325.13]R.T                             |
| 0.999144 | 0.9958 K.KAK[325.13]KPAAAGVK.K                               |
| 0.999143 | 0.9983 K.TVPK[325.13]TVDNFVALATGEK.G                         |
| 0.999143 | 0.9995 K.AFAVGQVQVLLK[325.13]VLYQYK.E                        |
| 0.999142 | 0.9884 R.NPDDITQEEYGEFYK[325.13]SLTNDWEDHLAVK.H              |
| 0.999142 | 0.9935 R.K[325.13]QVVNIPSFIVR.L                              |
| 0.999142 | 0.9991 R.ITELMQVLK[325.13]DLNHGK.Y                           |
| 0.999142 | 0.9963 K.DGNASGTTLLEALDC[160.03]ILPPTRPTDK[325.13]PLRLP      |
| 0.99914  | 0.9992 R.LIHPK[325.13]SGR.S                                  |
| 0.999139 | 0.9994 R.LYQVEYAFK[325.13]AINQGGLTSVAVR.G                    |
| 0.999139 | 0.9994 R.GNTPK[325.13]YGLIFHSTFIGR.A                         |
| 0.999138 | 0.999 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K                     |
| 0.999138 | 0.9938 K.HK[325.13]SDFGK.F                                   |
| 0.999135 | 0.9985 K.LPDGYEFK[325.13]FPNR.L                              |
| 0.999132 | 0.9991 K.NISFTVWDVGGQDK[325.13]IRPLWR.H                      |
| 0.999132 | 0.9951 K.TYSAK[325.13]LDNAR.Q                                |
| 0.999131 | 0.9992 R.TDEAAFQK[325.13]LMSNLDNR.D                          |
| 0.999131 | 0.9946 K.YK[325.13]PAVNQIEC[160.03]HPYLTQEK.L                |
| 0.999131 | 0.9775 R.IFAPNHVVAK[325.13]SR.F                              |
| 0.99913  | 0.9977 K.FVADGIFK[325.13]AELNEFLTR.E                         |
| 0.999129 | 0.9424 R.TLLIK[325.13]TVETR.D                                |
| 0.999129 | 0.9978 R.HESGASIK[325.13]IDEPLEGSEDR.I                       |
| 0.999129 | 0.9993 R.TQIAPGSQTVLGIGPGPADLIDK[325.13]VTGHLK.L             |
| 0.999128 | 0.9287 R.ETNLDLPLVDTHSK[325.13]R.T                           |
| 0.999128 | 0.9992 R.AYAPGGPAYQPVEAFGTDILHK[325.13]DGIINR.K              |
| 0.999127 | 0.9829 R.GTK[325.13]VILHLKEDQTEYLEER.R                       |
| 0.999127 | 0.9985 R.LPSAHTC[160.03]FNQLDLPAYESFEK[325.13]LR.H           |
| 0.999126 | 0.9996 R.NSK[325.13]QQLSAEELDAQLDAYNAR.M                     |
| 0.999126 | 0.999 R.DFTVSALHGDMQK[325.13]ER.D                            |
| 0.999125 | 0.9886 K.MPILGLGTWK[325.13]SPPGQVTEAVK.V                     |
| 0.999125 | 0.9939 K.AHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D         |
| 0.999124 | 0.9996 R.GLQTVHINENFAK[325.13]LAEALYIADR.K                   |
| 0.999123 | 0.9962 R.YK[325.13]SYSPYDMLESIR.K                            |
| 0.999121 | 0.9984 K.IFVGGIK[325.13]EDTEEYNLR.D                          |
| 0.999121 | 0.9987 K.ISK[325.13]SPDGAHLTWEPPSVTSGK.I                     |
| 0.999121 | 0.9932 K.LWNTLGVK[160.03]K[325.13]YTVQDESHSEWVSC[160.03]IR.H |
| 0.999121 | 0.9996 R.LAYIAHPK[325.13]LGK.R                               |
| 0.99912  | 0.926 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAM         |
| 0.99912  | 0.997 R.SYSK[325.13]LLC[160.03]GLLAER.L                      |

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| 0.99912  | 0.9997 R.EYTINIHK[325.13]R.I                             |
| 0.99912  | 0.9997 K.ILK[325.13]TNHSNIMDDPFIR.E                      |
| 0.999119 | 0.9943 K.K[325.13]KHPDASVNFSEFSK.K                       |
| 0.999119 | 0.8683 R.ELPAQK[325.13]WWHTGALYR.I                       |
| 0.999119 | 0.9912 R.GVLK[325.13]VFLENVIR.D                          |
| 0.999118 | 0.9996 K.LLSATGESEK[325.13]QFQEAIIVFQEEFK.C              |
| 0.999118 | 0.9989 K.LGEFAK[325.13]VLELDNVK.S                        |
| 0.999118 | 0.9991 R.SLFSSIGEVESEK[325.13]LIR.D                      |
| 0.999118 | 0.9874 K.AFAETHIK[325.13]GFTLNDAAANSR.L                  |
| 0.999116 | 0.9996 R.DPLLLAIIPK[325.13]YLR.A                         |
| 0.999114 | 0.9942 R.FLQDYFDGNLK[325.13]R.Y                          |
| 0.999114 | 0.9986 K.ALAPLLAFVTK[325.13]PNSALESC[160.03]SFAR.H       |
| 0.999114 | 0.9964 R.C[160.03]FASNK[325.13]LGTAM[147.04]SHEIR.L      |
| 0.999113 | 0.9938 K.LLETK[325.13]WTLLQEQQ.S                         |
| 0.999113 | 0.0592 R.ADIK[325.13]EMGLSLQWLYSAR.G                     |
| 0.999112 | 0.9995 K.VVVNFAPTIQEI[325.13]SGTVTPGR.S                  |
| 0.999112 | 0.9996 R.EIQVQHPAAK[325.13]SMIEISR.T                     |
| 0.999109 | 0.9939 R.ALTVPILTQQVFDK[325.13]NMMAAC[160.03]DPR.H       |
| 0.999109 | 0.9984 K.GGPGSAVSPYPTFNPSSDVAALHK[325.13]AIMVK.G         |
| 0.999108 | 0.9963 R.LIFAGK[325.13]QLEDGR.T                          |
| 0.999107 | 0.9881 K.IK[325.13]IIAPPER.K                             |
| 0.999107 | 0.9988 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q                 |
| 0.999107 | 0.9378 R.SVPHLQK[325.13]VFDR.Y                           |
| 0.999105 | 0.9968 R.LK[325.13]GYLISGSSYAR.S                         |
| 0.999105 | 0.9936 R.ALLLPDYLVTVMLSGIK[325.13]C[160.03]PTFR.R        |
| 0.999103 | 0.9989 R.FLSHSLVELLNQISPTFK[325.13]K.N                   |
| 0.999103 | 0.9998 R.ILK[325.13]QPSTQSDTYSMLALGNVWLQTLHQPTR.D        |
| 0.999103 | 0.9886 K.EKYIDQEELNK[325.13]TKPIWTR.N                    |
| 0.999101 | 0.9992 R.HLK[325.13]IVYR.R                               |
| 0.999101 | 0.9993 R.K[325.13]PFPLVKPLPGEEPLFTIPTQEAFFR.T            |
| 0.999101 | 0.9921 K.IYK[325.13]IGQGYLIK.D                           |
| 0.999101 | 0.9991 R.YLGIPGDK[325.13]EYC[160.03]ISSDDLFLPYC[160.03]P |
| 0.9991   | 0.9992 R.VGC[160.03]K[325.13]YQAEIPDR.L                  |
| 0.9991   | 0.9962 K.LDK[325.13]SQIHDLVLVGGSTR.I                     |
| 0.999099 | 0.9991 K.TPLK[325.13]IHPLVR.L                            |
| 0.999098 | 0.9992 R.TMGVMFTPLTVK[325.13]YAYYDTER.I                  |
| 0.999098 | 0.9996 R.IVDPEIALK[325.13]ILHR.Q                         |
| 0.999097 | 0.9981 R.GTQDK[325.13]TTMVTSTFTNEDLLR.G                  |
| 0.999097 | 0.9983 R.SDTPLIYK[325.13]AVPSWFVR.V                      |
| 0.999096 | 0.9961 K.VYIYHSSSK[325.13]GLLR.Q                         |
| 0.999096 | 0.998 K.AK[325.13]LASLEELKR.Q                            |
| 0.999092 | 0.9996 K.ATPEEK[325.13]LKLEDFAR.N                        |
| 0.999091 | 0.9994 K.HGFSDNQK[325.13]LWER.N                          |
| 0.99909  | 0.9997 R.K[325.13]DSVWGSQGGQSVNHLVK.E                    |
| 0.99909  | 0.9995 K.LTSLALIDGK[325.13]NFSAGGHK.V                    |
| 0.999089 | 0.9766 K.DLPEHAVLK[325.13]MK.G                           |
| 0.999088 | 0.9937 R.DAVTYTEHAK[325.13]R.K                           |

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| 0.999088 | 0.9991 R.TLTNYK[325.13]AFSQFVRPLIAAK.N                   |
| 0.999088 | 0.9991 R.TLTNYK[325.13]AFSQFVRPLIAAK.N                   |
| 0.999087 | 0.9961 K.GDLASVPSMK[325.13]VHAPGLNLSGVGGK.M              |
| 0.999086 | 0.9991 K.NISFTVWDVGGQDK[325.13]IRPLWR.H                  |
| 0.999086 | 0.9948 K.AHLGTALK[325.13]ANPFGGASHAK.G                   |
| 0.999085 | 0.9995 R.RLEHSK[325.13]NVNTEK.L                          |
| 0.999085 | 0.9931 R.RLEDGEDFNLDALDSSNSMQTIQK[325.13]TTTR.R          |
| 0.999085 | 0.9993 R.NIK[325.13]SHLGNVHDQDN.-                        |
| 0.999085 | 0.9993 K.ALSK[325.13]QPLWNHLLNYYK.E                      |
| 0.999084 | 0.9952 R.M[147.04]IAGQVLDINLAAEPK[325.13]VNR.G           |
| 0.999084 | 0.9954 K.YMNSGPVVMVWEGLNVVK[325.13]TGR.V                 |
| 0.999084 | 0.9996 K.VLAFGAK[325.13]PDSTLHTYFPSFLSR.A                |
| 0.999083 | 0.9981 K.RPPSAFFLFC[160.03]SEYRPK[325.13]IK.G            |
| 0.999083 | 0.9995 K.IVEIPFNSTNK[325.13]YQLSIHK.N                    |
| 0.999083 | 0.9994 R.EQVPSLGSNVAC[160.03]GLAYTDYHK[325.13]AAMGLG.    |
| 0.999083 | 0.9997 K.K[325.13]NNPAIVIIGNNGQIHYDHQNDGASQALASC[160     |
| 0.999082 | 0.9934 K.HK[325.13]SDFGK.F                               |
| 0.999082 | 0.9984 R.ITK[325.13]VLNMKPPEILSMIEEAAGTR.M               |
| 0.999081 | 0.9959 K.AK[325.13]LKPGAPLRPK.L                          |
| 0.99908  | 0.9958 K.VDVGKDQEFTVK[325.13]SK.G                        |
| 0.999079 | 0.9982 R.ALTVPELTQQMFDAK[325.13]NMMAAC[160.03]DPR.H      |
| 0.999079 | 0.9957 R.LNVLEK[325.13]SSPGHR.A                          |
| 0.999078 | 0.9997 K.TPALK[325.13]YQQLFEDIR.G                        |
| 0.999075 | 0.9497 R.LQLETEIEALK[325.13]EELLFM[147.04]K.K            |
| 0.999072 | 0.985 K.ESWHGKPLPK[325.13]NMAEQIIQEISQIQSK.K             |
| 0.999072 | 0.9992 K.INALIK[325.13]AAGVNVEPFWPGLFAK.A                |
| 0.999072 | 0.9992 K.INALIK[325.13]AAGVNVEPFWPGLFAK.A                |
| 0.999071 | 0.998 R.QVLDLEDLVFTQGSFHMANK[325.13]R.C                  |
| 0.99907  | 0.9991 -.MK[325.13]HYEVEILDAK.T                          |
| 0.999069 | 0.9948 R.IAESNHIK[325.13]LSGSNPYTTVTPQIINSK.W            |
| 0.999069 | 0.9978 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.999069 | 0.9932 K.NTHC[160.03]SSLPHYQK[325.13]LK.K                |
| 0.999068 | 0.9991 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L         |
| 0.999068 | 0.9991 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L         |
| 0.999068 | 0.9372 K.KTESHHK[325.13]AK.G                             |
| 0.999067 | 0.9984 R.LFLLPHK[325.13]DQR.Q                            |
| 0.999067 | 0.9826 R.TLLIK[325.13]TVETR.D                            |
| 0.999067 | 0.9995 K.FGK[325.13]HGGTIPVPTAEFQDR.I                    |
| 0.999066 | 0.9947 R.FPGAYLK[325.13]GK.K                             |
| 0.999065 | 0.9991 R.MALIGLVSHPVLK[325.13]QVAEQFLNMR.G               |
| 0.999065 | 0.9963 K.VIADNVK[325.13]DWSK.V                           |
| 0.999063 | 0.9998 K.ELWFSDDPNVTK[325.13]TLR.F                       |
| 0.999063 | 0.996 R.EAMQQADDWLGIQVITPEEIVDPNVDEHSVMTYLSQFPK          |
| 0.999063 | 0.9993 K.K[325.13]YHNVGLSK.C                             |
| 0.999062 | 0.9996 K.TILALMK[325.13]TPVLFDIYEIK.E                    |
| 0.99906  | 0.9991 R.GREC[160.03]VDK[325.13]C[160.03]NLLEGEP.R       |
| 0.999059 | 0.9971 R.NNFEGEVTK[325.13]ENLLDFIK.H                     |

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| 0.999059 | 0.9816 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y              |
| 0.999059 | 0.9924 K.FIDTTSK[325.13]FGHGR.F                           |
| 0.999057 | 0.9985 K.K[325.13]AHLGTALK.A                              |
| 0.999056 | 0.9993 K.KETLLAMFK[325.13]YNK.F                           |
| 0.999055 | 0.9969 K.FEDENFILK[325.13]HTGPGILSM[147.04]ANAGPNTNGSI    |
| 0.999053 | 0.9996 R.K[325.13]FIC[160.03]HVVGITYQHIDR.W               |
| 0.999053 | 0.9969 K.FVGDPALVLNDIHK[325.13]K.I                        |
| 0.999052 | 0.9971 R.INVYYNEATGGK[325.13]YVPR.A                       |
| 0.999051 | 0.9911 R.K[325.13]ESYSVYVYK.V                             |
| 0.99905  | 0.9983 R.KVAHSDK[325.13]PGSTSTASFR.D                      |
| 0.99905  | 0.9995 R.K[325.13]FYGPEGPYGVFAGR.D                        |
| 0.999049 | 0.9995 R.SLK[325.13]SVQLYGPTNFAPVINHVAR.Y                 |
| 0.999047 | 0.6704 K.FLK[325.13]SGDAAIVDMVPGKPMC[160.03]VESFSDYPP     |
| 0.999046 | 0.9993 R.SGYIAIDDIQVLSYPC[160.03]DK[325.13]SPHFRL.L       |
| 0.999046 | 0.9938 R.FLMK[325.13]SYDQVHSGK.L                          |
| 0.999046 | 0.9872 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTSGSGFTS    |
| 0.999045 | 0.9975 K.VM[147.04]SQNFTNC[160.03]HTK[325.13]IR.H         |
| 0.999043 | 0.9946 R.GSK[325.13]DHNIR.A                               |
| 0.999043 | 0.9991 K.LVEHFC[160.03]AEFK[325.13]TK.Y                   |
| 0.999043 | 0.9087 R.M[147.04]VNHFIAEFK[325.13]R.K                    |
| 0.999042 | 0.9993 R.K[325.13]YTLPPGVDPTQVSSSLSPEGTLTVEAPMPK.L        |
| 0.99904  | 0.9998 R.ALAAPAAEEK[325.13]EEAR.E                         |
| 0.99904  | 0.9959 K.SRQELEQHSVDASTSDAVTFITYVQSLK[325.13]R.K          |
| 0.999039 | 0.9885 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E          |
| 0.999038 | 0.9994 R.LQGDVVLK[325.13]IAR.L                            |
| 0.999038 | 0.9853 R.ASLSK[325.13]LGDVYVNDAFGTAHR.A                   |
| 0.999036 | 0.9983 R.RK[325.13]QYPISLV LAPTR.E                        |
| 0.999036 | 0.999 K.NISFTVWDVGGQDK[325.13]IRPLWR.H                    |
| 0.999036 | 0.9956 R.LAK[325.13]SDPMVQC[160.03]IIEESGEHIIAGAGELHLEI   |
| 0.999035 | 0.9977 R.AVDDGVNTFK[325.13]VLTR.D                         |
| 0.999035 | 0.998 K.KAVLFC[160.03]LSEDK[325.13]K.N                    |
| 0.999032 | 0.9995 R.LGLPPK[325.13]IVIGYQSHADTATK.S                   |
| 0.999032 | 0.9995 R.LGLPPK[325.13]IVIGYQSHADTATK.S                   |
| 0.999032 | 0.9992 R.ELTDYLMK[325.13]ILTR.G                           |
| 0.999031 | 0.9931 K.TLHPDLGTDKDK[325.13]EQWK.E                       |
| 0.999031 | 0.815 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR        |
| 0.999031 | 0.9948 K.IWDLEGK[325.13]IIVDELKQEVISTSSK.A                |
| 0.99903  | 0.9844 R.LDYLSSLK[325.13]VK.G                             |
| 0.999029 | 0.9994 K.KPLKPC[160.03]C[160.03]AC[160.03]PETK[325.13]K.A |
| 0.999029 | 0.9994 K.KPLKPC[160.03]C[160.03]AC[160.03]PETK[325.13]K.A |
| 0.999029 | 0.9974 R.GLTSVINQK[325.13]LKDEVAQLK.K                     |
| 0.999029 | 0.9 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                    |
| 0.999029 | 0.9936 R.LREK[325.13]LQEEM[147.04]LQR.E                   |
| 0.999027 | 0.984 K.SK[325.13]GIAYIEFK.T                              |
| 0.999026 | 0.9967 R.K[325.13]AHLTNQYM[147.04]QR.V                    |
| 0.999026 | 0.9984 R.FDMAENVVIVASQK[325.13]RPLGGR.E                   |
| 0.999024 | 0.9291 K.NQK[325.13]DDVAQTDLLQIDPNFGSK.E                  |



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| 0.999023 | 0.9991 R.SLGK[325.13]YGIIC[160.03]MEDLIHEIYTVGK.R  |
| 0.999022 | 0.9991 K.YDPNVYSIK[325.13]YNNQLATR.T               |
| 0.999022 | 0.9991 K.YDPNVYSIK[325.13]YNNQLATR.T               |
| 0.999022 | 0.9939 K.FK[325.13]MPEMHFK.T                       |
| 0.999021 | 0.9745 R.K[325.13]GHAVGDIPGVR.F                    |
| 0.99902  | 0.9993 K.LYNNITFEELGALLEIPAAK[325.13]AEK.I         |
| 0.999019 | 0.9926 R.YK[325.13]LLGGLAVR.R                      |
| 0.999018 | 0.9948 R.KIFVGTK[325.13]GIPHLVTHDAR.T              |
| 0.999018 | 0.986 R.TGGMAFHSYFMEAIAPLLQELK[325.13]K.V          |
| 0.999017 | 0.999 K.IDGSANLK[325.13]SQDDRDK.F                  |
| 0.999016 | 0.9991 R.VTIK[325.13]AGIHAR.L                      |
| 0.999015 | 0.9976 K.FLSPVVPNYDNVHPNYHK[325.13]EPFLQQLK.V      |
| 0.999015 | 0.995 R.TREGNDLYHEMIESGVINLK[325.13]DATSK.V        |
| 0.999015 | 0.9955 R.IK[325.13]VFGPGIEGK.D                     |
| 0.999015 | 0.998 K.VEYSEEELKTHISK[325.13]GTLGK.F              |
| 0.999015 | 0.3671 R.LLLPGELAK[325.13]HAVSEGK.A                |
| 0.999011 | 0.999 R.LC[160.03]IEHFDK[325.13]LLVEDINK.D         |
| 0.99901  | 0.9986 R.RNK[325.13]LDHYAIK.F                      |
| 0.99901  | 0.9157 R.LVYLVENPGGYVAYSK[325.13]AATVTGK.L         |
| 0.999007 | 0.9991 K.LHYC[160.03]VSC[160.03]AIHSK[325.13]VVR.N |
| 0.999007 | 0.9995 K.LVGGTTPGK[325.13]GGQTHLGLPVFNTVK.E        |
| 0.999007 | 0.9997 R.ADLK[325.13]QLMVHAFIK.R                   |
| 0.999006 | 0.9448 K.NVTLPAVFK[325.13]APIRPDIVNFVHTNLR.K       |
| 0.999006 | 0.9995 K.NVQDIK[325.13]NVVLQTLEGHLR.S              |
| 0.999005 | 0.9995 K.LK[325.13]HILILQNK.I                      |
| 0.999004 | 0.9848 R.VISGVLQLGNIVFK[325.13]K.E                 |
| 0.999004 | 0.9996 R.LHPELSGPGVAAK[325.13]VLAASVR.R            |
| 0.999002 | 0.9931 R.TFSWASVTSK[325.13]NLPPSGAVPVTGIPPHVVK.V   |
| 0.999001 | 0.9823 K.K[325.13]GDVVIVLTGWRPGSGFTNTMR.V          |
| 0.999    | 0.9996 K.FLALK[325.13]QTPDFHTVIGDVTGLLER.C         |
| 0.998999 | 0.9998 R.GQAFVIFK[325.13]EVSSATNALR.S              |
| 0.998998 | 0.9935 K.ALKPPPIK[325.13]LYR.E                     |
| 0.998997 | 0.9671 R.HNGTGGK[325.13]SIYGEK.F                   |
| 0.998996 | 0.5341 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK |
| 0.998994 | 0.9993 R.AELRDDPIISTHLAK[325.13]LYDNLLEQNLIR.V     |
| 0.998993 | 0.9338 R.LQSTLK[325.13]TLSFSFPPNTVTGSER.V          |
| 0.998992 | 0.9986 K.NIK[325.13]HSGNITFDEIVNIAR.Q              |
| 0.998992 | 0.998 R.DKTIIMWK[325.13]LTR.D                      |
| 0.998991 | 0.985 K.VFGNEIK[325.13]LEKPK.G                     |
| 0.998989 | 0.9761 K.K[325.13]KPQKVAGGAAPSKPASAK.K             |
| 0.998989 | 0.9995 K.SSMSVTSLEAELQAK[325.13]IQESHPELR.R        |
| 0.998988 | 0.9861 K.K[325.13]LGEMWNNTAADDKQPYEK.K             |
| 0.998988 | 0.9078 K.TVTAMDVVYALK[325.13]R.Q                   |
| 0.998987 | 0.9954 K.ISIPDVGLHLK[325.13]GPK.M                  |
| 0.998987 | 0.9996 K.EILTLK[325.13]EVFQIASNDHDAAINR.Y          |
| 0.998986 | 0.9937 R.GHYTIGK[325.13]EIIDPVLDR.I                |
| 0.998986 | 0.9848 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V          |

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| 0.998984 | 0.8417 R.FLEQQNK[325.13]ILLAELEQLK.G                       |
| 0.998984 | 0.9932 R.KK[325.13]NLQYYDISAK.S                            |
| 0.998984 | 0.9943 K.TLVLLMGK[325.13]EGVHGGLINK.K                      |
| 0.998983 | 0.9972 R.KPSAPK[325.13]KGDSSAEELK.L                        |
| 0.998982 | 0.9886 R.EVTVPVFYPTTEK[325.13]VWLEVEPVGM[147.04]LK.E       |
| 0.998982 | 0.8999 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]LK.E |
| 0.998981 | 0.9996 K.K[325.13]YDVDTLDMVFLDHWK.D                        |
| 0.998979 | 0.9303 R.GNPTVEVDLFTSK[325.13]GLFR.A                       |
| 0.998979 | 0.9992 R.GFK[325.13]LPDTPQGLLGEAR.M                        |
| 0.998978 | 0.9993 K.MHLAGK[325.13]TEQAK.A                             |
| 0.998977 | 0.9976 K.KYHNVGLSK[325.13]C[160.03]EIK.V                   |
| 0.998976 | 0.9977 K.K[325.13]GADSLEDFLYHEGYAC[160.03]TSIHGDR.S        |
| 0.998973 | 0.9835 K.DGNASGTTLEALDC[160.03]ILPPTRPDTK[325.13]PLR.L     |
| 0.998971 | 0.9953 R.VLADPSDDTK[325.13]GFFDPNTHENLTYLQLLER.C           |
| 0.998971 | 0.9918 R.ASVPDGFLSELTTQLAQATGK[325.13]PPQYIAVHVVPDQ        |
| 0.998969 | 0.668 K.WGDAGAEYVVESTGVFTTMEK[325.13]AGAHQLGGAK.R          |
| 0.998967 | 0.9946 R.SYDVPPPPMEPDHPFYNSISK[325.13]DRR.Y                |
| 0.998966 | 0.9991 R.GNVGFVFTK[325.13]EDLTEIR.D                        |
| 0.998966 | 0.9979 K.DVK[325.13]GSYVSIHSSGFR.D                         |
| 0.998965 | 0.9996 K.YGLFAPVHK[325.13]VTK.I                            |
| 0.998964 | 0.995 K.SRLDQELK[325.13]LIGEYGLR.N                         |
| 0.99896  | 0.9963 R.HPFIVNHPK[325.13]VGR.V                            |
| 0.99896  | 0.9991 R.HISPSAK[325.13]PFENGQYLDIYGITR.D                  |
| 0.998959 | 0.9955 R.DIFNK[325.13]GFGFGLVK.L                           |
| 0.998956 | 0.9978 R.TDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A                |
| 0.998956 | 0.9991 R.KGAAPAPPGK[325.13]TGPAVAK.A                       |
| 0.998954 | 0.9957 K.KLK[325.13]EVFSMAGVVVR.A                          |
| 0.998951 | 0.9981 R.SGK[325.13]SPILVATAVAAR.G                         |
| 0.99895  | 0.9943 R.VTGNFK[325.13]HASPILPITEFSDIPR.R                  |
| 0.998949 | 0.7448 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                   |
| 0.998949 | 0.9991 K.FGEVVDC[160.03]TIK[325.13]MDPNTGR.S               |
| 0.998949 | 0.9963 K.TC[160.03]SLPGTALK[325.13]VSC[160.03]FNVR.F       |
| 0.998948 | 0.9991 K.ISAWHNNVEK[325.13]TLPSTK.A                        |
| 0.998946 | 0.9994 K.DTFLGPVLK[325.13]QMYITYVR.N                       |
| 0.998945 | 0.9973 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T           |
| 0.998945 | 0.9992 R.LYPWGVVEVENPEHNDFLK[325.13]LR.T                   |
| 0.998945 | 0.9992 R.LYPWGVVEVENPEHNDFLK[325.13]LR.T                   |
| 0.998944 | 0.6387 K.EITALAPSTMKIK[325.13]IIAPPER.K                    |
| 0.998944 | 0.9234 R.SIFSAVLDELK[325.13]VAQAPWK.A                      |
| 0.998944 | 0.998 R.GSGSGSHNWGTVKDELTESPK[325.13]YIQK.Q                |
| 0.998943 | 0.9932 K.VIPSPFK[325.13]HADIVTTTHK.T                       |
| 0.998943 | 0.9911 R.K[325.13]LLEGEESR.I                               |
| 0.998943 | 0.9856 R.RYQK[325.13]STELLIR.K                             |
| 0.998942 | 0.9943 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S        |
| 0.998942 | 0.9927 K.NK[325.13]ITITNDQNR.L                             |
| 0.998942 | 0.9993 R.DVFLPK[325.13]PTWGNHTPIFR.D                       |
| 0.998941 | 0.9964 K.GVVEVTHDLQK[325.13]HLAGLGLTEAIDK.N                |

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| 0.998939 | 0.9994 K.K[325.13]LPPLPLTLALGAFLNHR.K              |
| 0.998938 | 0.9994 R.GIIAK[325.13]AVDHATNR.T                   |
| 0.998936 | 0.9939 R.EDSQRPGAHLTVK[325.13]K.I                  |
| 0.998935 | 0.1666 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E  |
| 0.998933 | 0.9967 R.DLNK[325.13]SINPDEAVAYGAAVQAAILMGDK.S     |
| 0.99893  | 0.9933 -.MQIFVK[325.13]TLTGK.T                     |
| 0.99893  | 0.999 R.VTASDRDK[325.13]GSNAVHVHYSIMSGNAR.G        |
| 0.998929 | 0.9183 K.K[325.13]EDLYLKPIQR.T                     |
| 0.998928 | 0.9926 R.K[325.13]LTATPTPLGGMTGFHMQTEDR.T          |
| 0.998927 | 0.9993 R.LPNFGSHVLTPEAMEAFK[325.13]QR.H            |
| 0.998925 | 0.9991 R.LVC[160.03]YNNK[325.13]ITASYEDR.V         |
| 0.998925 | 0.9915 R.AAAEK[325.13]LFGNMEGDC[160.03]PSDWK.T     |
| 0.998925 | 0.9927 R.NLPGLVQEGEPFSEATLFTK[325.13]ELVLQR.E      |
| 0.998925 | 0.9994 R.AFQAHK[325.13]EENWALPVMYAVALDLR.V         |
| 0.998923 | 0.9993 R.AVSDASAGDYGSAIETLVTAISLIK[325.13]QSK.V    |
| 0.998922 | 0.9992 R.SSSILK[325.13]GMELSVLDSLNR.M              |
| 0.998922 | 0.9911 R.IQEIEQLDVTTSEYEKEK[325.13]LNER.L          |
| 0.998922 | 0.9992 R.TGTK[325.13]IIHILK.S                      |
| 0.99892  | 0.9875 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H          |
| 0.998919 | 0.9902 K.GSFK[325.13]TLTLPSLPLNSADEIYELR.V         |
| 0.998919 | 0.9974 R.FLM[147.04]K[325.13]SYDQVHSGK.L           |
| 0.998919 | 0.9976 R.VGK[325.13]VEHGSVALPAIMR.S                |
| 0.998918 | 0.9992 K.NKPK[325.13]WLLQGIFSTTVLC[160.03]QK.L     |
| 0.998917 | 0.9982 K.AKDPFAHLPK[325.13]STFVLDEFK.R             |
| 0.998917 | 0.9851 K.K[325.13]ALAAAGYDVEK.N                    |
| 0.998917 | 0.9983 R.IVGSK[325.13]PLYVALAQR.K                  |
| 0.998916 | 0.7891 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M          |
| 0.998916 | 0.9946 K.GYEK[325.13]KPYC[160.03]NAHYPK.Q          |
| 0.998916 | 0.9047 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C  |
| 0.998915 | 0.9945 R.LTLYDIAHTPGVAADLSHIETK[325.13]AAVK.G      |
| 0.998912 | 0.9925 K.IQQLVK[325.13]EFFNGKEPSR.G                |
| 0.998912 | 0.9989 R.IHLEIK[325.13]QLNR.Q                      |
| 0.998911 | 0.9996 R.TELLNVC[160.03]MNAK[325.13]HHK.E          |
| 0.998911 | 0.9991 R.ELTDYLMK[325.13]ILTER.G                   |
| 0.998911 | 0.9991 R.ELTDYLMK[325.13]ILTER.G                   |
| 0.99891  | 0.997 K.LHQAM[147.04]K[325.13]GVGTR.H              |
| 0.99891  | 0.9972 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L |
| 0.998909 | 0.9982 K.LHIEVGQPAAGNQPFVK[325.13]K.A              |
| 0.998908 | 0.9995 K.IHLFDIDVPGK[325.13]ITFQESK.T              |
| 0.998902 | 0.9998 R.HWFFK[325.13]GQLHVDGQK.L                  |
| 0.998901 | 0.9973 R.YPMAVGLNK[325.13]GHK.V                    |
| 0.998901 | 0.9937 R.DIQQHK[325.13]EEAWVIGSVVAR.A              |
| 0.998901 | 0.9995 K.FDEC[160.03]VLDK[325.13]LGWVRPDLGELSK.V   |
| 0.998901 | 0.9995 R.AK[325.13]EMDLVGLGLHPLFSSR.F              |
| 0.998899 | 0.9957 K.DAK[325.13]TAASGIPYHSEVPVSLK.E            |
| 0.998898 | 0.9977 R.NVESYTK[325.13]LGNPTR.S                   |
| 0.998898 | 0.9991 K.AILNGIDSINK[325.13]VLDHFR.R               |

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| 0.998898 | 0.9938 R.HQEGEIFDTEK[325.13]EKYEITEQR.K                   |
| 0.998896 | 0.9853 R.LVSNHSLHETSSVFDLSLK[325.13]ATC[160.03]APQHGA     |
| 0.998896 | 0.9824 K.NAQK[325.13]SNQNGKDSKPSSTPR.S                    |
| 0.998896 | 0.9987 K.HPAK[325.13]PDPSGEC[160.03]NPDLR.L               |
| 0.998895 | 0.9933 R.GC[160.03]ALQC[160.03]AILSPAFAK[325.13]VR.E      |
| 0.998895 | 0.9777 K.NMAEQIIQEISQIQSK[325.13]K.K                      |
| 0.998895 | 0.9994 R.VYGLESLEK[325.13]DLFPNLTVIR.G                    |
| 0.998895 | 0.9325 R.LAHYNK[325.13]R.S                                |
| 0.998891 | 0.9934 R.FDDPGLMLMGFK[325.13]PLVLLK.K                     |
| 0.998889 | 0.9994 R.DGHDQHVLELEAK[325.13]MDQLR.T                     |
| 0.998888 | 0.9546 R.LK[325.13]VPPAINQFTQALDR.Q                       |
| 0.998888 | 0.9963 K.YGIIC[160.03]MEDLIHEIYTVGK[325.13]R.F            |
| 0.998887 | 0.9959 K.K[325.13]KPRPPPALGPEETSASAGLPK.K                 |
| 0.998884 | 0.9968 R.FQTK[325.13]IPNIYAIGDVVAGPMLAHK.A                |
| 0.99888  | 0.9941 R.REEAAVDAQQQK[325.13]R.S                          |
| 0.998878 | 0.9989 R.AGEIK[325.13]GFTGIDSDYEKPETPER.V                 |
| 0.998878 | 0.9747 R.HYGGLTGLNK[325.13]AETAAG.H                       |
| 0.998878 | 0.9949 K.MPDLHLK[325.13]APK.I                             |
| 0.998874 | 0.9905 K.K[325.13]HPDASVNFSEFSK.K                         |
| 0.998874 | 0.9993 R.VVVSGLPPSGSWQDLK[325.13]DHMR.E                   |
| 0.998873 | 0.9728 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.998873 | 0.8902 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.]      |
| 0.998872 | 0.9994 R.TGLK[325.13]ITSLTEVVC[160.03]GLDLC[160.03]NQGN.  |
| 0.998872 | 0.9829 K.MPK[325.13]FSMPGFK.A                             |
| 0.99887  | 0.9911 R.VLEQHK[325.13]LNKDQWEER.I                        |
| 0.998869 | 0.9954 K.VINTGIK[325.13]VWC[160.03]R.N                    |
| 0.998868 | 0.9915 R.KQLATK[325.13]AAR.K                              |
| 0.998867 | 0.9992 R.GGRPNEIEPPPEMPPWQK[325.13]R.Q                    |
| 0.998867 | 0.9992 R.GGRPNEIEPPPEMPPWQK[325.13]R.Q                    |
| 0.998866 | 0.9855 K.STHDHWK[325.13]ALVTK.K                           |
| 0.998865 | 0.9981 R.NSQFAGGPLGNPNTTAK[325.13]VQQR.L                  |
| 0.998865 | 0.9729 R.ILGLLDAYLK[325.13]TR.T                           |
| 0.998865 | 0.9923 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D         |
| 0.998863 | 0.9983 R.VLPSITTEILK[325.13]SVVAR.F                       |
| 0.998862 | 0.9996 K.ILTGADK[325.13]NVVVFVK.S                         |
| 0.998862 | 0.9857 K.EVK[325.13]GDLENAFLNLVQC[160.03]IQNKPLYFADR.L    |
| 0.998861 | 0.9995 K.DNPK[325.13]IVHAFDMEDLGDK.A                      |
| 0.99886  | 0.7346 R.MVNHFAIEFK[325.13]R.K                            |
| 0.998858 | 0.9996 K.HQPHK[325.13]VTQYK.K                             |
| 0.998858 | 0.9965 K.ILIANTGMDTDKIK[325.13]IFGSR.V                    |
| 0.998856 | 0.9948 R.DNK[325.13]DGSC[160.03]SAEYIPFAPGDYDVNITYGGAI    |
| 0.998855 | 0.9756 R.LLGAALPLLTK[325.13]EQLHLVMQGDVIR.H               |
| 0.998855 | 0.9994 K.VQQAK[325.13]EMVLELIR.D                          |
| 0.998855 | 0.9995 K.VLAFGAK[325.13]PDSTLHTYFPSFLSR.A                 |
| 0.998853 | 0.9974 R.TAK[325.13]LWALPQC[160.03]QLLGVSFSGHR.R          |
| 0.998852 | 0.9981 K.NLK[325.13]PIKPMQFLGDEETVRK.A                    |
| 0.998852 | 0.991 K.HVVFVK[325.13]VK.E                                |

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| 0.998852 | 0.9994 K.HFVGMLPEK[325.13]DC[160.03]R.Y                  |
| 0.998851 | 0.999 R.GNVGFVFTK[325.13]EDLTEIR.D                       |
| 0.99885  | 0.9879 K.EIK[325.13]ILNIFGVIK.G                          |
| 0.99885  | 0.9993 R.LTGVSISQVNHK[325.13]PLR.T                       |
| 0.998849 | 0.9991 R.HIITVDGK[325.13]PPTWSEFPK.G                     |
| 0.998847 | 0.9992 R.YVAQAHDK[325.13]PR.Y                            |
| 0.998847 | 0.9959 K.FGDPVVQSDMK[325.13]HWPQVINDGDKPK.V              |
| 0.998846 | 0.9863 K.YGK[325.13]SLYYYIQQDTK.G                        |
| 0.998846 | 0.9994 K.RPLEDGDQPDAK[325.13]K.V                         |
| 0.998846 | 0.7873 R.HQGVMVGM[147.04]GQK[325.13]DSYVGDEAQSKR.G       |
| 0.998845 | 0.9995 K.LWNEVLASLK[325.13]DRPASGSPFLFLSK.V              |
| 0.998844 | 0.9917 K.HK[325.13]SDFGK.F                               |
| 0.998843 | 0.9992 R.GAK[325.13]EEHGGLIR.S                           |
| 0.998842 | 0.9274 R.LVNHFVEEFK[325.13]R.K                           |
| 0.998842 | 0.9986 R.C[160.03]YLLVHQAK[325.13]R.L                    |
| 0.998838 | 0.9847 R.VVDLMAHMASK[325.13]E.-                          |
| 0.998838 | 0.5318 R.K[325.13]DGNASGTTLEALDC[160.03]ILPPTRPTDKPLR.   |
| 0.998835 | 0.9991 R.VNSK[325.13]FDTIYQILLK.K                        |
| 0.99883  | 0.9965 R.K[325.13]TVTAM[147.04]DVVYALK.R                 |
| 0.998829 | 0.9989 R.K[325.13]PISTHTVDFTFNK.F                        |
| 0.998828 | 0.9969 K.ILPTLEAVAALGNK[325.13]VVESLR.A                  |
| 0.998828 | 0.9992 R.EQC[160.03]C[160.03]YNC[160.03]GK[325.13]PGHLAR |
| 0.998826 | 0.9964 R.GLK[325.13]M[147.04]AVTFIGNSTAIQELFK.R          |
| 0.998825 | 0.9866 K.FDLMYAK[325.13]R.A                              |
| 0.998824 | 0.9947 K.KELNYFAK[325.13]ALESERPFLAILGGAK.V              |
| 0.998824 | 0.9924 K.HK[325.13]PGGGDVK.I                             |
| 0.998823 | 0.9729 R.LDHK[325.13]FDLMYAK.R                           |
| 0.998822 | 0.9991 K.LNNLVLFDK[325.13]ATYDK.L                        |
| 0.998822 | 0.9229 R.TLLIK[325.13]TVETR.D                            |
| 0.998821 | 0.9699 K.DLPEHAVLK[325.13]MK.G                           |
| 0.99882  | 0.9937 K.NFATSLYSMIK[325.13]GDTSGDYKK.A                  |
| 0.998818 | 0.999 K.AATKK[325.13]PVVNIITPSHVEER.G                    |
| 0.998816 | 0.9995 R.DRDVDVLSAALK[325.13]EQLSHSR.Q                   |
| 0.998816 | 0.9995 K.NLVLAGIK[325.13]AVTIHDTEK.C                     |
| 0.998815 | 0.9955 R.LFC[160.03]VGFTK[325.13]K.R                     |
| 0.998815 | 0.9754 R.QLFHPEQLITGK[325.13]EDAANNYAR.G                 |
| 0.998814 | 0.9912 R.KAHEILPNLVC[160.03]C[160.03]SAK[325.13]NLR.D    |
| 0.998814 | 0.999 R.IGK[325.13]VTSEELHYFVQNHFTSAR.M                  |
| 0.998814 | 0.9942 K.WHDK[325.13]QYK.K                               |
| 0.998813 | 0.9955 R.HLTGEFEK[325.13]K.Y                             |
| 0.998813 | 0.7894 R.HQGVM[147.04]VGMGQKDSYVGDEAQSK[325.13]R.G       |
| 0.998812 | 0.9994 K.LQTYK[325.13]TAVETAVLLLR.I                      |
| 0.998809 | 0.9987 K.TSFVNFTDIC[160.03]K[325.13]LLHR.Q               |
| 0.998806 | 0.9833 K.GVSK[325.13]AVEHINK.T                           |
| 0.998806 | 0.9836 R.ALM[147.04]LQGVDLLADAVAVTMGPK[325.13]GR.T       |
| 0.998805 | 0.9981 K.K[325.13]AHLGTALK.A                             |
| 0.998805 | 0.9949 K.K[325.13]QHLVEVR.S                              |

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| 0.998804 | 0.9933 R.MVLAAAGGVEHQQLDLAQK[325.13]HLGGIPWTYAEDA        |
| 0.998804 | 0.9918 R.YK[325.13]LLGGLAVR.R                            |
| 0.998804 | 0.983 R.LPMNK[325.13]EWPSNLDLR.K                         |
| 0.998801 | 0.9979 R.LQHAAELIK[325.13]TVASR.Y                        |
| 0.998799 | 0.9944 K.HKLDELYPQGYPESVIQHLGYLFLK[325.13]MSPEDIR.K      |
| 0.998798 | 0.9996 R.FGALTAEK[325.13]LR.S                            |
| 0.998798 | 0.9993 R.SHISDQSPLSSK[325.13]R.K                         |
| 0.998797 | 0.9991 R.K[325.13]FGVVLDEIKPSSAPELQAVR.M                 |
| 0.998797 | 0.9993 R.NK[325.13]THTLC[160.03]R.R                      |
| 0.998796 | 0.9746 R.KQSLGELIGTLNAAK[325.13]VPADTEVVC[160.03]APPTA   |
| 0.998796 | 0.9993 R.YEAK[325.13]YLSGIAHFLEK.L                       |
| 0.998794 | 0.9945 K.LDSGK[325.13]ELHINLIPNK.Q                       |
| 0.998792 | 0.9996 R.HGNQYIQVNEPWK[325.13]R.I                        |
| 0.998792 | 0.9991 R.IGYPK[325.13]PALLHSTFFPALQGAQTK.M               |
| 0.998791 | 0.9409 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGGGFG.    |
| 0.998788 | 0.7585 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR      |
| 0.998786 | 0.4141 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I            |
| 0.998785 | 0.952 R.IFAPNHVVAK[325.13]SR.F                           |
| 0.998785 | 0.9992 K.TK[325.13]DGLEVAVLPHNIR.A                       |
| 0.998785 | 0.9518 R.GTK[325.13]VILHLK.E                             |
| 0.998784 | 0.9963 K.NLFTK[325.13]THPQWYPAR.Q                        |
| 0.998781 | 0.9948 K.TGISDVFAK[325.13]NDLAVVDVR.I                    |
| 0.998781 | 0.9994 K.K[325.13]DILLPFQGQLDSIPVSNPSC[160.03]PM[147.04] |
| 0.998781 | 0.9988 K.NISFTVWDVGGQDK[325.13]IRPLWR.H                  |
| 0.998779 | 0.9957 R.YIGIVK[325.13]QAGLER.M                          |
| 0.998778 | 0.9926 R.ILK[325.13]HGINC[160.03]FINR.Q                  |
| 0.998778 | 0.9701 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I  |
| 0.998776 | 0.9976 K.RPSSVK[325.13]VFSGK.S                           |
| 0.998773 | 0.9996 R.DK[325.13]VAGHSLGYGFVNYVTAK.D                   |
| 0.998772 | 0.9979 K.TEVNSGFFYK[325.13]SAEER.E                       |
| 0.998772 | 0.9993 R.FTSYQK[325.13]ATEEHSTR.Q                        |
| 0.998772 | 0.9709 R.K[325.13]LAVNMVPFPR.L                           |
| 0.998771 | 0.9874 K.SAFLC[160.03]GVMK[325.13]TYR.Q                  |
| 0.998771 | 0.9987 K.ALVKPK[325.13]EVKPK.I                           |
| 0.99877  | 0.9992 R.AVSDASAGDYGSAIETLVTAISLIK[325.13]QSK.V          |
| 0.998767 | 0.9996 K.IDLHK[325.13]YLTVK.D                            |
| 0.998766 | 0.9996 K.IHNFTSK[325.13]C[160.03]LYC[160.03]NR.Y         |
| 0.998765 | 0.9693 K.SGDAAIVDM[147.04]VPGK[325.13]PMC[160.03]VESFS   |
| 0.998765 | 0.9994 K.AVVPK[325.13]YLDEDTIYHLQPSGR.F                  |
| 0.998763 | 0.994 K.VFQFLNAK[325.13]C[160.03]ESAFLSK.R               |
| 0.998761 | 0.999 K.FFEVILIDPFHK[325.13]AIR.R                        |
| 0.998761 | 0.9953 R.LQAAYAGDK[325.13]ADDIQKR.E                      |
| 0.99876  | 0.9975 R.DKPLK[325.13]DVIIADC[160.03]GK.I                |
| 0.99876  | 0.9961 R.SSK[325.13]QHYNLC[160.03]EHSK.I                 |
| 0.998759 | 0.9979 K.HK[325.13]SETDTSLIR.G                           |
| 0.998756 | 0.998 R.WLK[325.13]GGVVLK.E                              |
| 0.998754 | 0.9396 R.FGFPEGSVELYAEK[325.13]VATR.G                    |

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| 0.998754 | 0.9896 K.KPAPEKK[325.13]PAEK.K                      |
| 0.998752 | 0.9974 R.AHWK[325.13]FLK.T                          |
| 0.998751 | 0.9976 K.AAYLQETGK[325.13]PLDETLKK.A                |
| 0.99875  | 0.9992 K.SLFVGHMDYK[325.13]YLR.W                    |
| 0.998748 | 0.979 R.LK[325.13]LLLPWLEAR.I                       |
| 0.998746 | 0.9976 R.IRDPNQGGK[325.13]DITEEIMSGAR.T             |
| 0.998745 | 0.9994 K.NAK[325.13]FYPVTR.E                        |
| 0.998744 | 0.9995 K.YELGRPAANTK[325.13]IGPR.R                  |
| 0.998742 | 0.9913 R.EIAQDFK[325.13]TDLR.F                      |
| 0.998742 | 0.9867 R.K[325.13]VESLQEEIAFLK.K                    |
| 0.998742 | 0.53 R.DALSDLALHFLNK[325.13]MK.I                    |
| 0.99874  | 0.9976 K.VK[325.13]EGMNIVEAMER.F                    |
| 0.99874  | 0.994 R.ETLMDLSTK[325.13]AFAMTNQILVEK.S             |
| 0.998739 | 0.9946 R.DVFTK[325.13]GYGFGLIK.L                    |
| 0.998739 | 0.9793 K.LLLQGEADQSLLTFIDK[325.13]AMHGELQK.A        |
| 0.998737 | 0.9981 R.HSQYHVDGSLEK[325.13]DR.T                   |
| 0.998736 | 0.9901 K.HVVFGK[325.13]VK.E                         |
| 0.998732 | 0.9971 R.KFVADGIFK[325.13]AELNEFLTR.E               |
| 0.998729 | 0.8689 R.APQC[160.03]LGK[325.13]FIEIAR.K            |
| 0.998728 | 0.9933 R.VYLFTIKK[325.13]GILGQHQFLEGPEGIENTR.F      |
| 0.998727 | 0.9995 K.K[325.13]YDVDTLDMVFLDHWK.D                 |
| 0.998726 | 0.999 R.VGLHK[325.13]VFK.L                          |
| 0.998725 | 0.9913 R.KPEDWDERPK[325.13]IPDPEAVKPDDEWEDAPAK.I    |
| 0.998725 | 0.9946 R.VEFATLQEALAHALTEK[325.13]EGK.D             |
| 0.998725 | 0.9946 K.K[325.13]EKEHASGSGAQSEAAGR.T               |
| 0.998724 | 0.999 R.GFK[325.13]LPDTPQGLLGEAR.M                  |
| 0.998721 | 0.9946 R.K[325.13]PVTVHSR.A                         |
| 0.99872  | 0.9996 R.YGGQPLFSEK[325.13]FPTLWSGAR.S              |
| 0.998717 | 0.8989 R.QTVAVGVK[325.13]AVDKK.A                    |
| 0.998716 | 0.9921 K.IGKPHTVPC[160.03]K[325.13]VTGR.C           |
| 0.998716 | 0.9942 K.K[325.13]AAVTPGKK.A                        |
| 0.998715 | 0.9998 R.AHFK[325.13]ELVNAVATVR.V                   |
| 0.998714 | 0.9303 R.HAYYVTEAAPYWLHK[325.13]PQSHLYGPGETAR.L     |
| 0.99871  | 0.997 -.M[147.04]QIFVK[325.13]TLTGK.T               |
| 0.998709 | 0.7747 R.HQGVMM[147.04]VGMGQKDSYVGDEAQSK[325.13]R.G |
| 0.998709 | 0.5219 R.DALSDLALHFLNK[325.13]MK.I                  |
| 0.998709 | 0.9994 K.GPLK[325.13]TPIAAGHPSMNLLLR.K              |
| 0.998708 | 0.9833 K.AVKPK[325.13]AAKPK.A                       |
| 0.998707 | 0.9974 K.DLIPYLEK[325.13]LSDSTLK.E                  |
| 0.998707 | 0.9941 K.FLSAIVSSVDK[325.13]IPYGM.R.F               |
| 0.998707 | 0.9941 K.VHAPGLNLSGVGGK[325.13]MQVGGDGVK.V          |
| 0.998706 | 0.999 K.IC[160.03]QFK[325.13]LVLLGESAVGK.S          |
| 0.998704 | 0.8146 R.AAAEVAGQFVK[325.13]LTHDVELNLDYER.Y         |
| 0.998703 | 0.9998 R.MAFK[325.13]GWSAHPGVVR.A                   |
| 0.998703 | 0.9996 K.HTGGK[325.13]ILGFFF.-                      |
| 0.998703 | 0.9963 K.RPK[325.13]NFGIGQDIQPK.R                   |
| 0.998702 | 0.9759 R.AK[325.13]HHAISAK.L                        |

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| 0.9987   | 0.9969 R.K[325.13]EFSPFGTITSAK.V                        |
| 0.9987   | 0.9996 R.SWHDIEK[325.13]DNAR.F                          |
| 0.9987   | 0.9802 K.HPVTGQFLYQDSNWASK[325.13]VEK.L                 |
| 0.9987   | 0.9998 R.K[325.13]QVMGLITHDTPYIR.A                      |
| 0.998699 | 0.9973 R.SNPK[325.13]IWNVHSVLNLHSLVDK.S                 |
| 0.998699 | 0.9974 K.K[325.13]LSVAC[160.03]FYGGTPYGGQFER.M          |
| 0.998697 | 0.9994 K.YHPGYFGK[325.13]VGMK.H                         |
| 0.998696 | 0.9973 R.AELIVQPELK[325.13]YGDGIQLTR.S                  |
| 0.998696 | 0.9971 K.GTVLIK[325.13]TAEELMNFSK.G                     |
| 0.998696 | 0.9997 R.VAGC[160.03]SVHK[325.13]GYAFVQYSNER.H          |
| 0.998696 | 0.9996 R.ADLTEYLSTHYK[325.13]APR.M                      |
| 0.998696 | 0.9827 K.ITLPVDFVTADKFDENAK[325.13]TGQATVASGIPAGWMC     |
| 0.998695 | 0.9912 R.HLILPEK[325.13]YPPPTELLDLQPLVPSALR.N           |
| 0.998694 | 0.9992 R.MPTPVIK[325.13]AFGILK.R                        |
| 0.998694 | 0.9998 R.IVAAHNK[325.13]C[160.03]PR.D                   |
| 0.998692 | 0.8859 R.NLQNLILTAK[325.13]ADR.T                        |
| 0.99869  | 0.9113 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K         |
| 0.99869  | 0.9994 K.QLPDK[325.13]WQHDLFDSGFGGGAGVETGGK.L           |
| 0.99869  | 0.9801 R.VISGVLQLGNIVFK[325.13]K.E                      |
| 0.99869  | 0.9994 K.GTLGGMFGMLK[325.13]GLVGSK.S                    |
| 0.99869  | 0.9992 R.DAVHNK[325.13]LWLQR.R                          |
| 0.99869  | 0.9994 K.IHLFDIDVPGK[325.13]ITFQESK.T                   |
| 0.998689 | 0.9961 R.GTNLNK[325.13]AM[147.04]TLQEAEAFVGAER.C        |
| 0.998687 | 0.9753 R.DQHFKV[325.13]IQVK.D                           |
| 0.998686 | 0.9922 R.AVNYFSK[325.13]VK.Q                            |
| 0.998684 | 0.9892 K.K[325.13]LNC[160.03]QVIGASVDSHFC[160.03]HLAWVI |
| 0.998683 | 0.9986 R.VTSLGK[325.13]DWHRPC[160.03]LK.C               |
| 0.998683 | 0.9988 R.K[325.13]VTNVLSR.Y                             |
| 0.998683 | 0.9484 K.SIYGEK[325.13]FEDENFILK.H                      |
| 0.998682 | 0.9975 K.QEWPK[325.13]HWPTFISDIVGASR.T                  |
| 0.998681 | 0.9941 R.SFVGK[325.13]QFSANDK.V                         |
| 0.998678 | 0.9909 K.IGYNPDTVAFPISGWNGDNM[147.04]LEPSANMPWFK[       |
| 0.998676 | 0.9925 R.LLLSK[325.13]GHSC[160.03]YRPR.R                |
| 0.998672 | 0.9787 R.IAAYLFK[325.13]GNNR.W                          |
| 0.998671 | 0.9997 R.ILVGSLEK[325.13]NEFITLAHVNPQSFPAPK.E           |
| 0.998671 | 0.9971 R.IGNFIVK[325.13]KPMVLGHEASGTVEK.V               |
| 0.99867  | 0.9905 K.SAPATGGVK[325.13]KPHR.Y                        |
| 0.99867  | 0.9994 K.GFVEFAAK[325.13]PPAR.K                         |
| 0.99867  | 0.9993 R.K[325.13]FYGPEGPYGVFAGR.D                      |
| 0.99867  | 0.9973 K.RNPGVK[325.13]EGYK.F                           |
| 0.998669 | 0.9985 R.IDFYFDENPYFENK[325.13]VLSK.E                   |
| 0.998668 | 0.9946 R.KSAPATGGVK[325.13]KPHR.Y                       |
| 0.998668 | 0.9814 K.GVSK[325.13]AVEHINK.T                          |
| 0.998666 | 0.9991 R.HISSK[325.13]VEELSQALSQK.E                     |
| 0.998665 | 0.9754 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I          |
| 0.998664 | 0.9943 K.GTLVQTK[325.13]GTGASGSFK.L                     |
| 0.998664 | 0.9993 K.VQQAK[325.13]EMVLELIR.D                        |



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| 0.998663 | 0.9995 R.IWSLEGK[325.13]SIMTIVGHTDVVK.D                |
| 0.998662 | 0.9988 R.VLPSITTEILK[325.13]SVVAR.F                    |
| 0.998661 | 0.9964 K.EGFEKISK[325.13]GANPVEIR.R                    |
| 0.998657 | 0.9995 K.VLTPTQVK[325.13]NRPTSISWDGLDSGK.L             |
| 0.998656 | 0.9904 R.VIFGLFGK[325.13]TVPK.T                        |
| 0.998654 | 0.9966 R.HGESGSMVAFHQQTGPSYSESK[325.13]R.L             |
| 0.998654 | 0.9995 R.NSSHAGAFVIVTEEAIK[325.13]GIR.R                |
| 0.99865  | 0.9997 R.K[325.13]AIQISQQTPYWHC[160.03]R.L             |
| 0.998649 | 0.9993 R.K[325.13]GLEFPMTDLMLSPIHTPQR.T                |
| 0.998647 | 0.9303 K.RVTIMPK[325.13]DIQLAR.R                       |
| 0.998646 | 0.997 R.THQK[325.13]FVIATSTK.I                         |
| 0.998645 | 0.9991 K.K[325.13]VLC[160.03]LAVAVGHVK.M               |
| 0.998644 | 0.9998 R.K[325.13]EWVLDC[160.03]HR.M                   |
| 0.998644 | 0.9997 K.HK[325.13]GFAFVEYEVPEAAQLALEQMNSVMLGGR.N      |
| 0.998641 | 0.4546 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK     |
| 0.998641 | 0.999 R.KTGQAPGYSYTAANK[325.13]NK.G                    |
| 0.99864  | 0.9991 R.DVFLPK[325.13]PTWGNHTPIFR.D                   |
| 0.998638 | 0.9955 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R    |
| 0.998638 | 0.9998 R.YHSYK[325.13]DLSEFLR.G                        |
| 0.998637 | 0.9929 R.K[325.13]YAYSAASGGR.R                         |
| 0.998636 | 0.9758 K.HPVTGQFLYQDSNWASK[325.13]VEK.L                |
| 0.998636 | 0.9975 K.GVLFGVPGAFTPGC[160.03]SK[325.13]THLPGFVEQAEA  |
| 0.998635 | 0.9985 R.HSHALVSLFLK[325.13]NLR.L                      |
| 0.998634 | 0.9991 R.LK[325.13]GLLQSGQIPGR.E                       |
| 0.998633 | 0.9958 R.LLEDGEDFNLGDALDSSNSM[147.04]QTIQK[325.13]TTTI |
| 0.998632 | 0.9987 R.KLERPPETPTVDPTVK[325.13]YER.Q                 |
| 0.998632 | 0.9923 K.VMTK[325.13]DGQWFTDWDVPHSR.H                  |
| 0.998632 | 0.9994 K.VK[325.13]SLSVYHPQLAYC[160.03]VVQFLEK.E       |
| 0.998629 | 0.9168 R.LAHYNK[325.13]R.S                             |
| 0.998629 | 0.9923 R.K[325.13]KNLQYYDISAK.S                        |
| 0.998627 | 0.9897 R.KQLATK[325.13]AAR.K                           |
| 0.998626 | 0.9995 K.VLVADK[325.13]SGDVYSFSVLEPHGC[160.03]GR.L     |
| 0.998626 | 0.9578 R.TMPVEQVFAK[325.13]NFR.V                       |
| 0.998622 | 0.9774 R.EHSSWDLVGLEK[325.13]WTEYR.V                   |
| 0.998621 | 0.9904 R.GYPTIK[325.13]FFR.N                           |
| 0.99862  | 0.9997 R.GKNPPPEFAK[325.13]VSPC[160.03]LPVLSR.L        |
| 0.998618 | 0.9998 K.TDWLDGK[325.13]HVVFGHVK.E                     |
| 0.998618 | 0.9928 K.VFQFLNAK[325.13]C[160.03]ESAFLSK.R            |
| 0.998615 | 0.997 R.EAGLSWK[325.13]EFLPEGQDIGAFVAEQK.V             |
| 0.998615 | 0.9997 R.DC[160.03]FK[325.13]TIISYIDEQFER.Y            |
| 0.998613 | 0.9051 R.LNFSHGTHEYHAETIK[325.13]NVR.T                 |
| 0.99861  | 0.9942 K.ATGQK[325.13]AAPAPK.A                         |
| 0.99861  | 0.9948 K.SLTGVVNAQALTSAFSPHTK[325.13]PWIGLAEALGTLMR.   |
| 0.998608 | 0.9883 R.K[325.13]LLEGEESR.I                           |
| 0.998608 | 0.9948 K.SLYYYIQQDTK[325.13]GDYQK.A                    |
| 0.998608 | 0.9944 R.KK[325.13]TATAVAHC[160.03]K.R                 |
| 0.998607 | 0.9976 R.FSNISAAK[325.13]AVADAIR.T                     |

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| 0.998606 | 0.9988 K.NVPNLHVMK[325.13]AMQSLK.S                      |
| 0.998605 | 0.9818 R.DAK[325.13]LDKSQIHIDIVLVGGSTR.I                |
| 0.998604 | 0.9957 R.IC[160.03]ANK[325.13]YMKV.S                    |
| 0.998602 | 0.9544 R.HNGTGGK[325.13]SIYGEK.F                        |
| 0.998601 | 0.9903 R.AIMKDPDDHTVC[160.03]HLLFANQTEK[325.13]DILLRPE  |
| 0.9986   | 0.9895 K.HK[325.13]SDFGK.F                              |
| 0.998595 | 0.9992 K.DTFLGPVLK[325.13]QMYITYVR.N                    |
| 0.998594 | 0.996 R.FQSSAVMALQEAC[160.03]EAYLVGLFEDTNLC[160.03]A    |
| 0.998593 | 0.9991 R.NIVDK[325.13]TASFVAR.N                         |
| 0.998592 | 0.9995 K.FHPDK[325.13]NKSPQAEK.F                        |
| 0.998591 | 0.9931 K.LTLDKLDVK[325.13]GK.R                          |
| 0.998589 | 0.9918 R.VYKAPEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03] |
| 0.998588 | 0.9933 R.FAK[325.13]QYINAIKDYELQLVTYK.A                 |
| 0.998587 | 0.9966 K.IPGK[325.13]DSVIC[160.03]LK.G                  |
| 0.998586 | 0.9988 K.IK[325.13]SDYAQLLED MQNAFR.S                   |
| 0.998585 | 0.8341 K.LAQMFSDMVLK[325.13]DGFQPSR.S                   |
| 0.998584 | 0.9939 R.YEEIVK[325.13]EVSTYIK.K                        |
| 0.998582 | 0.9977 R.RPFTK[325.13]NLGLEELGIELDPR.G                  |
| 0.998579 | 0.9914 R.ILK[325.13]HGINC[160.03]FINR.Q                 |
| 0.998577 | 0.9995 K.ILTGGADK[325.13]NVVVFVK.S                      |
| 0.998577 | 0.9995 R.GLGFSIAGGK[325.13]GSTPYR.A                     |
| 0.998573 | 0.9992 R.ALAIYK[325.13]QVLR.N                           |
| 0.998573 | 0.999 K.FNK[325.13]IVHSSMTR.A                           |
| 0.998572 | 0.9972 K.RPSSVK[325.13]VFSGK.S                          |
| 0.998571 | 0.9993 R.LVFVPLLLC[160.03]NIK[325.13]PR.R               |
| 0.998571 | 0.9926 R.LGDK[325.13]HATLQK.S                           |
| 0.99857  | 0.9932 K.LTFDSSFSPNTGK[325.13]K.N                       |
| 0.99857  | 0.9992 K.TTWAIK[325.13]HAASNPSK.K                       |
| 0.998569 | 0.9939 K.LGEK[325.13]ILPEIIPILEEGLR.S                   |
| 0.998568 | 0.9997 K.GVHQK[325.13]EGWPSSAYGVTK.I                    |
| 0.998566 | 0.9997 K.GTDYQLSK[325.13]EYTLDVYR.L                     |
| 0.998565 | 0.57 K.EITALAPSTMK[325.13]IKIIPPER.K                    |
| 0.998565 | 0.9741 R.K[325.13]VSQPIEGHAASFAQFK.M                    |
| 0.998565 | 0.9131 R.LAHYNK[325.13]R.S                              |
| 0.998562 | 0.0875 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I           |
| 0.998562 | 0.9992 K.TAGVK[325.13]HLIVLINK.M                        |
| 0.998561 | 0.9726 R.RYQK[325.13]STELLIR.K                          |
| 0.99856  | 0.9723 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T               |
| 0.99856  | 0.9929 R.EHPFLVK[325.13]GGEDLR.Q                        |
| 0.998559 | 0.9996 K.AHTLILQPPSEK[325.13]GR.Q                       |
| 0.998557 | 0.9973 K.GYISHQHVK[325.13]LVVSK.Q                       |
| 0.998556 | 0.9804 R.RYQK[325.13]STELLIR.K                          |
| 0.998551 | 0.9797 R.QHFPATPLLDYALEVEK[325.13]ITTSK.K               |
| 0.99855  | 0.9986 R.HGK[325.13]QVLDGNSNPYDIFLK.D                   |
| 0.99855  | 0.9995 R.FEHQEWK[325.13]AAIEAFNK.C                      |
| 0.998549 | 0.9974 R.LTPK[325.13]LFHEVVQAFA.A                       |
| 0.998549 | 0.9981 K.KGWK[325.13]EGTK.I                             |

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| 0.998548 | 0.9959 K.TDK[325.13]TLVLLM[147.04]GK.E                     |
| 0.998548 | 0.9973 K.K[325.13]GYPEVALHFVK.D                            |
| 0.998548 | 0.9672 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I          |
| 0.998547 | 0.9991 R.M[147.04]GVVEC[160.03]AK[325.13]HELLQPFNVLYEK.    |
| 0.998547 | 0.996 K.ANIK[325.13]HKPGGGDVK.I                            |
| 0.998545 | 0.9993 R.EGLLAIFK[325.13]SGGIPALVR.M                       |
| 0.998545 | 0.9965 R.FLM[147.04]K[325.13]SYDQVHSGK.L                   |
| 0.998542 | 0.9939 R.K[325.13]YAYSAASGGR.R                             |
| 0.998542 | 0.9992 R.AVLLGPPGAGK[325.13]GTQAPR.L                       |
| 0.998541 | 0.9973 K.TLSDLK[325.13]LDYLDLYLIHWPTGFKPGK.E               |
| 0.99854  | 0.9998 K.GSK[325.13]FYGPAGPYGIFAGR.D                       |
| 0.998538 | 0.9976 R.QIYGAK[325.13]GFSLSDPQAEISGEHLR.I                 |
| 0.998536 | 0.9991 R.DAVSGMGVIVHIEK[325.13]DK.I                        |
| 0.998534 | 0.9031 K.KPVGAAGK[325.13]KPK.K                             |
| 0.998534 | 0.9936 K.DWHRPC[160.03]LK[325.13]C[160.03]EK.C             |
| 0.998534 | 0.9968 R.IGNFIVK[325.13]KPMVLGHEASGTVEK.V                  |
| 0.998532 | 0.9479 K.LLSK[325.13]TPELNLDQFHDK.T                        |
| 0.998532 | 0.9924 R.LGDK[325.13]HATLQK.S                              |
| 0.998531 | 0.9933 K.LTSLALDGGK[325.13]NVNAGGHK.L                      |
| 0.99853  | 0.9982 R.DMHSAKK[325.13]HADGK.K                            |
| 0.99853  | 0.9973 R.EDSVK[325.13]PGAHLTVK.K                           |
| 0.99853  | 0.991 R.VVLIGGK[325.13]PDR.V                               |
| 0.998529 | 0.9893 R.DDSFFGETSHNYHK[325.13]FDSEYER.M                   |
| 0.998522 | 0.9993 K.LSLNLDHK[325.13]SR.I                              |
| 0.998521 | 0.9966 K.AK[325.13]DPFAHLPK.S                              |
| 0.99852  | 0.9946 K.VMSQNFTNC[160.03]HTK[325.13]IR.H                  |
| 0.998519 | 0.085 K.QVHPDTGISSK[325.13]AMGIMNSFVNDIFER.I               |
| 0.998518 | 0.999 R.FQTK[325.13]IPNIYAIGDVVAGPM[147.04]LAHK.A          |
| 0.998517 | 0.9958 K.ATILDLSC[160.03]NK[325.13]LTTLPSTDFC[160.03]GLTHL |
| 0.998513 | 0.982 K.TVTAM[147.04]DVVYALK[325.13]R.Q                    |
| 0.998512 | 0.8925 R.LESGMQNMSIHTK[325.13]TTSYGAGGLSSAYGGLTSPGLS       |
| 0.99851  | 0.9996 K.YSNSALGHVNC[160.03]TIK[325.13]ELR.R               |
| 0.99851  | 0.9996 K.YSNSALGHVNC[160.03]TIK[325.13]ELR.R               |
| 0.99851  | 0.9993 R.K[325.13]LHELTVMQDR.R                             |
| 0.998509 | 0.9998 R.ETQAQPPDGDHSPGNHEQSYVGK[325.13]R.S                |
| 0.998509 | 0.9998 R.EPFVAQFSLPSNVLPVPLVPLHTTPK[325.13]AVEK.E          |
| 0.998505 | 0.9997 K.VK[325.13]LEGHELPADLPPHLVPPSK.R                   |
| 0.998505 | 0.9969 K.IK[325.13]DPDASKPEDWDER.A                         |
| 0.998504 | 0.9913 R.FVGHTK[325.13]DVLSVAFSSDNR.Q                      |
| 0.998501 | 0.9924 R.NLATTVTEEILEK[325.13]SFSEFGK.L                    |
| 0.998499 | 0.9972 R.KAVLVALK[325.13]ER.G                              |
| 0.998499 | 0.9313 K.TEWLDGK[325.13]HVVFGK.V                           |
| 0.998497 | 0.9989 R.MNK[325.13]AGQVMC[160.03]VAQGSGHTHSVGTVC[1        |
| 0.998496 | 0.997 R.FSTPEQAAK[325.13]NR.I                              |
| 0.998494 | 0.9925 R.GGEPNQRPELK[325.13]NHIDR.V                        |
| 0.998492 | 0.9975 R.VSLDVNHFAPELTVK[325.13]TK.D                       |
| 0.998491 | 0.9936 K.AAEVLNK[325.13]HSLSGRPLK.V                        |

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| 0.998491 | 0.9902 R.DIMLATGK[325.13]LSPDAIPGK.W                          |
| 0.998488 | 0.9896 K.IQQLVK[325.13]EFFNGKEPSR.G                           |
| 0.998488 | 0.9938 K.FVIHC[160.03]NSPVWGADK[325.13]C[160.03]EELLEK.T      |
| 0.998487 | 0.9269 R.LVNHFVEEFK[325.13]R.K                                |
| 0.998486 | 0.9974 K.YRPLFDYFLK[325.13]C[160.03]K.E                       |
| 0.998486 | 0.9993 R.AVFQANQENLPILK[325.13]R.A                            |
| 0.998486 | 0.9961 K.VVNPLFEK[325.13]RPK.N                                |
| 0.998485 | 0.9867 K.VGLQVVAVK[325.13]APGFGDNRK.N                         |
| 0.998484 | 0.9949 R.AITIAGVPQSVTEC[160.03]VK[325.13]QIC[160.03]LVML      |
| 0.998484 | 0.9781 R.SKGQESFK[325.13]K.Q                                  |
| 0.998481 | 0.9994 R.SLENYHFVDEHGK[325.13]DQGINIR.Q                       |
| 0.99848  | 0.8615 R.M[147.04]VNHFAIEFK[325.13]R.K                        |
| 0.99848  | 0.9992 K.RPAC[160.03]TLK[325.13]PEC[160.03]VQQLLVC[160.03]    |
| 0.998478 | 0.9985 K.YQAVTATLEEK[325.13]RK.E                              |
| 0.998478 | 0.9992 R.TGAHYILFPC[160.03]ASSLC[160.03]GC[160.03]SVK[325.13] |
| 0.998478 | 0.5337 R.K[325.13]LFIGGLSFETTEESLR.N                          |
| 0.998478 | 0.9978 R.LVQLLVK[325.13]AHQDAQR.H                             |
| 0.998478 | 0.9976 K.K[325.13]FVLLSAQGSMLFHK.L                            |
| 0.998476 | 0.9889 R.LLLNNGAK[325.13]MPILGLGTWK.S                         |
| 0.998476 | 0.9994 K.ALK[325.13]ASAPAPGHH.-                               |
| 0.998475 | 0.9935 R.GDGMK[325.13]VEYTPYEEGLHSVDVTYDGSPVPSSPFQ            |
| 0.998475 | 0.9995 K.TFGK[325.13]AAGPSLSHTSGGTQSK.V                       |
| 0.998475 | 0.9976 R.C[160.03]LPTPK[325.13]C[160.03]HTPPLYR.M             |
| 0.998473 | 0.9761 R.LQAEIEGLK[325.13]GQR.A                               |
| 0.998473 | 0.998 K.AMK[325.13]QYNGVPLDGRPMNIQLVTSQIDAQR.R                |
| 0.998472 | 0.9987 R.VVVK[325.13]YC[160.03]DPDSYHR.R                      |
| 0.998472 | 0.9993 K.IHLFDIDVPGK[325.13]ITFQESK.T                         |
| 0.99847  | 0.9906 R.DAVTYTEHAK[325.13]RK.T                               |
| 0.998469 | 0.9965 R.RLDPNK[325.13]YPVPENWLHK.E                           |
| 0.998468 | 0.999 K.SDGIYIINLK[325.13]R.T                                 |
| 0.998467 | 0.9997 K.TGTLSC[160.03]TVALRPK[325.13]TGSQDQEVHR.T            |
| 0.998463 | 0.999 R.THTGK[325.13]YWTLTATGGVQSTASSK.N                      |
| 0.998463 | 0.9838 K.FASFIDK[325.13]VR.F                                  |
| 0.998462 | 0.9997 R.DLLHPSLEEEK[325.13]KK.H                              |
| 0.99846  | 0.9993 R.LNDYIFSFDK[325.13]MLDDR.G                            |
| 0.998459 | 0.9922 R.K[325.13]QVVNIPSFIVR.L                               |
| 0.998458 | 0.9967 K.TGFYC[160.03]K[325.13]LC[160.03]SLFYTNEEVAK.N        |
| 0.998457 | 0.9933 K.ATGQK[325.13]AAPAPK.A                                |
| 0.998457 | 0.9867 R.DAVTYTEHAK[325.13]R.K                                |
| 0.998457 | 0.7824 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y                  |
| 0.998457 | 0.9991 K.K[325.13]GLMPYPIFHVLTG.G                             |
| 0.998453 | 0.911 R.HAYYVTEAAPYWLHK[325.13]PQSHLYGPGETAR.L                |
| 0.998453 | 0.9996 R.IC[160.03]VK[325.13]VQDHLNSLR.N                      |
| 0.998453 | 0.97 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I                |
| 0.998452 | 0.9968 R.IVDGK[325.13]VVSETNDTK.V                             |
| 0.998451 | 0.9948 R.K[325.13]LPAIALDLLR.L                                |
| 0.998448 | 0.9973 R.K[325.13]NGVQAMVEFDSVQSAQR.A                         |

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| 0.998448 | 0.998 K.LGVQVVITDPEK[325.13]LDQIR.Q                     |
| 0.998447 | 0.9992 R.MVILLC[160.03]NLKPAK[325.13]MR.G               |
| 0.998447 | 0.9992 R.MVILLC[160.03]NLKPAK[325.13]MR.G               |
| 0.998446 | 0.9938 K.SNQNGKDSK[325.13]PSSTPR.S                      |
| 0.998443 | 0.996 R.HGESGSM[147.04]AVFHQTQGPSYSESK[325.13]R.L       |
| 0.998442 | 0.9968 K.AGLQVYNK[325.13]C[160.03]WK.F                  |
| 0.998442 | 0.992 K.K[325.13]SADTLWDIQK.D                           |
| 0.998441 | 0.8466 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I               |
| 0.998438 | 0.9856 R.RMEELHNQEVQK[325.13]R.K                        |
| 0.998438 | 0.9993 K.HK[325.13]FMVQSMFAPTDTSMEAVWK.E                |
| 0.998433 | 0.9894 K.KVSYSHIQSK[325.13]C[160.03]GSK.D               |
| 0.99843  | 0.9988 R.SNLPAK[325.13]AIGHR.I                          |
| 0.99843  | 0.9984 K.SVGK[325.13]IEHSFWR.S                          |
| 0.998428 | 0.9876 R.AAAEK[325.13]LFGNMEGDC[160.03]PSDWK.T          |
| 0.998424 | 0.9981 K.APK[325.13]SAC[160.03]GVC[160.03]PGR.L         |
| 0.998424 | 0.9992 K.MVSGMVK[325.13]HITGSYK.V                       |
| 0.998424 | 0.8496 K.VMIGENVDEK[325.13]HLPTLDHPIIPADYVAIK.A         |
| 0.998423 | 0.9994 R.K[325.13]LVILEGELER.A                          |
| 0.998423 | 0.9993 K.AFQYVETHGEVC[160.03]PANWTPDSPTIKPSPAASK[325    |
| 0.998422 | 0.9743 R.VFSGLVSTGLK[325.13]VR.I                        |
| 0.998421 | 0.9995 R.YLYTLVITDK[325.13]EK.A                         |
| 0.99842  | 0.9916 K.VSHVSTGGGASLELLEGGK[325.13]VLPGVDALSNI.-       |
| 0.99842  | 0.9961 R.LAK[325.13]AAFDDAIAELDTLSEESYK.D               |
| 0.99842  | 0.9991 K.DTFLGPVLK[325.13]QMYITYVR.N                    |
| 0.998416 | 0.9456 R.K[325.13]LPIDVTEGEVISLGLPFGK.V                 |
| 0.998415 | 0.9975 R.NIIHGSDSVK[325.13]SAEK.E                       |
| 0.998415 | 0.9991 R.K[325.13]YFTC[160.03]DEGHGIFVR.Q               |
| 0.998414 | 0.9976 R.ASFITVPGGVGPMTVAMLMQSTVESAK[325.13]R.F         |
| 0.998413 | 0.9993 R.YSYVC[160.03]PDLVK[325.13]EFNKYDTDGSK.W        |
| 0.99841  | 0.9982 K.VK[325.13]ADRDESSPYAAMLAAQDVAQR.C              |
| 0.99841  | 0.9943 R.VHTVEDYQAIVDAEWNILYDK[325.13]LEK.I             |
| 0.998409 | 0.9953 K.YLAIAPPIIK[325.13]QSTIVC[160.03]HNR.V          |
| 0.998408 | 0.9949 R.NYYEQWGK[325.13]LTDC[160.03]VVMR.D             |
| 0.998408 | 0.9143 R.TLSDYNIQK[325.13]ESTLHLVLR.L                   |
| 0.998404 | 0.9998 R.LADHFGGK[325.13]LHLGFIQIR.E                    |
| 0.998404 | 0.9991 R.IFGSNK[325.13]WTTEQQQR.F                       |
| 0.998404 | 0.9998 R.AHAAQVTC[160.03]VAASPHK[325.13]DSVFLSC[160.03] |
| 0.998404 | 0.9998 R.HYSIK[325.13]VVPVGASR.G                        |
| 0.998404 | 0.9998 R.TFFPEYTHQLFGDDETAFGYK[325.13]GLK.I             |
| 0.998403 | 0.9425 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                 |
| 0.998401 | 0.9774 K.VVLKSK[325.13]DDQVTVIGAGVTLHEALAAELLK.K        |
| 0.9984   | 0.8813 R.LEKPAK[325.13]YDDIKK.V                         |
| 0.998399 | 0.9968 R.ILVK[325.13]KEELTLEGIR.Q                       |
| 0.998398 | 0.9967 K.K[325.13]QGGLGPMNIPLVSDPK.R                    |
| 0.998393 | 0.9988 K.TEFLSFMNTELAFTK[325.13]NQK.D                   |
| 0.998391 | 0.9991 R.YALYDASFETK[325.13]ESR.K                       |
| 0.998388 | 0.9994 R.YIK[325.13]EYVTC[160.03]HTC[160.03]R.S         |

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| 0.998388 | 0.999 R.GVEVDPSLIK[325.13]DTWHQVYR.R                          |
| 0.998387 | 0.9932 R.LPPK[325.13]VESLESlyFTPIPAR.S                        |
| 0.998387 | 0.9992 R.VK[325.13]TTGIVETHFTFK.D                             |
| 0.998384 | 0.9969 R.HEVEK[325.13]SEISENTDASGK.I                          |
| 0.998382 | 0.9994 R.QMSGAIK[325.13]IANPVEGSTDR.Q                         |
| 0.998381 | 0.996 K.TC[160.03]TTVAFTQVNSEDKGALAK[325.13]LVEAIR.T          |
| 0.998381 | 0.9926 K.NKYEDEINK[325.13]R.T                                 |
| 0.998379 | 0.9991 K.FLDASGAK[325.13]LDYR.R                               |
| 0.998379 | 0.9629 R.AK[325.13]VTLNGVPAQPLGPR.A                           |
| 0.998379 | 0.9921 R.IAEDDGKPRPAFSNALEPDFK[325.13]ATSITVTGSGSC[160.03]R.S |
| 0.998379 | 0.9023 R.LAHYNK[325.13]R.S                                    |
| 0.998378 | 0.9954 R.GHLDNISNNLLIGAINIENGK[325.13]ANSVR.N                 |
| 0.998377 | 0.9903 R.LPSGNHM[147.04]K[325.13]ESR.E                        |
| 0.998377 | 0.9966 R.RLLELGPK[325.13]PEVAQQTR.K                           |
| 0.998376 | 0.9771 R.YLEGTSC[160.03]IAGVLVPAK[325.13]DQPGRQEK.M           |
| 0.998374 | 0.987 R.SSFYVNGLTGGQK[325.13]C[160.03]SVIR.D                  |
| 0.998373 | 0.9739 K.FAAK[325.13]GEGQLGPAER.A                             |
| 0.99837  | 0.9995 R.ADLTEYLSTHYK[325.13]APR.M                            |
| 0.99837  | 0.9387 R.LK[325.13]VPPAINQFTQALDR.Q                           |
| 0.99837  | 0.999 R.DIFISK[325.13]IVHK.S                                  |
| 0.99837  | 0.9938 K.KEQTPEHGK[325.13]K.K                                 |
| 0.998368 | 0.9857 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D               |
| 0.998366 | 0.9953 R.INK[325.13]MLSC[160.03]AGADR.L                       |
| 0.998366 | 0.9733 R.KASGPPVSELITK[325.13]AVAASK.E                        |
| 0.998366 | 0.995 R.LAAIVAK[325.13]QVLLGR.K                               |
| 0.998365 | 0.9888 R.TAQSTPSAPPQK[325.13]VMC[160.03]VSM[147.04]GST        |
| 0.998364 | 0.9468 R.HNGTGGK[325.13]SIYGEK.F                              |
| 0.998363 | 0.9993 R.THVDSHGHNVEFK[325.13]ER.I                            |
| 0.998363 | 0.9995 R.FRPAGAAPRPPK[325.13]PM.-                             |
| 0.998359 | 0.9995 K.DVPFGFQTVTSDVNK[325.13]LSSFYSLK.L                    |
| 0.998359 | 0.9973 R.FYVPPTQEDGVDPVEAFAQNVLSK[325.13]ADVQATGDA            |
| 0.998359 | 0.9998 R.GK[325.13]FIYITPEELAANFIR.Q                          |
| 0.998357 | 0.9974 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K                     |
| 0.998356 | 0.9899 R.DAVTYTEHAK[325.13]RK.T                               |
| 0.998355 | 0.9982 K.SYSMIVNNLLKPISVEGSSK[325.13]K.V                      |
| 0.998354 | 0.997 R.HGIPTAQWK[325.13]AFTKPEEAC[160.03]SFILSADFPAL         |
| 0.998345 | 0.9977 K.KYEDIC[160.03]PSTHNMDVPMK[325.13]R.N                 |
| 0.998344 | 0.9961 R.GGK[325.13]LMITYTR.K                                 |
| 0.998344 | 0.9993 R.GIYQK[325.13]AIEVLSDEHAR.E                           |
| 0.998344 | 0.9941 K.LLVP GK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E       |
| 0.998343 | 0.9993 R.DRDVDVLSAALK[325.13]EQLSHSR.Q                        |
| 0.998341 | 0.8452 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]R.N     |
| 0.99834  | 0.9925 K.ANPFGGASHAK[325.13]GIVLEK.V                          |
| 0.998339 | 0.998 K.HLIPAANTGESK[325.13]VFYK.M                            |
| 0.998338 | 0.9217 R.LIPDGC[160.03]GVK[325.13]YIPNR.G                     |
| 0.998335 | 0.9753 K.TVDGPSGK[325.13]LWR.D                                |
| 0.998332 | 0.9935 R.GGEPNQRPELK[325.13]NHIDR.V                           |

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| 0.99833  | 0.9984 K.TPQHVK[325.13]ITDFGLAK.L                             |
| 0.998329 | 0.9661 R.ILGLLDAYLK[325.13]TR.T                               |
| 0.998328 | 0.9919 K.APLK[325.13]IFAQDGEGQR.I                             |
| 0.998325 | 0.9992 K.LLEHSK[325.13]GAGSK.T                                |
| 0.998321 | 0.9927 K.K[325.13]LGEM[147.04]WNNTAADDKQPYEK.K                |
| 0.998321 | 0.997 K.VLLPEYGGTK[325.13]VVLDDKDYFLFR.D                      |
| 0.998321 | 0.976 R.YAIC[160.03]SALAASALPALVM[147.04]SK[325.13]GHR.       |
| 0.998321 | 0.9993 K.MLALK[325.13]DPVHTVSLQQFIYEK.L                       |
| 0.998321 | 0.9992 R.K[325.13]LALQLHPDRNPDDPQAEK.F                        |
| 0.99832  | 0.9996 K.YPHYFPVMK[325.13]K.C                                 |
| 0.998318 | 0.959 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG          |
| 0.998315 | 0.9993 R.GVTQFGNK[325.13]YIQQTKPLTLER.T                       |
| 0.998313 | 0.9996 K.FALLK[325.13]GSFSEQGINEFLR.E                         |
| 0.998312 | 0.9995 K.DVAIKEPLVDVDPK[325.13]QLVTNAC[160.03]LIK.E           |
| 0.998311 | 0.9996 R.K[325.13]ILSHTEEHK.K                                 |
| 0.998311 | 0.9996 R.K[325.13]ILSHTEEHK.K                                 |
| 0.998311 | 0.9964 K.TLGDFAAEYAK[325.13]SNR.S                             |
| 0.998311 | 0.9964 R.IK[325.13]KPEGKPDQK.F                                |
| 0.998308 | 0.9743 K.KAK[325.13]AAAKPK.K                                  |
| 0.998306 | 0.9962 K.IQGEYK[325.13]YTQVGPDHNR.S                           |
| 0.998306 | 0.9993 K.K[325.13]VPTVSRPYSFIEDTFIQK.T                        |
| 0.998305 | 0.9936 K.SMK[325.13]FVDGLMIHSGDPVNYVDTAVR.H                   |
| 0.998303 | 0.9912 K.AETAAK[325.13]HGEAQVK.I                              |
| 0.998301 | 0.9989 R.KTINQWVK[325.13]GQTEGK.I                             |
| 0.998297 | 0.9882 K.FETLQAQAGK[325.13]HGDDL.R.N                          |
| 0.998296 | 0.9951 R.INK[325.13]MLSC[160.03]AGADR.L                       |
| 0.998295 | 0.9994 R.VQPEAQAK[325.13]VDVFREDLC[160.03]TK.T                |
| 0.998294 | 0.8745 R.GENSWFSTQVDTVATK[325.13]VK.D                         |
| 0.998294 | 0.9993 R.FK[325.13]GQILMPNIGYGSNKK.T                          |
| 0.998294 | 0.9997 K.VVMEFLHEC[160.03]MVNK[325.13]FK.K                    |
| 0.998294 | 0.985 R.ELAILGMLDPAEKDEK[325.13]GMPVTAR.V                     |
| 0.998291 | 0.9759 K.AGGTKPK[325.13]KPVGA.K.K                             |
| 0.99829  | 0.9773 R.TAVDSGIPLLTNFQVTK[325.13]LFAEAVQK.S                  |
| 0.99829  | 0.9888 R.VK[325.13]VFQSSANYAENFIQSIISTVEPAQR.Q                |
| 0.99829  | 0.0983 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                      |
| 0.998288 | 0.9991 R.TGAHYILFPC[160.03]ASSLC[160.03]GC[160.03]SVK[325.13] |
| 0.998288 | 0.9996 R.K[325.13]QHPYTFPGSGTVFAR.N                           |
| 0.998288 | 0.9888 K.KEDLVFIFWAPESAPLK[325.13]SK.M                        |
| 0.998286 | 0.9927 R.NPDDITNEEYGEFYK[325.13]SLTNDWEDHLAVK.H               |
| 0.998286 | 0.997 K.KAGEIWK[325.13]GMSK.E                                 |
| 0.998283 | 0.9968 R.HIAMEK[325.13]VASR.T                                 |
| 0.998282 | 0.9994 R.LK[325.13]QLQAAAHWQQHQQHR.V                          |
| 0.998282 | 0.9948 R.IVDGKVVSETNDTK[325.13]VLR.H                          |
| 0.998282 | 0.9992 R.K[325.13]WC[160.03]ELIPGAEFR.C                       |
| 0.998281 | 0.9994 R.ASC[160.03]ESDVLHFTSTTTSK[325.13]NR.I                |
| 0.998281 | 0.9958 R.EVK[325.13]EWHGC[160.03]R.A                          |
| 0.99828  | 0.9933 R.GGEPNQRPELK[325.13]NHIDR.V                           |

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| 0.998279 | 0.0977 R.IGDLQAFQGHGAGNLAGLK[325.13]GR.L                  |
| 0.998279 | 0.9991 R.SQNPGLK[325.13]QIGLDQIWDDL.R.A                   |
| 0.998279 | 0.9903 R.VTGNFK[325.13]HASPILPITEFSDIPR.R                 |
| 0.998277 | 0.9356 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L       |
| 0.998275 | 0.5897 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E                  |
| 0.998275 | 0.9965 K.DVK[325.13]GSYVSIHSSGFR.D                        |
| 0.998271 | 0.9991 R.RLSQPESA EK[325.13]HVTQR.L                       |
| 0.998269 | 0.9968 K.YELHLK[325.13]SFEK.A                             |
| 0.998268 | 0.9987 K.AAIDWFDGK[325.13]EFSGNPIK.V                      |
| 0.998267 | 0.9963 K.AEDKEWM[147.04]PVTK[325.13]LGR.L                 |
| 0.998267 | 0.9995 R.GWVLGPNNYYSFASQQQKPEDTTIPSTELAK[325.13]QVIE      |
| 0.998266 | 0.9996 R.SLGLK[325.13]MLQC[160.03]GYSVVFGSR.N             |
| 0.998265 | 0.8539 K.VK[325.13]DALEFWLQAGVDGFQVR.D                    |
| 0.998264 | 0.9966 K.AVASAAAALVLK[325.13]AK.S                         |
| 0.998264 | 0.9741 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V                 |
| 0.998264 | 0.9994 K.NQMSK[325.13]LISEMHFSIQIK.K                      |
| 0.998263 | 0.9421 K.HGEVC[160.03]PAGWKPGSDTIKPDVQK[325.13]SK.E       |
| 0.998263 | 0.9965 K.VSYSHIQSK[325.13]C[160.03]GSK.D                  |
| 0.998263 | 0.9926 K.KTK[325.13]FENLC[160.03]K.I                      |
| 0.998259 | 0.9875 R.SSIAGLLLK[325.13]ATNEK.L                         |
| 0.998259 | 0.9984 K.VVLDVGS GTGILC[160.03]MFAAK[325.13]AGAR.K        |
| 0.998258 | 0.9993 K.DLLHPSPEEEK[325.13]RK.H                          |
| 0.998256 | 0.9793 R.AGKPVIC[160.03]ATQMLES MIKK[325.13]PRPTR.A       |
| 0.998255 | 0.9952 R.KPSAPK[325.13]KGDSSAEELK.L                       |
| 0.998252 | 0.9994 R.KTPC[160.03]GEGSK[325.13]TWDR.F                  |
| 0.998251 | 0.9972 R.KVAHSDK[325.13]PGSTSTASFR.D                      |
| 0.99825  | 0.9863 R.LGGIGQFLAK[325.13]AIEPPPLDAVIEAEHTLR.E           |
| 0.998249 | 0.9995 K.IEISQHAK[325.13]YTC[160.03]SFC[160.03]GK.T       |
| 0.998245 | 0.6409 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E                  |
| 0.998245 | 0.997 K.FEK[325.13]LIVALMKPSR.L                           |
| 0.998244 | 0.9961 K.K[325.13]LISPESTMVLLLEAQAATGGIIDPHR.N            |
| 0.998243 | 0.9676 K.EITALAPSTM[147.04]K[325.13]IK.I                  |
| 0.998242 | 0.2308 K.VK[325.13]DALEFWLQAGVDGFQVR.D                    |
| 0.998241 | 0.9993 K.EK[325.13]EQC[160.03]C[160.03]VSLAAGLPHFSSGIFR.( |
| 0.998238 | 0.9982 K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPM[147.(    |
| 0.998235 | 0.9566 R.VIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I            |
| 0.998234 | 0.9535 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V            |
| 0.998233 | 0.8604 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI     |
| 0.998233 | 0.9996 K.VWPHK[325.13]DYPLIPVGK.L                         |
| 0.998231 | 0.1021 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E         |
| 0.99823  | 0.9992 K.YEK[325.13]PDGSPVFIAFR.S                         |
| 0.998228 | 0.9928 K.SAPELK[325.13]TGISDVFAK.N                        |
| 0.998228 | 0.9993 R.EILTLLQGVHQGAGFQDIPK[325.13]R.C                  |
| 0.998226 | 0.9868 R.AIIPC[160.03]IK[325.13]GYDVIAQAQSGTGK.T          |
| 0.998225 | 0.9995 R.IFDSEEILAGYK[325.13]R.E                          |
| 0.998224 | 0.999 R.AVSEGNLLLLHEALAK[325.13]HEAFFIR.C                 |
| 0.998224 | 0.9997 K.YRPQTLNDLISHQDILSTIQK[325.13]FINEDR.L            |



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| 0.998219 | 0.9996 R.MLHFLTAVVGSTC[160.03]DVK[325.13]VK.N              |
| 0.998218 | 0.9991 K.LQTYK[325.13]TAVETAVLLLR.I                        |
| 0.998218 | 0.9913 K.WHDK[325.13]QYK.K                                 |
| 0.998217 | 0.9996 K.TLK[325.13]ISELGSQLSDEAVEDGLFHEFKR.F              |
| 0.998217 | 0.9985 R.KYEAQLTFK[325.13]QVSK.N                           |
| 0.998217 | 0.9979 R.IHIMPSMNPDGFEAVKK[325.13]PDC[160.03]YYSIGR.E      |
| 0.998216 | 0.9953 R.GLFIIDGK[325.13]GVLR.Q                            |
| 0.998216 | 0.9923 R.DIFNK[325.13]GFGFGLVK.L                           |
| 0.998215 | 0.9996 R.AKGDK[325.13]IAIWTTEC[160.03]ENR.E                |
| 0.998214 | 0.9966 R.YVIGQK[325.13]GSGIR.K                             |
| 0.99821  | 0.9991 K.LK[325.13]HILILQNK.I                              |
| 0.998209 | 0.9924 K.LTLSALLDGK[325.13]NVNAGGHK.L                      |
| 0.998206 | 0.9867 K.VTLDWAK[325.13]PK.G                               |
| 0.998203 | 0.9996 K.K[325.13]HLLIGVSSDR.G                             |
| 0.998202 | 0.4166 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTRPDKPLR.     |
| 0.998201 | 0.9964 K.K[325.13]GHQFSC[160.03]VC[160.03]LHGDR.K          |
| 0.998201 | 0.9991 K.SSEQILATLK[325.13]GHTK.K                          |
| 0.9982   | 0.9991 K.VVAC[160.03]TSAFLLWDPTK[325.13]VPPR.L             |
| 0.998199 | 0.9967 R.EINDC[160.03]IGGTVLNISK[325.13]SGSC[160.03]SAIR.I |
| 0.998199 | 0.9903 K.IWDLEGK[325.13]IIVDELKQEVISTSSK.A                 |
| 0.998197 | 0.9912 R.GC[160.03]TATLGNFAK[325.13]ATFDAISK.T             |
| 0.998197 | 0.9996 R.FC[160.03]LSKPGVYK[325.13]VTPR.S                  |
| 0.998196 | 0.997 K.KPPK[325.13]PQLMANYYNK.V                           |
| 0.998195 | 0.9964 K.HDTK[325.13]LLILALER.L                            |
| 0.998194 | 0.9996 K.AQVARPGGDTIFGK[325.13]IIR.K                       |
| 0.998193 | 0.9992 K.K[325.13]LAPPLVTLLEAEPELQYVALR.N                  |
| 0.998192 | 0.9923 R.K[325.13]VEDLFLTFK.K                              |
| 0.998186 | 0.9976 K.GK[325.13]GFSVVADTPELQR.I                         |
| 0.998183 | 0.8683 R.GALQNIIPASTGAAK[325.13]AVGK.V                     |
| 0.998183 | 0.9781 R.K[325.13]MFTLLDVVNR.K                             |
| 0.998183 | 0.9881 R.GFGFVTFDDHDPVDK[325.13]IVLQK.Y                    |
| 0.998179 | 0.9925 K.GYLGPEQLPDC[160.03]LK[325.13]GC[160.03]DVVVIPA    |
| 0.998177 | 0.9951 K.AFFK[325.13]GAWSNVLR.G                            |
| 0.998177 | 0.9917 R.RK[325.13]DPELWGSVLLESNPYR.R                      |
| 0.998176 | 0.9977 R.IK[325.13]MIASDSHRPEVK.L                          |
| 0.998175 | 0.9937 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A               |
| 0.998171 | 0.9983 R.EPVGTC[160.03]FLQDGTK[325.13]TVEYAPC[160.03]R.S   |
| 0.99817  | 0.9974 R.DK[325.13]LPQPVPQDPVSHC[160.03]K.E                |
| 0.998169 | 0.9981 R.VVVK[325.13]AVDPTSGQLYGLAR.E                      |
| 0.998169 | 0.9881 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                   |
| 0.998169 | 0.9972 R.KK[325.13]EAISDLQQLWK.Q                           |
| 0.998168 | 0.9884 R.FPGAYLK[325.13]GK.K                               |
| 0.998164 | 0.9917 R.M[147.04]LQTLK[325.13]ELEAHSAEAR.A                |
| 0.99816  | 0.986 R.DLQQYQSQAK[325.13]QLFR.K                           |
| 0.998156 | 0.9991 R.K[325.13]FVIPDFMSFTSHIDELYESAK.K                  |
| 0.998153 | 0.9993 K.DSK[325.13]AYFHLLNQIAPK.G                         |
| 0.998152 | 0.8477 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.]       |

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| 0.998151 | 0.9944 K.K[325.13]GLTPSQIGVILR.D                         |
| 0.99815  | 0.9922 K.K[325.13]TESHHK.A                               |
| 0.99815  | 0.9746 R.FHILFK[325.13]ALGEEK.G                          |
| 0.99815  | 0.9941 K.LLVPGK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E   |
| 0.998148 | 0.9888 K.K[325.13]HGVYNPNK.I                             |
| 0.998147 | 0.9888 K.IMLPWDPTGK[325.13]IGPK.K                        |
| 0.998146 | 0.9739 K.GLGLSK[325.13]AYVGQK.S                          |
| 0.998146 | 0.978 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E          |
| 0.998142 | 0.9817 R.FLEGK[325.13]IKPHLMSQELPEDWDKQPVK.V             |
| 0.998139 | 0.9994 R.K[325.13]YGTC[160.03]PHGGYGLGLER.F              |
| 0.998135 | 0.9995 R.IK[325.13]IQHMELQLIK.K                          |
| 0.998133 | 0.9991 K.IK[325.13]EWVDKYDPGALVIPFSGALELK.L              |
| 0.998133 | 0.9993 R.RGPLVK[325.13]YSSDYFQAPSDYR.Y                   |
| 0.998133 | 0.9837 K.LVINGNPITIFQERDPSK[325.13]IK.W                  |
| 0.998131 | 0.9967 K.GFQQILAGEYDHLPEQAFYMGVPIEEAVAK[325.13]ADK.L     |
| 0.998131 | 0.9954 R.KENPLQFK[325.13]FR.A                            |
| 0.998129 | 0.9835 R.FHILFK[325.13]ALGEEK.G                          |
| 0.998129 | 0.9997 K.K[325.13]YLLSQSSPAPLTAAEEELR.Q                  |
| 0.998127 | 0.9887 K.DSEDNPQTLLFSATC[160.03]PHWVFNVAK[325.13]K.Y     |
| 0.998123 | 0.9997 R.TDEQALLSSILAK[325.13]TASNIIDVSAADSQGMEQHEYM     |
| 0.998122 | 0.9996 R.AGK[325.13]VEAQHILASAPTDR.N                     |
| 0.998121 | 0.9961 R.IKDHIQNGK[325.13]LDLTK.L                        |
| 0.998121 | 0.3852 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSK.L      |
| 0.998121 | 0.9995 R.WK[325.13]QLSLPQQEAQK.I                         |
| 0.998121 | 0.9961 K.DHFTK[325.13]LAVEAVLR.L                         |
| 0.998119 | 0.9851 K.WQSLK[325.13]DLVK.E                             |
| 0.998118 | 0.9736 R.K[325.13]AKLGDSHDLQR.F                          |
| 0.998115 | 0.9996 K.EHLLQSNIGTGEK[325.13]ELGLR.T                    |
| 0.998115 | 0.9992 R.TVITEEFKVPDK[325.13]MVGFIIGR.G                  |
| 0.998111 | 0.9948 R.M[147.04]AQEVLTHLK[325.13]EHPDAWTR.V            |
| 0.998111 | 0.9954 R.VLALSVETDYTFPLAEK[325.13]VK.A                   |
| 0.998111 | 0.9299 R.LLIHQSLAGGIIGVK[325.13]GAK.I                    |
| 0.998108 | 0.9995 R.HLETGGQK[325.13]IEADSR.T                        |
| 0.998107 | 0.9976 R.VQLTTC[160.03]IHHIK[325.13]HDYPSR.W             |
| 0.998105 | 0.939 K.KK[325.13]EVAGAKPHITAAEGK.L                      |
| 0.998102 | 0.9957 R.TAK[325.13]LWALPQC[160.03]QLLGVFSGHR.R          |
| 0.9981   | 0.9784 K.AVTK[325.13]YTSSK.-                             |
| 0.9981   | 0.9951 R.M[147.04]ATEVAADALGEEWK[325.13]GYVVR.I          |
| 0.9981   | 0.9994 R.GK[325.13]SGPLFNFDVHDDVR.L                      |
| 0.998099 | 0.9959 R.HM[147.04]YHSLYLK[325.13]VK.G                   |
| 0.998099 | 0.9963 R.AK[325.13]ELLGQGLLLR.S                          |
| 0.998097 | 0.9919 R.AGLVGPEFHEK[325.13]LLSAEK.A                     |
| 0.998096 | 0.9965 R.EVSGIK[325.13]AAYEAE LGDAR.K                    |
| 0.998096 | 0.9987 R.EQC[160.03]C[160.03]YNC[160.03]GK[325.13]PGHLAR |
| 0.998095 | 0.9836 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L            |
| 0.998092 | 0.9996 K.GVHQB[325.13]EGWPSSAYGVTK.I                     |
| 0.998091 | 0.9991 R.K[325.13]AIVIC[160.03]PTDEDLKDR.T               |

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| 0.998091 | 0.9987 K.VK[325.13]FTQQNYHDR.L                            |
| 0.99809  | 0.9904 R.K[325.13]VIDDTNITR.L                             |
| 0.99809  | 0.8752 K.EITALAPSTM[147.04]KIK[325.13]HAPPER.K            |
| 0.998089 | 0.9913 K.AATVTGK[325.13]LVHANFGTK.K                       |
| 0.998088 | 0.9905 K.GYEK[325.13]KPYC[160.03]NAHYPK.Q                 |
| 0.998085 | 0.9996 R.YLSQLK[325.13]DAHR.S                             |
| 0.998084 | 0.9551 R.FVPQEMGVHTVSVK[325.13]YR.G                       |
| 0.998083 | 0.9564 K.VVLAYEPVWAIGTGK[325.13]TATPQQAQEVHEK.L           |
| 0.99808  | 0.9971 K.SPAVKPAAAPK[325.13]QPVGGGQK.L                    |
| 0.99808  | 0.9777 K.ELASALK[325.13]SALSGHLETVILGLK.T                 |
| 0.998079 | 0.9942 R.KTVTAM[147.04]DVVYALK[325.13]R.Q                 |
| 0.998078 | 0.9996 K.K[325.13]GQTHLTEDFQR.V                           |
| 0.998077 | 0.9991 R.HEVININLK[325.13]NKPEWFFK.K                      |
| 0.998073 | 0.9962 R.AK[325.13]VEFNIR.K                               |
| 0.998072 | 0.998 R.VVVK[325.13]AVDPTSGQLYGLAR.E                      |
| 0.998071 | 0.9767 K.TVTAM[147.04]DVVYALK[325.13]R.Q                  |
| 0.998069 | 0.9997 R.NSDPTYGQQGHPNTWK[325.13]R.E                      |
| 0.998067 | 0.9395 K.AGAHLQGGAK[325.13]R.V                            |
| 0.998066 | 0.9946 K.KQK[325.13]KPLVGK.K                              |
| 0.998066 | 0.9086 R.EVTVPVFYPTK[325.13]VWLEVEPVGMLK.E                |
| 0.998066 | 0.9995 R.K[325.13]GLPLGSAVSSPVLFSPVGR.R                   |
| 0.998066 | 0.9996 K.TTLLHMLK[325.13]DDR.L                            |
| 0.998063 | 0.9994 R.LTTINC[160.03]EEGDKLK[325.13]LTC[160.03]FELAPK.S |
| 0.998063 | 0.9206 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I     |
| 0.99806  | 0.9975 R.YPVNSVNILK[325.13]AHGR.S                         |
| 0.99806  | 0.9979 R.LHGGK[325.13]DSASPR.Y                            |
| 0.998055 | 0.9753 R.AEAESMYQIK[325.13]YEELQSLAGK.H                   |
| 0.998053 | 0.9982 R.K[325.13]FLPLFDR.V                               |
| 0.998053 | 0.9993 R.C[160.03]K[325.13]ELGITALHIK.L                   |
| 0.998052 | 0.9994 R.K[325.13]FFLSHPAYR.H                             |
| 0.998042 | 0.9995 R.LSMSLMEQLLK[325.13]TLR.Y                         |
| 0.998041 | 0.9978 R.K[325.13]GISLNPEQWSQLK.E                         |
| 0.99804  | 0.9993 K.VVVVQAISALC[160.03]QK[325.13]YPR.K               |
| 0.998039 | 0.9743 K.AEQPDGLILGMGGQTALNC[160.03]GVELFK[325.13]R.G     |
| 0.998038 | 0.9971 K.IVLTNPVC[160.03]TEVGEEK[325.13]IALSR.R           |
| 0.998038 | 0.9996 K.K[325.13]KPFVYTQQAVALNR.A                        |
| 0.998038 | 0.9878 R.KIEEIK[325.13]DFLLTAR.R                          |
| 0.998036 | 0.999 R.NEK[325.13]IAVHC[160.03]TVR.G                     |
| 0.998035 | 0.9992 R.ASDTEAGK[325.13]YQC[160.03]VAELWR.K              |
| 0.998033 | 0.9992 R.TSK[325.13]LLSDPNYGVHLPVK.L                      |
| 0.998031 | 0.9996 R.LGAGNK[325.13]IGGR.R                             |
| 0.99803  | 0.9991 R.GLQTVHINENFAK[325.13]LAEALYIADR.K                |
| 0.99803  | 0.9954 K.HVVFGK[325.13]VLEGMEVVR.K                        |
| 0.998029 | 0.9991 K.KAEGAQNQGK[325.13]K.V                            |
| 0.998029 | 0.9991 R.LTHQIQELTDPYFK[325.13]IQAR.N                     |
| 0.998028 | 0.9937 R.YHVK[325.13]DSSR.H                               |
| 0.998027 | 0.9268 R.SVGELPSTVESLQK[325.13]VQEQVHTLLSQDQAQAAR.L       |

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| 0.998027 | 0.974 K.GLGILSLK[325.13]QQEMMAALTDAIQDK.K              |
| 0.998027 | 0.996 K.KVQAAQSEAK[325.13]VVSQYHELVVQAR.D              |
| 0.998027 | 0.996 R.K[325.13]AHQLWLSVEALK.Y                        |
| 0.998024 | 0.996 K.TSSAETPTIPLGSAVEAIK[325.13]ANC[160.03]SDNEFTQA |
| 0.998022 | 0.9946 K.WPKETVK[325.13]PVEVEEGESVVLPC[160.03]NPPPSAEI |
| 0.998019 | 0.9739 R.LAAVALINAAIQK[325.13]GVAEK.T                  |
| 0.998019 | 0.9994 K.LVLISK[325.13]LYEEGSNKR.L                     |
| 0.998019 | 0.9986 R.GGRPNEIEPPPEMPWQK[325.13]R.Q                  |
| 0.998018 | 0.9797 K.LFVGGIK[325.13]EDTEEHHLR.D                    |
| 0.998015 | 0.9995 K.EIYHFTLEK[325.13]IQPR.V                       |
| 0.998008 | 0.7312 R.VIHLSNLP HSGYSDSAVLK[325.13]LAEPYGK.I         |
| 0.998008 | 0.9967 R.NLHHYK[325.13]LHGVNINVEASK.N                  |
| 0.998008 | 0.9915 K.HAAENPGK[325.13]YNILGTNTIMDK.M                |
| 0.998008 | 0.9996 R.HGK[325.13]NC[160.03]TAGAVYTYHEK.K            |
| 0.998004 | 0.9995 R.NLGFTAIP LHGQMSQSK[325.13]R.L                 |
| 0.998002 | 0.9992 K.LQGK[325.13]EVGVYEALKDDSWLK.G                 |
| 0.998002 | 0.987 R.FLMK[325.13]SYDQVHSGK.L                        |
| 0.997998 | 0.9991 R.GVVHK[325.13]SLPPR.T                          |
| 0.997996 | 0.9961 R.HGVSHK[325.13]VDDSSGSIGR.R                    |
| 0.997995 | 0.9994 K.AC[160.03]PRPEGLNFQDLK[325.13]NQLK.H          |
| 0.997993 | 0.9224 R.GTK[325.13]VILHLK.E                           |
| 0.99799  | 0.9996 R.AGGEPWGAK[325.13]KPR.H                        |
| 0.997985 | 0.9942 R.IAWPPPTELGS SGALEEGIKMSK[325.13]PK.W          |
| 0.997981 | 0.9862 K.EGKPLLK[325.13]AVM[147.04]R.R                 |
| 0.99798  | 0.9997 K.FVDPSAALDLLK[325.13]GAFR.S                    |
| 0.997979 | 0.9994 R.K[325.13]PTDGASSNC[160.03]VTDISHLVR.K         |
| 0.997978 | 0.999 K.SIAK[325.13]FFDHSGTLVMDAYEPEISR.L              |
| 0.997977 | 0.9694 K.KAK[325.13]AAAKPK.K                           |
| 0.997976 | 0.9873 R.NLK[325.13]ASLENSLR.E                         |
| 0.997975 | 0.9992 K.ILK[325.13]SLHHPNIVGYR.A                      |
| 0.997975 | 0.9992 R.K[325.13]LHGTAQQLQDSK.T                       |
| 0.997972 | 0.9997 R.LVIGDHK[325.13]STSHFR.T                       |
| 0.997971 | 0.9993 K.TIYEK[325.13]LASAFTEEQAVLYNQR.V               |
| 0.997968 | 0.9896 K.AC[160.03]VK[325.13]TYHYHC[160.03]GVQDK.A     |
| 0.997966 | 0.9997 R.AAHVFFTDSC[160.03]PDALFNELVK[325.13]SR.A      |
| 0.997966 | 0.9479 R.VK[325.13]GGGHVAQIYAIR.Q                      |
| 0.99796  | 0.9988 R.IREPALLSK[325.13]QDIVLTTYNILTHDYGTK.G         |
| 0.997959 | 0.9716 K.GATYGK[325.13]PVHHGVNQLK.F                    |
| 0.997959 | 0.987 K.AYAALAALEK[325.13]LFPDTPLALDANK.K              |
| 0.997959 | 0.9997 K.K[325.13]NYVHFAATQVQNR.I                      |
| 0.997958 | 0.9991 R.VLFLIPK[325.13]NNPPTLVGDFTK.S                 |
| 0.997957 | 0.9894 R.K[325.13]AYGQALAK.L                           |
| 0.997957 | 0.9916 R.HC[160.03]IAK[325.13]SQER.V                   |
| 0.997957 | 0.9991 K.YHSDDYIK[325.13]FLR.S                         |
| 0.997956 | 0.9879 R.FDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V           |
| 0.997952 | 0.9996 R.YSYQYTVANK[325.13]EYVAYSHTGR.I                |
| 0.99795  | 0.9993 R.ISGK[325.13]MALNHPYFNDLDNQIK.K                |

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| 0.997947 | 0.9765 K.SYK[325.13]VSTSGPR.A                             |
| 0.997945 | 0.9985 K.YAGK[325.13]DGYNYTLK.T                           |
| 0.997942 | 0.9961 K.IGDTSVSYK[325.13]YTSR.Y                          |
| 0.997942 | 0.9995 K.HAASTVQILGAEK[325.13]ALFR.A                      |
| 0.997941 | 0.9896 R.KITIGQAPTEK[325.13]GHTR.T                        |
| 0.99794  | 0.9955 K.VTYK[325.13]APVPTGEVYFADSFDR.G                   |
| 0.997939 | 0.9913 R.RGPPEK[325.13]EWR.R                              |
| 0.997937 | 0.9892 R.YISPDQLADLYKSFIK[325.13]DYPVVSIEDPFDQDDWGAM      |
| 0.997935 | 0.9705 R.GIFPVLC[160.03]K[325.13]DPVQEAWAEDVDLR.V         |
| 0.997933 | 0.9721 R.SGK[325.13]YDLDFK.S                              |
| 0.997932 | 0.9912 K.GGSWIQEINVAEK[325.13]NWYPR.Q                     |
| 0.997932 | 0.9997 R.LAAEVTk[325.13]LVHGR.E                           |
| 0.99793  | 0.9984 R.TLFGHLHSQK[325.13]R.N                            |
| 0.99793  | 0.8666 K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T     |
| 0.997928 | 0.9883 R.QDLMNIAGTTLSSK[325.13]LLTHHK.D                   |
| 0.997928 | 0.9762 R.TM[147.04]PVEQVFAK[325.13]NFR.V                  |
| 0.997927 | 0.9931 R.FGLPAAAPC[160.03]PK[325.13]GSFGTAVR.H            |
| 0.997925 | 0.9991 R.DQLASIFLAC[160.03]TSHK[325.13]VR.R               |
| 0.997925 | 0.986 K.SIPIC[160.03]TLK[325.13]NFPNAIEHTLQWAR.D          |
| 0.997924 | 0.9892 R.NLLSVAYK[325.13]NVVGAR.R                         |
| 0.997923 | 0.9964 R.KLFNLK[325.13]EDDVR.Q                            |
| 0.997919 | 0.9997 R.LDDLFLSFETDVKPLK[325.13]GDHLR.A                  |
| 0.997913 | 0.9831 R.IPK[325.13]EQGVLSFWR.G                           |
| 0.997908 | 0.9947 R.QIEYEYK[325.13]LAQALHEMR.E                       |
| 0.997907 | 0.9131 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF          |
| 0.997904 | 0.9936 K.FTVPMLK[325.13]EAC[160.03]R.A                    |
| 0.997904 | 0.9964 K.SLK[325.13]FATEAAITILR.I                         |
| 0.997903 | 0.9937 K.ATILDLSK[160.03]NK[325.13]LTTLPSDFC[160.03]GLTHL |
| 0.997903 | 0.9484 R.KYGGPPPSVYSGVQPGIGTEVFVGK[325.13]IPR.D           |
| 0.997902 | 0.9967 R.NLHK[325.13]LLYNRPSTVSSLK.K                      |
| 0.997902 | 0.3715 R.DALSDLALHFLNK[325.13]MK.I                        |
| 0.997901 | 0.9909 K.ATGQK[325.13]AAPAPK.A                            |
| 0.9979   | 0.9994 R.DALAK[325.13]ALHAR.V                             |
| 0.997899 | 0.999 R.LNAIYQNNLTk[325.13]SHIEIR.G                       |
| 0.997897 | 0.9754 R.GVNASAK[325.13]FATDGEGYKPC[160.03]DPQVIR.D       |
| 0.997896 | 0.9987 R.QYK[325.13]IPDWFLNR.Q                            |
| 0.997895 | 0.9992 R.IHMOVSK[325.13]R.S                               |
| 0.997887 | 0.8577 K.SVHELEK[325.13]SKR.A                             |
| 0.997884 | 0.9957 K.YGVSGYPTLK[325.13]IFR.D                          |
| 0.997873 | 0.9904 R.MPSLPSYK[325.13]VGDK.I                           |
| 0.997873 | 0.9862 R.VHK[325.13]ISNVNK.A                              |
| 0.997866 | 0.8399 R.ETNLDLPLVDTHSK[325.13]R.T                        |
| 0.997866 | 0.9985 R.LLLETHLPSK[325.13]K.K                            |
| 0.997864 | 0.7595 R.WLPAGDALLQMITIHLSPVTAQK[325.13]YR.C              |
| 0.997862 | 0.9996 R.K[325.13]PALELLHYLK.N                            |
| 0.99786  | 0.9912 R.HC[160.03]IAK[325.13]SQER.V                      |
| 0.997859 | 0.9962 R.ILQEHEQIK[325.13]K.K                             |

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| 0.997856 | 0.9856 K.VIHDNFGIVEGLM[147.04]TTVHAITATQK[325.13]TVDGI  |
| 0.997855 | 0.9733 R.YLEGTSC[160.03]IAGVLVPAK[325.13]DQPGR.Q        |
| 0.997854 | 0.9872 R.LPSGNHM[147.04]K[325.13]ESR.E                  |
| 0.997854 | 0.9582 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H               |
| 0.997853 | 0.9992 K.VLTPTQVK[325.13]NRPTSISWDGLDSGK.L              |
| 0.997849 | 0.9958 R.RVLEC[160.03]LASGIVMPDGSGIYDPC[160.03]EK[325.1 |
| 0.997848 | 0.9938 K.K[325.13]EM[147.04]QPTHPIR.L                   |
| 0.997844 | 0.9968 K.KVK[325.13]TDTVLILC[160.03]R.K                 |
| 0.997843 | 0.9919 K.DISLSDYK[325.13]GK.Y                           |
| 0.997841 | 0.9889 K.LGLAK[325.13]SIHHAR.V                          |
| 0.997841 | 0.9716 K.IK[325.13]IAPPER.K                             |
| 0.997837 | 0.9991 R.LAAC[160.03]VNLIPQITSIYEWK[325.13]GK.I         |
| 0.997837 | 0.9302 R.HNGTGGK[325.13]SIYGEK.F                        |
| 0.997836 | 0.9963 R.DFRPLK[325.13]DSR.F                            |
| 0.997834 | 0.9975 K.AGLQVYNK[325.13]C[160.03]WKFEHC[160.03]NFNDVT  |
| 0.997833 | 0.9943 R.K[325.13]NQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLC     |
| 0.997829 | 0.9993 R.FRLDYLPNPQFSTAK[325.13]R.E                     |
| 0.997828 | 0.999 K.EILK[325.13]WEALHAAEC[160.03]PC[160.03]GPSLIR.F |
| 0.997823 | 0.9716 K.AKKPAGAAK[325.13]KPK.K                         |
| 0.997821 | 0.9993 R.NLLSVAYK[325.13]NVVGGQR.A                      |
| 0.997814 | 0.9994 R.K[325.13]WRPIASDEIVPGDIVSIGR.S                 |
| 0.99781  | 0.9963 K.K[325.13]IFVGGIKEDTEEYNLR.D                    |
| 0.99781  | 0.0828 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E       |
| 0.997809 | 0.9985 K.K[325.13]VNAVFEWHITK.G                         |
| 0.997808 | 0.9994 R.IC[160.03]K[325.13]GDHWTTTR.C                  |
| 0.997803 | 0.9735 K.SK[325.13]FADLSEAANR.N                         |
| 0.997802 | 0.6944 R.DLTDYLM[147.04]K[325.13]ILTER.G                |
| 0.9978   | 0.9824 K.NK[325.13]GLWVPEGQR.A                          |
| 0.997799 | 0.9959 R.HIAMEK[325.13]VASR.T                           |
| 0.997798 | 0.9996 R.SLPGPAPC[160.03]LK[325.13]HFPLDLR.T            |
| 0.997798 | 0.9996 R.LQLGSK[325.13]AIYHLEAFVAK.F                    |
| 0.997792 | 0.9843 R.VIFGLFGK[325.13]TVPK.T                         |
| 0.997792 | 0.9996 R.KQAAAK[325.13]FYSFLVLK.K                       |
| 0.997791 | 0.9988 R.INFDK[325.13]YHPGYFGK.V                        |
| 0.997788 | 0.9947 R.RNPDTQWITKPVHK[325.13]HR.E                     |
| 0.997788 | 0.9832 R.DLQQYQSQAK[325.13]QLFR.K                       |
| 0.997788 | 0.9976 R.FFSDC[160.03]K[325.13]IQNGAQGIR.F              |
| 0.997788 | 0.9722 K.AVKPK[325.13]AAKPK.A                           |
| 0.997787 | 0.9904 K.K[325.13]HLLVHAPEDKK.E                         |
| 0.997782 | 0.9981 K.FHTVSGSK[325.13]C[160.03]EIK.V                 |
| 0.99778  | 0.9655 R.LGQSDPAPLQHQMIDIYQK[325.13]R.C                 |
| 0.997779 | 0.9956 R.C[160.03]K[325.13]DDEFTHLYTLIVRPDNTYEVK.I      |
| 0.997773 | 0.9906 R.RGPPEK[325.13]EWR.R                            |
| 0.997771 | 0.9885 R.GVQDIVVGEGTHFLIPWVQK[325.13]PIIFDC[160.03]R.S  |
| 0.997771 | 0.9992 R.SQGTGPK[325.13]PPTPLTVSFGGNPLHC[160.03]NC[160  |
| 0.997767 | 0.9481 R.K[325.13]LAVNMVFPFR.L                          |
| 0.997767 | 0.4136 R.K[325.13]LFIGGLSFETTEESLR.N                    |

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| 0.997767 | 0.9996 R.FHEIC[160.03]SNLVK[325.13]TR.R                  |
| 0.997766 | 0.9957 R.FSPNSSNPIIVSC[160.03]GWDK[325.13]LVK.V          |
| 0.997765 | 0.9996 R.GFAFVYFENVDDAK[325.13]EAK.E                     |
| 0.997764 | 0.9279 R.HNGTGGK[325.13]SIYGEK.F                         |
| 0.997763 | 0.999 K.GLESTTLADKDGEIYC[160.03]K[325.13]GC[160.03]YAK.I |
| 0.997763 | 0.9997 K.DKLEFAPK[325.13]AVLNR.N                         |
| 0.997761 | 0.9882 R.K[325.13]YSNEDTLSVALPYFWEHFDK.D                 |
| 0.997761 | 0.9686 R.SIVDYK[325.13]PNLDLLEQQHQLIQEALIFDNK.H          |
| 0.99776  | 0.9967 R.K[325.13]NNFSDTGNFGFGIQEHIDLGK.Y                |
| 0.997756 | 0.9909 K.VINTGIK[325.13]VWC[160.03]R.N                   |
| 0.997755 | 0.9995 K.KVPDK[325.13]LLDSSTVTHLFK.I                     |
| 0.997755 | 0.9977 R.YYVGHK[325.13]GK.F                              |
| 0.997755 | 0.998 R.GQTVK[160.03]NVK[325.13]LLHR.V                   |
| 0.997754 | 0.9989 R.DRDVDVLSAALK[325.13]EQLSHSR.Q                   |
| 0.997748 | 0.9948 R.LIK[325.13]VHLDK.A                              |
| 0.997748 | 0.9791 R.HGK[325.13]YM[147.04]AC[160.03]C[160.03]LLYR.G  |
| 0.997747 | 0.8945 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGPGGFG.   |
| 0.997743 | 0.9807 R.TGNK[325.13]YNVYPTYDFAC[160.03]PIVDSIEGVTHALR   |
| 0.997735 | 0.9637 K.AGAHLQGGAK[325.13]R.V                           |
| 0.997734 | 0.9897 K.GYAFIEFASFEDAK[325.13]EALNSC[160.03]NKR.E       |
| 0.997732 | 0.9864 R.TIAQDYGVLK[325.13]ADEGISFR.G                    |
| 0.997732 | 0.999 K.ATPEEK[325.13]LKLEDFAR.N                         |
| 0.997731 | 0.9877 R.TVVTGIEM[147.04]FHK[325.13]SLER.A               |
| 0.997731 | 0.9573 R.RYQK[325.13]STELLIR.K                           |
| 0.997727 | 0.9844 R.DAVTYTEHAK[325.13]R.K                           |
| 0.997724 | 0.9933 R.TFK[325.13]TVFAEHISDEC[160.03]K.R               |
| 0.99772  | 0.9979 R.FPK[325.13]TLFATEDALEVR.R                       |
| 0.997719 | 0.9827 R.TFK[325.13]TVFAEHISDEC[160.03]KR.R              |
| 0.997719 | 0.9927 R.NYEQWGK[325.13]LTDC[160.03]VVMR.D               |
| 0.997715 | 0.9817 R.LDHK[325.13]FDLM[147.04]YAK.R                   |
| 0.997711 | 0.9942 R.RNPDTQWITK[325.13]PVHK.H                        |
| 0.997709 | 0.986 R.MC[160.03]TLIDK[325.13]FDEHDPVR.G                |
| 0.997705 | 0.9995 K.IFSGSSHQDLSQK[325.13]IADR.L                     |
| 0.997701 | 0.9995 K.AFDK[325.13]HMNLILC[160.03]DC[160.03]DEFK.I     |
| 0.997701 | 0.8641 R.LAHYNK[325.13]R.S                               |
| 0.997697 | 0.9987 K.VVVNFAPTIQEI[325.13]SGTVTPGR.S                  |
| 0.997693 | 0.9881 R.GVQDIVVGEGTHFLIPWVQK[325.13]PIIFDC[160.03]R.S   |
| 0.997692 | 0.9892 R.LPVEVAYK[325.13]R.G                             |
| 0.997692 | 0.9968 K.INEEISVK[325.13]HLPSTEPDPHVVR.I                 |
| 0.997681 | 0.9953 K.THISK[325.13]GTLGK.F                            |
| 0.997678 | 0.9929 K.K[325.13]EMQPTHPIR.L                            |
| 0.997678 | 0.9956 K.LTLK[325.13]GGAAVDPDSGLEHSAHVLEK.G              |
| 0.997676 | 0.9723 K.FSK[325.13]SATSPEGK.K                           |
| 0.997676 | 0.9943 R.YPMAVGLNK[325.13]GHK.V                          |
| 0.997674 | 0.9936 R.M[147.04]RGETTLWNPGC[160.03]DHAGIATQVVVEK[3.    |
| 0.997672 | 0.7321 R.GGMGSGGLATGIAGGLAGMGGIQNEK[325.13]ETMQSLI       |
| 0.997671 | 0.9901 K.YFEGVSPK[325.13]SLK.H                           |

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| 0.997669 | 0.9826 K.HK[325.13]SDFGK.F                              |
| 0.997667 | 0.9871 R.DLVLSGDLGSLYAMTQDK[325.13]VFR.L                |
| 0.997665 | 0.9674 R.K[325.13]AKLGDSHDLQR.F                         |
| 0.997661 | 0.9997 R.IVPASSHHFLK[325.13]HLVPGADYDLC[160.03]LLALSPA  |
| 0.997659 | 0.9965 R.VLPSITTEILK[325.13]SVVAR.F                     |
| 0.997658 | 0.9957 R.GFGFVYSC[160.03]VEEVDAAMC[160.03]ARPHK[325.1   |
| 0.997658 | 0.9995 R.FGEVVDC[160.03]TIK[325.13]TDPVTGR.S            |
| 0.997658 | 0.999 K.TPVLFDIYEIK[325.13]EAIK.G                       |
| 0.997657 | 0.9943 K.FLSPVVPNYDNVHPNYHK[325.13]EPFLQQLK.V           |
| 0.997656 | 0.993 R.K[325.13]TVTAM[147.04]DVVYALK.R                 |
| 0.997655 | 0.9774 K.K[325.13]QGGLGPMNIPLVSDPKR.T                   |
| 0.997655 | 0.999 K.NLMK[325.13]HGYP LIYDVFPDAC[160.03]K.E          |
| 0.997652 | 0.99 K.NGQDLGVAFK[325.13]ISK.E                          |
| 0.997652 | 0.9762 R.VLGEAQT[325.13]AQHQALSSLELLNVLF.R.T            |
| 0.99765  | 0.8586 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVLR.L |
| 0.997649 | 0.9989 R.K[325.13]ALHSDRPPSASQPR.G                      |
| 0.997644 | 0.999 R.TVITEEFKVPDK[325.13]MVGFIIGR.G                  |
| 0.997642 | 0.9871 R.GC[160.03]TATLGNFAK[325.13]ATFDAISK.T          |
| 0.99764  | 0.9835 K.K[325.13]QPHGGQKPSYSGYQSHQGQQSYNQSPYSI         |
| 0.997639 | 0.9974 R.FSVLPPTFHPGDQK[325.13]QYGGFDNR.G               |
| 0.997638 | 0.9661 K.EKLC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325. |
| 0.997635 | 0.9991 R.STGEAFVQFASK[325.13]EIAENALGK.H                |
| 0.997634 | 0.9645 K.EPLFGISTGNLITGLAAGAK[325.13]TYK.M              |
| 0.997634 | 0.9694 K.EKYIDQEELNK[325.13]TKPIWTR.N                   |
| 0.99763  | 0.997 K.VNK[325.13]KLETAVNLAWTAGNSNTR.F                 |
| 0.99763  | 0.7613 K.VK[325.13]GLVLGPIHK.N                          |
| 0.99763  | 0.9874 R.LLSDATVEKDESHAGK[325.13]VVLR.S                 |
| 0.997629 | 0.9567 R.TLLIK[325.13]TVETR.D                           |
| 0.997629 | 0.995 R.SGEPQTFTLK[325.13]FK.R                          |
| 0.997629 | 0.9961 R.AGVK[325.13]MVMIQDGPQNTGADKPLR.I               |
| 0.997627 | 0.978 R.HGK[325.13]YM[147.04]AC[160.03]C[160.03]LLYR.G  |
| 0.997623 | 0.9768 R.AK[325.13]VTLNGVPAQPLGPR.A                     |
| 0.99762  | 0.9984 K.DVHMPK[325.13]HPELADK.N                        |
| 0.997619 | 0.9989 R.GHTK[325.13]LAFPSFGHLSEGFSHSR.W                |
| 0.997617 | 0.9745 R.EMAGDNK[325.13]LLGQFTLIGIPPAPR.G               |
| 0.997613 | 0.9833 R.SSGPYGGGGQYFAK[325.13]PR.N                     |
| 0.997611 | 0.999 K.SELPLDPLVPTEEGNPLLK[325.13]HYR.G                |
| 0.99761  | 0.9944 K.FGEVVDC[160.03]TLK[325.13]LDPITGR.S            |
| 0.99761  | 0.8966 R.SLDLDGIIAEVK[325.13]AQYEEMAK.C                 |
| 0.997608 | 0.9996 R.K[325.13]SWLWQHDEPC[160.03]YWR.L               |
| 0.997608 | 0.9996 K.LNPNFLVDFGK[325.13]EPLGPALAEHLR.Y              |
| 0.997606 | 0.9876 K.LSDVDRDGMMLDDEEFALASHLIEAK[325.13]LEGHGLPANL   |
| 0.997606 | 0.9996 R.K[325.13]AENPQC[160.03]LLGDFVTEFFK.I           |
| 0.997603 | 0.9457 R.AK[325.13]VTLNGVPAQPLGPR.A                     |
| 0.997603 | 0.9989 K.GKLPK[325.13]QPVIVK.A                          |
| 0.997601 | 0.9996 R.FGQVYTEAK[325.13]RPPGFDR.V                     |
| 0.9976   | 0.9898 K.DTELAEEELLQWFLQEEK[325.13]R.E                  |



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| 0.9976   | 0.9994 K.WK[325.13]GFSEEHNTWEPEK.N                      |
| 0.997594 | 0.999 K.EVHIK[325.13]NLPSLFK.K                          |
| 0.997593 | 0.9995 R.QYYTLLNK[325.13]APEYLHR.F                      |
| 0.997593 | 0.9945 R.KFVADGIFK[325.13]AELNEFLTR.E                   |
| 0.997592 | 0.9747 R.IAK[325.13]AVNEK.S                             |
| 0.997592 | 0.9914 R.IIGDPYK[325.13]VQQAC[160.03]EMVMDILR.E         |
| 0.997592 | 0.9964 K.ETVFTK[325.13]SPYQEFTDHLVK.T                   |
| 0.997592 | 0.7483 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |
| 0.99759  | 0.9995 R.MLFKDDYPSSPPK[325.13]C[160.03]K.F              |
| 0.997586 | 0.9995 R.LEK[325.13]HLDALLR.Q                           |
| 0.997584 | 0.9995 K.TTLLHMLK[325.13]DDR.L                          |
| 0.997581 | 0.9959 K.LHNSLIGTK[325.13]GR.L                          |
| 0.997579 | 0.989 R.APGSGLALLPLK[325.13]ITFR.S                      |
| 0.997579 | 0.9969 R.SIRPDNMSEYSK[325.13]QMQR.F                     |
| 0.997576 | 0.9994 K.AMTAK[325.13]GGDISVC[160.03]EWYQR.V            |
| 0.997575 | 0.9853 K.AYAALAALEK[325.13]LFPDTPLALDANK.K              |
| 0.997574 | 0.9918 R.IIAQK[325.13]IYGADDIELLPEAQHK.A                |
| 0.997573 | 0.9949 R.LYK[325.13]EELEQTYHAK.L                        |
| 0.997572 | 0.9607 K.WSLLQQQK[325.13]TAR.S                          |
| 0.997568 | 0.9988 R.TLTGTVIDSGDGVTHVIPVAEGYVIGSC[160.03]IK[325.13] |
| 0.997565 | 0.9914 R.HLK[325.13]STHSELLEDYYQSGR.M                   |
| 0.997565 | 0.8704 R.LMAEGAPKWPKETVK[325.13]PVEVEEGESVVLPC[160.03]  |
| 0.997563 | 0.9933 K.GRPC[160.03]K[325.13]IVEMSTSK.T                |
| 0.997557 | 0.9984 R.LYQVEYAFK[325.13]AINQGGLTSVAVR.G               |
| 0.997555 | 0.9995 R.HLPK[325.13]SIYSQIQEQR.I                       |
| 0.997554 | 0.9915 K.VC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M     |
| 0.997553 | 0.7531 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M               |
| 0.997553 | 0.7974 K.TVTAMDVVYALK[325.13]R.Q                        |
| 0.997553 | 0.9966 K.YHEEFK[325.13]SR.M                             |
| 0.997553 | 0.9896 K.VPK[325.13]ISMPDVDLHLK.G                       |
| 0.99755  | 0.9993 K.IEISQHAK[325.13]YTC[160.03]SFC[160.03]GK.T     |
| 0.99755  | 0.9961 R.K[325.13]NNFSDTGNFGFGIQEHIDLGK.Y               |
| 0.99755  | 0.8605 K.K[325.13]AKVAKPK.K                             |
| 0.99755  | 0.9918 R.YIEVFK[325.13]SHR.T                            |
| 0.99755  | 0.9988 K.FLEVIK[325.13]PFC[160.03]VILPEIQKPER.K         |
| 0.997548 | 0.9884 R.FAK[325.13]QYINAIKDYLQLVTYK.A                  |
| 0.997547 | 0.9886 R.K[325.13]FNALFAQGNYSEAAK.V                     |
| 0.997545 | 0.9993 K.TVAGGAWTYNTTSAVTVK[325.13]SAIR.R               |
| 0.997545 | 0.9858 R.VYK[325.13]APEEPNIQVNPLGIPVNSKEPEEVATC[160.03] |
| 0.997543 | 0.999 K.ATGRPEC[160.03]FLTIQEGLASK[325.13]FTSLTK.V      |
| 0.997542 | 0.9993 R.GGLGLSGAK[325.13]ANYR.G                        |
| 0.997542 | 0.998 K.GKTPALK[325.13]YQQLFEDIR.G                      |
| 0.997542 | 0.9973 K.ANGTTVHVGIHPSK[325.13]VVITR.L                  |
| 0.997539 | 0.9987 K.TLLPHDPTADVFTPAEEK[325.13]PIEIQWVKPEPK.V       |
| 0.997539 | 0.9888 R.LLGAALPLLTK[325.13]EQLHLVM[147.04]QGDVIR.H     |
| 0.997538 | 0.9992 K.IGSLIDVNQSK[325.13]DPEGLR.V                    |
| 0.997536 | 0.9859 R.RTK[325.13]TEISEMNR.N                          |

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| 0.997534 | 0.9799 K.K[325.13]LNC[160.03]QVIGASVDSHFC[160.03]HLAWVI |
| 0.997531 | 0.9173 R.GPVLQLHDLK[325.13]R.E                          |
| 0.997529 | 0.9895 K.GGLK[325.13]GSEVGFHGAAPDISVK.G                 |
| 0.997529 | 0.9895 R.AGAISASGPQLGAGHSG[325.13]LQVTMPGIK.V           |
| 0.997527 | 0.9987 R.YPM[147.04]AVGLNK[325.13]GHK.V                 |
| 0.997527 | 0.9818 K.GHLSGLAK[325.13]R.A                            |
| 0.997526 | 0.9994 R.YFK[325.13]VWLYHDGR.L                          |
| 0.997522 | 0.9855 K.HLNMK[325.13]LTR.A                             |
| 0.99752  | 0.9966 R.YK[325.13]APFHQLR.I                            |
| 0.997519 | 0.9996 K.SK[325.13]INVNEIFYDLVR.Q                       |
| 0.997517 | 0.9986 R.NSLK[325.13]ELWLVIHGR.V                        |
| 0.997517 | 0.9983 R.TVPVFESVEAAVLLPEEPVSQLGVK[325.13]SPGLYFLTAGD   |
| 0.997515 | 0.9655 R.VLEALLPLK[325.13]GLEER.V                       |
| 0.997511 | 0.9867 K.GETK[325.13]SFYPEEVSSMVLTK.M                   |
| 0.99751  | 0.9924 R.INVYYNEATGGK[325.13]YVPR.A                     |
| 0.99751  | 0.9992 R.NLLSVAYK[325.13]NVVGGQR.A                      |
| 0.99751  | 0.9963 R.K[325.13]TLGHNLLVSELYNQLK.F                    |
| 0.99751  | 0.9644 R.K[325.13]HGLEVIYMIEPIDEYC[160.03]VQQLK.E       |
| 0.997509 | 0.9957 R.SYSK[325.13]LLC[160.03]GLLAER.L                |
| 0.997508 | 0.9955 K.FRQDLMNIAGTTLSSK[325.13]LLTHHK.D               |
| 0.997502 | 0.9992 K.KVGDDIAK[325.13]ATGDWK.G                       |
| 0.997498 | 0.9976 R.AK[325.13]DINQEVYNFLATAGAK.Y                   |
| 0.997498 | 0.9903 R.IGKPAPDFK[325.13]ATAVVDGAFK.E                  |
| 0.997495 | 0.9976 R.GREC[160.03]VDK[325.13]C[160.03]NLLEGEP.R.E    |
| 0.997495 | 0.999 K.NLMK[325.13]HGYP LIYDVFPDAC[160.03]K.E          |
| 0.997495 | 0.9672 K.TK[325.13]DLPVTEAVFSALVTGHAR.A                 |
| 0.997493 | 0.9844 -.MQIFVK[325.13]TLTGK.T                          |
| 0.997493 | 0.9918 R.LQSLTENLTK[325.13]EHLMLLEEELR.N                |
| 0.997492 | 0.9994 R.NVTK[325.13]DHIMEIFSTYGK.I                     |
| 0.99749  | 0.999 K.TLVK[325.13]NC[160.03]IVLIDSTPYR.Q              |
| 0.99749  | 0.997 K.SNLMDAISFVLGEK[325.13]TSNLR.V                   |
| 0.997489 | 0.9976 K.VEQIK[325.13]TFSGQTHGFVHR.K                    |
| 0.997486 | 0.853 R.LLLPGELAKHAVSEGK[325.13]AVTK.Y                  |
| 0.997485 | 0.9919 K.KDIK[325.13]GSYVSIHSSGFR.D                     |
| 0.997483 | 0.9982 R.GLEAIC[160.03]AK[325.13]FTHESQR.Q              |
| 0.997483 | 0.9996 R.K[325.13]VPNQYTHLSGLLDIFK.S                    |
| 0.997482 | 0.9936 K.K[325.13]PGSKNFQNIFFSATLHLSNIPPSVSEEDLK.V      |
| 0.997478 | 0.9996 R.KLGINSLQELK[325.13]QNIAGK.G                    |
| 0.997473 | 0.9665 R.GAVGALLVYDIAK[325.13]HLTENVER.W                |
| 0.997471 | 0.9971 K.K[325.13]TGQPM[147.04]INLYTDR.E                |
| 0.99747  | 0.9994 K.DIVAAIQHNYK[325.13]MSAFK.E                     |
| 0.997467 | 0.9994 R.NHLTQFSPHFK[325.13]SGSLAVDNADPILK.I            |
| 0.997466 | 0.9936 K.HELQANC[160.03]YEEVK[325.13]DR.C               |
| 0.997462 | 0.9995 K.ISFK[325.13]FDHLR.K                            |
| 0.997461 | 0.9951 R.K[325.13]RVPDHHPC[160.03].-                    |
| 0.99746  | 0.9342 R.SIQLDGLVWGASK[325.13]LVPVGYGIR.K               |
| 0.997453 | 0.9966 K.K[325.13]NIFLLFK.K                             |

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| 0.997453 | 0.998 K.HK[325.13]ELAPYDENWFYTR.A                        |
| 0.997446 | 0.9976 R.YQTNPC[160.03]IGYK[325.13]LFPNC[160.03]VPSFGFR. |
| 0.997444 | 0.9986 K.VVGAK[325.13]VVTNAR.S                           |
| 0.997442 | 0.9863 R.HEMLPEFYK[325.13]TVSPALISR.F                    |
| 0.997441 | 0.9996 K.LK[325.13]DPANFQYPAESVLAYK.E                    |
| 0.997441 | 0.9467 R.KQSLGELIGTLNAAK[325.13]VPADTEVVC[160.03]APPTA   |
| 0.997439 | 0.9911 K.VC[160.03]QGTSNK[325.13]LTQLGTFEDHFLSLQR.M      |
| 0.997438 | 0.9665 R.LLLEAQAATGFLDPVK[325.13]GER.L                   |
| 0.997435 | 0.9965 R.LDQLIYIPLDEK[325.13]SR.V                        |
| 0.997435 | 0.9986 K.IGWEK[325.13]TGSHPQAR.G                         |
| 0.997434 | 0.9891 R.C[160.03]QHLQAEK[325.13]K.K                     |
| 0.997434 | 0.9995 R.KK[325.13]PALVSIPEDVVQAEAGGMHTVC[160.03]LSK.S   |
| 0.997434 | 0.9651 K.AAKPK[325.13]VVKPK.K                            |
| 0.997433 | 0.7891 K.TVTAMDVVYALK[325.13]R.Q                         |
| 0.997433 | 0.9983 K.EVEEISLLQPQVEESVLNLGK[325.13]FHSIVR.L           |
| 0.997433 | 0.9985 R.VADLADFVK[325.13]IAHPEPAFR.E                    |
| 0.997432 | 0.995 K.LK[325.13]GEMMDLQHGSFLR.T                        |
| 0.997428 | 0.9983 K.HGFSNQNK[325.13]LWER.N                          |
| 0.997427 | 0.9996 R.EVLHK[325.13]FTVDLPK.K                          |
| 0.997423 | 0.9885 K.NVNAGGHK[325.13]LGLGLEFQA.-                     |
| 0.997423 | 0.9268 K.IAPSFIVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S   |
| 0.997422 | 0.9389 K.KAK[325.13]KPAAAAGAK.K                          |
| 0.99742  | 0.9853 K.LQNK[325.13]EHVIEALR.R                          |
| 0.997419 | 0.9991 R.ELHGQNPVVTPC[160.03]NK[325.13]QFLSQFEMQSR.K     |
| 0.997418 | 0.9891 K.LVHANFGTK[325.13]K.D                            |
| 0.997415 | 0.1979 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G             |
| 0.997412 | 0.9504 K.EK[325.13]PYFPIPEEYTFIQNPLED.R.V                |
| 0.997411 | 0.9992 R.FLTDTSHLLSAVK[325.13]GQER.F                     |
| 0.99741  | 0.9988 R.K[325.13]WC[160.03]ELIPGAEFR.C                  |
| 0.997409 | 0.9992 R.FASENDLPEWK[325.13]ER.G                         |
| 0.997408 | 0.9991 R.K[325.13]QMVIDVLHPGK.A                          |
| 0.997403 | 0.9903 R.IFLC[160.03]QGK[325.13]RPR.S                    |
| 0.997401 | 0.9939 R.LVVPATQC[160.03]GSLIGK[325.13]GGC[160.03]K.I    |
| 0.9974   | 0.9463 K.TM[147.04]QNVK[325.13]HPVTGQFLYQDSNWASK.V       |
| 0.9974   | 0.9903 K.SLTGVVNAQALTSFSPHTK[325.13]PWIGLAEALGTLMR.      |
| 0.997397 | 0.9996 K.LHIVK[325.13]VVAK.K                             |
| 0.997396 | 0.9972 K.LIDIFYPGDQQSVTFGTK[325.13]SR.V                  |
| 0.997396 | 0.9883 R.IK[325.13]NPFLSLAAC[160.03]VMPSR.L              |
| 0.997395 | 0.9992 R.ADLTEYLSTHYK[325.13]APR.M                       |
| 0.997387 | 0.9992 K.TGHSK[325.13]GFGFVR.F                           |
| 0.997383 | 0.9612 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V                |
| 0.99738  | 0.9989 K.NLETPLC[160.03]K[325.13]NGFLLDGFP.R.T           |
| 0.997379 | 0.8394 K.KTESHHK[325.13]AK.G                             |
| 0.997379 | 0.9937 R.KESYSIYVYK[325.13]VLK.Q                         |
| 0.997379 | 0.9996 R.LDILK[325.13]IHSR.K                             |
| 0.997378 | 0.9959 R.LPK[325.13]SPPYTAFLGNLPYDVTEESIK.E              |
| 0.997378 | 0.9938 R.VTFLPTGITFK[325.13]SVTR.E                       |

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| 0.997377 | 0.9012 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                |
| 0.997366 | 0.9801 R.GHNC[160.03]PK[325.13]PVLNFYEANFPANVMDVIAR.C    |
| 0.997363 | 0.9487 R.RQQEGFK[325.13]GTFPDAR.E                        |
| 0.99736  | 0.9953 R.KGVAINFVK[325.13]NDDIR.I                        |
| 0.997358 | 0.9857 R.IFHELTQTDK[325.13]ALFNR.L                       |
| 0.997357 | 0.9632 K.SLVSK[325.13]GTLVQTK.G                          |
| 0.997356 | 0.9941 K.LLK[325.13]NHDEESLEC[160.03]LC[160.03]R.L       |
| 0.997356 | 0.9777 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V                  |
| 0.997354 | 0.9988 K.ILK[325.13]SLHHPNIVGYR.A                        |
| 0.997352 | 0.9817 R.ALSTGEK[325.13]GFGYK.G                          |
| 0.997351 | 0.9974 R.LK[325.13]GLGAFVIDSDHLGHR.A                     |
| 0.997348 | 0.9995 K.DAHSIHGTNPQYLVEK[325.13]IIR.T                   |
| 0.997346 | 0.9943 K.FLYQLHETEK[325.13]EDLIR.E                       |
| 0.997344 | 0.9869 K.QIFLGGVDK[325.13]HTQFWR.Y                       |
| 0.997342 | 0.9801 R.YALYDATYETK[325.13]ESK.K                        |
| 0.997342 | 0.9991 R.ADK[325.13]QHVLDMLFSAFEK.H                      |
| 0.99734  | 0.9963 K.KLQK[325.13]AALLK.A                             |
| 0.997339 | 0.9938 R.YIEIFK[325.13]SSR.A                             |
| 0.997337 | 0.9996 R.VPIWDQDIQFLPGSQK[325.13]LVTC[160.03]TGYHQVR.I   |
| 0.997335 | 0.9996 R.K[325.13]APQHTAVGFK.Q                           |
| 0.997334 | 0.9993 R.TTHYTPLAC[160.03]GSNPLK[325.13]R.E              |
| 0.997333 | 0.9035 K.TAWLDGK[325.13]HVVFGK.V                         |
| 0.99733  | 0.9703 K.FEDENFILK[325.13]HTGPGILSMANAGPNTNGSQFFIC[16    |
| 0.997329 | 0.9995 R.K[325.13]LVEALC[160.03]AAGHR.A                  |
| 0.997329 | 0.9845 R.KEEQEVQATLESEEVDL NAGLHGNWTLEN AK[325.13]AR.I   |
| 0.997327 | 0.996 R.RK[325.13]DGVFLYFEDNAGVIVNNK.G                   |
| 0.997325 | 0.9883 R.ISLGLPVGAVINC[160.03]ADNTGAK[325.13]NLYIISVK.G  |
| 0.997323 | 0.999 R.TM[147.04]GVMFTPLTVK[325.13]YAYYDTER.I           |
| 0.997323 | 0.9824 K.FLK[325.13]SGDAAIVDMVPGKPM[147.04]C[160.03]VE   |
| 0.997319 | 0.993 K.VM[147.04]SQNFTNC[160.03]HTK[325.13]IR.H         |
| 0.997318 | 0.987 R.K[325.13]FVADGIFK.A                              |
| 0.997317 | 0.9649 K.IK[325.13]IIAPPER.K                             |
| 0.997316 | 0.9696 R.SAPGGGSK[325.13]VPQKK.V                         |
| 0.997316 | 0.999 R.YIK[325.13]EYVTC[160.03]HTC[160.03]R.S           |
| 0.997315 | 0.994 R.GC[160.03]RPGK[325.13]IVQMTEAEVR.G               |
| 0.997314 | 0.8405 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R.L |
| 0.99731  | 0.9979 K.K[325.13]TGKPMINLYTDKDTGKPK.G                   |
| 0.99731  | 0.9922 R.LSFFGLEK[325.13]LLTNLGLGER.K                    |
| 0.997307 | 0.9932 R.HGESGSM AVFHQTQGPSYSESK[325.13]R.L              |
| 0.997306 | 0.9991 R.ITGDAFK[325.13]VQQAR.E                          |
| 0.997304 | 0.9908 R.NLFNVVDC[160.03]K[325.13]LHWQK.N                |
| 0.9973   | 0.9865 K.SIYGEKFEDENFILK[325.13]HTGPGILSMANAGPNTNGSQ     |
| 0.9973   | 0.9438 R.FHK[325.13]LQNVQIALDYLR.H                       |
| 0.997299 | 0.9165 R.ETAQAIK[325.13]GMHIR.K                          |
| 0.997294 | 0.9993 R.K[325.13]GLPLGSAVSSPVLFSPVGR.R                  |
| 0.997293 | 0.992 K.KPTSQIPETK[325.13]HPFSFPLENQAR.E                 |
| 0.997292 | 0.9884 K.ITGEAFVQFASQELAEK[325.13]ALGK.H                 |

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| 0.997292 | 0.9964 K.NFLEK[325.13]FVQGLDIGPTK.T                       |
| 0.99729  | 0.9877 R.HK[325.13]PLLIDMNK.V                             |
| 0.997281 | 0.9948 K.DRVEK[325.13]VGQVIR.V                            |
| 0.997281 | 0.755 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I                  |
| 0.99728  | 0.9943 R.DWVLNEFK[325.13]HGK.A                            |
| 0.997278 | 0.9958 K.HADIVTTTHK[325.13]TLR.G                          |
| 0.997276 | 0.9612 R.SKGQESFK[325.13]K.Q                              |
| 0.997275 | 0.9659 R.YLEGTSC[160.03]IAGVLVPAK[325.13]DQPGR.Q          |
| 0.997275 | 0.9971 R.KIGLETGVVK[325.13]INEK.T                         |
| 0.997274 | 0.9831 R.WYHPGC[160.03]FVK[325.13]NR.E                    |
| 0.997273 | 0.9877 R.AVTGYK[325.13]DPYTGQQISLFQAMQK.G                 |
| 0.997272 | 0.9991 R.K[325.13]DSVWGSQGGQSVNHLVK.E                     |
| 0.997272 | 0.9708 K.LTPK[325.13]IGFPWSEIR.N                          |
| 0.997266 | 0.9961 R.GQHTK[325.13]TTGR.R                              |
| 0.997265 | 0.9992 R.VTK[325.13]QYLPHVAR.L                            |
| 0.997265 | 0.9826 R.VAPEEHPVLLTEAPLNPK[325.13]ANREK.M                |
| 0.997263 | 0.9909 R.FGLPAAAPC[160.03]PK[325.13]GSFGTAVR.H            |
| 0.997263 | 0.9632 R.LQLETEIEALK[325.13]EELLFMK.K                     |
| 0.997259 | 0.9852 R.LSMQK[325.13]SMQNHA AVFR.V                       |
| 0.997258 | 0.9855 R.INSQGGK[325.13]LPNFGFVVFDDSEPVQK.V               |
| 0.997258 | 0.9978 K.FMQASEDLLK[325.13]EHYVDLK.D                      |
| 0.997258 | 0.998 K.LPNLTHLNLSGNK[325.13]LK.D                         |
| 0.997257 | 0.9988 K.EVQEFYK[325.13]DTYNK.L                           |
| 0.997254 | 0.9939 K.EFGTNIK[325.13]LGVIEDHSNR.T                      |
| 0.997245 | 0.9992 R.FPHDK[325.13]LLLLDTQQEAGMLLR.Q                   |
| 0.997242 | 0.9616 R.KVDSK[325.13]SLFHVR.Q                            |
| 0.997241 | 0.9979 R.QGLTK[325.13]DAHNALLDIQSSGR.A                    |
| 0.99724  | 0.9757 R.VTQKSYK[325.13]VSTSGPR.A                         |
| 0.997239 | 0.9995 K.VYK[325.13]GHLFGPAPGEQTQAVAIK.T                  |
| 0.997236 | 0.9615 R.DPYSGSTISLFQAMQK[325.13]GLVLR.Q                  |
| 0.997233 | 0.9991 K.SQFEAQK[325.13]IWYEHR.L                          |
| 0.997231 | 0.9946 R.FVTGNK[325.13]ILR.I                              |
| 0.99723  | 0.9956 R.K[325.13]NGGLGHMNIALLSDLTK.Q                     |
| 0.99723  | 0.8598 R.LLLPGELAKHAVSEGK[325.13]AVTK.Y                   |
| 0.997228 | 0.9939 R.ALYK[325.13]AISVPR.V                             |
| 0.997228 | 0.9996 R.TVNC[160.03]LLVGAIAIPHC[160.03]VLK[325.13]C[160. |
| 0.997227 | 0.9996 R.ADGVTVTC[160.03]K[325.13]VEHESFEAPALIPVTLVR.Y    |
| 0.99722  | 0.9882 K.IPMPDFDLHLK[325.13]GPK.V                         |
| 0.997219 | 0.9994 R.DLDGNGYPDLIVGSFGVDK[325.13]AVVYR.G               |
| 0.997217 | 0.9992 R.YVTNK[325.13]FDTQLFHTIGVEFLNK.D                  |
| 0.997217 | 0.9965 R.K[325.13]HFGAGGNQR.I                             |
| 0.997216 | 0.9876 K.FK[325.13]MPDMHFK.A                              |
| 0.997215 | 0.9691 R.LPSGNHMK[325.13]ESR.E                            |
| 0.997214 | 0.9721 K.WKPPMIDNPSYQGIWK[325.13]PR.K                     |
| 0.997213 | 0.9482 R.VTYK[325.13]NVPNWHR.D                            |
| 0.997211 | 0.9991 R.SVNIK[325.13]EIC[160.03]WNLQNIR.L                |
| 0.997209 | 0.9912 R.RGPFEEAFYSDPQGVPEAK[325.13]IGR.F                 |

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| 0.997208 | 0.9949 R.LYDAYELK[325.13]HALK.G                         |
| 0.997207 | 0.9615 R.TAVDSGIPLLTNFQVTK[325.13]LFAEAVQK.S            |
| 0.997207 | 0.9994 R.FK[325.13]MADKDGDLIATK.E                       |
| 0.997201 | 0.9995 R.K[325.13]HINTWVAEK.T                           |
| 0.997201 | 0.9985 R.NIHSSDWPK[325.13]FFEK.Y                        |
| 0.997198 | 0.8801 R.SEGVVAVLLTK[325.13]K.S                         |
| 0.997197 | 0.9796 R.AIVDC[160.03]GFEHPSEVQHEC[160.03]IPQAILGMDVLC  |
| 0.997195 | 0.9891 R.GGEPNQRPELK[325.13]NHIDR.V                     |
| 0.997194 | 0.9996 K.HNELTGDNVGPLILK[325.13]K.K                     |
| 0.997191 | 0.9977 R.K[325.13]DLQHPNEFIR.G                          |
| 0.997183 | 0.9973 R.AGK[325.13]IVVNLTGR.L                          |
| 0.997182 | 0.9951 K.VK[325.13]FMKSKPGAAMVEMADGYAVDR.A              |
| 0.99718  | 0.9915 R.LSHYLQK[325.13]GC[160.03]R.L                   |
| 0.997169 | 0.9993 K.GGHFYSK[325.13]PEILR.A                         |
| 0.997166 | 0.9896 K.K[325.13]KPRPPPALGPEETSASAGLPK.K               |
| 0.997166 | 0.9987 R.TVLEHYALEDPLAAFK[325.13]QR.Q                   |
| 0.997163 | 0.9991 K.WVHAEMVVK[325.13]NSELK.L                       |
| 0.997162 | 0.9988 R.YPSLSLHGIEGAFSGSGAK[325.13]TVIPR.K             |
| 0.99716  | 0.6337 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y            |
| 0.997159 | 0.999 K.YSFK[325.13]GPHLVQSDGTVPFWAHAGNAIPSSDQIR.V      |
| 0.997153 | 0.9994 R.AVYIGVHVPFSK[325.13]ESR.R                      |
| 0.997153 | 0.9995 R.NILDFPQHVSPSK[325.13]DIR.T                     |
| 0.997152 | 0.9991 R.GK[325.13]SGPLFNFDVHDDVR.L                     |
| 0.997151 | 0.9991 R.LTEK[325.13]TVFPLADVSR.I                       |
| 0.99715  | 0.9722 K.LHQAMK[325.13]GVGTR.H                          |
| 0.99715  | 0.9578 R.LVNQLQHLDLLNNK[325.13]LVTLPVSFAQLK.N           |
| 0.997144 | 0.9928 K.GHK[325.13]FHHTIGGSR.R                         |
| 0.997141 | 0.9441 K.SVVLMSHLGRPDGVPM[147.04]PDK[325.13]YSLEPVAVI   |
| 0.99714  | 0.9935 R.AAATQPDAK[325.13]DTPDEPWAFPAR.E                |
| 0.997139 | 0.9829 K.ESYSIYVYK[325.13]VLK.Q                         |
| 0.997138 | 0.9981 K.DGTVLC[160.03]ELINALYPEGQAPVK[325.13]K.I       |
| 0.997132 | 0.9971 R.K[325.13]LVSIVHGC[160.03]R.S                   |
| 0.997127 | 0.9741 K.FIDTTSK[325.13]FGHGR.F                         |
| 0.997125 | 0.9878 K.FSMPGFK[325.13]AEGPEVDVNLPK.A                  |
| 0.997122 | 0.9539 R.VFSGLVSTGLK[325.13]VR.I                        |
| 0.997122 | 0.9992 K.AHTLILQPPSEK[325.13]GR.Q                       |
| 0.997111 | 0.999 K.LAAK[325.13]LIHTLDDR.T                          |
| 0.997109 | 0.9927 R.HGESGSMVAFHQQTGPSYSESK[325.13]R.L              |
| 0.997109 | 0.9992 R.MLFDYLADK[325.13]HGFR.Q                        |
| 0.997106 | 0.8151 K.GLVLGPIHK[325.13]NQK.D                         |
| 0.997104 | 0.9935 R.TSTQK[325.13]HTHLAVSFGR.S                      |
| 0.997103 | 0.8087 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E           |
| 0.997102 | 0.9994 K.TTLLHMLK[325.13]DDR.L                          |
| 0.997098 | 0.9976 R.ELTDYLMK[325.13]ILTER.G                        |
| 0.997098 | 0.9669 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H               |
| 0.997096 | 0.9982 R.M[147.04]GVVEC[160.03]AK[325.13]HELLQPFNVLYEK. |
| 0.997095 | 0.9891 R.TRPAANPIQFTLNK[325.13]EK.L                     |

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| 0.997092 | 0.9873 K.NLLHSLQSSGIGSK[325.13]AGVPSK.S                  |
| 0.99709  | 0.831 R.LAHYNK[325.13]R.S                                |
| 0.997087 | 0.995 R.IHAEIK[325.13]NSLK.I                             |
| 0.997086 | 0.9914 K.FLPPVLLK[325.13]LSSTQEGVR.K                     |
| 0.997085 | 0.9995 R.SHNK[325.13]VLNPPGGK.S                          |
| 0.99708  | 0.9829 R.SSFYVNGLTGGQK[325.13]C[160.03]SVIR.D            |
| 0.99708  | 0.9667 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                |
| 0.997079 | 0.9988 R.ATGLPSSLASIPGGK[325.13]PAYSFHVSADGQMGPVFPF      |
| 0.997074 | 0.9912 R.FK[325.13]EANNFLWPFK.L                          |
| 0.99707  | 0.9804 K.VIHDNFGIVEGLM[147.04]TTVHAITATQK[325.13]TVDGI   |
| 0.99707  | 0.9896 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q                |
| 0.997069 | 0.9875 K.C[160.03]DPRHGK[325.13]YMAC[160.03]C[160.03]LLY |
| 0.997068 | 0.9818 K.HK[325.13]PGGGDVK.I                             |
| 0.997067 | 0.9956 K.VLLPEYGGTK[325.13]VVLDDKDYFLFR.D                |
| 0.997066 | 0.9813 R.ADHPPAEVTSHAASGAK[325.13]ADQEEQIHPR.S           |
| 0.997066 | 0.9996 K.IFQGNK[325.13]DYHQDVR.N                         |
| 0.997062 | 0.9971 R.VTSLGK[325.13]DWHRPC[160.03]LK.C                |
| 0.99706  | 0.9937 K.MEADPELSK[325.13]FLYQLHETEKEDLIR.E              |
| 0.997052 | 0.9688 R.IPELNK[325.13]VAR.A                             |
| 0.997044 | 0.9954 K.EGLPVALDK[325.13]HILGFDTGDAVLNEAAQILR.L         |
| 0.99704  | 0.9996 K.K[325.13]C[160.03]QSWSSMTPHR.H                  |
| 0.997037 | 0.9979 K.FDYK[325.13]AHQR.Q                              |
| 0.997034 | 0.9749 K.KPAEK[325.13]KPTTEEK.K                          |
| 0.997033 | 0.9995 R.IIAHSNQK[325.13]SAAGYPDYYC[160.03]K.W           |
| 0.997031 | 0.9835 K.AVLFC[160.03]LSEDK[325.13]K.N                   |
| 0.997031 | 0.9987 R.STPAITLESPIK[325.13]YPLR.L                      |
| 0.99703  | 0.9862 R.VSVADHSLHLSK[325.13]AK.I                        |
| 0.997026 | 0.9612 K.IK[325.13]IIAPPER.K                             |
| 0.997023 | 0.9931 R.IESLSSQLSNLQK[325.13]ESR.A                      |
| 0.997023 | 0.9865 K.ALYEHLTAK[325.13]NTK.L                          |
| 0.997022 | 0.6108 R.DLTDYLM[147.04]K[325.13]ILTER.G                 |
| 0.997021 | 0.9996 R.NAIFHLLK[325.13]NFLR.L                          |
| 0.997021 | 0.9996 K.AELSK[325.13]LVIVAK.A                           |
| 0.997021 | 0.9996 R.TITK[325.13]QVPNESFFNFFNPLK.A                   |
| 0.997021 | 0.9996 R.SK[325.13]FALITWIGENVSGLQR.A                    |
| 0.997021 | 0.9996 K.KLLVK[325.13]VDAK.T                             |
| 0.997021 | 0.9996 R.K[325.13]ELVHLYPR.E                             |
| 0.99702  | 0.9996 R.GLTAHGINIK[325.13]DR.S                          |
| 0.997019 | 0.9996 R.DNSGMIDKNELK[325.13]QALSGFGYR.L                 |
| 0.997019 | 0.9996 K.TYGEIFEK[325.13]FHPIR.-                         |
| 0.997016 | 0.9943 K.DKFSFDLGK[325.13]GEVIK.A                        |
| 0.997011 | 0.9994 R.DMFYK[325.13]ILHGFK.D                           |
| 0.99701  | 0.9897 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A             |
| 0.99701  | 0.9995 R.C[160.03]GAHYK[325.13]LVPQQLAH.-                |
| 0.997008 | 0.9994 R.DKELEGLQVK[325.13]IQR.L                         |
| 0.997007 | 0.9995 K.VQK[325.13]VMVQPINLIFR.Y                        |
| 0.997006 | 0.9936 K.TGFYC[160.03]K[325.13]LC[160.03]SLFYTNEEVAK.N   |

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| 0.997005 | 0.9995 K.DKVNC[160.03]SFYFK[325.13]IGAC[160.03]R.H         |
| 0.997005 | 0.9705 R.GVLK[325.13]VFLENVIR.D                            |
| 0.996999 | 0.9799 R.KPEDWDERPK[325.13]IPDPEAVKPDDWDEDAPAK.I           |
| 0.996998 | 0.9995 R.IFK[325.13]GC[160.03]NIENAC[160.03]YPLGIC[160.03] |
| 0.996996 | 0.9924 R.QIEYEYK[325.13]LAQALHEMR.E                        |
| 0.996995 | 0.7545 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C          |
| 0.996994 | 0.9951 K.IGK[325.13]PHTVPC[160.03]K.V                      |
| 0.996993 | 0.9783 R.DDSFFGETSHNYHK[325.13]FDSEYER.M                   |
| 0.996992 | 0.9996 R.K[325.13]ILALLDALSTVHSQK.M                        |
| 0.996992 | 0.9892 K.ENLLDFIK[325.13]HNQLPLVIEFTEQTAPK.I               |
| 0.996989 | 0.9995 R.ELLGELDGDVLLQQLSVFK[325.13]R.H                    |
| 0.996989 | 0.9993 R.LGVHTK[325.13]GADIDALC[160.03]VAPR.H              |
| 0.996984 | 0.9987 R.VNHVTLSQPKIVK[325.13]WDR.D                        |
| 0.996981 | 0.9995 R.YPFHK[325.13]QPPTYVR.A                            |
| 0.99698  | 0.9607 R.GRLPLLAVC[160.03]DYK[325.13]QVEVTVHK.G            |
| 0.99698  | 0.998 R.DVFLPK[325.13]PTWGNHTPIFR.D                        |
| 0.996979 | 0.9986 R.TGK[325.13]C[160.03]HVQTIQLC[160.03]R.R           |
| 0.996978 | 0.9993 R.NHPQMIAVLVDK[325.13]MIR.T                         |
| 0.996976 | 0.9702 K.M[147.04]LK[325.13]DKFNEC[160.03]GHVLYADIK.M      |
| 0.996976 | 0.9303 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I    |
| 0.996971 | 0.8099 K.KPVGAAK[325.13]KPK.K                              |
| 0.996971 | 0.9968 R.GVEVTVGHEQEEGK[325.13]WPYAGTAEAIK.A               |
| 0.996969 | 0.9976 R.VALHLDEEDK[325.13]LR.H                            |
| 0.996965 | 0.981 K.TVDNFVALATGEK[325.13]GFGYK.N                       |
| 0.996964 | 0.9996 R.KLEAEADK[325.13]IGLLAAK.A                         |
| 0.996963 | 0.9996 -.MLWFQGAIPAAIATAK[325.13]R.S                       |
| 0.996961 | 0.9758 K.NK[325.13]GLWVPEGQR.A                             |
| 0.996956 | 0.9912 R.QTATQLLK[325.13]LAHK.Y                            |
| 0.996956 | 0.9993 R.GFGHIGIAVPDVYSAC[160.03]K[325.13]R.F              |
| 0.996949 | 0.9995 R.VSGK[325.13]YFAHIK.E                              |
| 0.996948 | 0.2987 K.EITALAPSTMKIK[325.13]IIAPPER.K                    |
| 0.996948 | 0.9978 R.VDK[325.13]ITEYLC[160.03]EPLRK.C                  |
| 0.996938 | 0.9951 R.IANFK[325.13]IEPPGLFR.G                           |
| 0.996935 | 0.9995 K.TLWK[325.13]HQFAWPFQQPVDVAVK.L                    |
| 0.996932 | 0.9996 R.K[325.13]VDIADAAYSIFQKPK.S                        |
| 0.99693  | 0.9803 R.FGWDC[160.03]HGLPVEYEIDK[325.13]TLGIR.G           |
| 0.996928 | 0.9827 K.SPYQEFTDHLVK[325.13]THTR.V                        |
| 0.996927 | 0.9978 R.FAGLHFFNPVPVMK[325.13]LVEVIK.T                    |
| 0.996924 | 0.9991 R.VTK[325.13]QYLPHVAR.L                             |
| 0.996924 | 0.9322 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I          |
| 0.996923 | 0.9986 R.ERPPSGTLEK[325.13]LVSEAK.A                        |
| 0.996919 | 0.9946 R.ESQLAHIK[325.13]DEPPPLSPAPLTPATPSSLDPPFSR.E       |
| 0.996917 | 0.956 R.GELAIK[325.13]DANAK.L                              |
| 0.996915 | 0.9907 R.KNQLK[325.13]DMAIATGGAVFGEEGLTLNLEDVQPHDLG        |
| 0.996911 | 0.9994 R.RFELYFQGPSSNK[325.13]PR.V                         |
| 0.996911 | 0.9993 K.VWPHK[325.13]DYPLIPVGK.L                          |
| 0.996908 | 0.9818 K.IGKPHTVPC[160.03]K[325.13]VTGR.C                  |



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| 0.996905 | 0.9994 R.EKDLEDLFYK[325.13]YGR.I                           |
| 0.996904 | 0.9996 K.FFADLLDYIK[325.13]ALNR.N                          |
| 0.996904 | 0.8672 R.LVNHFVEEFK[325.13]R.K                             |
| 0.996902 | 0.999 R.SVNIK[325.13]EIC[160.03]WNLQNIR.L                  |
| 0.996898 | 0.8817 R.KPAGAAK[325.13]KPK.K                              |
| 0.996894 | 0.9963 K.DK[325.13]MMNGGHHYTYSEN.R                         |
| 0.996891 | 0.9985 K.IK[325.13]EWVDKYDPGALVIPFSGALELK.L                |
| 0.99689  | 0.8677 K.IK[325.13]GEHPGLSIGDVAK.K                         |
| 0.99689  | 0.9808 R.FVGHTK[325.13]DVLSVAFSSDNR.Q                      |
| 0.996889 | 0.9888 K.YGK[325.13]IVGC[160.03]SVHK.G                     |
| 0.996887 | 0.997 K.NADPILISLK[325.13]HGYIPGK.N                        |
| 0.996887 | 0.9868 K.LSIYNALKK[325.13]DLLPSDMAVALLEAQAGTGHIIDPATS      |
| 0.996887 | 0.9601 R.DAK[325.13]LDKSQIHDIIVLVGGSTR.I                   |
| 0.996881 | 0.9936 K.AGLQVYNK[325.13]C[160.03]WK.F                     |
| 0.996879 | 0.975 R.EIAQDFK[325.13]TDLR.F                              |
| 0.996876 | 0.9967 K.LITQTFSHHNQLAQK[325.13]TR.R                       |
| 0.996875 | 0.9962 K.TILK[325.13]DATLTALDR.G                           |
| 0.996873 | 0.9877 K.KNNIK[325.13]LYVR.R                               |
| 0.99687  | 0.7947 R.LESGMQNMSIHTK[325.13]TTSYGAGGLSSAYGGTSPGLS        |
| 0.996867 | 0.9775 R.GLVM[147.04]VKPGSIK[325.13]PHQK.V                 |
| 0.996867 | 0.9824 R.VYKAPEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]    |
| 0.996865 | 0.9584 K.DKGEYTLVVK[325.13]WGDEHIPGSPYR.V                  |
| 0.996865 | 0.9971 R.K[325.13]FLPLFDR.V                                |
| 0.996861 | 0.99 R.SPK[325.13]LFYADHPFIFLVR.D                          |
| 0.99686  | 0.9993 R.MDLGEC[160.03]LK[325.13]VHDLALR.A                 |
| 0.996859 | 0.9865 K.QMADTGK[325.13]LNTLLQR.A                          |
| 0.996856 | 0.9642 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                  |
| 0.996855 | 0.9304 R.TMPVEQVFAK[325.13]NFR.V                           |
| 0.996854 | 0.9981 R.TC[160.03]LITFK[325.13]PGAFIPGAPVQPVVLR.Y         |
| 0.996853 | 0.9996 K.SVVQVK[325.13]NFFVNYR.R                           |
| 0.99685  | 0.9934 R.DWVLNEFK[325.13]HGK.A                             |
| 0.996848 | 0.9582 K.TLNNK[325.13]FASFIDK.V                            |
| 0.996846 | 0.9996 R.VVK[325.13]NFEHLNSDFDR.Y                          |
| 0.996843 | 0.9929 R.IVATK[325.13]PLYVALAQR.K                          |
| 0.996843 | 0.9921 R.YGK[325.13]SPYLYPLYGLGELPQGFAR.L                  |
| 0.996839 | 0.9866 K.DGSC[160.03]SVEIPIYEAGTYSLNVTYGGHQVPGSPFK[32]     |
| 0.996829 | 0.9995 R.GLFSANDWQC[160.03]K[325.13]TC[160.03]SNVNWAR      |
| 0.996823 | 0.9938 R.VHLSQK[325.13]YK.R                                |
| 0.996818 | 0.979 K.NQQFHK[325.13]ER.E                                 |
| 0.996817 | 0.9935 R.VIC[160.03]ILSHPIK[325.13]NTNDANSC[160.03]QIIIPQI |
| 0.996816 | 0.9933 R.GC[160.03]RPGK[325.13]IVQMTEAEVR.G                |
| 0.996813 | 0.9996 K.SPFAVC[160.03]K[325.13]HILETSK.V                  |
| 0.996813 | 0.9996 R.EK[325.13]LMHLFTSGDC[160.03]K.A                   |
| 0.996813 | 0.9996 K.VHLSTGELGIIDSAFGQSGK[325.13]FK.I                  |
| 0.996811 | 0.9927 K.AQAK[325.13]VGSLDNVGHLPAGGAVK.T                   |
| 0.996811 | 0.9801 R.NLK[325.13]ASLENSLR.E                             |
| 0.996811 | 0.9985 R.KILDPTGEPAPVLSSPPPADVSTFLAFPSPEK[325.13]LLR.I     |

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| 0.996807 | 0.8414 R.LLLPGELAKHAVSEGK[325.13]AVTK.Y                |
| 0.996804 | 0.9933 R.EANQAINPK[325.13]LLQLVEDR.G                   |
| 0.996803 | 0.7402 R.K[325.13]EVKGDLENAFLNLVQC[160.03]IQNKPLYFADR. |
| 0.996803 | 0.9995 K.IPETYPFNPPK[325.13]VR.F                       |
| 0.996798 | 0.7739 R.FLEQQNK[325.13]ILLAELEQLK.G                   |
| 0.996798 | 0.9995 K.K[325.13]LKQSMWSLLTALSGK.E                    |
| 0.996797 | 0.9942 K.VDLGVLGK[325.13]QQFDLENK.F                    |
| 0.996794 | 0.9966 R.IFSAYIK[325.13]EVEERPAPTPWGSK.M               |
| 0.99679  | 0.9569 K.K[325.13]LGEMWNNTAADDKQPYEK.K                 |
| 0.996786 | 0.9867 R.FLSNGHVTIPGQQDK[325.13]DMFQETMEAMR.I          |
| 0.996784 | 0.983 R.DISEASVFDAYVLPK[325.13]LYVK.L                  |
| 0.996784 | 0.9958 R.K[325.13]KNGPLEVAGAAVSAGHGLPAK.F              |
| 0.996782 | 0.9988 K.VLTPTQVK[325.13]NRPTSISWDGLDSGK.L             |
| 0.996781 | 0.9935 K.EGAK[325.13]HFSGLEEAVYR.N                     |
| 0.996773 | 0.9995 R.YNVPFLT FINK[325.13]LDR.M                     |
| 0.996773 | 0.9995 R.YNVPFLT FINK[325.13]LDR.M                     |
| 0.996773 | 0.5961 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y           |
| 0.996771 | 0.9258 R.TGLYNYDDKEK[325.13]LQIVEMPLAHK.L              |
| 0.99677  | 0.9947 R.VPHSLDLSSPNMANTVNAALK[325.13]PLETLR.I         |
| 0.996769 | 0.9843 R.GC[160.03]TATLGNFAK[325.13]ATFDAISK.T         |
| 0.996765 | 0.9992 K.GGHFYSK[325.13]PEILR.A                        |
| 0.996762 | 0.9867 K.KVEELEGEITTLNHK[325.13]LQDASAEVER.L           |
| 0.996761 | 0.9992 R.AK[325.13]C[160.03]YHNLD AFVR.L               |
| 0.996759 | 0.994 R.IKK[325.13]PEGKPDQK.F                          |
| 0.996757 | 0.9977 R.KYTLPPGVDPTQVSSLSPEGLTVEAPMPK[325.13]LATQ     |
| 0.996754 | 0.9917 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T       |
| 0.996753 | 0.9775 R.LAAFGQLHK[325.13]VLGMDPLPSK.M                 |
| 0.996747 | 0.9906 R.SVPTWLK[325.13]LTSDDVK.E                      |
| 0.996745 | 0.9992 K.HC[160.03]VDPTSFLKPIAK[325.13]LFSVIK.N        |
| 0.996744 | 0.7818 R.LEK[325.13]PAKYDDIKK.V                        |
| 0.996743 | 0.9971 R.HLK[325.13]IVYR.R                             |
| 0.99674  | 0.999 K.ATFNPAQDK[325.13]C[160.03]GIR.L                |
| 0.996738 | 0.9966 K.GILAADESTGSIK[325.13]R.L                      |
| 0.996736 | 0.9549 K.LK[325.13]NKHEAMITDLEER.L                     |
| 0.996726 | 0.9768 K.SNYNFEK[325.13]PFLWLAR.K                      |
| 0.996718 | 0.9972 K.K[325.13]LPIQEFHLSR.I                         |
| 0.996716 | 0.3446 R.KDGNASGTTLLEALDC[160.03]ILPPTRPDK[325.13]PLR. |
| 0.996715 | 0.9946 R.EYSLQVLK[325.13]NAR.A                         |
| 0.996711 | 0.7681 K.KTESHHK[325.13]AK.G                           |
| 0.996703 | 0.985 K.NKYEDEINK[325.13]R.T                           |
| 0.9967   | 0.9851 K.AK[325.13]YHGNVMLLR.A                         |
| 0.996689 | 0.9964 K.LTSMHFYGWK[325.13]QGLK.T                      |
| 0.996688 | 0.5998 R.FLEQQNK[325.13]ILLAELEQLK.G                   |
| 0.996688 | 0.9853 R.IYTTK[325.13]IKPR.L                           |
| 0.996688 | 0.9994 K.VYK[325.13]GHLFGPAPGEQTQAVAIK.T               |
| 0.996686 | 0.9946 K.IGK[325.13]PHTVPC[160.03]K.V                  |
| 0.996684 | 0.981 R.TVPQYK[325.13]YAAGVR.N                         |

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| 0.996684 | 0.9984 K.IK[325.13]EWVDKYDPGALVIPFSGALELK.L             |
| 0.996677 | 0.992 K.LMELHGESSSGK[325.13]ATGDETGAK.V                 |
| 0.996677 | 0.9974 R.TYVGPMTESLFGYHTK[325.13]AR.A                   |
| 0.996676 | 0.9777 K.ETAENYLGH TAK[325.13]NAVITVPAYFNDSQR.Q         |
| 0.996675 | 0.9964 R.LHGGK[325.13]DSASPR.Y                          |
| 0.996668 | 0.9993 K.HANAK[325.13]PFEVPFLK.F                        |
| 0.996667 | 0.9214 K.KAKK[325.13]PAAAAGAK.K                         |
| 0.996666 | 0.3324 K.WGDAGAEYVVESTGVFTTMEK[325.13]AG AHLQGGAK.R     |
| 0.996662 | 0.9678 K.ESYSVYVYK[325.13]VLK.Q                         |
| 0.996661 | 0.9968 K.QDLPNAMNAAEITDK[325.13]LGLHSLR.H               |
| 0.996658 | 0.9993 R.NK[325.13]IADLC[160.03]HTFIK.D                 |
| 0.996654 | 0.9912 R.GLFIIDGK[325.13]GVLR.Q                         |
| 0.996652 | 0.9932 R.SPPNVQFTFQQPK[325.13]PLSVEPQQGPQAGGTTLIHG      |
| 0.996651 | 0.9983 K.SQGK[325.13]VLQATVVAVGSGSK.G                   |
| 0.99665  | 0.9925 R.DHC[160.03]VAHK[325.13]LFNNLK.-                |
| 0.996643 | 0.9994 R.K[325.13]HINTWVAEK.T                           |
| 0.996643 | 0.9848 R.LYSLALHPNAFK[325.13]R.L                        |
| 0.996635 | 0.9438 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK. |
| 0.996634 | 0.9485 K.K[325.13]AKAAAKPK.K                            |
| 0.996633 | 0.9882 K.TC[160.03]SLPGTALK[325.13]VSC[160.03]FNVR.F    |
| 0.996633 | 0.9994 R.KPVAGALDVSFNK[325.13]FIPLSEPAPVPPIPNEQQLAR.L   |
| 0.996632 | 0.9793 R.LDHLAEK[325.13]FR.Q                            |
| 0.996632 | 0.9731 R.RAPFDLFENK[325.13]K.K                          |
| 0.996628 | 0.9996 K.LVSFSK[325.13]LC[160.03]TSYSHSSTR.D            |
| 0.996623 | 0.9992 R.DAFPVAGQK[325.13]LIYAGK.I                      |
| 0.996623 | 0.9993 R.HPDLK[325.13]TDGFGIDTC[160.03]R.S              |
| 0.996618 | 0.9927 R.DHC[160.03]VAHK[325.13]LFNNLK.-                |
| 0.996617 | 0.9925 R.DQLEAAQEAVPPADIVFSVK[325.13]SPPSAGYLVMSR.G     |
| 0.996617 | 0.9981 R.ALSSVGLHMTK[325.13]GLALWEAYR.E                 |
| 0.996611 | 0.9971 K.ISAWHNNVEK[325.13]TLPSTK.A                     |
| 0.99661  | 0.9837 R.ERHPGSFDVVHVK[325.13]DANGNSFATR.L              |
| 0.99661  | 0.9888 R.FELSC[160.03]YSLAPQIK[325.13]VIAPWR.M          |
| 0.996607 | 0.9736 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T            |
| 0.996605 | 0.9981 K.MIQLGK[325.13]TVHYLPILFIDQLSNR.V               |
| 0.996605 | 0.3413 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI   |
| 0.996604 | 0.9342 R.NTDQASMPDNTAAQK[325.13]VSHLLGINVTDFTR.G        |
| 0.996601 | 0.9971 K.K[325.13]LPIQEFHLSR.I                          |
| 0.996597 | 0.9954 K.VGDK[325.13]VLLPEYGGTK.V                       |
| 0.996596 | 0.955 R.SGK[325.13]YDLDFK.S                             |
| 0.996595 | 0.9939 R.TDGK[325.13]VFQFLNAK.C                         |
| 0.996594 | 0.9965 R.RTEITIVK[325.13]PQESAHR.R                      |
| 0.996594 | 0.9992 R.GK[325.13]ASFLYSLPHR.H                         |
| 0.996591 | 0.9747 K.HK[325.13]SDFGK.F                              |
| 0.996591 | 0.4389 R.M[147.04]VNHFIAEFK[325.13]R.K                  |
| 0.996585 | 0.9994 R.NILDFPQHVSPSK[325.13]DIR.T                     |
| 0.99658  | 0.9936 K.MVVESAYEVIK[325.13]LK.G                        |
| 0.99658  | 0.996 K.VDVFREDLC[160.03]TK[325.13]TENLLGSYFPK.K        |

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| 0.99658  | 0.9896 R.SSK[325.13]QHYNCL[160.03]EHSK.I                 |
| 0.99658  | 0.9772 K.TLHPDLGTDK[325.13]DKEQWK.E                      |
| 0.996577 | 0.9855 R.ILDDDTIITLENLK[325.13]R.E                       |
| 0.996575 | 0.9991 R.TTHYTPLAC[160.03]GSNPLK[325.13]R.E              |
| 0.996566 | 0.9932 R.AALLK[325.13]SMLNFK.K                           |
| 0.996566 | 0.9946 R.GIVK[325.13]HLEGLSEEAIM[147.04]ELNLPTGIPIVYELDI |
| 0.996566 | 0.9955 R.KLIK[325.13]DGLIIR.K                            |
| 0.996564 | 0.9844 K.IK[325.13]WGDAGAEYVVESTGVFTTMEK.A               |
| 0.996563 | 0.9857 R.RQVDQLTNDK[325.13]AR.V                          |
| 0.996559 | 0.9974 K.VGAVDADK[325.13]HHSLGGQYGVQGFPTIK.I             |
| 0.996558 | 0.9791 R.AIVDC[160.03]GFEHPSEVQHEC[160.03]IPQAILGMDVLC   |
| 0.996554 | 0.9932 K.FNADEFEDMVAEK[325.13]R.L                        |
| 0.996554 | 0.9995 K.HGDPGDAAQQEAK[325.13]HR.E                       |
| 0.996552 | 0.9995 R.SQNPPQSK[325.13]GC[160.03]C[160.03]FVTFYTR.K    |
| 0.996552 | 0.9995 R.SQNPPQSK[325.13]GC[160.03]C[160.03]FVTFYTR.K    |
| 0.99655  | 0.9941 R.LNTGILNK[325.13]HLQDLMEGLTAK.V                  |
| 0.996545 | 0.9914 K.GALAK[325.13]LVEAIR.T                           |
| 0.996544 | 0.9803 R.RTK[325.13]TEISEMNR.N                           |
| 0.996541 | 0.9992 K.ILLEK[325.13]LMLAQDEER.Q                        |
| 0.996541 | 0.9983 R.ILALEK[325.13]LGAVFNQVAFPLQYTPR.K               |
| 0.996541 | 0.9772 K.NQQFHK[325.13]ER.E                              |
| 0.996541 | 0.9809 R.NRPPLPAGTNSK[325.13]GPPDFSSDEEREPTPVLGSGAAA     |
| 0.996538 | 0.985 R.AVTGYTDPYTGGQISLFQAMQK[325.13]GLIVR.E            |
| 0.996538 | 0.9992 R.SLGLK[325.13]MLQC[160.03]GYSVVFGSR.N            |
| 0.996535 | 0.9818 R.MVQEA EK[325.13]YKAEDEK.Q                       |
| 0.996535 | 0.9995 R.APGAAPSAAAK[325.13]SHR.C                        |
| 0.996535 | 0.9901 R.FQTK[325.13]IPNIYAIGDVVAGPMLAHK.A               |
| 0.996534 | 0.9433 R.GKDHVVSDFFSEHGSLK[325.13]YLHENLPIQR.N           |
| 0.996534 | 0.9993 R.KLK[325.13]ELEVAEGGK.A                          |
| 0.996533 | 0.9961 K.VK[325.13]TDTVLILC[160.03]R.K                   |
| 0.996529 | 0.9952 K.FHNELNAHIK[325.13]LSNLYK.S                      |
| 0.996523 | 0.9963 K.HLSPYATLTVGDSSHK[325.13]TK.T                    |
| 0.996523 | 0.9993 R.YEFSNK[325.13]GADVFLAALR.L                      |
| 0.996522 | 0.9995 R.K[325.13]IIIPPFLAYGEK.G                         |
| 0.996521 | 0.9986 K.NFQNIFFPSATLHLSNIPPSVTVDLKL[325.13]NLFIEAGC[1   |
| 0.99652  | 0.9983 R.K[325.13]FVIPDFMSFTSHIDELYESAK.K                |
| 0.996515 | 0.9978 R.SNDPK[325.13]SQNHPGWLMR.G                       |
| 0.996514 | 0.99 K.TC[160.03]SLPGTALK[325.13]VSC[160.03]FNVR.F       |
| 0.996511 | 0.9957 K.TWK[325.13]FVEGLPINDFSR.E                       |
| 0.996508 | 0.9935 R.HIAMEK[325.13]VASR.T                            |
| 0.996507 | 0.9995 K.ALETNTHVK[325.13]C[160.03]FSLAATR.S             |
| 0.996503 | 0.962 K.K[325.13]C[160.03]GHTNNLRPK.K                    |
| 0.996496 | 0.999 K.TVAGGAWTYNTTSAVTVK[325.13]SAIR.R                 |
| 0.996494 | 0.9971 R.ELTDYLMK[325.13]ILTER.G                         |
| 0.996493 | 0.9994 R.K[325.13]AIHEVFEVGVTSR.S                        |
| 0.996493 | 0.9909 R.LSM[147.04]QK[325.13]SMQNHA AVFR.V              |
| 0.996492 | 0.9991 R.GGIQELIGLIK[325.13]HTK.I                        |

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| 0.996488 | 0.9757 R.LAAFGQLHK[325.13]VLGMDPLPSK.M                  |
| 0.996485 | 0.9773 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                |
| 0.996485 | 0.9936 K.MAILQIMK[325.13]ELNKR.G                        |
| 0.99648  | 0.9667 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.996476 | 0.9993 R.IAAQTLLGTAK[325.13]MLLHEGQHPAQLR.S             |
| 0.996473 | 0.9791 K.GFVLHK[325.13]SK.S                             |
| 0.996472 | 0.9992 K.VWPHK[325.13]DYPLIPVGK.L                       |
| 0.996469 | 0.9746 R.RLYWDDLK[325.13]R.K                            |
| 0.996468 | 0.9171 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I |
| 0.996467 | 0.998 R.VLAKPQNTAEVQK[325.13]VQLTGEPVPMAR.C             |
| 0.996465 | 0.9972 K.K[325.13]PVVNIITPSHVEER.G                      |
| 0.996459 | 0.9974 R.SGYIAIDDIQVLSYPC[160.03]DK[325.13]SPHFLR.L     |
| 0.996458 | 0.9514 R.VLEALLPLK[325.13]GLEER.V                       |
| 0.996458 | 0.9756 K.DLPEHAVLK[325.13]M[147.04]K.G                  |
| 0.996443 | 0.9968 R.RVELSGPK[325.13]AAEPVSR.R                      |
| 0.996438 | 0.998 R.K[325.13]VAQVPLGPEC[160.03]SR.A                 |
| 0.996436 | 0.9948 K.AGLQVYNK[325.13]C[160.03]WK.F                  |
| 0.996435 | 0.8517 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                  |
| 0.996435 | 0.9995 K.AVTHQVK[325.13]FGQQNPR.Q                       |
| 0.996434 | 0.922 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M        |
| 0.996422 | 0.9995 R.MGAHAGK[325.13]HSSP.-                          |
| 0.996419 | 0.5625 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIK    |
| 0.996417 | 0.9928 R.NQSFC[160.03]PTVNLDK[325.13]LWTLVSEQTR.V       |
| 0.996416 | 0.9994 R.VRPDYTAQNLDHGK[325.13]AWGILTFK.G               |
| 0.996416 | 0.9988 R.VYGSFLVNPESGYNVSLLYDLENLPASK[325.13]DSIVHQAC   |
| 0.996416 | 0.9994 R.KTPQGPPEIYSDTQFPSLQSTAK[325.13]HVESR.K         |
| 0.996412 | 0.9994 R.VPLHQVPYAVK[325.13]GC[160.03]FR.F              |
| 0.996404 | 0.9967 R.QNEINNPK[325.13]FNFLNPNDPYHAYR.H               |
| 0.996397 | 0.9989 R.TDLVSPK[325.13]HALMVFR.V                       |
| 0.996393 | 0.9926 K.AGLQVYNK[325.13]C[160.03]WK.F                  |
| 0.996393 | 0.999 R.LQEVIELLSLEK[325.13]QTR.T                       |
| 0.99639  | 0.985 K.AVK[325.13]EEGFPIRPHYFWPLLVGR.R                 |
| 0.996386 | 0.9976 K.DGTVLC[160.03]ELINALYPEGQAPVK[325.13]K.I       |
| 0.996383 | 0.9986 K.YGLFAPVHK[325.13]VTK.I                         |
| 0.996383 | 0.9995 K.HTK[325.13]QSLQVIESAMER.D                      |
| 0.996378 | 0.9984 R.GVMINK[325.13]DVTHPR.M                         |
| 0.996377 | 0.9978 R.LATALQK[325.13]LEEAEK.A                        |
| 0.996375 | 0.9579 K.TLQLLK[325.13]VGEEDDGEYR.C                     |
| 0.996368 | 0.9937 K.SSGEIVYC[160.03]GQVFEK[325.13]SPLR.V           |
| 0.996364 | 0.9954 R.VMTVSFHK[325.13]YGEYFPGTGLR.D                  |
| 0.996353 | 0.9835 K.YSLEPVAVELK[325.13]SLLGK.D                     |
| 0.996351 | 0.9947 R.TGLYNYDDKEK[325.13]LQIVEM[147.04]PLAHK.L       |
| 0.99635  | 0.9995 K.K[325.13]LGALLDSFITISEAAK.E                    |
| 0.996348 | 0.9993 K.NNHSK[325.13]SGTSTLR.L                         |
| 0.996348 | 0.9991 K.K[325.13]GPSGYGFNLHSDK.S                       |
| 0.996347 | 0.9906 R.M[147.04]ATEVAADALGEEWK[325.13]GYVVR.I         |
| 0.996346 | 0.9964 K.ILTFDQLALDSPK[325.13]GC[160.03]GTVLLSGPR.K     |

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| 0.996344 | 0.9987 K.FHPDK[325.13]NKSPQAEEK.F                      |
| 0.996344 | 0.9815 K.K[325.13]SADTLWDIQQ.D                         |
| 0.996344 | 0.973 R.FVPQEM[147.04]GVHTVSVK[325.13]YR.G             |
| 0.996342 | 0.9794 K.KAQLNIGNVLPVGTMPGIVC[160.03]C[160.03]LEEK[3   |
| 0.99634  | 0.969 K.KAASGEAK[325.13]PK.A                           |
| 0.996337 | 0.9972 K.AAIDWFDGK[325.13]EFHGNIK.V                    |
| 0.996336 | 0.9933 R.HVVHK[325.13]WHYK.L                           |
| 0.996336 | 0.977 R.AFDSAVAK[325.13]ALEHHR.S                       |
| 0.996336 | 0.9884 R.KADGYNQPSK[325.13]R.R                         |
| 0.996334 | 0.776 R.ADEARPNTIDFGKDDQHFTVTGLHK[325.13]GTTYIFR.L     |
| 0.996329 | 0.9987 R.K[325.13]C[160.03]VPSVVVGVMGHVPGIEK.N         |
| 0.996325 | 0.9496 K.FINYVK[325.13]NC[160.03]FR.M                  |
| 0.996325 | 0.9992 K.IHMGSC[160.03]AENTAK[325.13]K.L               |
| 0.996323 | 0.9888 K.FTVPMLK[325.13]EAC[160.03]R.A                 |
| 0.996318 | 0.9995 R.LK[325.13]GLGC[160.03]QTLGPHNPTPPSLDMFAEELA   |
| 0.996304 | 0.9723 K.ERQEAEAK[325.13]EALLQASR.D                    |
| 0.996304 | 0.997 R.LLDHMQNTPGFMKY[325.13]NLQC[160.03]LVIDEADR.I   |
| 0.996303 | 0.9988 K.K[325.13]TSFVNFTDIC[160.03]K.L                |
| 0.996301 | 0.995 K.VGDK[325.13]VLLPEYGGTK.V                       |
| 0.996295 | 0.9991 R.VLYAYGYTGEPK[325.13]R.S                       |
| 0.996288 | 0.9965 R.NSVIQK[325.13]SC[160.03]AFAMGHLVR.T           |
| 0.996282 | 0.9461 K.TVDGPSGK[325.13]LWR.D                         |
| 0.996282 | 0.98 R.LSMQK[325.13]SMQNHAHVFR.V                       |
| 0.996281 | 0.9887 R.FK[325.13]EANNFLWPFK.L                        |
| 0.996279 | 0.9995 K.KLLVK[325.13]VDAK.T                           |
| 0.996278 | 0.9995 R.FLILPDMLK[325.13]NAPMLK.S                     |
| 0.996277 | 0.9985 R.TAAQC[160.03]LEHYEFLLDK[325.13]AAQR.D         |
| 0.996267 | 0.9985 R.LC[160.03]HDKETYK[325.13]LQR.R                |
| 0.996267 | 0.9758 K.K[325.13]VNVTVDYIRPASPATETVPAFSE.T            |
| 0.996266 | 0.9826 R.LPVEVAYK[325.13]R.G                           |
| 0.99626  | 0.8854 K.KK[325.13]EVAGAKPHITAAEGK.L                   |
| 0.996259 | 0.9869 K.TC[160.03]SLPGTALK[325.13]VSC[160.03]FNVR.F   |
| 0.996257 | 0.8628 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T              |
| 0.996253 | 0.9943 R.DKEC[160.03]GQLLISENQK[325.13]VAAHHK.C        |
| 0.996249 | 0.9995 R.HK[325.13]IISIFSGTEK.G                        |
| 0.996247 | 0.1398 R.ADIK[325.13]EM[147.04]GLSLQWLYSAR.G           |
| 0.996247 | 0.9287 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I       |
| 0.996244 | 0.9837 K.DWHRPC[160.03]LK[325.13]C[160.03]EK.C         |
| 0.99624  | 0.7609 R.LESGMQNMSIHTK[325.13]TTSGYAGGLSSAYGGLTSPGL    |
| 0.99624  | 0.9992 K.HPVSC[160.03]K[325.13]DTPGFIVNR.L             |
| 0.996233 | 0.9749 K.VIHDNFGIVEGLM[147.04]TTVHAITATQK[325.13]TVDGI |
| 0.996232 | 0.8756 R.GTK[325.13]VILHLK.E                           |
| 0.996223 | 0.9994 R.YFTLGLPTGSTPLGC[160.03]YK[325.13]K.L          |
| 0.996223 | 0.9963 K.LFKPGQEAVK[325.13]YQGPR.D                     |
| 0.996221 | 0.9949 R.NLLQELK[325.13]VIQENEHALQK.D                  |
| 0.996219 | 0.982 K.IPVQLVFK[325.13]NK.I                           |
| 0.996218 | 0.9993 K.YPPGK[325.13]VIEPGC[160.03]VR.V               |

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| 0.996218 | 0.9837 R.VHIPNDDAQFDASHC[160.03]DSDK[325.13]GEFGGFGSV   |
| 0.996216 | 0.993 R.IPLSLDLTHQISK[325.13]DYGVYLED SGHTLR.G          |
| 0.996211 | 0.9887 K.LRVDK[325.13]AAAAAALQAK.S                      |
| 0.996208 | 0.9992 R.AVYIGVHVVPFSK[325.13]ESR.R                     |
| 0.996194 | 0.999 R.SEFYK[325.13]HIVLSGGSTM[147.04]YPGLPSR.L        |
| 0.996184 | 0.933 R.LVNLQHLDLLNNK[325.13]LVTLPVSFAQLK.N             |
| 0.996183 | 0.9924 R.FSTPEQAAK[325.13]NR.I                          |
| 0.996177 | 0.9876 R.NLFNVVDC[160.03]K[325.13]LHWQK.N               |
| 0.996176 | 0.9748 K.GATLK[325.13]ITLDNAYM[147.04]EK.C              |
| 0.996171 | 0.9995 R.EK[325.13]TYSEC[160.03]EDGTYSPEISWHHR.K        |
| 0.996167 | 0.9828 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y             |
| 0.996166 | 0.9994 K.ATC[160.03]IGNNSAAAVSMLK[325.13]QDYK.E         |
| 0.996164 | 0.9941 K.ISDSEGFK[325.13]ANLSLLR.R                      |
| 0.996164 | 0.9854 K.K[325.13]LASQGDSISSQLGPIHPPPR.T                |
| 0.996162 | 0.9992 K.DC[160.03]LHGIEAK[325.13]SYSVGASGSSSR.K        |
| 0.996158 | 0.9994 R.SVVALHNLINNK[325.13]IANR.D                     |
| 0.996157 | 0.992 R.TEK[325.13]LLETIDQLYLEYAK.R                     |
| 0.996155 | 0.9994 R.LGMDLTK[325.13]VVLPTFILER.R                    |
| 0.996154 | 0.9991 R.K[325.13]QHPYTFPGSGTVFAR.N                     |
| 0.996151 | 0.9975 R.MHC[160.03]C[160.03]DEVQPK[325.13]HVK.E        |
| 0.996147 | 0.9837 R.DPYTGQSVSLFQALK[325.13]K.G                     |
| 0.996145 | 0.9965 R.QVRPVTEK[325.13]LPANHPLLTGQR.V                 |
| 0.996141 | 0.8714 K.ANEVISK[325.13]LYAVHQEGNK.N                    |
| 0.996123 | 0.9984 R.VGFQYEGTYK[325.13]WVNPHKL.-                    |
| 0.99612  | 0.9863 R.KHYASEEIK[325.13]EK.L                          |
| 0.996118 | 0.9471 R.DGSIDLVINLPNNNTK[325.13]FVHDNYVIR.R            |
| 0.996109 | 0.909 K.TMQNVK[325.13]HPVTGQFLYQDSNWASK.V               |
| 0.996104 | 0.8477 R.FSGWYDADLSPAGHEEAK[325.13]R.G                  |
| 0.996104 | 0.9914 R.IEPHTGLLLSVQK[325.13]R.S                       |
| 0.996101 | 0.9975 R.C[160.03]VK[325.13]IFQGNVHNFEK.N               |
| 0.99609  | 0.9631 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                |
| 0.996086 | 0.9463 K.EDLYLK[325.13]PIQR.T                           |
| 0.996086 | 0.9557 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H               |
| 0.996086 | 0.9638 K.K[325.13]ISSIQSIVPALEIANAHR.K                  |
| 0.996085 | 0.9601 K.HPK[325.13]NPEVGLKPVWYSPK.V                    |
| 0.996083 | 0.9149 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPM[147. |
| 0.996074 | 0.9995 R.GSIPEFFHIMK[325.13]R.K                         |
| 0.99607  | 0.999 K.ILTAK[325.13]QALSEVTAALR.E                      |
| 0.996069 | 0.8764 R.HNGTGGK[325.13]SIYGEK.F                        |
| 0.996067 | 0.9978 K.VGDMLEK[325.13]AAELLMSC[160.03]FR.V            |
| 0.996066 | 0.9984 R.LAAVQLLQFLAPK[325.13]IR.A                      |
| 0.996066 | 0.9955 K.K[325.13]PRPPPALGPEETSASAGLPK.K                |
| 0.996062 | 0.998 K.SQ GK[325.13]VLQATVVAVGSGSK.G                   |
| 0.996058 | 0.9924 R.K[325.13]RVPDHHPC[160.03].-                    |
| 0.996056 | 0.9894 R.IGK[325.13]PAPDFK.A                            |
| 0.996056 | 0.9993 R.LVK[325.13]DVFISAAER.D                         |
| 0.99605  | 0.9793 R.KIFVGTK[325.13]GIPHLVTHDAR.T                   |

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| 0.996048 | 0.9942 R.TDFKEEPEPGFK[325.13]R.L                          |
| 0.996042 | 0.9489 R.IMK[325.13]AQALR.D                               |
| 0.996041 | 0.2239 K.VIHDNFGIVEGLMTTVHAITATQK[325.13]TVDGPGSGK.L      |
| 0.996039 | 0.9918 K.ALSTDPAAPNLK[325.13]SQLAAAR.A                    |
| 0.996038 | 0.9992 K.K[325.13]TMLHLTDIQLQDNK.T                        |
| 0.996038 | 0.9825 K.GNK[325.13]PWISLPR.G                             |
| 0.996036 | 0.996 R.IIGVK[325.13]VHPGQR.K                             |
| 0.996034 | 0.7487 K.SPAKPK[325.13]AVKPK.A                            |
| 0.996023 | 0.9988 R.AAALK[325.13]LGQELC[160.03]GMLHRPR.H             |
| 0.996023 | 0.9741 R.VTQK[325.13]SYKVSTSGPR.A                         |
| 0.996019 | 0.9995 R.AYTSETYLMK[325.13]HMR.K                          |
| 0.996019 | 0.9995 R.LGLSTLGELK[325.13]QNLSR.S                        |
| 0.996019 | 0.9995 R.ILTMDGLIEDIK[325.13]HR.R                         |
| 0.996009 | 0.9991 K.KIK[325.13]LQVWDTAGQER.F                         |
| 0.996001 | 0.9797 R.KAMK[325.13]GLGTDEESILTLLTSR.S                   |
| 0.995991 | 0.9993 K.GSVAIWSGK[325.13]PPIC[160.03]EK.V                |
| 0.995987 | 0.9452 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L             |
| 0.995986 | 0.9975 R.FDSKDEILLTLEK[325.13]HGGIC[160.03]DC[160.03]QTSI |
| 0.995985 | 0.975 R.TIAQDYGVLK[325.13]ADEGISFR.G                      |
| 0.995972 | 0.9922 R.GLDIPEVDLVIQSSPPK[325.13]DVESYIHR.S              |
| 0.995972 | 0.9992 K.HC[160.03]ILDVSGNAIK[325.13]R.L                  |
| 0.995971 | 0.9927 K.GGQK[325.13]ISPDTVLHLILPESPGSHEESR.E             |
| 0.995965 | 0.9903 R.K[325.13]MGVPYC[160.03]IHK.G                     |
| 0.995961 | 0.8129 K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V    |
| 0.99596  | 0.9979 R.IVGC[160.03]IC[160.03]EEDNTSVVFWFLHK[325.13]GE   |
| 0.99596  | 0.9898 K.SC[160.03]GK[325.13]DGFHIR.V                     |
| 0.995956 | 0.9981 K.AK[325.13]DQTKAQAAAPASVPAQAPK.R                  |
| 0.995954 | 0.9719 R.SSGPYGGGGQYFAK[325.13]PR.N                       |
| 0.995953 | 0.9964 K.LKTK[325.13]DEPQR.E                              |
| 0.995951 | 0.9682 R.MPK[325.13]VQQTVDLFR.A                           |
| 0.995951 | 0.9991 R.K[325.13]DHPFGFVAVPTK.N                          |
| 0.995947 | 0.9993 R.VGTHGGTLSSYIVK[325.13]NIALDK.T                   |
| 0.995942 | 0.974 R.YVEPIEDVPC[160.03]GNIVGLVGVDQFLVK[325.13]TGTI     |
| 0.99594  | 0.5506 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E                  |
| 0.99594  | 0.9991 K.AYPLADAHLTK[325.13]K.L                           |
| 0.995939 | 0.9929 K.IAAK[325.13]HYQFASGAFLHIK.E                      |
| 0.995936 | 0.9647 R.K[325.13]LAVNM[147.04]VPFPR.L                    |
| 0.995933 | 0.975 R.KQLATK[325.13]AAR.K                               |
| 0.995928 | 0.9829 R.NTTIPTK[325.13]QTQTFTTYSNQPVGVLIVYEGER.A         |
| 0.995928 | 0.9828 K.GEHVPGFC[160.03]LPK[325.13]K.G                   |
| 0.995927 | 0.9616 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                  |
| 0.995927 | 0.9816 K.GIYQSLEGAVQAGQLK[325.13]VPPGYHPLDVEK.E           |
| 0.995923 | 0.9988 K.SESGDWHC[160.03]TASWK[325.13]THSGSVWR.V          |
| 0.995918 | 0.9918 R.NQSFC[160.03]PTVNLDK[325.13]LWTLVSEQTR.V         |
| 0.995904 | 0.9909 K.AK[325.13]QFLPFLQR.A                             |
| 0.995899 | 0.999 R.NPQQQESLK[325.13]HATR.I                           |
| 0.995895 | 0.9789 R.LIFAGK[325.13]QLEDGR.T                           |



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| 0.995884 | 0.9916 R.VIC[160.03]ILSHPIK[325.13]NTNDANSC[160.03]QIIIPQI |
| 0.995871 | 0.9991 K.HVK[325.13]EAFR.L                                 |
| 0.995869 | 0.999 K.LSAAIVLK[325.13]NHHSR.L                            |
| 0.995869 | 0.9908 K.DLDFEK[325.13]AKPR.M                              |
| 0.995869 | 0.9964 K.TFNQVEIK[325.13]PEMIGHYLGEFSITYKPVK.H             |
| 0.995868 | 0.9975 R.VC[160.03]EGPK[325.13]AVAAPRPDR.L                 |
| 0.99586  | 0.6171 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M          |
| 0.995857 | 0.9919 R.YC[160.03]KNK[325.13]PYPK.S                       |
| 0.995857 | 0.998 K.IK[325.13]EWVDKYDPGALVIPFSGALELK.L                 |
| 0.995848 | 0.2052 R.DALSDLALHFLNK[325.13]MK.I                         |
| 0.995846 | 0.9929 K.EYGFC[160.03]IMDNHK[325.13]ER.I                   |
| 0.995843 | 0.9796 K.GYEK[325.13]KPYC[160.03]NAHYPK.Q                  |
| 0.995843 | 0.9692 R.K[325.13]LTWVNEGLVDGWDDPRFPTVR.G                  |
| 0.995838 | 0.9992 R.K[325.13]YAVLYQPLFDKR.F                           |
| 0.99583  | 0.9921 K.NPNGPYPYTLK[325.13]LC[160.03]FSTAQHAS.-           |
| 0.995826 | 0.979 R.GLVMVKPGSIK[325.13]PHQK.V                          |
| 0.995826 | 0.9905 R.TAK[325.13]LWALPQC[160.03]QLLGVFSGHR.R            |
| 0.995817 | 0.999 R.RNPEMLK[325.13]QWEYC[160.03]GQPK.V                 |
| 0.995815 | 0.9991 R.FK[325.13]MADKDGDLIATK.E                          |
| 0.995812 | 0.4774 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR        |
| 0.995812 | 0.9919 K.FYGDEEKDK[325.13]GLQTSQDAR.F                      |
| 0.995808 | 0.9974 R.M[147.04]GVVEC[160.03]AK[325.13]HELLQPFNVLYEK.    |
| 0.995807 | 0.9957 R.SLFSSIGEVESEAK[325.13]LIR.D                       |
| 0.995807 | 0.9764 R.LLMTEVAWTK[325.13]DELKEALDDVTLPR.L                |
| 0.995806 | 0.9989 R.LNTDPMLLQFFK[325.13]SQGYR.D                       |
| 0.995799 | 0.7814 K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V     |
| 0.995799 | 0.9993 R.KDPGVPNSAPFK[325.13]EALLR.E                       |
| 0.99579  | 0.9927 R.HDGK[325.13]LWNLNNYR.T                            |
| 0.995789 | 0.9859 R.AITIAGVPQSVTEC[160.03]VK[325.13]QIC[160.03]LVML   |
| 0.995781 | 0.9994 K.VPLK[325.13]C[160.03]LAQEVNIPDWIVDLR.H            |
| 0.995774 | 0.9638 K.IYK[325.13]IGQGYLIK.D                             |
| 0.995771 | 0.981 K.VTRK[325.13]DGNASGTTLEALDC[160.03]ILPPTRPDTKI      |
| 0.995768 | 0.8605 R.KVDWLTEK[325.13]MHAR.D                            |
| 0.995764 | 0.9736 K.HKPGGGDVK[325.13]IESQK.L                          |
| 0.995764 | 0.9762 R.IYC[160.03]KPHFNQLFK[325.13]SK.G                  |
| 0.995757 | 0.7922 R.TLSDYNIQK[325.13]ESTLHLVLR.L                      |
| 0.995756 | 0.4685 R.HQGVM[147.04]VGMGQK[325.13]DSYVGDEAQSQR.G         |
| 0.995754 | 0.9868 K.NLYIISVK[325.13]GIK.G                             |
| 0.995749 | 0.9973 R.ELFVQSEIFPLETPAFAIK[325.13]EQGFR.A                |
| 0.99574  | 0.9955 K.LITQTFSHHNQLAQK[325.13]TR.R                       |
| 0.995737 | 0.5005 R.DLTDYLM[147.04]K[325.13]ILTER.G                   |
| 0.995734 | 0.9925 R.AIEALKEFNEDGALAVLQQFK[325.13]DSDLSHVQNK.S         |
| 0.995732 | 0.9974 R.SSPK[325.13]ALNFGGIGVVVGHETHAFDDQGR.E             |
| 0.995728 | 0.9845 K.VMSQNFTNC[160.03]HTK[325.13]IR.H                  |
| 0.995726 | 0.9777 R.RK[325.13]QEELQQLEQQR.R                           |
| 0.995716 | 0.4714 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR        |
| 0.995716 | 0.8829 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S     |

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| 0.995715 | 0.9819 K.YTPVQQGPVGVNVTYGGDPIPK[325.13]SPFSVAVSPSLDL    |
| 0.99571  | 0.9991 K.GTDYQLSK[325.13]EYTLDVYR.L                     |
| 0.995699 | 0.5486 R.ELPAQK[325.13]WWHTGALYR.I                      |
| 0.995697 | 0.9993 K.K[325.13]KDTAASGYGTQNR.L                       |
| 0.995696 | 0.9866 K.SMTEAEQQQLIDDHFLFDK[325.13]PVSPLLASGMAR.D      |
| 0.995696 | 0.9713 R.KFGEAIGMGFPVK[325.13]VPYR.K                    |
| 0.995694 | 0.7211 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V          |
| 0.995688 | 0.9978 K.K[325.13]C[160.03]HIAVGSPGR.I                  |
| 0.995684 | 0.9766 R.DVQNTFYDIVAELGAMEHAQAVDYIK[325.13]K.L          |
| 0.995676 | 0.9968 R.FLNK[325.13]QAPQTIHLPSGEILDVFDAAER.Y           |
| 0.995674 | 0.9922 K.IK[325.13]AIPQLQGYLR.S                         |
| 0.995673 | 0.9976 R.TGC[160.03]IGAK[325.13]HR.I                    |
| 0.995672 | 0.9932 K.LNNC[160.03]GMGIGGGK[325.13]ILAAALTEC[160.03]F |
| 0.995668 | 0.3971 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S        |
| 0.995667 | 0.9817 R.IIGLDQVAGMSETALPGAFK[325.13]TR.K               |
| 0.995667 | 0.9968 R.LNELLVK[325.13]ALER.H                          |
| 0.995667 | 0.9985 K.K[325.13]QVAPEKPVKK.Q                          |
| 0.995666 | 0.9987 R.ELSGTIK[325.13]EILGTAQSVGC[160.03]NVDGR.H      |
| 0.995666 | 0.9986 R.K[325.13]YGTC[160.03]PHGGYGLGLER.F             |
| 0.995659 | 0.9904 K.IQASTMAFK[325.13]QMEQISQFLQAAER.Y              |
| 0.995657 | 0.9703 K.FETLQAQAGK[325.13]HGDDL.R.N                    |
| 0.995652 | 0.9959 K.VLDFHNLDPGITK[325.13]TTGFC[160.03]ATR.R        |
| 0.995651 | 0.9532 K.KPAAATVTK[325.13]K.V                           |
| 0.995645 | 0.9991 K.TDFFWK[325.13]DIVAAIQHNYK.M                    |
| 0.995643 | 0.9864 K.YLAIAPPIK[325.13]QSTIVC[160.03]HNR.V           |
| 0.995639 | 0.9829 K.SK[325.13]IAHLAGVK.D                           |
| 0.995632 | 0.7468 K.KEDLYLK[325.13]PIQR.T                          |
| 0.995631 | 0.8957 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.995619 | 0.9407 R.LSAEAEK[325.13]VLALPEPSPAAPTLR.S               |
| 0.995615 | 0.1964 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK      |
| 0.995615 | 0.8612 R.ETAQAIK[325.13]GMHIR.K                         |
| 0.995614 | 0.9824 K.YDYNSGEELESYK[325.13]GHFGPIHC[160.03]VR.F      |
| 0.995606 | 0.992 R.LVEC[160.03]GSLFK[325.13]GIC[160.03]ALR.A       |
| 0.995601 | 0.998 K.LLSATGESEK[325.13]QFQEAIIVFQEEFK.C              |
| 0.995597 | 0.9914 K.LLQPPAPIMPLDTNWPLLTVSK[325.13]GFFEGTIASK.G     |
| 0.995596 | 0.9909 R.TDRGDSIGETPTPGASK[325.13]R.K                   |
| 0.995596 | 0.9886 K.HLK[325.13]ALTSELANAR.D                        |
| 0.995589 | 0.9807 R.EK[325.13]LQEEMLQR.E                           |
| 0.995585 | 0.9981 R.ELVGHK[325.13]VNLQMVYDSPLC[160.03]R.L          |
| 0.995582 | 0.9953 R.NGNPAPK[325.13]ITWYR.N                         |
| 0.995576 | 0.8361 R.GLDISNVK[325.13]HVINFDLPSDIEEYVHR.I            |
| 0.995569 | 0.9976 R.ELVHK[325.13]ANPIR.K                           |
| 0.995567 | 0.999 K.KIK[325.13]LQVWDTAGQER.F                        |
| 0.995567 | 0.9695 R.LGGHGPSFPLK[325.13]GITEQQK.E                   |
| 0.995566 | 0.9743 K.ALKPPPIK[325.13]LYR.E                          |
| 0.995562 | 0.9957 K.SM[147.04]TEAEQQQLIDDHFLFDK[325.13]PVSPLLASC   |
| 0.995561 | 0.9991 R.AK[325.13]SDLLGKPLGPR.T                        |

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| 0.995557 | 0.998 R.GVVHK[325.13]SLPPR.T                          |
| 0.995554 | 0.9911 R.VMEHFIK[325.13]LYK.K                         |
| 0.995553 | 0.7907 R.LLLPGELAKHAVSEGTK[325.13]AVTK.Y              |
| 0.995549 | 0.9924 K.ALAGC[160.03]DFLTISPK[325.13]LLGELLQDNAK.L   |
| 0.995547 | 0.9709 R.ALSTGEK[325.13]GFGYK.G                       |
| 0.995544 | 0.9933 K.FPHSAHQK[325.13]YVR.Q                        |
| 0.995542 | 0.991 K.VPTTEK[325.13]PTVTVNFR.K                      |
| 0.995538 | 0.9994 R.LQDQGPSWASGDSSNNHK[325.13]PR.E               |
| 0.995537 | 0.9994 R.NAIFHLLK[325.13]NFLR.L                       |
| 0.995537 | 0.9994 R.TITK[325.13]QVPNESFFNFFNPLK.A                |
| 0.995537 | 0.9994 R.SLK[325.13]AYGELPEHAK.I                      |
| 0.995537 | 0.9994 R.SLK[325.13]AYGELPEHAK.I                      |
| 0.995537 | 0.9994 R.ETQAQPPDGDHSPGNHEQSYVGK[325.13]R.S           |
| 0.995537 | 0.9994 R.KYDK[325.13]AWLLSMIQSK.C                     |
| 0.995536 | 0.7272 R.VHIQSSQTVESGLYTLQSILK[325.13]AQLVK.E         |
| 0.995536 | 0.9994 R.SVIRPPFK[325.13]K.F                          |
| 0.995532 | 0.9391 K.VQQLVPK[325.13]RDHALLEEQSK.Q                 |
| 0.995532 | 0.9953 K.ADDGRFPQVIK[325.13]SK.G                      |
| 0.995531 | 0.9986 R.YGGQPLFSEK[325.13]FPTLWSGAR.S                |
| 0.995531 | 0.9456 R.TPHVQAVQGPLGSPPK[325.13]R.G                  |
| 0.99553  | 0.9973 R.SK[325.13]SYSFHQSQHR.K                       |
| 0.99553  | 0.9993 R.MTLAHIK[325.13]DQK.E                         |
| 0.995529 | 0.995 R.AK[325.13]LWC[160.03]STTADYDRDHEWGF[160.03]F  |
| 0.995528 | 0.9991 R.HGK[325.13]NC[160.03]TAGAVYTYHEK.K           |
| 0.995527 | 0.9874 R.K[325.13]LTWVNEGLVDGWDDPR.F                  |
| 0.995527 | 0.9905 R.M[147.04]HAPGK[325.13]GLSQSALPYR.R           |
| 0.995525 | 0.9992 R.HGLQSLGK[325.13]VGISR.R                      |
| 0.995516 | 0.9887 K.HELQANC[160.03]YEEVK[325.13]DR.C             |
| 0.995515 | 0.9993 R.IFDANTKPNLNLQVLSNPEFLAEGTAIKDLK[325.13]NPDR. |
| 0.9955   | 0.9912 R.HVVHK[325.13]WHYK.L                          |
| 0.995499 | 0.9356 K.SK[325.13]DDQVTIGAGVTLHEALAAELLK.K           |
| 0.995498 | 0.9991 K.FTRPLFK[325.13]DLAAFDK.S                     |
| 0.995498 | 0.9993 R.YGHSLALYK[325.13]DK.I                        |
| 0.995498 | 0.9993 R.DAK[325.13]HTNFVEFR.N                        |
| 0.995496 | 0.9682 K.NK[325.13]ITITNDQNR.L                        |
| 0.995495 | 0.9914 R.NPYYGGESASITPLEDLYK[325.13]R.F               |
| 0.995495 | 0.9992 K.LYQHEINLFK[325.13]SK.T                       |
| 0.995493 | 0.9994 K.VLMEK[325.13]ELPGFLQSGK.D                    |
| 0.995491 | 0.9993 R.ESK[325.13]MEHLAQLR.K                        |
| 0.99549  | 0.9992 K.MAIQTQQSK[325.13]FVNWQVDGEYR.G               |
| 0.995487 | 0.9968 R.NALQQENHIIDGVK[325.13]VQVHTR.R               |
| 0.995487 | 0.9993 K.VHFFNSFFYDK[325.13]LR.T                      |
| 0.995478 | 0.9822 R.NFGTK[325.13]ISAR.A                          |
| 0.995478 | 0.9989 R.HFEATDILVSK[325.13]ISR.Q                     |
| 0.995468 | 0.9994 K.K[325.13]DNVAGVTLPVFEHYHEGTDSYELTGLAR.G      |
| 0.995463 | 0.9796 R.EVGEHLVSIK[325.13]K.N                        |
| 0.995461 | 0.993 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT |

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| 0.995455 | 0.9795 K.ALAAAGYDVEK[325.13]NNSR.I                     |
| 0.995452 | 0.9951 R.YHPDK[325.13]NKEPGAEEK.F                      |
| 0.995451 | 0.9808 R.VRTELADK[325.13]VTK.L                         |
| 0.995443 | 0.9977 K.AQAAAPASVPAQAPK[325.13]R.T                    |
| 0.995443 | 0.9937 K.IVK[325.13]PGMKLTELYNAYVETQDQLLEK.L           |
| 0.995444 | 0.9662 R.YALYDATYETK[325.13]ESK.K                      |
| 0.995444 | 0.7572 R.NRPLSDEELDAMFPEGYK[325.13]VLPPPAGYVPIR.T      |
| 0.995439 | 0.9992 R.IGIFGQDEDVTSK[325.13]AFTGR.E                  |
| 0.995438 | 0.9591 R.KESYSVYVYK[325.13]VLK.Q                       |
| 0.995437 | 0.9992 R.K[325.13]SFTPDHVYAR.S                         |
| 0.995437 | 0.9927 R.K[325.13]VC[160.03]GDSDKGFVVINQK.G            |
| 0.995432 | 0.9903 R.M[147.04]HAPGK[325.13]GLSQSALPYR.R            |
| 0.995429 | 0.9903 R.GAGM[147.04]PGQHGQITQQELDTVVK[325.13]TQHEIL   |
| 0.995429 | 0.9948 K.FLVQNIHTLAELK[325.13]MTGNC[160.03]LK.G        |
| 0.995428 | 0.0887 R.LLLPGELAK[325.13]HAVSEGK.A                    |
| 0.995426 | 0.9975 K.IVEIPFNSTNK[325.13]YQLSIHK.N                  |
| 0.995425 | 0.9915 K.KVQSDGQIVLVDDWIK[325.13]LQISHEAAAC[160.03]ITC |
| 0.995422 | 0.9857 K.SLKDEDVLQK[325.13]LPVGTATLYFR.D               |
| 0.995419 | 0.974 K.VMTK[325.13]DGQWFTDWDAPHSR.H                   |
| 0.995409 | 0.9332 R.AALQEELQLC[160.03]K[325.13]GLVQALQTK.V        |
| 0.995405 | 0.8625 R.KVDWLTEK[325.13]MHAR.D                        |
| 0.995398 | 0.9937 K.LMNESLMLVTALNPHIGYDK[325.13]AAK.I             |
| 0.995393 | 0.3482 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T               |
| 0.995392 | 0.9991 K.K[325.13]VLAQYYTVTDEHHR.S                     |
| 0.995391 | 0.9951 K.AMK[325.13]GLGTDEDTIIDIITHR.S                 |
| 0.995387 | 0.979 R.AQDGDFFFSK[325.13]EHTDTFNFR.I                  |
| 0.995382 | 0.998 R.KLTALDYHNPAGFNC[160.03]K[325.13]DETEFR.N       |
| 0.995378 | 0.9715 R.YQK[325.13]STELLIR.K                          |
| 0.995374 | 0.9683 K.DLPEHAVLK[325.13]M[147.04]K.G                 |
| 0.995373 | 0.9372 K.LGLK[325.13]SLVSK.G                           |
| 0.995369 | 0.8654 R.LREK[325.13]LQEEMLQR.E                        |
| 0.995367 | 0.9964 R.AK[325.13]LNWLSVDFNNWK.D                      |
| 0.995367 | 0.9844 R.K[325.13]AHLTNQYM[147.04]QR.V                 |
| 0.995355 | 0.9556 K.NSSYFVEWIPNNVK[325.13]TAVC[160.03]DIPPR.G     |
| 0.995352 | 0.9727 K.FFGNLMDASK[325.13]LSLC[160.03]GEESFGTGSDBIR.E |
| 0.995353 | 0.3986 R.DLTDYLMK[325.13]ILTER.G                       |
| 0.995349 | 0.9993 R.LFYGVK[325.13]AGPGVGAPR.R                     |
| 0.995341 | 0.9983 K.EK[325.13]QQHIEQLLAER.D                       |
| 0.995338 | 0.9994 R.NK[325.13]VLNHFSIMQQR.R                       |
| 0.995336 | 0.2514 K.WGDAGAERYVVESTGVFTTMEK[325.13]AGAHLQGGAK.R    |
| 0.995332 | 0.9971 R.GVEVDPSLIK[325.13]DTWHQVYR.R                  |
| 0.995333 | 0.9544 R.AIPC[160.03]IK[325.13]GYDVIAQAQSGTGK.T        |
| 0.995327 | 0.9255 K.VGINYQPPTVVPGGDLAK[325.13]VQR.A               |
| 0.995315 | 0.9916 R.VMDQHK[325.13]LTR.D                           |
| 0.995314 | 0.969 K.NLQYYDISAK[325.13]SNYNFEKPFLWLAR.K             |
| 0.995301 | 0.9698 K.LYEEK[325.13]TGNAWHSK.N                       |
| 0.995296 | 0.9956 R.VTASDRDK[325.13]GSNAVHVHYSIMSGNAR.G           |

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| 0.995294 | 0.9678 R.ALSTGEK[325.13]GFGYK.G                        |
| 0.995293 | 0.9994 R.K[325.13]GLPPSHTQYDFVELLDGSR.L                |
| 0.995291 | 0.9403 R.K[325.13]VDSKSLFHYR.Q                         |
| 0.995288 | 0.9965 R.SIQGHHVC[160.03]LLVK[325.13]K.G               |
| 0.995288 | 0.9901 R.TDAVLPLTVAEVQK[325.13]LLGPHVEGLK.A            |
| 0.995281 | 0.9705 R.TADGIVSHLK[325.13]K.Q                         |
| 0.995276 | 0.4458 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR    |
| 0.99527  | 0.9925 K.QHYIDLK[325.13]DRPFFPGLVK.Y                   |
| 0.995266 | 0.853 R.HNGTGGK[325.13]SIYGEK.F                        |
| 0.995264 | 0.9902 K.TFHHVYSGK[325.13]DLIAQAR.T                    |
| 0.995264 | 0.9848 K.EVDEQMLNVQNK[325.13]NSSYFVEWIPNNVK.T          |
| 0.995257 | 0.9907 K.K[325.13]LIYFQLHR.A                           |
| 0.995252 | 0.9946 R.IFSAYIK[325.13]EVEERPAPTPWGSK.M               |
| 0.995249 | 0.9895 R.THQK[325.13]FVIATSTK.I                        |
| 0.995245 | 0.907 K.LLGK[325.13]VTIAQGGVLPNIQAVLLPK.K              |
| 0.995236 | 0.971 R.TK[325.13]IDC[160.03]DNLEQYFIQQGGGPDKK.G       |
| 0.995234 | 0.9799 R.MIK[325.13]LGLGIDEDEVAEEPNAAVPDEIPPLEGDEDA    |
| 0.995234 | 0.9867 K.ENDAVTIQVLNQLIQK[325.13]IR.E                  |
| 0.99523  | 0.9584 K.DIEK[325.13]AC[160.03]QSIYPLHDVFVR.K          |
| 0.995226 | 0.9994 K.VTAHWHK[325.13]GTTLMIK.F                      |
| 0.995226 | 0.9905 R.FSTPEQAAK[325.13]NR.I                         |
| 0.995226 | 0.9994 K.DVPDWK[325.13]VGESVFHTTR.W                    |
| 0.995226 | 0.9994 R.TGVVTDGVK[325.13]HSMNPFC[160.03]EIAVEEAVR.L   |
| 0.995226 | 0.9994 R.LLFGIAQPQLPPK[325.13]C[160.03]LLSGPTSEGLMTWEL |
| 0.995226 | 0.9994 K.EPSEVPTPK[325.13]RPR.G                        |
| 0.995226 | 0.9994 R.LSGPLK[325.13]EQYAEHGLNFQR.L                  |
| 0.995226 | 0.9994 R.FFHSNQK[325.13]DTSEYIIQAYK.Y                  |
| 0.995226 | 0.9994 R.SHASK[325.13]SHGSGGGGGGGGGGGGNR.K             |
| 0.995225 | 0.9992 K.RPNK[325.13]PLFTALVTQC[160.03]QK.M            |
| 0.995222 | 0.9982 R.DTGVMVK[325.13]LYPNMTAVLLHNTQLDQR.K           |
| 0.995219 | 0.9992 K.YPHYFPLLK[325.13]K.C                          |
| 0.995215 | 0.9257 K.AGAHLQGGAK[325.13]R.V                         |
| 0.99521  | 0.972 K.IGKPHTVPC[160.03]K[325.13]VTGR.C               |
| 0.995197 | 0.9978 R.K[325.13]FVIPDFMSFTSHIDELYESAK.K              |
| 0.995188 | 0.9179 R.TYTWLK[325.13]GHQK.S                          |
| 0.995188 | 0.9347 R.IWDTLQK[325.13]LGAVYDVSHYNALLK.V              |
| 0.995186 | 0.9993 R.LAAEVTK[325.13]LVHGR.E                        |
| 0.995185 | 0.9347 K.NVK[325.13]LTVSNVLK.E                         |
| 0.995185 | 0.9797 R.DHASNIYK[325.13]VEGGC[160.03]ITK.L            |
| 0.995182 | 0.995 R.VVVK[325.13]AVDPTSGQLYGLAR.E                   |
| 0.995182 | 0.0877 K.VK[325.13]DALEFWLQAGVDGFQVR.D                 |
| 0.995173 | 0.4402 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR    |
| 0.995171 | 0.999 K.WC[160.03]TVTK[325.13]C[160.03]AGGHDDATLAR.L   |
| 0.995171 | 0.9782 K.MSPYK[325.13]DILETHLR.E                       |
| 0.995169 | 0.9245 R.VFSGLVSTGLK[325.13]VR.I                       |
| 0.995162 | 0.9992 R.K[325.13]IHIDLPEQAR.L                         |
| 0.995159 | 0.9981 R.VIPVK[325.13]LGIIGVVNR.S                      |

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| 0.995144 | 0.9757 R.K[325.13]QVVNIPSFIVR.L                        |
| 0.995143 | 0.9978 K.YEK[325.13]PDGSPVFIAFR.S                      |
| 0.995142 | 0.9915 K.FGK[325.13]GGQAGR.C                           |
| 0.995138 | 0.9739 K.IGQGYLIK[325.13]DGK.L                         |
| 0.995137 | 0.857 K.AGAHLQGGAK[325.13]R.V                          |
| 0.995135 | 0.9969 R.LNK[325.13]C[160.03]GVISPR.F                  |
| 0.995133 | 0.9975 K.FIEEHATK[325.13]LSR.T                         |
| 0.99513  | 0.9609 K.KQPHGGQK[325.13]PSYSGYQSHQGGQQSYNQSPYSI       |
| 0.995123 | 0.9949 K.AAFHK[325.13]SIR.S                            |
| 0.995122 | 0.9746 R.VYLFTIKK[325.13]GILGQHQFLEGPEGIENTR.F         |
| 0.995114 | 0.9969 R.HISSK[325.13]VEELSQUALSQK.E                   |
| 0.99511  | 0.9988 K.WPGDILAYK[325.13]EHLK.S                       |
| 0.995109 | 0.9992 R.VPLHK[325.13]PTDWQK.K                         |
| 0.995109 | 0.9688 R.HVM[147.04]QPYYK[325.13]DILPC[160.03]LDGYLK.T |
| 0.995106 | 0.9399 K.FSK[325.13]SATSPEGK.K                         |
| 0.995101 | 0.8918 K.GFGYK[325.13]GSC[160.03]FHR.I                 |
| 0.995101 | 0.9944 K.LISQK[325.13]AFFAK.M                          |
| 0.995095 | 0.9588 K.TAIGK[325.13]AGYTDK.V                         |
| 0.99509  | 0.996 K.NPILWNVADVVIK[325.13]FPEEEAPSTVLSQNLFTP.K      |
| 0.995086 | 0.9804 R.GYWGNK[325.13]IGKPHTVPC[160.03]K.V            |
| 0.995085 | 0.9804 R.NDLMEYAK[325.13]QHGIPIVTPK.N                  |
| 0.995084 | 0.9981 K.YK[325.13]YGYEIPVDM[147.04]LC[160.03]K.R      |
| 0.995082 | 0.9929 R.IVSRPEELREDDVGTGAGLLEIK[325.13]K.I            |
| 0.995081 | 0.9971 K.SLPK[325.13]GPFTYISPSNTELTLMIQER.G            |
| 0.995069 | 0.9994 R.K[325.13]FLDTSHYSTAGSSSVR.E                   |
| 0.995066 | 0.9867 R.FNVLK[325.13]VTK.A                            |
| 0.995066 | 0.9792 K.LNEINEK[325.13]IAPSFIVESIEDALK.A              |
| 0.99506  | 0.9949 R.VAHFLEK[325.13]QGFK.Q                         |
| 0.995058 | 0.999 K.IMGK[325.13]ILDQGEDFPASEMTR.I                  |
| 0.995049 | 0.9963 R.VLTVINQTQK[325.13]ENLR.K                      |
| 0.995045 | 0.9938 K.K[325.13]AADHLKPFLDDSTLR.F                    |
| 0.995043 | 0.9977 R.K[325.13]WC[160.03]ELIPGAEFR.C                |
| 0.99504  | 0.9741 R.LSNIFVIGK[325.13]GNKPWISLPR.G                 |
| 0.995038 | 0.9969 R.IAAK[325.13]FITHAPPGEFNEVFNDVR.L              |
| 0.995035 | 0.9979 R.SLENYHFVDEHGK[325.13]DQGINIR.Q                |
| 0.995035 | 0.9447 R.AGK[325.13]ITFAEK.V                           |
| 0.995031 | 0.6535 R.VTGALQFGELQK[325.13]QGAGGVEGAEWWTQAFHQF       |
| 0.99503  | 0.9992 R.FALPTAHHTLGLPVGK[325.13]HIYLSTR.I             |
| 0.995027 | 0.9834 K.MIYASSK[325.13]DAIKK.K                        |
| 0.995026 | 0.9991 R.AK[325.13]AQELIQATNQILSHR.K                   |
| 0.995025 | 0.9756 K.SHLAK[325.13]EGLYQYK.N                        |
| 0.995022 | 0.933 R.TAVDSGIPLLTNFQVTK[325.13]LFAEAVQK.S            |
| 0.995018 | 0.9899 R.KGVAINMVTEDK[325.13]R.T                       |
| 0.995017 | 0.9914 R.SYSK[325.13]LLC[160.03]GLLAER.L               |
| 0.995016 | 0.9978 R.VLFLIPK[325.13]NNPPTLVGDFTK.S                 |
| 0.995008 | 0.9914 K.K[325.13]YRPLFDYFLK.C                         |
| 0.995008 | 0.9801 R.VKVEPSHDASK[325.13]VK.A                       |

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| 0.995003 | 0.988 K.K[325.13]VVNPLFEK.R                                    |
| 0.994996 | 0.9927 K.FLDGNELTLADC[160.03]NLLPK[325.13]LHIVQVVC[160.03]K.N  |
| 0.994992 | 0.9991 R.FPSHFSSDLK[325.13]DLLR.N                              |
| 0.994992 | 0.989 R.SK[325.13]LILFPR.K                                     |
| 0.994991 | 0.9975 K.K[325.13]YAWQGVALLPFVDER.R                            |
| 0.994982 | 0.979 R.SVQNHNNK[325.13]SVNESLNNLFITEEDYQALR.T                 |
| 0.99498  | 0.8201 R.KPAGAAK[325.13]KPK.K                                  |
| 0.99498  | 0.9797 R.AAVIGPDVFAK[325.13]LLSAER.A                           |
| 0.994976 | 0.9991 K.KSQEGKPK[325.13]EHTEPK.S                              |
| 0.994975 | 0.9907 R.VAAPK[325.13]HWMLDK.L                                 |
| 0.994971 | 0.9628 K.GIVEFSGK[325.13]PAAR.K                                |
| 0.994959 | 0.9977 K.TTLLK[325.13]HIANR.A                                  |
| 0.994953 | 0.9786 R.DVFTK[325.13]GYGFGLIK.L                               |
| 0.994941 | 0.9152 R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V                     |
| 0.994941 | 0.998 K.ALK[325.13]ASAPAPGHH.-                                 |
| 0.994941 | 0.999 K.VHK[325.13]ISNPWQSPSGTLPALR.T                          |
| 0.994936 | 0.9362 K.K[325.13]LLEAQSHFR.K                                  |
| 0.994929 | 0.9951 K.AAIDWFDGK[325.13]EFHGNIK.V                            |
| 0.994923 | 0.9959 K.EQSGQK[325.13]C[160.03]FLAQPVTLDDIYTHWQQTSEL          |
| 0.994923 | 0.9526 R.LPSGNHMK[325.13]ESR.E                                 |
| 0.994919 | 0.641 K.SGDAAIVDMVPGK[325.13]PMC[160.03]VESFSDYPPLGF           |
| 0.994919 | 0.9969 R.LTGVSISQVNHK[325.13]PLR.T                             |
| 0.994909 | 0.9706 K.K[325.13]AKKPALVAK.S                                  |
| 0.994907 | 0.9394 R.NTDQASM[147.04]PDNTAAQK[325.13]VSHLLGINVTDF           |
| 0.994901 | 0.9912 R.SYSK[325.13]LLC[160.03]GLLAER.L                       |
| 0.994901 | 0.9912 R.SYSK[325.13]LLC[160.03]GLLAER.L                       |
| 0.9949   | 0.9971 R.TC[160.03]TDIKPEWLVK[325.13]IAPQYYDMSNFPQC[160.03]K.N |
| 0.994898 | 0.9992 R.FK[325.13]YGGC[160.03]LGNMNNFETLEEC[160.03]K.N        |
| 0.994896 | 0.989 R.K[325.13]SLVMHTPPVLK.K                                 |
| 0.994894 | 0.9992 R.VANHQK[325.13]DLFR.R                                  |
| 0.994893 | 0.9312 K.K[325.13]GWLYYEAGQR.F                                 |
| 0.994888 | 0.9966 K.K[325.13]VLC[160.03]LAVAVGHVK.M                       |
| 0.994886 | 0.997 R.VWNEEGEDGLPRPK[325.13]DPVIPSIQLFPGLR.E                 |
| 0.994885 | 0.9541 K.KPAGATPK[325.13]K.A                                   |
| 0.99488  | 0.7862 K.NVTLPVAFK[325.13]APIRPDIVNFVHTNLR.K                   |
| 0.99488  | 0.9927 R.GQHTK[325.13]TTGR.R                                   |
| 0.994874 | 0.1987 K.EITALAPSTMKIK[325.13]IIAPPER.K                        |
| 0.994869 | 0.9757 K.ETGEHLVHVK[325.13]K.N                                 |
| 0.994864 | 0.9906 R.NKPSDLGTK[325.13]LQDPR.I                              |
| 0.994863 | 0.9961 K.GYIWNYGAIPTWEDPGHNDK[325.13]HTGC[160.03]C[160.03]K.N  |
| 0.99486  | 0.9993 K.IK[325.13]LGHYATQLQNTYDR.C                            |
| 0.994853 | 0.9477 K.HVSLNK[325.13]AK.K                                    |
| 0.994846 | 0.9977 R.LDDLFK[325.13]LGEPHHR.K                               |
| 0.994846 | 0.6413 R.LFDHPESPTPNPTEPLFLAQAEVYK[325.13]ELR.L                |
| 0.994838 | 0.9374 R.LQALDTGWNELHK[325.13]MWENR.Q                          |
| 0.994832 | 0.9908 R.ELAVQIQK[325.13]GLLALGDYMNVC[160.03]HAC[160.03]K.N    |
| 0.994827 | 0.9922 K.AAVK[325.13]GYLGPEQLPDC[160.03]LK.G                   |

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| 0.994821 | 0.9708 K.HFVALSTNTTK[325.13]VK.E                           |
| 0.994818 | 0.9988 K.ILEK[325.13]LMLAQDEER.Q                           |
| 0.994812 | 0.9498 R.TIC[160.03]SHVQNMNIK[325.13]GVTLGFR.Y             |
| 0.994811 | 0.9795 R.IIGDPYK[325.13]VQQAC[160.03]EMVMDILR.E            |
| 0.994811 | 0.9898 R.K[325.13]LFIGGLSFETDDSLR.E                        |
| 0.994805 | 0.992 R.TLQIQK[325.13]AHGDHMASSR.N                         |
| 0.994797 | 0.9993 K.GQYFGELALVTNK[325.13]PR.A                         |
| 0.994797 | 0.9993 R.IQC[160.03]VPK[325.13]EPHSFQSR.L                  |
| 0.994796 | 0.9993 K.EVC[160.03]HPDIGGK[325.13]IIMC[160.03]PQC[160.03] |
| 0.994796 | 0.9904 R.DPVWK[325.13]YLQTVQYGVHGNFPR.L                    |
| 0.994795 | 0.9928 R.DIDFLKEEHDC[160.03]FLEEIMTK[325.13]R.E            |
| 0.99479  | 0.9948 R.K[325.13]HIC[160.03]PYR.T                         |
| 0.994787 | 0.9553 R.GTLK[325.13]GHNGWVTQIATTPQFPDMILSASR.D            |
| 0.994785 | 0.9766 R.EVGEHLVSIK[325.13]K.N                             |
| 0.994784 | 0.9759 K.SAEFLLHMLK[325.13]NAESNAELK.G                     |
| 0.99478  | 0.9973 R.MVILLC[160.03]NLKPAK[325.13]MR.G                  |
| 0.994772 | 0.9981 R.HAGGLGK[325.13]EFSR.S                             |
| 0.994764 | 0.9129 R.RFDDAVVQSDMK[325.13]HWPFM[147.04]VVNDAGRP         |
| 0.994764 | 0.9992 R.HLYFWGYSEAAK[325.13]K.R                           |
| 0.99475  | 0.9968 K.K[325.13]IGSGGFGLIYLAFTNKPEK.D                    |
| 0.994749 | 0.9991 K.LLEHK[325.13]EIDGR.L                              |
| 0.994747 | 0.9707 K.NLHSEISGK[325.13]R.D                              |
| 0.994746 | 0.9992 K.SVWGSLAVQNSPK[325.13]GC[160.03]HR.D               |
| 0.99473  | 0.9814 R.LAAIVAK[325.13]QVLLGR.K                           |
| 0.994726 | 0.9471 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                  |
| 0.994724 | 0.938 K.LNILK[325.13]LAPGGHVGR.F                           |
| 0.994718 | 0.9917 R.NLHK[325.13]LLYNRP GTVSSLK.K                      |
| 0.994707 | 0.9762 K.VK[325.13]C[160.03]SGPGLSPGMVR.A                  |
| 0.994705 | 0.9949 R.LVEGILHAPDAGWGNLVYVVNYPK[325.13]DNKR.K            |
| 0.994705 | 0.1934 K.EITALAPSTMKIK[325.13]IIAPPER.K                    |
| 0.994704 | 0.9777 R.QNISPDKIPWSALK[325.13]TLMAQSIYGGR.V               |
| 0.994704 | 0.997 K.K[325.13]HEEEAKAER.E                               |
| 0.994701 | 0.9339 R.SHAQK[325.13]NENAR.Q                              |
| 0.9947   | 0.9978 K.SK[325.13]NILFVITKPDVYK.S                         |
| 0.9947   | 0.9945 R.K[325.13]IHESAGLPFFEIVDAPLNIC[160.03]ESR.D        |
| 0.994698 | 0.959 R.FEPYANPTK[325.13]R.Y                               |
| 0.99469  | 0.9974 R.DLQANVEHLVQK[325.13]MK.T                          |
| 0.994676 | 0.9884 K.VTYK[325.13]APVPTGEVYFADSFDR.G                    |
| 0.994671 | 0.9982 R.NVNLVLLC[160.03]SEKPSK[325.13]TLLSR.I             |
| 0.994668 | 0.7179 R.GAEVHLPWNHDFTK[325.13]MEYDGILIAGGP GNPALAI        |
| 0.994668 | 0.9986 R.SLNYC[160.03]GHIYTPISC[160.03]K[325.13]IR.D       |
| 0.994667 | 0.9674 R.KQLATK[325.13]AAR.K                               |
| 0.994667 | 0.9891 K.AQPLEDLA GLK[325.13]ELFQTPVC[160.03]TDKPTTHEK.    |
| 0.994663 | 0.9992 K.ADPSHFELLK[325.13]VLGQGSFGK.V                     |
| 0.994662 | 0.9812 R.SEVDMLK[325.13]IR.S                               |
| 0.994662 | 0.76 R.LQLETEIEALK[325.13]EELLFM[147.04]K.K                |
| 0.994648 | 0.9916 K.LPDGYEFK[325.13]FPNR.L                            |



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| 0.994638 | 0.9715 K.KPVVGK[325.13]K.G                              |
| 0.994635 | 0.9985 R.GLASK[325.13]AAELEMELNEHSLVIDTLK.E             |
| 0.994633 | 0.9463 K.WK[325.13]PPMIDNPSYQGIWKPR.K                   |
| 0.994631 | 0.9698 K.SK[325.13]GYAFIEFASFEDAK.E                     |
| 0.99463  | 0.9759 K.AK[325.13]YHGNVMLLR.A                          |
| 0.994629 | 0.9991 R.K[325.13]SFYSSHYAR.E                           |
| 0.994624 | 0.9964 R.GNWEQPQNQNQTQHK[325.13]QRPQATAEQIR.L           |
| 0.99462  | 0.9658 R.HIVK[325.13]EFK.R                              |
| 0.994619 | 0.9765 R.DMFC[160.03]K[325.13]ILHGFK.N                  |
| 0.994617 | 0.9984 K.TFEEDPAVGAIVLTGGDK[325.13]AFAAGADIK.E          |
| 0.994613 | 0.9931 R.K[325.13]VVVSHSTHR.T                           |
| 0.994609 | 0.9913 K.K[325.13]DEEGQKEEDKPR.K                        |
| 0.994608 | 0.9909 R.LSYNTASNK[325.13]TR.L                          |
| 0.994603 | 0.9992 R.ATAGAYIASQTVK[325.13]K.V                       |
| 0.994603 | 0.0784 K.VK[325.13]DALEFWLQAGVDGFQVR.D                  |
| 0.994595 | 0.9987 R.K[325.13]GDSWAYIQYESLDAHAHAWTHMR.G             |
| 0.994595 | 0.594 R.APQC[160.03]LGK[325.13]FIEIAAR.K                |
| 0.994586 | 0.913 K.K[325.13]GIIRPGTAFELLEQAATGYVIDPIK.G            |
| 0.994579 | 0.9715 R.LK[325.13]LYLPK.E                              |
| 0.994578 | 0.9981 K.IIAGDKEVVIAQNDK[325.13]HTGPVR.A                |
| 0.994569 | 0.9963 K.AIHYNLC[160.03]C[160.03]GLAGGVEQFISDIC[160.03] |
| 0.994568 | 0.9913 R.GLFIDPNGVIK[325.13]HLSVNDLPVGR.S               |
| 0.99456  | 0.9984 R.FVPLPASAK[325.13]WASGLTPAQNC[160.03]PR.A       |
| 0.994556 | 0.9632 R.TADGIVSHLK[325.13]K.Q                          |
| 0.994554 | 0.9993 R.ALFEK[325.13]VQPTHVIHLAAMVGGLFR.N              |
| 0.99454  | 0.9756 R.HGYIK[325.13]GIVK.D                            |
| 0.99454  | 0.9991 K.TYFNILIKPETLAK[325.13]DVR.L                    |
| 0.994536 | 0.9149 K.WSLLQQQK[325.13]TAR.S                          |
| 0.994533 | 0.8924 K.TM[147.04]QNVK[325.13]HPVTGQFLYQDSNWASK.V      |
| 0.994528 | 0.9452 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H               |
| 0.994516 | 0.9977 K.SELPLDPLVPTEEGNPLLK[325.13]HYR.G               |
| 0.994515 | 0.9862 R.C[160.03]K[325.13]IQPHPR.T                     |
| 0.994513 | 0.9668 K.K[325.13]VHVIFNYK.G                            |
| 0.99451  | 0.9991 K.TK[325.13]PHLFYIPGR.M                          |
| 0.994506 | 0.997 R.FIK[325.13]PLSNAYHELAQVYSTNNPSEL.R.N            |
| 0.994505 | 0.9953 K.VLSEAAISASLEK[325.13]FEIPVK.I                  |
| 0.994505 | 0.9342 R.SFPFVSK[325.13]TLGVDFIDVATK.V                  |
| 0.994504 | 0.9316 R.MVTSESKNVK[325.13]LTVSNVLK.E                   |
| 0.994493 | 0.999 R.LHQLK[325.13]VPTK.R                             |
| 0.994489 | 0.9958 K.DGVVEITGK[325.13]HEER.Q                        |
| 0.994481 | 0.8063 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T               |
| 0.994476 | 0.2388 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI   |
| 0.994474 | 0.9979 K.DSK[325.13]AYFHLLNQIAPK.G                      |
| 0.994461 | 0.9771 R.QLSQSLLPAIVELAEDAK[325.13]WR.V                 |
| 0.994459 | 0.9921 R.GQHTK[325.13]TTGR.R                            |
| 0.994459 | 0.9903 R.ESQLAHIK[325.13]DEPPPLSPAPLTPATPSSLDPPFSR.E    |
| 0.994454 | 0.9992 R.K[325.13]TLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR.R     |

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| 0.994453 | 0.9888 K.TSSAETPTIPLGSAVEAIK[325.13]ANC[160.03]SDNEFTQA |
| 0.994449 | 0.9991 K.MIQHAVFK[325.13]ELVK.L                         |
| 0.994447 | 0.9838 R.K[325.13]FGDPVVQSDMK.H                         |
| 0.994447 | 0.9644 R.SGLAAK[325.13]HFIDVGAGVIDEDYR.G                |
| 0.994444 | 0.998 R.VQEK[325.13]QHPVPPPAQNQNQVR.S                   |
| 0.994444 | 0.9971 K.GAGAFGYFEVTHDITK[325.13]YSK.A                  |
| 0.994435 | 0.9993 R.MIPK[325.13]VEWSAFLEAADNLR.L                   |
| 0.994433 | 0.9988 R.FMTK[325.13]IYHPNVDK.L                         |
| 0.994421 | 0.9886 R.TPSAGK[325.13]AMHTPKPAVSGEK.N                  |
| 0.994419 | 0.7335 R.LLLPGELAK[325.13]HAVSEGTKAVTK.Y                |
| 0.994417 | 0.9989 R.EVFSK[325.13]YGPIADVSIYDQQSR.R                 |
| 0.994408 | 0.9966 K.HLSASQK[325.13]ALK.E                           |
| 0.994402 | 0.9968 R.EVSGIK[325.13]ALYESELADAR.R                    |
| 0.994396 | 0.5732 K.GLVLGPIHK[325.13]NQK.D                         |
| 0.994389 | 0.9764 K.GC[160.03]SVSLWDLLESEYVGADK[325.13]R.R         |
| 0.99437  | 0.9651 K.LK[325.13]TNHIGHTGYLNTVTVSPDGSLC[160.03]ASGGK  |
| 0.994367 | 0.9943 R.TQIAPGSQTVLGIGPGPADLIDK[325.13]VTGHLK.L        |
| 0.994362 | 0.9881 R.GLK[325.13]MSATFIGNSTAIQELFK.R                 |
| 0.994362 | 0.9969 R.VFQSLPHENK[325.13]PLTLSNYQTNK.A                |
| 0.994352 | 0.9972 R.FLLHEPIVNK[325.13]FR.E                         |
| 0.994351 | 0.9552 R.IPK[325.13]EQGVLSFWR.G                         |
| 0.994348 | 0.9734 K.FTASAGIQVVGDDLTVTNPK[325.13]R.I                |
| 0.994346 | 0.9 R.DQHFK[325.13]IQVK.D                               |
| 0.994342 | 0.9925 R.AGGK[325.13]ILTFDQLALDSPK.G                    |
| 0.994342 | 0.9918 K.AAEEIGIK[325.13]ATHIK.L                        |
| 0.994341 | 0.895 K.TPSSDVLVFDYTK[325.13]HPAKPDPSGEC[160.03]NPDLF   |
| 0.994337 | 0.985 R.GGM[147.04]GSGGLATGIAGGLAGMGGIQNEK[325.13]I     |
| 0.994325 | 0.9059 R.EIFNFVLK[325.13]AIRPQIDLK.R                    |
| 0.994323 | 0.9903 K.GTGNKNK[325.13]ITITNDQNR.L                     |
| 0.994318 | 0.9771 R.LSC[160.03]LPAFK[325.13]DLIAK.V                |
| 0.994318 | 0.9841 K.FQEHIIQAPK[325.13]PVEAIK.R                     |
| 0.994317 | 0.9752 R.DMFC[160.03]K[325.13]ILHGFK.N                  |
| 0.994308 | 0.9947 K.TLTSGGHAHEGK[325.13]PYC[160.03]NHPC[160.03]YA  |
| 0.994306 | 0.9992 K.AVTHQVK[325.13]FGQQNPR.Q                       |
| 0.994301 | 0.7453 R.LLLPGELAKHAVSEGK[325.13]AVTK.Y                 |
| 0.994289 | 0.9892 R.LPPGFSASSTVEKPSK[325.13]VHR.A                  |
| 0.994289 | 0.9281 R.K[325.13]FVHLLDQSDQDFQEELDMK.M                 |
| 0.994288 | 0.9463 K.K[325.13]QGGLGPMNIPLVSDPKR.T                   |
| 0.994285 | 0.9958 R.SGYIAIDDIQVLSYPC[160.03]DK[325.13]SPHFLR.L     |
| 0.994279 | 0.9826 K.IHK[325.13]NSSTYWEGK.A                         |
| 0.994276 | 0.9945 R.IIGLK[325.13]PEGVPR.I                          |
| 0.994274 | 0.9991 R.FEPVHFVASSSK[325.13]DER.Q                      |
| 0.994267 | 0.9169 K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q          |
| 0.994258 | 0.9991 R.HIK[325.13]EYAENIGDGR.S                        |
| 0.994257 | 0.9991 R.SISQQK[325.13]SGVSITIDDPVR.T                   |
| 0.994251 | 0.9957 K.LVEK[325.13]PSPLTLAPHDFANIK.A                  |
| 0.994249 | 0.9991 R.GIFETK[325.13]FLSQIESDC[160.03]LALLQVR.A       |

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| 0.994249 | 0.9276 R.RPISADSAIMNPASK[325.13]VIALK.A                |
| 0.994243 | 0.9402 K.SAFLC[160.03]GVMK[325.13]TYR.Q                |
| 0.99424  | 0.9882 R.SGK[325.13]APILIATDVASR.G                     |
| 0.994235 | 0.9625 R.RGEEGHDPK[325.13]EPEQLR.K                     |
| 0.994233 | 0.9891 R.GLGHQVATDALVAMEK[325.13]AMK.R                 |
| 0.99423  | 0.9959 K.DKDFAIIDIK[325.13]STHDHWK.A                   |
| 0.994228 | 0.9881 R.HESVSK[325.13]ISTISSVR.N                      |
| 0.994227 | 0.9895 R.HGIPTAQWK[325.13]AFTKPEEAC[160.03]SFILSADFPAL |
| 0.994226 | 0.9991 R.DDHGLFGLDVK[325.13]SR.G                       |
| 0.994225 | 0.9766 K.K[325.13]NIHPWVK.Q                            |
| 0.994223 | 0.8472 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S |
| 0.994222 | 0.9959 K.FDYK[325.13]AHQR.Q                            |
| 0.994221 | 0.9799 K.EMYK[325.13]TDLEKDIISDTSGDFR.K                |
| 0.99422  | 0.9722 K.SAPSTGGVK[325.13]KPHR.Y                       |
| 0.99422  | 0.9957 R.VK[325.13]IQDAHR.L                            |
| 0.994217 | 0.9103 K.WSLLQQQK[325.13]TAR.S                         |
| 0.994214 | 0.9707 R.GLVMVKPGSIK[325.13]PHQK.V                     |
| 0.994214 | 0.9954 R.TAWVFDDK[325.13]YK.R                          |
| 0.994212 | 0.9976 R.FYVK[325.13]DHR.N                             |
| 0.994206 | 0.9509 K.HPK[325.13]NPEVGLKPVWYSPK.V                   |
| 0.994204 | 0.9992 K.DHSFFIPDIEYLSDIK[325.13]GLIK.Y                |
| 0.994202 | 0.9908 R.K[325.13]NGGLGHMNIALLSDLTK.Q                  |
| 0.994201 | 0.9866 R.RLDPNK[325.13]YPVPENWLHK.E                    |
| 0.994199 | 0.9439 R.GVLK[325.13]VFLENVIR.D                        |
| 0.994196 | 0.962 K.EGVHGGLINK[325.13]K.C                          |
| 0.994187 | 0.9221 R.LAAVVSAC[160.03]K[325.13]QLHR.A               |
| 0.994186 | 0.9991 R.GQYC[160.03]YELDEK[325.13]AVRPGYPK.L          |
| 0.994183 | 0.999 R.DSK[325.13]LTHLFK.N                            |
| 0.994172 | 0.963 K.ALKPPPIK[325.13]LYR.E                          |
| 0.994172 | 0.963 K.ALKPPPIK[325.13]LYR.E                          |
| 0.994169 | 0.995 K.FHTVSGSK[325.13]C[160.03]EIK.V                 |
| 0.994168 | 0.9686 K.TLVLLMGK[325.13]EGVHGGLINK.K                  |
| 0.994167 | 0.9912 K.SPAVKPAAAPK[325.13]QPVGGGQK.L                 |
| 0.994166 | 0.9985 K.GKDSLQAQGK[325.13]R.R                         |
| 0.994163 | 0.9793 R.LAHEVGWK[325.13]YQAVTATLEEK.R                 |
| 0.994161 | 0.9652 K.DAIHFYNK[325.13]SLAEHR.T                      |
| 0.99415  | 0.9956 R.SIFGEDALANVSIEK[325.13]PIHQGPDAAVTGHIR.I      |
| 0.99415  | 0.9623 R.NLK[325.13]ASLENSLR.E                         |
| 0.994144 | 0.974 R.EGDYVLFHHEGGVDVDVDAK[325.13]AQK.L              |
| 0.994141 | 0.9737 R.LTTDFGNAEK[325.13]TDR.F                       |
| 0.994137 | 0.9736 K.ITLQDVVSHSK[325.13]K.L                        |
| 0.994136 | 0.998 R.LK[325.13]GHTSFVNSC[160.03]YPAR.R              |
| 0.994134 | 0.9991 K.LPPYDIPGMVSVVELK[325.13]QSSVMQR.L             |
| 0.99413  | 0.9955 R.NIK[325.13]SHLGNVHDQDN.-                      |
| 0.994129 | 0.907 R.LK[325.13]LLLPWLEAR.I                          |
| 0.994129 | 0.9979 R.HLK[325.13]TSGGQGYK.F                         |
| 0.994117 | 0.9978 K.K[325.13]PIPDEHLILK.T                         |

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| 0.994105 | 0.9838 K.AEGIEK[325.13]SYSQSILLDLTDNR.L                   |
| 0.994105 | 0.9672 K.NLHSEISGK[325.13]R.D                             |
| 0.994104 | 0.9992 R.HGLINFGIYK[325.13]R.I                            |
| 0.994102 | 0.9973 K.KAEGAQNQGK[325.13]K.V                            |
| 0.994096 | 0.9992 K.K[325.13]C[160.03]QSWSSMTPHR.H                   |
| 0.994095 | 0.8689 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.994092 | 0.9287 R.TSPEDTVITYK[325.13]C[160.03]EESFVK.I             |
| 0.994089 | 0.9991 R.LEC[160.03]VAFSHQNLK[325.13]LK.W                 |
| 0.994086 | 0.2217 R.KDGNASGTTLEALDC[160.03]ILPPTRPDK[325.13]PLR.     |
| 0.994082 | 0.9739 K.NNIK[325.13]LYVR.R                               |
| 0.994072 | 0.9633 R.GFC[160.03]FLEYEDHK[325.13]TAAQAR.R              |
| 0.994072 | 0.9737 R.ETWHK[325.13]LSELEPGTGDLR.F                      |
| 0.994058 | 0.988 R.TFNTSTGGLLLPSDTK[325.13]R.S                       |
| 0.994057 | 0.9992 R.FLILPDMLK[325.13]NAPMLK.S                        |
| 0.994057 | 0.9992 R.KYDK[325.13]AWLLSMIQSK.C                         |
| 0.994056 | 0.9992 R.INAGMLAQFIDK[325.13]PVC[160.03]FVGR.L            |
| 0.994055 | 0.9992 K.HTWQK[325.13]ANDQFLESQR.L                        |
| 0.994052 | 0.9991 K.RPQYC[160.03]SETQSK[325.13]K.V                   |
| 0.994049 | 0.968 K.SAPATGGVKK[325.13]PHR.Y                           |
| 0.994047 | 0.9992 R.K[325.13]SALGPGVPHINTK.L                         |
| 0.994044 | 0.9896 R.AAVGRPLDK[325.13]HEGALETLLR.Y                    |
| 0.994039 | 0.9883 K.RQELVTK[325.13]IDHILDAL.-                        |
| 0.994035 | 0.9913 K.AGLQVYNK[325.13]C[160.03]WK.F                    |
| 0.994034 | 0.9113 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I         |
| 0.994033 | 0.9991 R.FSEFK[325.13]SHSGEFR.Q                           |
| 0.994031 | 0.9892 K.VTEGLTDVILYHQPDDK[325.13]KK.N                    |
| 0.99403  | 0.9797 R.VYSTALSSFLTK[325.13]R.N                          |
| 0.994027 | 0.9979 K.HQPHK[325.13]VTQYK.K                             |
| 0.994023 | 0.9942 K.LLGGVTIAQGGVLPNIQAVLLPK[325.13]K.T               |
| 0.994008 | 0.9743 R.K[325.13]GNLQLQGTR.L                             |
| 0.994    | 0.9972 R.KADALK[325.13]AMK.Q                              |
| 0.993999 | 0.9636 K.SIVNYK[325.13]PKIDQLEGDHQLIQEALIFDNK.H           |
| 0.993997 | 0.9756 K.FLK[325.13]HWDHLTQVK.K                           |
| 0.993997 | 0.9936 R.AALQELLSK[325.13]GLIK.L                          |
| 0.993996 | 0.9967 K.LVGGTTPGK[325.13]GGQTHLGLPVFNTVK.E               |
| 0.993995 | 0.9739 K.YGK[325.13]IVGC[160.03]SVHK.G                    |
| 0.99399  | 0.9914 R.NSQGK[325.13]GAHRPEHASGR.R                       |
| 0.993983 | 0.9709 R.INEILSNALK[325.13]R.G                            |
| 0.993977 | 0.9195 K.KAEVEGK[325.13]DLPEHAVLK.M                       |
| 0.993974 | 0.9194 K.AVGK[325.13]VIPELNGK.L                           |
| 0.99397  | 0.9243 R.K[325.13]VSQPIEGHAASFAQFK.M                      |
| 0.993964 | 0.974 K.VYIYHSSSK[325.13]GLLR.Q                           |
| 0.993963 | 0.9918 R.NGNPAPK[325.13]ITWYR.N                           |
| 0.99396  | 0.9942 R.ENFC[160.03]NIHVSVPQPSSTGEQK[325.13]TKPTQNSV     |
| 0.993953 | 0.9746 R.KQAEIEGK[325.13]LHR.T                            |
| 0.99395  | 0.9439 R.LPSGNHMK[325.13]ESR.E                            |
| 0.993944 | 0.9989 R.ELENLQK[325.13]LNVSHNK.L                         |

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| 0.993935 | 0.996 R.TTIHEMFLSTLDPK[325.13]TISFR.S                     |
| 0.993922 | 0.9809 K.M[147.04]VINHLEK[325.13]LFVTNDAATILR.E           |
| 0.993913 | 0.9968 K.GTKPFK[325.13]PLEQLMGVFPAASGNFLPPSWR.K           |
| 0.993906 | 0.999 K.LGK[325.13]AHATTSENTVSK.L                         |
| 0.993904 | 0.9508 K.KAAATK[325.13]KPAPEK.K                           |
| 0.993892 | 0.9991 K.LPVHK[325.13]LYIEYGIQR.I                         |
| 0.993891 | 0.973 R.RK[325.13]PDTIEVQQMK.A                            |
| 0.993883 | 0.9783 R.ALANSLAC[160.03]QGK[325.13]YTPSGQAGAAAASESLFV.   |
| 0.993881 | 0.9412 R.MFAPTK[325.13]TWR.R                              |
| 0.993879 | 0.9992 K.EVHLGAC[160.03]GALK[325.13]NISFGR.D              |
| 0.993876 | 0.9622 K.IMLPWDPTGK[325.13]IGPK.K                         |
| 0.993874 | 0.9908 R.HSQYHVDGSLEK[325.13]DR.T                         |
| 0.993871 | 0.9977 R.IWSLEGK[325.13]SIMTIVGHTDVVK.D                   |
| 0.993867 | 0.9865 K.AK[325.13]LASLEELKR.Q                            |
| 0.993864 | 0.9989 K.KIK[325.13]LQIWDTAGQER.F                         |
| 0.993863 | 0.9919 R.SSPSFSSLHYQDAGNYVC[160.03]ETALQEVEGLK[325.13]    |
| 0.993859 | 0.9964 R.ETGVIEK[325.13]LLTSYGFIQC[160.03]SER.Q           |
| 0.993856 | 0.9383 K.KATK[325.13]SPAKPK.A                             |
| 0.993854 | 0.9668 R.GFIYVHK[325.13]PPVHIR.F                          |
| 0.993848 | 0.9952 R.K[325.13]PFPLVKPLPGEEPLFTIPHTQEAFR.T             |
| 0.993848 | 0.9363 K.SAFLC[160.03]GVMK[325.13]TYR.Q                   |
| 0.993844 | 0.9804 R.EM[147.04]AGDNK[325.13]LLGQFTLIGIPPAPR.G         |
| 0.993844 | 0.9794 K.GRPC[160.03]K[325.13]JIVEMSTSK.T                 |
| 0.993843 | 0.9912 R.NK[325.13]LDHYAIK.F                              |
| 0.99384  | 0.9875 K.K[325.13]SQIFSTASDNQPTVTIK.V                     |
| 0.993808 | 0.9981 R.LVSGWVK[325.13]PIIIGR.H                          |
| 0.993808 | 0.993 R.LK[325.13]GIEEEEILPGFILC[160.03]DPNNLC[160.03]HS  |
| 0.993808 | 0.9688 R.KAMK[325.13]GLGTDEESILTLLTSR.S                   |
| 0.993796 | 0.8982 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV      |
| 0.993794 | 0.9813 K.SLKDEDLQK[325.13]LPVGTATLYFR.D                   |
| 0.993791 | 0.9039 R.RFDDAVVQSDM[147.04]K[325.13]HWPFMVVNDAGRP        |
| 0.99378  | 0.9897 K.IVADFSASVKK[325.13]PHTLLQR.V                     |
| 0.993775 | 0.9882 R.HEVLLISAEQDK[325.13]R.A                          |
| 0.993762 | 0.9444 R.IYDLNKPEAEPK[325.13]EISGHTSGIK.K                 |
| 0.993761 | 0.9926 K.HGEVC[160.03]PAGWKPGSETIIPDPAGK[325.13]LK.Y      |
| 0.993748 | 0.9981 K.GK[325.13]FGHEFLEFEFRPDGK.L                      |
| 0.993746 | 0.8847 R.RQQEGFK[325.13]GTFPDAR.E                         |
| 0.993738 | 0.9992 R.VK[325.13]IETALSLHQR.I                           |
| 0.993736 | 0.7285 R.LQLETEIEALK[325.13]EELLFM[147.04]K.K             |
| 0.993736 | 0.9967 R.YPM[147.04]AVGLNK[325.13]GHK.V                   |
| 0.993729 | 0.9986 R.IHNQNNEQAWK[325.13]EILK.W                        |
| 0.993728 | 0.9573 R.AEAESM[147.04]YQIK[325.13]YEELQSLAGK.H           |
| 0.993722 | 0.9582 R.KPEDWDERPK[325.13]IPDPEAVKPDDWDEDAPAK.I          |
| 0.993717 | 0.9894 R.LSYNTASNK[325.13]TR.L                            |
| 0.993699 | 0.9881 K.SEFEQNLSEK[325.13]LSEQELQFR.R                    |
| 0.993688 | 0.9933 K.TGKPMINLYTDK[325.13]DTGKPK.G                     |
| 0.993683 | 0.9897 R.GTK[325.13]LMC[160.03]SLC[160.03]HC[160.03]PGATI |

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| 0.993681 | 0.9894 K.LVPVLSAK[325.13]AAQASDLEK.I                     |
| 0.993675 | 0.973 R.YK[325.13]SYSPYDMLESIR.K                         |
| 0.993675 | 0.9932 K.FASYLTFSPSEVK[325.13]SLR.T                      |
| 0.993661 | 0.975 R.IVSQLLTMDGLK[325.13]QR.A                         |
| 0.993648 | 0.9864 K.DQLIYNLLK[325.13]EEQTPQNK.I                     |
| 0.993645 | 0.9782 R.VINEEYK[325.13]IWK.K                            |
| 0.993644 | 0.9992 R.LRPVNPPLATK[325.13]GSFFK.V                      |
| 0.993644 | 0.9132 R.LQAEIEGLK[325.13]GQR.A                          |
| 0.993644 | 0.9992 R.TPLHLAK[325.13]SK.L                             |
| 0.993637 | 0.9813 K.IAVMELFRPK[325.13]GESK.D                        |
| 0.993636 | 0.8846 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V                |
| 0.993635 | 0.9967 K.LLK[325.13]GAEHITTYTFNTHK.A                     |
| 0.99363  | 0.9936 R.ANLVK[325.13]NGC[160.03]GGEIESPASSFHVLR.S       |
| 0.993625 | 0.9991 R.GYDQSAYDGK[325.13]DYIALNEDLR.S                  |
| 0.993625 | 0.9793 K.FEDENFILK[325.13]HTGPGILSM[147.04]ANAGPNTNGSI   |
| 0.993623 | 0.9718 R.TNEK[325.13]VELQELNDR.F                         |
| 0.99362  | 0.9726 K.GIVEFASK[325.13]PAAR.K                          |
| 0.993616 | 0.9636 R.IGSSM[147.04]K[325.13]SVGEVMAIGR.T              |
| 0.99361  | 0.9775 R.LAAIVAK[325.13]QVLLGR.K                         |
| 0.993609 | 0.996 K.LFNHLSAVSESIQALGWVAMAPK[325.13]PGPYVK.E          |
| 0.993607 | 0.9762 R.TRPAANPIQFTLNK[325.13]EK.L                      |
| 0.993595 | 0.9284 K.LSPDAIPGK[325.13]WTSQDSLLGMEFSGR.D              |
| 0.993586 | 0.9982 K.SLENAIEWSVK[325.13]SGQIR.N                      |
| 0.993581 | 0.9668 R.REEAAVDAQQK[325.13]R.S                          |
| 0.993578 | 0.9989 K.DFLGK[325.13]SDPFLEFFR.Q                        |
| 0.993578 | 0.9954 R.QYEQQTYQVIPEVIK[325.13]NFIQYFHK.T               |
| 0.993565 | 0.9838 K.SC[160.03]GK[325.13]DGFHIR.V                    |
| 0.993544 | 0.9945 K.DKTTGQSK[325.13]GFAFISFHR.R                     |
| 0.993534 | 0.9945 R.K[325.13]LNVNAKPFVNPVHAAEFVPSFLR.G              |
| 0.993527 | 0.9991 R.NLPYK[325.13]ITAEEMYDIFGK.Y                     |
| 0.993517 | 0.97 K.QFAEMYVAK[325.13]FAAK.G                           |
| 0.993517 | 0.9688 K.AVIVK[325.13]NIDDGTSDRPYSHALVAGIDR.Y            |
| 0.993516 | 0.9964 R.TGC[160.03]IGAK[325.13]HR.I                     |
| 0.993513 | 0.999 R.TQK[325.13]TPPGLQHEYAAPADYFR.I                   |
| 0.993512 | 0.9991 R.FDSK[325.13]PAPSAQPAPPPHPPSR.L                  |
| 0.993507 | 0.9991 K.HTK[325.13]QSLQVIESAMER.D                       |
| 0.9935   | 0.999 R.IDDYEEEPILKPGC[160.03]K[325.13]EYFWLLC[160.03]K. |
| 0.993491 | 0.9974 K.YELGRPAANTK[325.13]IGPR.R                       |
| 0.993491 | 0.9727 R.QK[325.13]HSQAVEELAEQLEQTKR.V                   |
| 0.993481 | 0.9566 R.K[325.13]M[147.04]C[160.03]LFAGFQR.K            |
| 0.993481 | 0.9557 R.K[325.13]ISNQFDWALMR.L                          |
| 0.993476 | 0.9676 R.LLLSK[325.13]GHSC[160.03]YRPR.R                 |
| 0.993468 | 0.9693 K.SAPSTGGVK[325.13]KPHR.Y                         |
| 0.993466 | 0.9726 R.DYETATLSDIK[325.13]ALIR.K                       |
| 0.993458 | 0.9991 K.FASC[160.03]VDASGGLK[325.13]C[160.03]HR.S       |
| 0.993451 | 0.9758 K.ASMK[325.13]GLGTDEDSLIEIC[160.03]SR.T           |
| 0.993451 | 0.9657 R.LLSDATVEKDESHAGK[325.13]VVLR.S                  |

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| 0.993446 | 0.9965 R.LTGVSSISQVNHK[325.13]PLR.T                    |
| 0.993444 | 0.9813 K.HWPFQVINDGDK[325.13]PK.V                      |
| 0.993442 | 0.9725 R.SEAANGNLDFVLSFLK[325.13]SNTLPISLQSIR.S        |
| 0.993438 | 0.9991 R.ELVPQDLWAAK[325.13]AWLITAR.S                  |
| 0.993437 | 0.9417 K.VHLVGIDIFTGK[325.13]K.Y                       |
| 0.99343  | 0.9706 R.DNK[325.13]DGSC[160.03]SAEYIPFAPGDYDVNITYGGAI |
| 0.993421 | 0.9905 R.MEELHNQEMQK[325.13]R.K                        |
| 0.993385 | 0.9035 K.AAKPK[325.13]AAKPK.A                          |
| 0.993366 | 0.9582 K.K[325.13]KHPDASVNFSEFSK.K                     |
| 0.993365 | 0.9542 K.NTHC[160.03]SSLPHYQK[325.13]LK.K              |
| 0.993364 | 0.9587 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R    |
| 0.993363 | 0.9513 K.AAGAGK[325.13]VTK.S                           |
| 0.99336  | 0.9866 K.KQELLEALTK[325.13]HFQD.-                      |
| 0.993344 | 0.9721 K.RGLKPSC[160.03]TIIPLMK[325.13]K.D             |
| 0.993344 | 0.998 K.SLLAK[325.13]IFYDR.A                           |
| 0.993338 | 0.9633 R.KVLRDNIQGITK[325.13]PAIR.R                    |
| 0.993336 | 0.9743 K.DAK[325.13]TAASGIPYHSEVPVSLK.E                |
| 0.99333  | 0.9968 R.K[325.13]HGVVPLATYM[147.04]R.I                |
| 0.993327 | 0.9968 K.NAK[325.13]FYPVTR.E                           |
| 0.993319 | 0.9991 K.TK[325.13]FGYHIIMVEGR.K                       |
| 0.993313 | 0.9908 K.TGVHHYSGNNIELGTAC[160.03]GK[325.13]YYR.V      |
| 0.993305 | 0.9073 R.LDYSSLKVK[325.13]GLVLGPIHK.N                  |
| 0.993302 | 0.9907 K.TQDQISNIK[325.13]YHEEFK.S                     |
| 0.993294 | 0.9762 K.ILVDISNNLK[325.13]INQYPESNAEYLAHLVPGAHVVK.A   |
| 0.993284 | 0.9978 R.K[325.13]IQALQQQADEAEDR.A                     |
| 0.993273 | 0.9255 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H              |
| 0.993273 | 0.0994 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAW   |
| 0.993261 | 0.9965 R.VMDGLLVIAMNK[325.13]HR.E                      |
| 0.993259 | 0.9856 K.K[325.13]LTQTSGETTHTDKVPGGEDK.S               |
| 0.993255 | 0.994 K.TEISFRPNDPK[325.13]SYEAYVLNIVR.F               |
| 0.99325  | 0.933 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H               |
| 0.993247 | 0.9991 K.LELQGVK[325.13]GGVDHAAAFGR.I                  |
| 0.993245 | 0.9991 R.HVTDYK[325.13]TSESTGSLPSPFLR.A                |
| 0.993241 | 0.9875 R.K[325.13]NLNYLHLDYNFNLKPVK.T                  |
| 0.993235 | 0.9954 R.NK[325.13]IAGYVTHLMK.R                        |
| 0.993235 | 0.9759 K.ENLLDFIK[325.13]HNQLPLVIEFTEQTAPK.I           |
| 0.993232 | 0.9797 K.LK[325.13]SIAFPSIGSGR.N                       |
| 0.993226 | 0.8602 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG! |
| 0.993219 | 0.9868 K.KLTGIK[325.13]HELQANC[160.03]YEEVK.D          |
| 0.993218 | 0.8518 R.ILGLLDAYLK[325.13]TR.T                        |
| 0.993208 | 0.9236 R.GGK[325.13]NSTWSGESK.T                        |
| 0.993199 | 0.9928 K.SK[325.13]GLAPDLPEDLYHLIK.K                   |
| 0.99318  | 0.9988 K.K[325.13]NISHDTFGTTYGR.I                      |
| 0.993173 | 0.9948 K.LIK[325.13]GIHQSTIDLK.N                       |
| 0.993168 | 0.8966 K.SK[325.13]DDQVTVIGAGVTLHEALAAELLK.K           |
| 0.993164 | 0.9975 R.FSVGGMTDVAEIK[325.13]GHR.R                    |
| 0.993161 | 0.9974 K.FKLDLDFPNLPYLLDGK[325.13]NK.I                 |

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| 0.993158 | 0.9954 R.HLQSLHK[325.13]FVSR.A                         |
| 0.993148 | 0.9907 K.HGEVC[160.03]PAGWK[325.13]PGSETIIPDPAGK.L     |
| 0.993147 | 0.9943 R.NPGGQMEGPWC[160.03]FTQNK[325.13]NVR.M         |
| 0.993147 | 0.9989 K.K[325.13]LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I     |
| 0.993146 | 0.9956 R.C[160.03]VK[325.13]IFQGNVHNFEK.N              |
| 0.993142 | 0.9887 R.AHSIQIMK[325.13]VEEIAASK.C                    |
| 0.993141 | 0.9451 R.YM[147.04]AQGK[325.13]HIGK.V                  |
| 0.993138 | 0.974 K.KPLVGK[325.13]K.A                              |
| 0.993131 | 0.4174 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIK.F |
| 0.993129 | 0.9924 K.VDVFREDLC[160.03]TK[325.13]TENLLGSYFPK.K      |
| 0.993125 | 0.9712 K.VDVSAPDVEAHGPEWNLK[325.13]MPK.M               |
| 0.993107 | 0.999 K.NLHK[325.13]VSPSLK.G                           |
| 0.993104 | 0.9713 R.K[325.13]PVTVHSR.A                            |
| 0.993101 | 0.9589 R.VVLIGGK[325.13]PDR.V                          |
| 0.993091 | 0.6471 R.LAHYNK[325.13]R.S                             |
| 0.99309  | 0.9557 R.LREK[325.13]LQEEM[147.04]LQR.E                |
| 0.993089 | 0.9531 R.AEAESM[147.04]YQIK[325.13]YEELQSLAGK.H        |
| 0.993088 | 0.9932 R.K[325.13]AGNFYVPAEPK.L                        |
| 0.993085 | 0.9895 K.EFSPFGSITSK[325.13]VMLEDGR.S                  |
| 0.993085 | 0.9804 R.TDDVHAK[325.13]DNTRPGANSPEM[147.04]WSEAIK.I   |
| 0.993071 | 0.9956 K.NSTIVFPLPIDMLQGIIGAK[325.13]HSHLG.-           |
| 0.993068 | 0.5909 K.YPIEHGIITNWDDMEK[325.13]IWHHTFYNELR.V         |
| 0.993061 | 0.9991 R.VYNASSTIVPSLK[325.13]HR.L                     |
| 0.99306  | 0.9635 K.GETK[325.13]SFYPEEVSSMVLTK.M                  |
| 0.993056 | 0.9975 R.VQEK[325.13]QHPVPPPAQNQNQVR.S                 |
| 0.993052 | 0.9288 R.IPELNK[325.13]VAR.A                           |
| 0.99305  | 0.9 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V                 |
| 0.993045 | 0.6635 K.ADK[325.13]DYHFKVDNDENEHQLSLR.T               |
| 0.993045 | 0.9372 R.RGPC[160.03]IYNEDNGIHK[325.13]AFR.N           |
| 0.993042 | 0.986 K.LK[325.13]DYAFIHFDER.D                         |
| 0.993034 | 0.9184 R.SAPGGGSK[325.13]VPQKK.V                       |
| 0.99303  | 0.9822 R.YYK[325.13]NIGLGFK.T                          |
| 0.993027 | 0.9902 K.FK[325.13]YDDAERR.F                           |
| 0.993025 | 0.9971 K.NILFVITK[325.13]PDVYK.S                       |
| 0.993023 | 0.994 K.EAPPMKPEVVK[325.13]THLR.D                      |
| 0.993019 | 0.9681 R.GK[325.13]PLPEYHVR.I                          |
| 0.99301  | 0.9926 K.SK[325.13]GLAPDLPEDLYHLIK.K                   |
| 0.993008 | 0.9991 K.KSEAAVPPWVDTNDEETIQQILALSADK[325.13]R.N       |
| 0.993003 | 0.9598 K.HLNMK[325.13]LTR.A                            |
| 0.993002 | 0.9946 K.VLTFALSEEVRPQDTVSVIGGVAGGSK[325.13]HGR.K      |
| 0.993    | 0.9708 K.LVHANFGTK[325.13]K.D                          |
| 0.992993 | 0.7448 R.LLMHGK[325.13]EVGSIIGK.K                      |
| 0.99299  | 0.9989 R.LMNSK[325.13]GEYQGVFHC[160.03]AVETAK.L        |
| 0.992981 | 0.9657 K.GYEK[325.13]KPYC[160.03]NAHYPK.Q              |
| 0.992978 | 0.9668 R.QLMWSATWPK[325.13]EVR.Q                       |
| 0.992977 | 0.9553 R.GLKPSC[160.03]TIPLM[147.04]K[325.13]K.D       |
| 0.992966 | 0.9381 R.K[325.13]TVTAMDVVYALK.R                       |



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| 0.992965 | 0.9948 R.LNELLVK[325.13]ALER.H                            |
| 0.992958 | 0.9579 K.HGK[325.13]APILIATDVASR.G                        |
| 0.992956 | 0.8466 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.992955 | 0.5005 K.VK[325.13]GLVLGPCHK.N                            |
| 0.992951 | 0.9126 R.VLDPFTIK[325.13]PLDR.K                           |
| 0.992946 | 0.9964 K.FHVDISLTDIFIQK[325.13]YSHLQPGDHLTDITLK.V         |
| 0.992935 | 0.9991 K.SPFSVHPK[325.13]TGR.I                            |
| 0.992933 | 0.9484 R.YK[325.13]LLGGLAVR.R                             |
| 0.992932 | 0.8953 K.NAQK[325.13]SNQNGKDSKPSSTPR.S                    |
| 0.992931 | 0.9536 K.TVDNFVALATGEK[325.13]GFGYK.N                     |
| 0.992931 | 0.981 R.FNVLK[325.13]VTK.A                                |
| 0.992929 | 0.9887 K.HTLTQIK[325.13]DAVR.D                            |
| 0.992925 | 0.9968 R.YVQK[325.13]GEYR.T                               |
| 0.992916 | 0.9913 R.YHPDK[325.13]NKEPGAEEK.F                         |
| 0.992908 | 0.9965 R.TLQEDLVK[325.13]DVLSNAHIQNELER.E                 |
| 0.992907 | 0.989 K.MGAK[325.13]AMNWMMSGK.I                           |
| 0.992899 | 0.9119 R.VVDLMAHMASK[325.13]E.-                           |
| 0.992897 | 0.993 K.IFK[325.13]SQGAALDK.Y                             |
| 0.992897 | 0.9483 K.HK[325.13]SDFGK.F                                |
| 0.992888 | 0.9991 R.VTILC[160.03]DK[325.13]FSGHPK.G                  |
| 0.992875 | 0.9777 K.LGETYKDHENIVIAK[325.13]MDSTANEVEAVK.V            |
| 0.992874 | 0.9455 R.AAAEK[325.13]LFGNMEGDC[160.03]PSDWK.T            |
| 0.992872 | 0.9241 R.EVTVPVFYPTK[325.13]VWLEVEPVGM[147.04]LK.E        |
| 0.992858 | 0.9078 K.K[325.13]LGEMWNNTAADDKQPYEK.K                    |
| 0.992857 | 0.9646 R.LLLSK[325.13]GHSC[160.03]YRPR.R                  |
| 0.992855 | 0.9991 K.IYNC[160.03]HVLLNSK[325.13]GAVVATYR.K            |
| 0.992855 | 0.9991 R.K[325.13]LHNSYTDVMC[160.03]NPFYNPGDR.I           |
| 0.992855 | 0.9991 R.EHTTSSSVSK[325.13]KPR.L                          |
| 0.992841 | 0.0935 K.SSEHINEGETAMLVC[160.03]K[325.13]SESVPVTDWAV      |
| 0.992838 | 0.9952 R.GNWEQPQNQNQTQHK[325.13]QRPQATAEQIR.L             |
| 0.992829 | 0.9848 R.M[147.04]HAPGK[325.13]GLSQSALPYR.R               |
| 0.99282  | 0.9721 K.ELNK[325.13]SINPDEAVAYGAAVQAAILSGDK.S            |
| 0.992811 | 0.9969 K.HLPNDPMFK[325.13]LVAQLYK.I                       |
| 0.992801 | 0.9984 R.GYSFSLTTFSPSGK[325.13]LVQIEYALAAGGAPSVGIK.A      |
| 0.992799 | 0.9601 R.LLLSK[325.13]GHSC[160.03]YRPR.R                  |
| 0.992799 | 0.9955 R.HISPSAK[325.13]PFENGQYLDIYGITR.D                 |
| 0.992794 | 0.9955 R.MVVGGAQAGDAGTYHC[160.03]TAAEWIQDPDGSWAQ          |
| 0.992793 | 0.9844 K.K[325.13]YSQFINFPIYVWSSK.T                       |
| 0.992784 | 0.1482 K.EITALAPSTMKIK[325.13]IIAPPER.K                   |
| 0.992783 | 0.9672 K.VINTGIK[325.13]VWC[160.03]R.N                    |
| 0.992781 | 0.9971 K.KTEFK[325.13]TLEGVITR.T                          |
| 0.992767 | 0.9925 R.VGSK[325.13]LFFDKR.D                             |
| 0.992742 | 0.9961 R.NIHSSDWPK[325.13]FFEK.Y                          |
| 0.992731 | 0.99 K.C[160.03]STPSTDATVQGNVEDTVQVK[325.13]VLADSLH       |
| 0.992713 | 0.9801 K.ANIK[325.13]HKPGGGDVK.I                          |
| 0.992713 | 0.999 K.LEPEAWK[325.13]HVEAVYIDIADR.S                     |
| 0.992698 | 0.9933 R.KREDC[160.03]SPADK[325.13]PYIDEAR.R              |

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| 0.992697 | 0.9967 R.MHFSK[325.13]TK.H                                |
| 0.992692 | 0.9953 R.IFYHPETTQLMILSASEATVK[325.13]R.V                 |
| 0.992685 | 0.9694 K.LLQAQK[325.13]LVQYLR.E                           |
| 0.992672 | 0.9919 K.EK[325.13]ISMFC[160.03]HVEPEQVIC[160.03]VHDVSSI  |
| 0.992669 | 0.9949 K.DGPLNM[147.04]ILDDGGDLTNLIHTK[325.13]YPQLLPGI    |
| 0.992666 | 0.9982 K.LK[325.13]FGIGDGNLQYYLYNWK.C                     |
| 0.992665 | 0.8677 R.WLPAGDALLQM[147.04]ITIHLPSVTAQK[325.13]YR.C      |
| 0.992665 | 0.9645 R.EHPFLVK[325.13]GGEDLR.Q                          |
| 0.992664 | 0.9829 K.FGEVVDC[160.03]TLK[325.13]LDPITGR.S              |
| 0.99266  | 0.9693 K.NK[325.13]YEDEINKR.T                             |
| 0.992658 | 0.9524 K.GATLK[325.13]ITLDNAYM[147.04]EK.C                |
| 0.992658 | 0.9063 R.RYQK[325.13]STELLIR.K                            |
| 0.992643 | 0.9915 K.VK[325.13]C[160.03]YRC[160.03]GETGHVAINC[160.03] |
| 0.99264  | 0.9941 K.RPFAYHK[325.13]LLK.D                             |
| 0.992633 | 0.9912 K.GLK[325.13]DMGYGNWISKPQEEK.N                     |
| 0.992632 | 0.9089 K.VDIDAPDVDVHGPDWHLK[325.13]MPK.M                  |
| 0.992631 | 0.9569 R.LPSGNHM[147.04]K[325.13]ESR.E                    |
| 0.992621 | 0.9988 R.TK[325.13]QTLGYHVYPTC[160.03]R.N                 |
| 0.992617 | 0.9283 R.K[325.13]AC[160.03]QIFVR.N                       |
| 0.992615 | 0.9943 K.VLTFALSEEVRPQDTVSVIGGVAGGSK[325.13]HGR.K         |
| 0.992613 | 0.9453 K.LAQM[147.04]FSDMVLK[325.13]DGFQPSR.S             |
| 0.992605 | 0.9977 R.AK[325.13]HSGDYFTLLR.H                           |
| 0.992604 | 0.9954 R.IFGGLDMLAEK[325.13]LPNLTHLNLSGNK.L               |
| 0.992603 | 0.9942 R.LKEIEHNLSK[325.13]IMK.L                          |
| 0.992603 | 0.9987 R.K[325.13]SFTPDHVYAR.S                            |
| 0.992602 | 0.9606 R.YTILIK[325.13]YGGDEIPFSPYR.V                     |
| 0.992587 | 0.969 K.ITALDEFATK[325.13]LIQNNHYAMEDVATR.R               |
| 0.992586 | 0.8966 K.VILHLK[325.13]EDQTEYLEER.W                       |
| 0.992582 | 0.999 R.NDVAHK[325.13]QLSAFGEYVAEILPK.Y                   |
| 0.992582 | 0.994 K.EAPPMKPEVVK[325.13]THLR.D                         |
| 0.992576 | 0.9914 K.AGLQVYNK[325.13]C[160.03]WKFEHC[160.03]NFNDVT    |
| 0.992574 | 0.9299 R.EVTVPVFYPTK[325.13]VWLEVEPVGM[147.04]LK.E        |
| 0.992574 | 0.999 R.NGVSEENLAK[325.13]LIQHANSVAHSSLIR.N               |
| 0.992571 | 0.9915 K.AYHLQK[325.13]STC[160.03]GK.C                    |
| 0.992568 | 0.9859 R.YVIGQK[325.13]GSGIR.K                            |
| 0.992567 | 0.9913 R.ADGYVLEGK[325.13]ELEFYLR.K                       |
| 0.99256  | 0.9766 R.KADGYNQPSK[325.13]R.R                            |
| 0.992556 | 0.841 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTC[160.03]LR.I    |
| 0.992555 | 0.9512 K.ETAENYLGHATK[325.13]NAVITVPAYFNDSQR.Q            |
| 0.99255  | 0.8689 K.VSASPLLYTLIEK[325.13]TMQNVK.H                    |
| 0.99255  | 0.9984 K.KLPK[325.13]NEPQNATGAPGR.N                       |
| 0.992548 | 0.9986 R.YLNIFGESQPNPK[325.13]TVELLSGVVDQTK.D             |
| 0.992548 | 0.9792 K.FQEHIIQAPK[325.13]PVEAIK.R                       |
| 0.992547 | 0.9314 K.IK[325.13]IIAPPERK.Y                             |
| 0.992543 | 0.9497 K.K[325.13]VNVTVDYIRPASPATETVPAFSER.T              |
| 0.992542 | 0.9567 K.FFGNLMASK[325.13]LSLC[160.03]GEESFGTGSDHIR.E     |
| 0.99254  | 0.9845 R.VTTVTEIGK[325.13]DVIGLR.I                        |

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| 0.99254  | 0.999  | R.MTELYDYPK[325.13]YSC[160.03]HFK.K                   |
| 0.992536 | 0.9435 | K.HVVFGK[325.13]VK.E                                  |
| 0.992536 | 0.9667 | K.MPDLHLK[325.13]APK.I                                |
| 0.992535 | 0.9988 | K.HVVLYPLVAK[325.13]SLR.N                             |
| 0.992529 | 0.9099 | R.SAPGGGSK[325.13]VPQK.K                              |
| 0.992525 | 0.9853 | K.YHPK[325.13]IIGR.K                                  |
| 0.992522 | 0.9361 | R.VTQKSYK[325.13]VSTSGPR.A                            |
| 0.992516 | 0.9642 | R.DPIIAK[325.13]QLFSSLSFGILK.E                        |
| 0.992512 | 0.9982 | R.MK[325.13]QELSSSELSTLLSSLSR.Y                       |
| 0.992503 | 0.9963 | K.KHEEEEAKE[325.13]AER.E                              |
| 0.992499 | 0.955  | R.DAVTYTEHAK[325.13]RK.T                              |
| 0.992497 | 0.9666 | K.FVIKPIDK[325.13]K.A                                 |
| 0.992497 | 0.2155 | R.KDGNASGTTLLEALDC[160.03]ILPPTTRPTDK[325.13]PLR.     |
| 0.992492 | 0.9492 | K.RGILTLK[325.13]YPIEHGIITNWDDMEK.I                   |
| 0.99249  | 0.9959 | K.HAEMVHTGLK[325.13]LER.A                             |
| 0.992479 | 0.9971 | K.FYK[325.13]ELQAHGADELLK.R                           |
| 0.99247  | 0.9849 | R.VEWK[325.13]FDQGDTR.L                               |
| 0.992463 | 0.9414 | K.RGILTLK[325.13]YPIEHGIITNWDDMEK.I                   |
| 0.992462 | 0.9866 | K.APLKPYPVSPSK[325.13]VLIQEK.T                        |
| 0.992462 | 0.8904 | K.K[325.13]AKAAAKPK.K                                 |
| 0.992461 | 0.9666 | R.FVPAEMGTHTVSVK[325.13]YK.G                          |
| 0.992446 | 0.9794 | K.LHQAM[147.04]K[325.13]GVGTR.H                       |
| 0.992442 | 0.8608 | R.K[325.13]MC[160.03]LFAGFQR.K                        |
| 0.992438 | 0.9771 | K.AM[147.04]QDAEVSK[325.13]SDIGEVLVGGMTR.M            |
| 0.992433 | 0.8895 | R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I            |
| 0.992431 | 0.9539 | R.YQK[325.13]STELLIR.K                                |
| 0.99243  | 0.999  | R.SLDIDTAK[325.13]SMLALLGR.T                          |
| 0.992429 | 0.9879 | R.VVIIGAGKPAAVVLQTK[325.13]GSPESR.L                   |
| 0.992422 | 0.9849 | K.K[325.13]GHQFSC[160.03]VC[160.03]LHGDR.K            |
| 0.992422 | 0.9961 | K.DFVLK[325.13]YALPLVGHR.K                            |
| 0.992422 | 0.9559 | K.EIRPALELLEPIEQK[325.13]FVSISDLLVPK.D                |
| 0.992421 | 0.9987 | R.VELSDVQNPAISITENVLHFK[325.13]AQGHGAK.G              |
| 0.99242  | 0.9896 | R.SLSGLILK[325.13]NNVK.A                              |
| 0.992417 | 0.6852 | R.LLLPGELAKHAVSEGTK[325.13]AVTK.Y                     |
| 0.992416 | 0.9275 | R.GVLK[325.13]VFLENVIR.D                              |
| 0.992413 | 0.6369 | R.LQSTLK[325.13]TSLFSFPNTVTGSR.V                      |
| 0.992408 | 0.9433 | K.LWNTLGVK[160.03]K[325.13]YTVQDESHSEWVSC[160.03]VSC. |
| 0.992406 | 0.9534 | R.DLFEDELVPLFEK[325.13]AGPIWDLR.L                     |
| 0.992406 | 0.9495 | K.IQQLVK[325.13]EFFNGKEPSR.G                          |
| 0.992404 | 0.9989 | R.APGAAPSAAAK[325.13]SHR.C                            |
| 0.992386 | 0.9003 | R.GVLK[325.13]EYGVKVLGTSVESIMATEDR.Q                  |
| 0.992383 | 0.9908 | K.KTATAVAHC[160.03]K[325.13]R.G                       |
| 0.992378 | 0.9987 | R.K[325.13]EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR.G       |
| 0.992367 | 0.9988 | R.EQLFAVSHDK[325.13]LLAVSDR.Y                         |
| 0.992366 | 0.9681 | K.EAFTNK[325.13]PNVFTVVTR.G                           |
| 0.992365 | 0.9693 | R.GPDWHLK[325.13]MPK.I                                |
| 0.992364 | 0.9968 | K.FLVHNVK[325.13]LEVLMLC[160.03]NK.S                  |

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| 0.992359 | 0.912 K.KPAAAGVK[325.13]K.V                             |
| 0.992351 | 0.9844 R.K[325.13]EKAQALEELTGFR.E                       |
| 0.992348 | 0.1833 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSA    |
| 0.992348 | 0.9652 K.VSGLLVLDYSK[325.13]DYNHWLATAK.S                |
| 0.992346 | 0.9841 R.VTTVTEIGK[325.13]DVIQLR.I                      |
| 0.992344 | 0.9861 K.WGTDEEK[325.13]FITIFGTR.S                      |
| 0.992341 | 0.9909 K.GVTIPYRPK[325.13]PSSSPVIFAGGQDR.Y              |
| 0.992336 | 0.9986 R.HETEQAEPLELAK[325.13]DYVC[160.03]SQFPTPEAVL    |
| 0.992326 | 0.8607 R.DLTDYLM[147.04]K[325.13]ILTER.G                |
| 0.992325 | 0.9982 K.K[325.13]PHIIIATPGR.L                          |
| 0.992311 | 0.9539 K.K[325.13]VHVIFNYK.G                            |
| 0.992299 | 0.9985 R.GGFC[160.03]NFMHLK[325.13]PISR.E               |
| 0.99229  | 0.983 K.IQASTMAFK[325.13]QMEQISQFLQAAER.Y               |
| 0.992287 | 0.9658 K.QSK[325.13]DGAGFLINLIDSPGHVDFSSEVTAALR.V       |
| 0.992286 | 0.8944 K.WSLLQQQK[325.13]TAR.S                          |
| 0.992272 | 0.9049 R.SHAQK[325.13]NENAR.Q                           |
| 0.992271 | 0.9787 R.GLK[325.13]MAVTFIGNSTAIQELFK.R                 |
| 0.992271 | 0.9656 R.VHFK[325.13]NTR.E                              |
| 0.992267 | 0.8717 R.LLFNDVQTLK[325.13]DGRHPQGEQMYR.R               |
| 0.992264 | 0.9727 K.VVLSK[325.13]LPIGDVATQYFADR.D                  |
| 0.992262 | 0.9987 R.GDEELDSLK[325.13]ATIAGGGVIPHIHK.S              |
| 0.992244 | 0.9945 K.YPASTVQILGAEK[325.13]ALFR.A                    |
| 0.992236 | 0.9931 R.DDHTLK[325.13]IR.K                             |
| 0.992226 | 0.9607 R.VLAEK[325.13]LAAIGEATR.L                       |
| 0.992225 | 0.9961 K.VVAC[160.03]TSAFLLWDPTK[325.13]VPPR.L          |
| 0.99222  | 0.987 R.FFK[325.13]LHQEDQAC[160.03]ATC[160.03]LILAC[160 |
| 0.992219 | 0.9675 R.K[325.13]GQVLSVC[160.03]VEEENIIPYITNVLQNPDLALF |
| 0.992203 | 0.9482 K.EGKPLLK[325.13]AVM[147.04]R.R                  |
| 0.992197 | 0.9143 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H               |
| 0.992193 | 0.9687 R.AGK[325.13]PVIC[160.03]ATQMLESNIK.K            |
| 0.992189 | 0.9894 K.HGEVC[160.03]PAGWK[325.13]PGSETIIPDPAGK.L      |
| 0.992179 | 0.9753 K.IQVTPPGFQLVFLPFADDK[325.13]R.K                 |
| 0.992178 | 0.985 R.FSPNSSNPIIVSC[160.03]GWDK[325.13]LVK.V          |
| 0.992176 | 0.8215 R.VK[325.13]GGGHVAQIYAIR.Q                       |
| 0.992167 | 0.9835 K.EKQDK[325.13]IYFMAGSSR.K                       |
| 0.992156 | 0.893 R.TK[325.13]TEISEMNR.N                            |
| 0.992155 | 0.9597 K.AENGK[325.13]LVINGNPITIFQER.D                  |
| 0.992152 | 0.3183 R.DLTDYLM[147.04]K[325.13]ILTER.G                |
| 0.992152 | 0.97 R.GSNTIASAAADKIPGLLGVFQK[325.13]LIASK.A            |
| 0.992151 | 0.9777 K.NQLK[325.13]DMAIATGGAVFGEEGLTLNLEDVQPHDLGK     |
| 0.992146 | 0.9482 K.LIPDSIGK[325.13]DIEKAC[160.03]QSIYPLHDVFVR.K   |
| 0.992131 | 0.9875 R.K[325.13]NNFSDTGNGFGIQEHLGLK.Y                 |
| 0.992126 | 0.9649 R.SGVSLAALK[325.13]K.A                           |
| 0.992126 | 0.9855 R.K[325.13]YEMFAQTLQQSR.G                        |
| 0.992108 | 0.9642 K.VINTGIK[325.13]VWC[160.03]R.N                  |
| 0.992105 | 0.9727 R.TYHYHC[160.03]ALHDK[325.13]AQIR.E              |
| 0.992103 | 0.9789 K.NAK[325.13]GSNYWR.N                            |

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| 0.992085 | 0.9961 R.NLSK[325.13]ILPALC[160.03]HDITDWVVGTR.V       |
| 0.992083 | 0.9988 R.DAVDWVHYK[325.13]GSLK.E                       |
| 0.992079 | 0.9727 R.DVQIGDIVTVGEC[160.03]RPLSK[325.13]TVR.F       |
| 0.992074 | 0.3975 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR    |
| 0.992068 | 0.6311 R.SEGVVAVLLTK[325.13]K.S                        |
| 0.992067 | 0.795 R.TLSDYNIQK[325.13]ESTLHLVLR.L                   |
| 0.992066 | 0.999 R.SKAEWGVQYVETSAK[325.13]TR.A                    |
| 0.992066 | 0.999 R.LMHK[325.13]LSVEAPPK.I                         |
| 0.992066 | 0.999 R.AYPHVFTK[325.13]GIPNVLR.R                      |
| 0.992061 | 0.9674 K.AFNQ GK[325.13]IFK.-                          |
| 0.992058 | 0.9988 R.FSEFK[325.13]SHSGEFR.Q                        |
| 0.992051 | 0.9734 K.LPSFELLHK[325.13]EMLGGEIIPR.S                 |
| 0.992046 | 0.9173 R.VIISAPSADAPM[147.04]FVMGVNHEK[325.13]YDNSLK.I |
| 0.992037 | 0.9843 K.KDSEDNPQTLLFSATC[160.03]PHWVFNVAK[325.13]K.Y  |
| 0.992032 | 0.9778 R.EK[325.13]QTVHSVFR.K                          |
| 0.992029 | 0.9986 R.LLVPTQYVGAIIGK[325.13]EGATIR.N                |
| 0.992028 | 0.9382 R.LDHK[325.13]FDLM[147.04]YAK.R                 |
| 0.992023 | 0.9394 R.RPDQQLQGEGK[325.13]IIDR.R                     |
| 0.992017 | 0.9883 R.RNEK[325.13]IAVHC[160.03]TVR.G                |
| 0.992015 | 0.9748 R.LALK[325.13]EDKFPR.F                          |
| 0.992014 | 0.9535 K.GFVLHK[325.13]SK.S                            |
| 0.99201  | 0.9011 R.TGVELGKPTHFTVNAK[325.13]AAGK.G                |
| 0.992009 | 0.9501 K.VIPSPFK[325.13]HADIVTTTHK.T                   |
| 0.992002 | 0.9283 R.RGPC[160.03]IYNEDNGIHK[325.13]AFR.N           |
| 0.991995 | 0.9498 K.MAVTFIGNSTAIQELFK[325.13]R.I                  |
| 0.991979 | 0.8573 R.IGSSMK[325.13]SVGEVMAIGR.T                    |
| 0.991976 | 0.9666 K.EDFDSLLQSAK[325.13]K.K                        |
| 0.991973 | 0.9868 R.ISADTIFVTAPHKPTSGIIGVVK[325.13]K.G            |
| 0.991958 | 0.9851 K.KK[325.13]WNLDELPK.F                          |
| 0.991954 | 0.9964 K.IK[325.13]SEHPGLSIGDTAK.K                     |
| 0.991953 | 0.9952 R.SPEEQC[160.03]LDVVTHWIEGEEGRPK[325.13]DDR.H   |
| 0.991952 | 0.9763 R.GTNLNK[325.13]AM[147.04]TLQEAFAFVGAER.C       |
| 0.991951 | 0.9982 R.APGSLIK[325.13]LQGC[160.03]R.E                |
| 0.991946 | 0.8654 R.ALQTGGPHVK[325.13]AR.V                        |
| 0.991943 | 0.0526 K.VK[325.13]DALEFWLQAGVDGFQVR.D                 |
| 0.991943 | 0.9917 R.NEC[160.03]NQC[160.03]KAPK[325.13]PDGPGGGPGG: |
| 0.991941 | 0.892 R.LQAEIEGLK[325.13]GQR.A                         |
| 0.991934 | 0.9916 R.WSPK[325.13]GTYLATFHQR.G                      |
| 0.991932 | 0.9971 R.EITSLK[325.13]EHFGAR.E                        |
| 0.991926 | 0.9529 R.LPSGNHM[147.04]K[325.13]ESR.E                 |
| 0.991918 | 0.9372 R.RAPFDLFENK[325.13]K.K                         |
| 0.991917 | 0.9897 K.K[325.13]DVLETFTVK.S                          |
| 0.991916 | 0.9868 K.LTLHGLQQYYVK[325.13]LKDNEK.N                  |
| 0.99191  | 0.9925 R.WNRPK[325.13]MSLAQK.K                         |
| 0.991903 | 0.9969 R.FVNVVPTFGK[325.13]K.K                         |
| 0.991897 | 0.8634 R.TLLIK[325.13]TVETR.D                          |
| 0.991885 | 0.9954 R.ESGYAGK[325.13]ISQMPVILTPLHFRDPLQK.Q          |

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| 0.991885 | 0.8112 K.VAHALAEGLGVIA[160.03]IGEK[325.13]LDER.E        |
| 0.991882 | 0.967 K.AGYTDK[325.13]VVIGMDVAASEFFR.S                  |
| 0.99188  | 0.9137 K.FEDENFILK[325.13]HTGPGILSMANAGPNTNGSQFFIC[16   |
| 0.991879 | 0.9978 R.K[325.13]GFSEGLWEIENNPTVK.A                    |
| 0.991877 | 0.9949 R.K[325.13]LYGKSPLFGQYFVLENPGTIK.V               |
| 0.991875 | 0.9842 R.NYEQWGK[325.13]LTDC[160.03]VVMRDPASK.R         |
| 0.991874 | 0.9876 R.HQKPAGAPATK[325.13]K.K                         |
| 0.991872 | 0.9934 R.FLTAVNLEHPEMLEK[325.13]ASR.E                   |
| 0.99187  | 0.3628 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E                |
| 0.991867 | 0.7322 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T               |
| 0.991849 | 0.9637 K.IWC[160.03]FGPDGTGPNILTDITK[325.13]GVQYLNEIK.C |
| 0.991837 | 0.9741 R.EM[147.04]AGDNK[325.13]LLGQFTLIGIPPAPR.G       |
| 0.991836 | 0.9514 K.IVADK[325.13]DYSVTANSK.I                       |
| 0.991828 | 0.9637 K.VTRK[325.13]DGNASGTTLEALDC[160.03]ILPPTRPDKI   |
| 0.991824 | 0.963 K.LIEK[325.13]LDIK.L                              |
| 0.991822 | 0.9542 K.MQASIEK[325.13]GGSLPK.V                        |
| 0.991821 | 0.9527 R.FDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V            |
| 0.991819 | 0.9939 R.LRPEDPVLK[325.13]DLYLSWGTVLER.D                |
| 0.991818 | 0.9662 K.K[325.13]HLLVHAPEDK.K                          |
| 0.991789 | 0.9361 R.EIAQDFK[325.13]TDLR.F                          |
| 0.991786 | 0.9901 R.VHIPNDDAQFDASHC[160.03]DSDKGEFGGFGSVTGK[32     |
| 0.991785 | 0.8146 R.DALSDLALHFLNK[325.13]M[147.04]K.I              |
| 0.991784 | 0.9635 K.FVIKPIDK[325.13]K.A                            |
| 0.991777 | 0.7626 K.HGEAQVK[325.13]IWR.R                           |
| 0.991776 | 0.9984 R.TKDIEDVFK[325.13]YGAIK.D                       |
| 0.991772 | 0.5567 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI   |
| 0.991765 | 0.9672 R.EDSQRPGAHLTVK[325.13]K.I                       |
| 0.99176  | 0.5699 R.LEK[325.13]PAKYDDIKK.V                         |
| 0.991747 | 0.9946 R.RGYHK[325.13]VSLQVHPDR.V                       |
| 0.991746 | 0.9957 R.IVGC[160.03]IC[160.03]EEDNTSVVFWLHK[325.13]GE  |
| 0.99174  | 0.9693 R.KK[325.13]TATAVAHC[160.03]K.R                  |
| 0.99173  | 0.9807 R.LVVPATQC[160.03]GSLIGK[325.13]GGC[160.03]K.I   |
| 0.99173  | 0.9541 K.ELNYFAK[325.13]ALESPERPFLAILGGAK.V             |
| 0.991728 | 0.9514 R.LLSDATVEKDESHAGK[325.13]VVLK.S                 |
| 0.991727 | 0.9655 R.LAALADQWQFLVQK[325.13]SAEK.S                   |
| 0.991726 | 0.8943 K.KPAAAGVK[325.13]K.V                            |
| 0.991719 | 0.9987 R.RPVHGESDTEQLQDDDIETTK[325.13]VEMLR.L           |
| 0.99171  | 0.9631 K.YNDK[325.13]HIPGSPFTAK.I                       |
| 0.99171  | 0.9984 R.KYAVLYQPLFDK[325.13]R.F                        |
| 0.991704 | 0.967 K.DAGKAPLK[325.13]IFAQDGEGQR.I                    |
| 0.991701 | 0.9655 K.SK[325.13]FGANAILGVSLAVC[160.03]K.A            |
| 0.991695 | 0.9984 R.AGLIPK[325.13]FVSFLGR.T                        |
| 0.99169  | 0.8603 R.TLLIK[325.13]TVETR.D                           |
| 0.99169  | 0.9573 R.REEAAVDAQQQK[325.13]R.S                        |
| 0.991687 | 0.9522 R.TK[325.13]TEISEM[147.04]NR.N                   |
| 0.991684 | 0.9424 K.NK[325.13]ITITNDQNR.L                          |
| 0.991682 | 0.9319 R.KLPIDVTEGEVISLGLPFGK[325.13]VTNLLM[147.04]LK.G |

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| 0.991673 | 0.9493 R.ASNGDAWVEAHGK[325.13]LYSPSQIGAFVLMK.M          |
| 0.991672 | 0.998 R.K[325.13]PFGAILNLVPLAESVVK.L                    |
| 0.991669 | 0.9938 R.TGTK[325.13]IIHLLK.S                           |
| 0.991663 | 0.9671 R.YIGIVK[325.13]QAGLER.M                         |
| 0.991644 | 0.9959 R.K[325.13]GLEFPMTDLMLSPIHTPQR.T                 |
| 0.991625 | 0.9355 R.SSFYVNGLTGGQK[325.13]C[160.03]SVIR.D           |
| 0.991616 | 0.9866 K.IVKPVK[325.13]VSAPR.V                          |
| 0.991614 | 0.9983 K.SVVFLNLSPLVWHLK[325.13]TER.L                   |
| 0.991611 | 0.9857 K.TEVNSGFFYK[325.13]SAEER.E                      |
| 0.991607 | 0.9567 K.VHLDK[325.13]AQQNNVEHK.V                       |
| 0.991606 | 0.9556 R.TLK[325.13]LTTPTYGDLNHLVSATM[147.04]SGVTTC[16  |
| 0.991604 | 0.9988 R.LQK[325.13]ILHSYVPEIR.D                        |
| 0.991597 | 0.9691 K.SLYYYIQQDTK[325.13]GDYQK.A                     |
| 0.991593 | 0.4296 R.WLPAGDALLQMITIHLPSPVTAQK[325.13]YR.C           |
| 0.991589 | 0.966 R.LRLPLDK[325.13]EPAR.E                           |
| 0.991588 | 0.8366 R.YVEPIEDVPC[160.03]GNIVGLVGVDQFLVK[325.13]TGTT  |
| 0.991584 | 0.964 K.LPVPSK[325.13]QHGGIR.G                          |
| 0.991583 | 0.9958 K.LLSATGESEK[325.13]QFQEAIVFQEEFK.C              |
| 0.991583 | 0.5116 R.VTGALQFGELQK[325.13]QGAGGVEGAEEWWATQAFHQF      |
| 0.99158  | 0.9936 K.GYIWNYGAIQPTWEDPGHNDK[325.13]HTGC[160.03]C[    |
| 0.991555 | 0.9648 K.SKLDQGGVIQDFINALDQLSNPELLFK[325.13]DWSNDVR.    |
| 0.991548 | 0.9194 R.KFGDPVVQSDMK[325.13]HWPFGVINDGDKPK.V           |
| 0.991541 | 0.6152 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGPGGFG,  |
| 0.991537 | 0.9826 R.IVDGK[325.13]VVSETNDTK.V                       |
| 0.991536 | 0.9143 R.IPELNK[325.13]VAR.A                            |
| 0.991533 | 0.9983 R.IEK[325.13]AYAQQLTEWAR.R                       |
| 0.99153  | 0.9587 K.YMNSGPVVAMVWEGLNVVK[325.13]TGR.V               |
| 0.99153  | 0.9942 K.YK[325.13]PLDLRPK.K                            |
| 0.991523 | 0.9136 K.K[325.13]C[160.03]GHTNNLRPK.K                  |
| 0.991509 | 0.997 R.DPTDEGIFISK[325.13]VSPTGAAGR.D                  |
| 0.991509 | 0.9981 R.GADAAQAK[325.13]VLTFLDSHC[160.03]EC[160.03]NEF |
| 0.991485 | 0.9839 R.RYLSPK[325.13]YIK.M                            |
| 0.991481 | 0.9956 R.GAGMPGQHGGITQQELDTVVVK[325.13]TQHEILR.Q        |
| 0.99148  | 0.9934 R.TLFGHLHSQK[325.13]R.N                          |
| 0.991465 | 0.9821 R.K[325.13]QFGAQANVIGPWIQTK.M                    |
| 0.991456 | 0.9747 R.ALK[325.13]MIVDPVEPHGEM[147.04]K.F             |
| 0.991451 | 0.9888 R.NFLGEK[325.13]YIR.R                            |
| 0.991448 | 0.7985 K.K[325.13]KEVAGAKPHITAAEGK.L                    |
| 0.991445 | 0.9968 R.YIK[325.13]EYVTC[160.03]HTC[160.03]R.S         |
| 0.99144  | 0.9962 K.MLALK[325.13]DPVHTVSLQQFIYEK.L                 |
| 0.991438 | 0.8726 K.VFGNEIK[325.13]LEKPK.G                         |
| 0.991434 | 0.9921 R.FPK[325.13]TLFATEDALEVR.R                      |
| 0.991433 | 0.9484 R.K[325.13]ESYSIYVYK.V                           |
| 0.991426 | 0.9436 R.WYHPGC[160.03]FVK[325.13]NR.E                  |
| 0.991417 | 0.8764 R.LQAEIEGLK[325.13]GQR.A                         |
| 0.991414 | 0.9142 K.DSYVGDEAQSK[325.13]R.G                         |
| 0.991406 | 0.9977 R.IEHLIGK[325.13]K.L                             |

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| 0.991382 | 0.9641 K.QKVEGTEPTTAFNLFVGNLNFNK[325.13]SAPELK.T       |
| 0.99137  | 0.9816 K.MEADPELSK[325.13]FLYQLHETEKEDLIR.E            |
| 0.991367 | 0.9985 K.WMEEQAQSLIDK[325.13]TTAAFQQGK.I               |
| 0.991356 | 0.9972 R.FRLDYLPNPQFSTAK[325.13]R.E                    |
| 0.991356 | 0.9932 K.IVQAEGEAEAAK[325.13]MLGEALSK.N                |
| 0.991351 | 0.9964 K.NILFVITK[325.13]PDVYK.S                       |
| 0.991351 | 0.9942 R.GNWEQPQNQNQTQHK[325.13]QRPQATAEQIR.L          |
| 0.991348 | 0.9625 K.WVK[325.13]HWVK.G                             |
| 0.991341 | 0.9464 R.FKK[325.13]PGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V  |
| 0.991326 | 0.8518 R.VTYK[325.13]NVPNWHR.D                         |
| 0.991323 | 0.995 R.VTDPVGDIVSFMHSFEELK[325.13]YGR.A               |
| 0.991314 | 0.9928 K.KGDSSAEELK[325.13]LATQLTGPMVMPVR.N            |
| 0.991312 | 0.8454 R.RQQEGFK[325.13]GTFPDAR.E                      |
| 0.99131  | 0.8989 R.GLFIIDDK[325.13]GILR.Q                        |
| 0.99131  | 0.9871 R.LGNDFHTNK[325.13]R.V                          |
| 0.991306 | 0.9754 K.VK[325.13]LIVLVPPSKPTVNIPSSATIGNR.A           |
| 0.991304 | 0.9647 R.GK[325.13]LGLVGVNLTDGVK.S                     |
| 0.991304 | 0.9926 K.IITFTK[325.13]NNQFQALLQYADPVNAHYAK.M          |
| 0.991293 | 0.8591 R.TYTWLK[325.13]GHQK.S                          |
| 0.991287 | 0.6623 R.KPAGAAK[325.13]KPK.K                          |
| 0.991286 | 0.9388 R.LLLNNGAK[325.13]MPILGLGTWK.S                  |
| 0.991277 | 0.9976 R.IC[160.03]K[325.13]GDHWTTTR.C                 |
| 0.991275 | 0.966 K.LK[325.13]EVFSMAGVVVR.A                        |
| 0.99126  | 0.9988 K.VKDGPGGK[325.13]EATWVVDVK.N                   |
| 0.991258 | 0.9644 R.YASLLK[325.13]YAGEPVPFIEPPESFEFYAQQLR.K       |
| 0.991257 | 0.9729 R.YHVK[325.13]DSSR.H                            |
| 0.99125  | 0.9957 R.MVIITGPPEAQFK[325.13]AQGR.I                   |
| 0.99123  | 0.1189 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTRPDKPLR. |
| 0.991212 | 0.926 R.K[325.13]LAVNM[147.04]VPFPR.L                  |
| 0.991206 | 0.9955 K.VGEFSGANK[325.13]EK.L                         |
| 0.991198 | 0.993 R.TLK[325.13]LTTPTYGDLNHLVSATMSGVTTSLR.F         |
| 0.991195 | 0.9837 K.QGFPMK[325.13]QGVLTGHR.V                      |
| 0.991183 | 0.8868 K.VK[325.13]VLPHTDASK.V                         |
| 0.991179 | 0.9985 R.NTLFNLSNFLDK[325.13]SGLQGYDMSTFIR.R           |
| 0.991175 | 0.9417 R.YK[325.13]LLGGLAVR.R                          |
| 0.991166 | 0.9949 R.GGRPNEIEPPPEMPPWQK[325.13]R.Q                 |
| 0.991164 | 0.9836 K.K[325.13]HPFPC[160.03]PTSYP.T                 |
| 0.99116  | 0.9533 R.LSMQK[325.13]SMQNHAHVFR.V                     |
| 0.991157 | 0.9431 K.NQQFHK[325.13]ER.E                            |
| 0.991148 | 0.9649 K.ITLDNAYMEK[325.13]C[160.03]DENILWLDYK.N       |
| 0.991139 | 0.9739 K.FHHK[325.13]MVDNR.G                           |
| 0.991138 | 0.9268 R.DAVTYTEHAK[325.13]R.K                         |
| 0.991131 | 0.9459 R.MVLAAAGGVEHQQLDLAQK[325.13]HLGGIPWTYAEDA      |
| 0.991122 | 0.9974 R.K[325.13]PAAGLSAAPVPTAPAAGAPLMDFGNDVFPPAPF    |
| 0.991091 | 0.0861 R.EHALLAYTLGVK[325.13]QLIVGVNK.M                |
| 0.991089 | 0.9187 K.GSFK[325.13]TLTLPSLPLNSADEIYELR.V             |
| 0.991086 | 0.9629 K.K[325.13]APDFVIFYAPR.L                        |



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| 0.991083 | 0.9329 K.FETLQAQAGK[325.13]HGDDL.R.N                   |
| 0.991075 | 0.9956 K.K[325.13]GKHDELADSLPC[160.03]AEGEFIFLR.L      |
| 0.991073 | 0.9912 K.IFK[325.13]SQGAALDK.Y                         |
| 0.991073 | 0.9988 K.HGLEK[325.13]PISFVK.N                         |
| 0.991071 | 0.9985 -.MK[325.13]PLVVFVLGGPGAGK.G                    |
| 0.991068 | 0.9463 R.LRENELTYYC[160.03]C[160.03]K[325.13]K.D       |
| 0.991055 | 0.992 K.QDLPNAMNAAEITDK[325.13]LGLHSLR.H               |
| 0.991053 | 0.5847 K.AFGQAK[325.13]HQPTAIIAK.T                     |
| 0.991036 | 0.9957 K.SWHK[325.13]AC[160.03]FR.C                    |
| 0.991025 | 0.998 R.MYSHPLHNDPNLETVYTLC[160.03]EK[325.13]K.A       |
| 0.991023 | 0.9915 K.K[325.13]LDTNSDGLDFSEFLNLIGGLAMAC[160.03]HD   |
| 0.99102  | 0.9958 R.DVPRPILLGASAPLK[325.13]IK.C                   |
| 0.991019 | 0.9987 K.YPWGPK[325.13]LR.I                            |
| 0.991017 | 0.5725 R.LAHYNK[325.13]R.S                             |
| 0.991013 | 0.998 K.AYPLADAHLTK[325.13]K.L                         |
| 0.99101  | 0.9957 R.SEHK[325.13]LSTDHIPILYR.T                     |
| 0.991007 | 0.9426 K.YK[325.13]PAVNQIEC[160.03]HPYLTQEK.L          |
| 0.990997 | 0.9816 R.SGK[325.13]APILIATDVASR.G                     |
| 0.990987 | 0.9855 R.LK[325.13]GFGYAEFEDLSLLSALSNEESLGNRR.I        |
| 0.990966 | 0.8806 K.TLNNK[325.13]FASFIDK.V                        |
| 0.990965 | 0.9629 K.VGDK[325.13]IATR.K                            |
| 0.990959 | 0.9448 K.RVIISAPSADAPMFVM[147.04]GVNHEK[325.13]YDNSLK  |
| 0.990959 | 0.9846 K.VYLPDGTSSSEYDSILVEINK[325.13]R.V              |
| 0.990952 | 0.9495 K.TLQIFNIEMK[325.13]SK.M                        |
| 0.990927 | 0.9396 R.EIAQDFK[325.13]TDLR.F                         |
| 0.990924 | 0.9392 R.TFIAIK[325.13]PDGVQR.G                        |
| 0.990916 | 0.8906 R.ISIEMNGTLEDQLSHLK[325.13]QYER.S               |
| 0.990905 | 0.9881 K.HVEDLLTK[325.13]LK.E                          |
| 0.990899 | 0.9927 K.RPFAYHK[325.13]LLK.D                          |
| 0.990895 | 0.9966 K.ELAC[160.03]K[325.13]MALELLTQEFGIPIER.L       |
| 0.990894 | 0.9861 R.HPAENGK[325.13]SNFLNC[160.03]YVSGFHPSDIEVDLLK |
| 0.990893 | 0.9596 K.ISIPDVGLHLK[325.13]GPK.M                      |
| 0.990884 | 0.9945 R.VLGVPIIVQASQAEK[325.13]NR.A                   |
| 0.990883 | 0.8883 R.IMK[325.13]AQALR.D                            |
| 0.990875 | 0.9952 K.LTLSALIDGK[325.13]NFSAGGHK.V                  |
| 0.990866 | 0.9784 R.K[325.13]EFSPFGTITSAK.V                       |
| 0.990855 | 0.8795 R.GELAIK[325.13]DANAK.L                         |
| 0.990848 | 0.8929 R.TSPEDTVITYK[325.13]C[160.03]EESFVK.I          |
| 0.990842 | 0.8732 K.NQSQGYNQWQQGQFWGQK[325.13]PWSQHYHQGY.-        |
| 0.99084  | 0.991 R.LEGC[160.03]SK[325.13]FVLAHGGR.R               |
| 0.990836 | 0.9945 K.VLDFEHFLPMLQTVAK[325.13]NKDQGTIEDYVEGLR.V     |
| 0.990835 | 0.8182 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M      |
| 0.990834 | 0.7311 R.K[325.13]LPIDVTEGEVISLGLPFGK.V                |
| 0.990829 | 0.9727 R.VKLPSGSK[325.13]K.V                           |
| 0.990817 | 0.8667 K.VEAK[325.13]FINYVK.N                          |
| 0.990816 | 0.884 R.LEK[325.13]HELIEFR.R                           |
| 0.990813 | 0.9636 K.TAPYK[325.13]NVNVQNFHISWK.D                   |

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| 0.990805 | 0.9625 R.TTEEDRGNYC[160.03]VVSATWK[325.13]QR.N           |
| 0.990803 | 0.9957 K.VVLDDK[325.13]DYFLFR.D                          |
| 0.990786 | 0.9932 R.IVQK[325.13]HPHTGDTKEEK.D                       |
| 0.990785 | 0.9762 R.GLPFGC[160.03]SK[325.13]EEIVQFFSGLEIVPNGITLPVDI |
| 0.990781 | 0.9134 R.MFAPTK[325.13]TWR.R                             |
| 0.990758 | 0.8598 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.990755 | 0.8924 K.TVTAM[147.04]DVVYALK[325.13]R.Q                 |
| 0.990747 | 0.9942 K.LPK[325.13]GTVSFHSHSDHR.F                       |
| 0.990744 | 0.9442 K.DKYK[325.13]NIGAK.L                             |
| 0.990741 | 0.9952 R.MVILLC[160.03]NLKPAK[325.13]MR.G                |
| 0.990739 | 0.5635 R.LAHYNK[325.13]R.S                               |
| 0.990737 | 0.9122 R.KFGDPVQSDMK[325.13]HWPQVINDGDKPK.V              |
| 0.990728 | 0.9934 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L         |
| 0.990727 | 0.8525 R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V               |
| 0.990723 | 0.9596 R.FKLPK[325.13]FNFSGSK.V                          |
| 0.990722 | 0.9373 R.IDFSK[325.13]LTSNLVK.Y                          |
| 0.99072  | 0.9874 R.NGNPAPK[325.13]ITWYR.N                          |
| 0.990703 | 0.88 K.FINYVK[325.13]NC[160.03]FR.M                      |
| 0.990699 | 0.9823 K.K[325.13]NFEWVAER.V                             |
| 0.990695 | 0.9838 R.LSSLDNLK[325.13]ASVSQVEADLK.M                   |
| 0.990695 | 0.9838 R.QTESLESLLSK[325.13]SQEHEQR.L                    |
| 0.990683 | 0.7613 R.TMPVEQVFAK[325.13]NFR.V                         |
| 0.990681 | 0.9692 R.YIEVFK[325.13]SHR.T                             |
| 0.990678 | 0.8834 R.GLFIDDK[325.13]GILR.Q                           |
| 0.990671 | 0.9925 R.GFGFILFK[325.13]DAASVEK.V                       |
| 0.990669 | 0.961 K.NGQDLGVAFK[325.13]ISK.E                          |
| 0.990661 | 0.9938 R.SNLPAK[325.13]AIGHR.I                           |
| 0.990653 | 0.9035 R.GGK[325.13]NSTWSGESK.T                          |
| 0.99064  | 0.9858 K.SFVLNLGK[325.13]DSNNLC[160.03]LHFNPR.F          |
| 0.990632 | 0.9306 K.APEEPNIQVNPGLIPVNSK[325.13]EPEEVATC[160.03]VG   |
| 0.990632 | 0.9802 K.AQNLIWNK[325.13]DELKK.V                         |
| 0.990631 | 0.9702 R.MISK[325.13]QFHHQLR.V                           |
| 0.990627 | 0.9928 R.SILIDESTQATEPEC[160.03]MVPVVLGAK[325.13]QLILVC  |
| 0.990625 | 0.9671 K.LLVPGK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E   |
| 0.99061  | 0.9903 K.KSDVEAIFSK[325.13]YGK.I                         |
| 0.990599 | 0.5678 R.SVPHLQK[325.13]VFDR.Y                           |
| 0.990587 | 0.9833 R.KGVAINFVK[325.13]NDDIR.I                        |
| 0.990584 | 0.9695 K.K[325.13]LVGSVNLFSDENVPR.L                      |
| 0.99058  | 0.9615 K.ATGQK[325.13]AAPAPK.A                           |
| 0.990575 | 0.9977 R.VLYAYGYTGEPK[325.13]R.S                         |
| 0.990572 | 0.9582 R.WC[160.03]NEHLK[325.13]C[160.03]VSK.R           |
| 0.990567 | 0.1533 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAN    |
| 0.990566 | 0.4706 K.K[325.13]IGYNPDTVAFVPISGWNGDNMLEPSANM[147.04]   |
| 0.990561 | 0.9952 R.VGVM[147.04]KPPKM[147.04]PQK[325.13]R.R         |
| 0.990559 | 0.9938 R.GFGGITHGPPEK[325.13]K.M                         |
| 0.990555 | 0.8631 R.LDYLSSLK[325.13]VK.G                            |
| 0.990543 | 0.9948 K.VVGAK[325.13]VVTNAR.S                           |

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| 0.990532 | 0.5664 R.ALMLQGVDLLADAVAVTMGPK[325.13]GR.T             |
| 0.99053  | 0.9668 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q              |
| 0.990529 | 0.9531 K.GKWKPPM[147.04]IDNPSYQGIWK[325.13]PRK.I       |
| 0.990519 | 0.9084 K.LFVGGIK[325.13]EDTEEHHLR.D                    |
| 0.990516 | 0.9606 R.LIGNESK[325.13]GEHVPGF[160.03]LPK.K           |
| 0.990505 | 0.9958 R.TK[325.13]TPGPGAQSALR.A                       |
| 0.990495 | 0.9954 K.NEEVLAVLGHELGHWK[325.13]LGHTVK.N              |
| 0.990493 | 0.9901 K.EHNVFQNK[325.13]IHVSQETQQMQMK.F               |
| 0.990492 | 0.444 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I               |
| 0.990491 | 0.98 R.MMK[325.13]LIINSLYK.N                           |
| 0.990476 | 0.989 K.LAK[325.13]TQGNVFATDAILATLMSC[160.03]TR.S      |
| 0.990468 | 0.5847 K.RK[325.13]ELEQVC[160.03]NPIISGLYQGAGGPGPGGF,  |
| 0.990454 | 0.8978 R.AGK[325.13]ITFAEK.V                           |
| 0.990447 | 0.9985 K.K[325.13]LKQSMWSLLTALSGK.E                    |
| 0.990442 | 0.6306 R.LLLPGELAKHAVSEGK[325.13]AVTK.Y                |
| 0.990427 | 0.9586 R.DMFC[160.03]K[325.13]ILHGFK.N                 |
| 0.990421 | 0.8049 R.FVPQEMGVHTVSVK[325.13]YR.G                    |
| 0.99042  | 0.9715 R.VKLPSSGSK[325.13]K.V                          |
| 0.99042  | 0.921 R.KLPIDVTEGEVISLGLPFGK[325.13]VTNLLM[147.04]LK.G |
| 0.990418 | 0.9332 R.RLYWDDLK[325.13]R.K                           |
| 0.990415 | 0.9981 R.FLENHEK[325.13]MTSTTR.Y                       |
| 0.990401 | 0.9982 K.K[325.13]GYFYIPPLATHIC[160.03]DR.N            |
| 0.9904   | 0.9898 R.LPISASHSSK[325.13]TR.S                        |
| 0.990394 | 0.9628 K.SK[325.13]IAHLAGVK.D                          |
| 0.990392 | 0.9601 K.VVVQVLAEPEAVLK[325.13]GAKPK.L                 |
| 0.99039  | 0.8701 K.NVK[325.13]LTVSNVLK.E                         |
| 0.990387 | 0.2609 R.K[325.13]DLYANTVLSGGTMYPGIADR.M               |
| 0.990386 | 0.9976 K.YLHVGYIVPPAPEK[325.13]SIVGMTK.V               |
| 0.990371 | 0.9493 R.TLK[325.13]LTTPTYGDLNHLVSATM[147.04]SGVTTC[16 |
| 0.990368 | 0.9422 R.QAERLKPYVAAQLDVLPEFTLGDK[325.13]K.N           |
| 0.990356 | 0.888 K.TVTAM[147.04]DVVYALK[325.13]R.Q                |
| 0.990349 | 0.8689 K.TVDGPSGK[325.13]LWR.D                         |
| 0.990348 | 0.9569 K.NKYEDEINK[325.13]R.T                          |
| 0.990348 | 0.996 K.NKGDSHLNVQVSNEK[325.13]SGK.G                   |
| 0.990343 | 0.5925 K.KTESHHK[325.13]AK.G                           |
| 0.990341 | 0.9933 R.GAK[325.13]EEHGGLIR.S                         |
| 0.99034  | 0.9959 K.FEQLTLDGHNLPVLC[160.03]VITGK[325.13]GPLR.E    |
| 0.990338 | 0.9893 R.DAGEYEC[160.03]HTPSTDK[325.13]QYFGSYSK.M      |
| 0.990326 | 0.9982 R.ALVSTK[325.13]WLAESIR.T                       |
| 0.990322 | 0.9989 R.YEVVNGKLTNTGTVK[325.13]MLPPLETPLFSGSAYFVVS.   |
| 0.990308 | 0.9807 R.YPEDK[325.13]ITPENLPQILLQK.R                  |
| 0.990307 | 0.9872 R.TAHSLEK[325.13]R.Y                            |
| 0.990303 | 0.9825 R.LQK[325.13]VMNHITDGPR.K                       |
| 0.990293 | 0.9973 R.MLFDYLADK[325.13]HGFR.Q                       |
| 0.990267 | 0.9596 K.IKEK[325.13]YIDQEELNK.T                       |
| 0.990258 | 0.8651 R.FANYIDK[325.13]VR.F                           |
| 0.990257 | 0.9966 R.NGPFGHNDIDSNTIQEILIPASK[325.13]VGLVIGR.G      |

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| 0.990244 | 0.9865 K.GVDDLDFFIGDEAIEKPTYATK[325.13]WPIR.H             |
| 0.990227 | 0.7406 K.AGAHLQGGAK[325.13]R.V                            |
| 0.990223 | 0.9573 R.K[325.13]QITMEELVR.S                             |
| 0.990216 | 0.8882 R.LK[325.13]LLLPWLEAR.I                            |
| 0.990206 | 0.9791 R.KSTGGK[325.13]APR.K                              |
| 0.990197 | 0.9655 R.GTLDPVEK[325.13]ALR.D                            |
| 0.99019  | 0.969 R.MISK[325.13]QFHHQLR.V                             |
| 0.990185 | 0.8642 R.FANYIDK[325.13]VR.F                              |
| 0.990159 | 0.939 K.HKPGGGDVK[325.13]IESQK.L                          |
| 0.990148 | 0.9982 R.AIILAAAPGEK[325.13]LPLFPEPLHVFAPR.A              |
| 0.990142 | 0.9672 R.LQLETEIEALKEELFM[147.04]K[325.13]K.N             |
| 0.990125 | 0.9844 R.ITALK[325.13]SQYEGR.I                            |
| 0.990123 | 0.5768 K.GLVLGPIHK[325.13]NQKDDVAQTDLLQIDPNFGSK.E         |
| 0.99011  | 0.9946 K.LLK[325.13]GAEHITTYTFNTHK.A                      |
| 0.99011  | 0.9567 K.EGK[325.13]LIMGIGHR.V                            |
| 0.990102 | 0.8306 R.FDASFFGVHPK[325.13]QAHTMDPQLR.L                  |
| 0.990096 | 0.908 R.VSFELFADK[325.13]VPK.T                            |
| 0.990085 | 0.9928 R.VK[325.13]TLHPAVHAGILAR.N                        |
| 0.990083 | 0.8266 R.RQQEGFK[325.13]GTFPDAR.E                         |
| 0.99008  | 0.9578 K.GIVEFASK[325.13]PAAR.K                           |
| 0.990065 | 0.9896 R.IIGLK[325.13]PEGVPR.I                            |
| 0.990059 | 0.9904 R.LNRPLTLSEK[325.13]IVYGHLD DPASQEIER.G            |
| 0.990032 | 0.9789 R.IK[325.13]KPEGKPDQK.F                            |
| 0.99003  | 0.9756 K.TC[160.03]TTVAFTQVNSDKGALAK[325.13]LVEAIR.T      |
| 0.990029 | 0.9567 K.EQLAK[325.13]LMATLR.N                            |
| 0.990018 | 0.9964 R.ALFGLYMSASHIASNPK[325.13]ASAK.T                  |
| 0.989986 | 0.86 R.IMK[325.13]AQALR.D                                 |
| 0.989976 | 0.9979 K.DHIMEIFSTYGK[325.13]IK.M                         |
| 0.989972 | 0.9946 R.KFAADAVK[325.13]LER.M                            |
| 0.989961 | 0.982 K.LIQLMEEIMAEK[325.13]ENK.T                         |
| 0.989929 | 0.984 R.LLPHK[325.13]VFEGNRPTNSIVFTK.L                    |
| 0.989921 | 0.9898 R.IHLEIK[325.13]QLNR.Q                             |
| 0.98992  | 0.98 K.AK[325.13]SIVFHR.K                                 |
| 0.989919 | 0.9932 R.LIEEK[325.13]GAVDALAAALAHISGASSFEPR.S            |
| 0.989918 | 0.9556 K.QSK[325.13]DGAGFLINLIDSPGHVDFSSEVTAALR.V         |
| 0.989907 | 0.9906 K.VVLDVGS GTGILC[160.03]MFAAK[325.13]AGAR.K        |
| 0.989907 | 0.9984 K.MK[325.13]NLIPFDQMTIEDLNEAFPETK.L                |
| 0.989894 | 0.9931 K.AIH YALNC[160.03]C[160.03]GLAGGVEQFISDIC[160.03] |
| 0.989882 | 0.9976 R.EHQK[325.13]GRPTSTNPIASIFAWTR.G                  |
| 0.989875 | 0.9948 R.AHVTGPVEDNEK[325.13]C[160.03]YPPPSVQSC[160.03]   |
| 0.989866 | 0.7232 R.K[325.13]LPIDVTEGEVISLGLPFGK.V                   |
| 0.98986  | 0.993 R.IFYHPETTQLMILSASEATVK[325.13]R.V                  |
| 0.98985  | 0.9372 K.VIPSPFK[325.13]HADIVTTTHK.T                      |
| 0.989846 | 0.9787 R.TLAEIAK[325.13]VELDNMPLR.G                       |
| 0.989832 | 0.8513 K.WK[325.13]PPM[147.04]IDNPSYQGIWKPR.K             |
| 0.989822 | 0.9865 R.VGLK[325.13]APGIIPR.I                            |
| 0.989817 | 0.9907 K.RAEVLGHK[325.13]TPEPAPR.R                        |

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| 0.989816 | 0.956 K.GFNK[325.13]VVLK.H                            |
| 0.989811 | 0.9702 R.VTFLPTGITFK[325.13]SVTR.E                    |
| 0.989803 | 0.9422 R.HDSPEDVK[325.13]R.R                          |
| 0.989781 | 0.9984 K.WARPPISMNFVFPFAPSGLK[325.13]VR.Y             |
| 0.98977  | 0.9958 R.NK[325.13]AMINLHIQK.D                        |
| 0.989753 | 0.9946 R.RLSQPESA EK[325.13]HVTQR.L                   |
| 0.989751 | 0.9796 R.YPEDK[325.13]ITPENLPQILLQLK.R                |
| 0.989749 | 0.948 R.SSGPYGGGGQYFAK[325.13]PR.N                    |
| 0.989749 | 0.9933 K.ETAIELGYLTAEQFDEWVKPK[325.13]DMLGPK.-        |
| 0.989729 | 0.9965 K.LTPLK[325.13]LIDSWMGK.G                      |
| 0.989719 | 0.9393 R.FFTVK[325.13]LPVALDPGAK.I                    |
| 0.989715 | 0.9743 K.GHK[325.13]FHHTIGGS.R                        |
| 0.9897   | 0.9971 K.FQMQLPQC[160.03]GHAVHEDAPDK[325.13]VAEAVA'   |
| 0.989696 | 0.9954 R.AGM[147.04]FVSK[325.13]FFGGYVPEMVLTPDDQR.L   |
| 0.98969  | 0.9843 R.DVQDFWISLPGLC[160.03]SEK[325.13]MALSTASDDR.C |
| 0.989687 | 0.9925 R.SC[160.03]SLVLEHQPDNIK[325.13]ALFR.K         |
| 0.989683 | 0.9689 K.AM[147.04]QDAEVSK[325.13]SDIGEVILVGGMTR.M    |
| 0.989669 | 0.9941 K.IQLEQVQEWK[325.13]SK.M                       |
| 0.989659 | 0.7509 K.IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK[325.13]C    |
| 0.989643 | 0.9473 R.GYLNK[325.13]DTHDQLSEPSEVR.S                 |
| 0.989641 | 0.9954 K.EFNKYDTDGSK[325.13]WIK.Q                     |
| 0.989641 | 0.9956 R.LLGLTGSTK[325.13]QVAQASHSYR.V                |
| 0.989635 | 0.8604 R.VFSGLVSTGLK[325.13]VR.I                      |
| 0.989634 | 0.9775 K.LIVLVPPSK[325.13]PTVNIPSSATIGNR.A            |
| 0.98963  | 0.9512 R.YQHLLK[325.13]GK.N                           |
| 0.989625 | 0.8621 K.WSLLQQQK[325.13]TAR.S                        |
| 0.989617 | 0.9959 K.K[325.13]KYDVDTLDMVFLDHWK.D                  |
| 0.989614 | 0.9946 R.EAVELPLTHFELYK[325.13]QIGIDPPR.G             |
| 0.9896   | 0.7059 R.HNGTGGK[325.13]SIYGEK.F                      |
| 0.9896   | 0.9931 K.KASAIK[325.13]LGSSKPK.E                      |
| 0.989595 | 0.8258 R.TK[325.13]TEISEMNR.N                         |
| 0.989588 | 0.8569 K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q        |
| 0.989588 | 0.8821 R.ALMLQGVDLLADAVAVTM[147.04]GPK[325.13]GR.T    |
| 0.989579 | 0.9968 K.LAAAILGGVDQIHIK[325.13]PGAK.V                |
| 0.989561 | 0.9803 K.DHWQK[325.13]YGR.N                           |
| 0.98956  | 0.9867 K.K[325.13]DVLETFTVK.S                         |
| 0.989549 | 0.7824 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S      |
| 0.989536 | 0.879 K.TVTAM[147.04]DVVYALK[325.13]R.Q               |
| 0.989522 | 0.8138 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I      |
| 0.989519 | 0.853 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V              |
| 0.989518 | 0.9827 R.NLHHYK[325.13]LHGVNINVEASK.N                 |
| 0.989515 | 0.997 R.TGAVYLC[160.03]PLTAHK[325.13]DDC[160.03]ER.M  |
| 0.989501 | 0.9406 K.RFDDPGLMLMGFK[325.13]PLVLLK.K                |
| 0.989498 | 0.9773 R.GPLDK[325.13]WR.A                            |
| 0.989497 | 0.9973 K.SLEK[325.13]MGYNAC[160.03]TLHGK.G            |
| 0.989493 | 0.983 R.QIYGAK[325.13]GFSLSVPQAEISGEHLR.I             |
| 0.989493 | 0.9821 R.DFRPLK[325.13]DSR.F                          |

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| 0.98949  | 0.9327 R.KK[325.13]NLQYYDISAK.S                         |
| 0.989473 | 0.9899 K.GNDISSGTVLSDYVGSPPK[325.13]GTGLHR.Y            |
| 0.989471 | 0.9535 K.TVTPAK[325.13]AVTTPGKK.G                       |
| 0.98947  | 0.9929 K.VGSSVK[325.13]HLKPGDR.V                        |
| 0.98947  | 0.9564 R.C[160.03]VRAPGSGLALLPLK[325.13]ITFR.S          |
| 0.989449 | 0.9896 K.NISFTVWDVGGQDK[325.13]IRPLWR.H                 |
| 0.989435 | 0.9948 K.FLEVIK[325.13]PFC[160.03]VILPEIQKPER.K         |
| 0.989433 | 0.9974 R.APQDPASMPK[160.03]TRPPSAPHYLTAVGMGAK[325.13]   |
| 0.989429 | 0.9794 K.RPSSVK[325.13]VFSGK.S                          |
| 0.989428 | 0.9947 K.GLIAAIC[160.03]AGPTALLAHEIGFGSK[325.13]VTTHPLA |
| 0.989426 | 0.9688 K.LRVDK[325.13]AAAAAALQAK.S                      |
| 0.989425 | 0.9651 R.K[325.13]LPAIALDLLR.L                          |
| 0.989417 | 0.9986 K.NTLPTK[325.13]ETIEQEK.R.S                      |
| 0.989408 | 0.9945 R.LGLPPK[325.13]IVIGYQSHADTATK.S                 |
| 0.989381 | 0.9549 K.FK[325.13]MPDLHLK.A                            |
| 0.989379 | 0.911 R.VTQKSYK[325.13]VSTSGPR.A                        |
| 0.989365 | 0.9777 R.TLAEIAK[325.13]VELDNMPLR.G                     |
| 0.989359 | 0.9767 R.LKPAQK[325.13]AFIGFEGVK.G                      |
| 0.989354 | 0.953 K.WLK[325.13]EDKLEC[160.03]SEELGDLVK.S            |
| 0.989352 | 0.9815 K.LSDFFK[325.13]THYR.L                           |
| 0.989335 | 0.9835 K.VSTVFWK[325.13]SGNALFHASTLHR.L                 |
| 0.989332 | 0.6285 R.FGFPEGSVELYAEK[325.13]VATR.G                   |
| 0.989326 | 0.9777 R.SPLVAAMQHFLPVLK[325.13]DR.F                    |
| 0.989311 | 0.9927 K.AIHYNLC[160.03]C[160.03]GLAGGVEQFISDIC[160.03] |
| 0.989307 | 0.9528 K.AKFENLC[160.03]K[325.13]LMK.E                  |
| 0.989302 | 0.9907 K.YGLIYHASLVGQTSPK[325.13]HK.G                   |
| 0.989301 | 0.8606 K.FYEAFSK[325.13]NLK.L                           |
| 0.989297 | 0.9976 K.K[325.13]HLLIGVSSDR.G                          |
| 0.989294 | 0.9976 R.GADAAQAK[325.13]VLTFLDSHC[160.03]EC[160.03]NEF |
| 0.98928  | 0.9777 R.K[325.13]GTVLLADNVIC[160.03]PGAPDFLAHRV.G      |
| 0.989257 | 0.9937 R.VADLADFVK[325.13]IAHPEPAFR.E                   |
| 0.989256 | 0.9967 K.IGEGTYGVVYK[325.13]AR.N                        |
| 0.989249 | 0.9443 K.K[325.13]SAEFLHMLK.N                           |
| 0.989248 | 0.9379 R.GLGK[325.13]GFVPSPTSQPGGHESLVDR.W              |
| 0.98924  | 0.9966 R.GK[325.13]NNTVGLIQLNRPK.A                      |
| 0.98924  | 0.3324 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I   |
| 0.989239 | 0.987 K.ALVAYYQK[325.13]YVDEASKK.E                      |
| 0.989236 | 0.8828 K.KATK[325.13]SPAKPK.A                           |
| 0.989231 | 0.9983 R.FEPVHFVASSSK[325.13]DER.Q                      |
| 0.989229 | 0.7107 K.TFVNITPAEVGVLVGK[325.13]DR.S                   |
| 0.989224 | 0.9837 K.GLAPDLPEDLYHLIK[325.13]K.A                     |
| 0.989219 | 0.9525 R.AVTGYK[325.13]DPYTGQQISLFQAMQK.G               |
| 0.989207 | 0.8186 R.TYTWLK[325.13]GHQK.S                           |
| 0.989197 | 0.9961 R.VQEK[325.13]QHPVPPPAQNQNQVR.S                  |
| 0.989187 | 0.8989 R.AIIPC[160.03]IK[325.13]GYDVIAQAQSGTGK.T        |
| 0.989175 | 0.6051 R.GTK[325.13]VILHLK.E                            |
| 0.989173 | 0.9118 K.DQVDIAVQELLQLK[325.13]AQYK.S                   |

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| 0.989173 | 0.9957 K.VSQAADLK[325.13]QFC[160.03]LQNAQHDPLLTGVSSS       |
| 0.989168 | 0.9967 K.LIHLEIK[325.13]PAIR.N                             |
| 0.989166 | 0.8547 K.DC[160.03]VGPEVEK[325.13]AC[160.03]ANPAAGSVILL    |
| 0.989166 | 0.8817 K.HAVSEGTK[325.13]AVTKYTSAK.-                       |
| 0.989153 | 0.5021 K.VK[325.13]GLVLGPIHK.N                             |
| 0.98915  | 0.9895 K.FYAPWC[160.03]GHC[160.03]K[325.13]TLAPTWEELSK.    |
| 0.989149 | 0.7941 R.FVPQEMGVHTVSVK[325.13]YR.G                        |
| 0.989148 | 0.9546 R.AQDGDFFFSK[325.13]EHTDTFNFR.I                     |
| 0.989147 | 0.8341 R.LPMNK[325.13]EWPSNLDLR.K                          |
| 0.98914  | 0.1 R.K[325.13]DLLFGSIVAVDEPTRPIYR.F                       |
| 0.989127 | 0.9773 R.HIYAK[325.13]VSGGPSLEQR.F                         |
| 0.989126 | 0.9982 R.VK[325.13]LQIWDTAGQER.F                           |
| 0.989121 | 0.9984 K.K[325.13]TTLALHHLSSGHLK.W                         |
| 0.989112 | 0.994 K.LVGGTTPGK[325.13]GGQTHLGLPVFNTVK.E                 |
| 0.989095 | 0.859 R.GELAIK[325.13]DANAK.L                              |
| 0.989081 | 0.4085 R.APQC[160.03]LGK[325.13]FIEIAAR.K                  |
| 0.989072 | 0.9951 K.K[325.13]HPDSSVNFAFSK.K                           |
| 0.989048 | 0.8405 K.WSLLQQQK[325.13]TAR.S                             |
| 0.989042 | 0.9878 K.LVLPMIK[325.13]EHIMQMLQNPDWK.Y                    |
| 0.989037 | 0.9796 K.SDEMNVK[325.13]VLDFEHFLPMLQTVAK.N                 |
| 0.989032 | 0.9424 R.TVVGTIEM[147.04]FHK[325.13]SLER.A                 |
| 0.989028 | 0.996 K.DYGALK[325.13]DIVINANPASPLSLVLHR.L                 |
| 0.989024 | 0.9967 R.K[325.13]VIGIEC[160.03]SSISDYAVK.I                |
| 0.989018 | 0.9809 K.SINDNIAIFTEVQK[325.13]R.S                         |
| 0.989001 | 0.9444 R.DIENLK[325.13]DASSFLAEWQNITK.G                    |
| 0.988994 | 0.9545 K.VC[160.03]LDIYK[325.13]MMPK.L                     |
| 0.988984 | 0.8315 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y          |
| 0.988976 | 0.958 R.ENVIMSQLPC[160.03]IK[325.13]ELVSDANQHVK.S          |
| 0.988969 | 0.8626 R.VVDLMAHMASK[325.13]E.-                            |
| 0.98896  | 0.9492 R.HGEK[325.13]VEEC[160.03]QR.F                      |
| 0.988945 | 0.9436 R.VYLFTIKK[325.13]GILGQHGFLEGPEGIENTR.F             |
| 0.988926 | 0.9443 R.K[325.13]AYGQALAK.L                               |
| 0.988923 | 0.9986 R.VLFRPSDTANSSNQDALSSNTSLK[325.13]LR.K              |
| 0.988908 | 0.9985 R.K[325.13]ELVHLYPR.E                               |
| 0.988907 | 0.9985 K.EVC[160.03]HPDIGGK[325.13]IIMC[160.03]PQC[160.03] |
| 0.988901 | 0.8235 R.LVNQLHLDLLNNK[325.13]LVTLPVSFQALK.N               |
| 0.988897 | 0.9944 R.KFGK[325.13]HGGTIPVPTAEFQDR.I                     |
| 0.988897 | 0.926 R.LGGHGPFPLK[325.13]GITEQQK.E                        |
| 0.988886 | 0.8603 R.VHK[325.13]INNVNK.A                               |
| 0.988877 | 0.9854 K.K[325.13]VHPAVVIR.Q                               |
| 0.988866 | 0.8604 K.LGLK[325.13]SLVSK.G                               |
| 0.988866 | 0.5283 K.AFGQAK[325.13]HQPTAIIAK.T                         |
| 0.98885  | 0.8631 R.GLFIIDDK[325.13]GILR.Q                            |
| 0.988833 | 0.9789 R.HEVLLISAEQDK[325.13]R.A                           |
| 0.988828 | 0.8615 K.KPAAAGVK[325.13]K.V                               |
| 0.988825 | 0.9762 K.NQALFPAC[160.03]VLK[325.13]NAELK.F                |
| 0.988811 | 0.7911 R.TVSLGAGAK[325.13]DELHIVEAEAMNYEGSPIK.V            |

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| 0.98881  | 0.8555 K.TLNNK[325.13]FASFIDK.V                        |
| 0.988803 | 0.9924 K.K[325.13]IKGC[160.03]WDSIHVVEVQEK.S           |
| 0.988801 | 0.9007 K.DQVDIAVQELLQLK[325.13]AQYK.S                  |
| 0.988799 | 0.9775 R.VHFEESK[325.13]LEDLLR.K                       |
| 0.988795 | 0.9372 R.TVVTGIEM[147.04]FHK[325.13]SLER.A             |
| 0.988787 | 0.9367 R.HDSPEDVK[325.13]R.R                           |
| 0.988782 | 0.8472 K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q         |
| 0.98878  | 0.8912 K.AVTK[325.13]YTSAK.-                           |
| 0.988736 | 0.9874 R.AK[325.13]LWC[160.03]STTADYDRDHEWGFC[160.03]F |
| 0.988736 | 0.9532 R.DNSTMGYMM[147.04]AK[325.13]K.H                |
| 0.988726 | 0.9752 K.TAK[325.13]LHVAVK.V                           |
| 0.988726 | 0.9808 R.DFRPLK[325.13]DSR.F                           |
| 0.988723 | 0.9981 K.RPNK[325.13]PLFTALVTQC[160.03]QK.M            |
| 0.988714 | 0.9746 K.K[325.13]FISDKDASIVGFFDDSFSEAHSEFLK.A         |
| 0.988711 | 0.9693 R.YQQFK[325.13]DFQR.R                           |
| 0.988683 | 0.8189 R.ALTQTGGPHVK[325.13]AR.V                       |
| 0.988679 | 0.8961 R.EVTVPVFYPTK[325.13]VWLEVEPVGM[147.04]LK.E     |
| 0.988664 | 0.1304 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI  |
| 0.98866  | 0.9984 R.GHEK[325.13]FGSC[160.03]QQGVAATFTK.D          |
| 0.988657 | 0.8578 K.LDSEDK[325.13]DKEGKPLLK.A                     |
| 0.988646 | 0.9551 K.SKEYFSK[325.13]QK.-                           |
| 0.988643 | 0.9961 K.IVSGEAESEVTPENLQDFVGK[325.13]PVFTVER.M        |
| 0.988639 | 0.8594 K.TVDGPSGK[325.13]LWR.D                         |
| 0.988618 | 0.9529 K.MQLAK[325.13]KEEELQAALAR.V                    |
| 0.988605 | 0.8799 R.AGK[325.13]ITFAEK.V                           |
| 0.9886   | 0.9927 K.GQLTTDQVFPYPSVLNEEQTQFLK[325.13]ELVEPVSR.F    |
| 0.988597 | 0.9912 R.C[160.03]IESLIAVFQK[325.13]YAGK.D             |
| 0.98859  | 0.996 R.AVALDEAISQSTQFHDK[325.13]IDQILESLE.I           |
| 0.988575 | 0.9508 R.DMFC[160.03]K[325.13]ILHGFK.N                 |
| 0.988557 | 0.9738 R.LIK[325.13]VHLDK.A                            |
| 0.988547 | 0.7527 R.HYGGLTGLNK[325.13]AETA.AK.H                   |
| 0.988542 | 0.9901 K.LNKSELK[325.13]ELLTR.E                        |
| 0.988541 | 0.8655 R.LAHYNK[325.13]R.S                             |
| 0.988528 | 0.9556 R.ALPK[325.13]GDFPPPERPQQLPHGLGGIGMGLGPGGQPI    |
| 0.988528 | 0.9169 K.LAQM[147.04]FSDMVLK[325.13]DGFQPSR.S          |
| 0.988508 | 0.8611 K.LTPK[325.13]IGFPWSEIR.N                       |
| 0.988501 | 0.9853 R.AGMFVSK[325.13]FFGGYVPEMVLTPDDQR.L            |
| 0.988497 | 0.9975 R.DLDGNGYPDLIVGSFGVDK[325.13]AVVYR.G            |
| 0.988497 | 0.8701 R.RPISADSAIMNPASK[325.13]VIALK.A                |
| 0.988489 | 0.8493 K.GVSK[325.13]AVEHINK.T                         |
| 0.988467 | 0.9524 K.VSELKEELK[325.13]K.R                          |
| 0.988464 | 0.8602 K.IK[325.13]IIAPPER.K                           |
| 0.98845  | 0.9935 K.VVNSYPLAHK[325.13]VFEEK.T                     |
| 0.988444 | 0.9942 R.LGAQALLGAAK[325.13]M[147.04]LLHSEQHPGQLK.D    |
| 0.988426 | 0.8904 K.SAFLC[160.03]GVMK[325.13]TYR.Q                |
| 0.988388 | 0.9559 R.IGKPAPDFK[325.13]ATAVVDGAFK.E                 |
| 0.988387 | 0.9803 K.K[325.13]TGC[160.03]NVLLIQK.S                 |



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| 0.988386 | 0.9784 K.EHK[325.13]MDQAIIFC[160.03]R.T                 |
| 0.988383 | 0.9645 K.SVSDYDGK[325.13]LSNFK.T                        |
| 0.988368 | 0.9539 R.TATESFASDPILYRPVAVALDTK[325.13]GPEIR.T         |
| 0.98836  | 0.9946 K.GFDALQYQEHLDEIISLNPEFNK[325.13]AVIR.V          |
| 0.988353 | 0.9652 R.AHQVVEDGYEFFAK[325.13]R.Q                      |
| 0.98835  | 0.838 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V                |
| 0.988347 | 0.9907 K.ELFSEK[325.13]HASLQNSQR.T                      |
| 0.988333 | 0.8501 K.TLNNK[325.13]FASFIDK.V                         |
| 0.988321 | 0.9887 K.AAIDWFDGK[325.13]EFHGNIK.V                     |
| 0.988316 | 0.9518 R.K[325.13]NILEESLC[160.03]ELVAK.Q               |
| 0.988315 | 0.9927 R.VLHK[325.13]LTTLHVYEEDPR.E                     |
| 0.988315 | 0.9649 K.NALESYAFNMK[325.13]SAVEDEGLK.G                 |
| 0.988299 | 0.9978 R.AAK[325.13]LHGELR.A                            |
| 0.988293 | 0.9936 K.K[325.13]PPVKPPTPIGFDLEIEKR.I                  |
| 0.98829  | 0.986 K.K[325.13]AADHLKPFLDDSTLR.F                      |
| 0.988289 | 0.8559 K.K[325.13]ALAAAGYDVEK.N                         |
| 0.988288 | 0.847 K.GVSK[325.13]AVEHINK.T                           |
| 0.988275 | 0.8621 R.K[325.13]AVVVC[160.03]PK.D                     |
| 0.988273 | 0.9564 K.KEQTPEHGK[325.13]K.K                           |
| 0.988255 | 0.803 K.EITALAPSTM[147.04]K[325.13]IK.I                 |
| 0.988249 | 0.9675 R.VK[325.13]ILFNKK.E                             |
| 0.988247 | 0.9929 R.VLGVPIIVQASQAEK[325.13]NR.A                    |
| 0.988228 | 0.9961 R.LVK[325.13]PGNQNTQVTEAWN.K.V                   |
| 0.988221 | 0.9952 R.LC[160.03]YSSDHEK[325.13]LKPQYLEELPGQLK.Q      |
| 0.98822  | 0.9933 R.SLSEGHPTAQHEK[325.13]MLC[160.03]DTWC[160.03]II |
| 0.988209 | 0.9983 K.VNLEVIKPWITK[325.13]R.V                        |
| 0.988196 | 0.9411 R.GREEYEGPNK[325.13]KPR.F                        |
| 0.988196 | 0.9909 K.IFVGGLSPDTPEEK[325.13]IR.E                     |
| 0.988195 | 0.9936 K.VVAC[160.03]TSAFLLWDPTK[325.13]VPPR.L          |
| 0.988193 | 0.9686 R.IGK[325.13]PAPDFK.A                            |
| 0.988188 | 0.9785 R.RFEK[325.13]PLEEK.G                            |
| 0.988187 | 0.9699 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T        |
| 0.988187 | 0.9286 R.K[325.13]FLVYVANFDEKDPR.T                      |
| 0.988179 | 0.8542 K.K[325.13]LGEMWNNTAADDKQPYEK.K                  |
| 0.988172 | 0.8546 R.LEK[325.13]HELIEFR.R                           |
| 0.988168 | 0.8584 K.SK[325.13]FADLSEAANR.N                         |
| 0.988168 | 0.9927 R.YHQIGSGK[325.13]C[160.03]EIK.V                 |
| 0.988161 | 0.9303 R.GLKPSC[160.03]TIPLMK[325.13]K.D                |
| 0.988158 | 0.9597 K.ITK[325.13]FENAFLSHVVSQHQAALLGTIR.A            |
| 0.98814  | 0.9985 R.HLSVVTAAK[325.13]VK.C                          |
| 0.988134 | 0.8522 K.VILHLK[325.13]EDQTEYLEER.W                     |
| 0.988128 | 0.9345 K.HLNMK[325.13]LTR.A                             |
| 0.98812  | 0.9447 R.GVQDIVVGEGTHFLIPWVQK[325.13]PIIFDC[160.03]R.S  |
| 0.988117 | 0.8603 R.RQFASQANVVGPIQTK[325.13]MEEIGR.I               |
| 0.988112 | 0.9965 R.QRDEK[325.13]DEHGR.A                           |
| 0.988109 | 0.9314 K.SGTIFDNFLITNDEAYAEFGNETWGVTK[325.13]AAEK.Q     |
| 0.988107 | 0.9279 R.FPGAYLK[325.13]GK.K                            |

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| 0.988094 | 0.97   | R.EVDRPGSK[325.13]VNKK.E                             |
| 0.988093 | 0.9912 | R.KTGQAPGYSYTAANK[325.13]NK.G                        |
| 0.988078 | 0.9242 | K.TAITVEHLAIK[325.13]C[160.03]HWTQR.A                |
| 0.988077 | 0.8634 | K.SYK[325.13]VSTSGPR.A                               |
| 0.988073 | 0.9973 | R.AIK[325.13]AAIWESQHEGPEGAR.S                       |
| 0.988071 | 0.9961 | K.IDLHK[325.13]YLTVK.D                               |
| 0.988065 | 0.9974 | R.MREEFDK[325.13]IGMR.R                              |
| 0.988064 | 0.928  | K.LK[325.13]TNHIGHTGYLNTVTVSPDGSLC[160.03]ASGGK      |
| 0.988062 | 0.8854 | R.MFAPTK[325.13]TWR.R                                |
| 0.988051 | 0.9879 | R.LC[160.03]IEHFDK[325.13]LLVEDINK.D                 |
| 0.988027 | 0.1252 | K.EITALAPSTMKIK[325.13]IIPPER.K                      |
| 0.988016 | 0.9871 | R.DKLC[160.03]GPYEK[325.13]FIC[160.03]EQDHQNFLR.L    |
| 0.987998 | 0.9663 | K.RPK[325.13]NFGIGQDIQPK.R                           |
| 0.987995 | 0.8379 | K.EIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q              |
| 0.987987 | 0.9218 | K.EGKPLLK[325.13]AVM[147.04]R.R                      |
| 0.98798  | 0.9954 | R.IHMOVSK[325.13]R.S                                 |
| 0.987974 | 0.9877 | K.TEFK[325.13]VDSDDQWGEYSC[160.03]VFLPEPM[147.04]R.R |
| 0.987969 | 0.9323 | R.HDSPEDVK[325.13]R.R                                |
| 0.987934 | 0.8595 | K.FDLMYAK[325.13]R.A                                 |
| 0.987919 | 0.9823 | K.EAEIHSK[325.13]PVFITVK.M                           |
| 0.987912 | 0.9497 | K.C[160.03]DPRHGK[325.13]YMAC[160.03]C[160.03]LLY    |
| 0.987887 | 0.9099 | R.FEPYANPTK[325.13]R.Y                               |
| 0.987875 | 0.998  | K.EDDLNSFNATDLK[325.13]DLSSHQLNEFLAQTLQR.A           |
| 0.987874 | 0.9244 | R.FK[325.13]IPGSPPEMGR.G                             |
| 0.987874 | 0.7884 | K.KLEDGPK[325.13]FLK.S                               |
| 0.987869 | 0.9924 | R.IAAK[325.13]FITHAPPGFNEVFNDVR.L                    |
| 0.987863 | 0.9759 | R.GIDIHGVPPYVINVTLPDEK[325.13]QNYVHR.I               |
| 0.987859 | 0.8296 | K.DGNASGTTLEALDC[160.03]ILPPTRPTDK[325.13]PLR.L      |
| 0.987853 | 0.9813 | K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT      |
| 0.98784  | 0.996  | K.TVK[325.13]HGAPSPSHPIAPQAAAAAALR.R                 |
| 0.987837 | 0.9499 | K.FGK[325.13]EVAVK.M                                 |
| 0.987814 | 0.9417 | R.KVLRDNIQGITK[325.13]PAIR.R                         |
| 0.987811 | 0.9965 | K.K[325.13]HNPGKPGEGTPISSR.E                         |
| 0.9878   | 0.9922 | R.LNK[325.13]C[160.03]GVISPR.F                       |
| 0.987786 | 0.9829 | R.K[325.13]VVVSHSTHR.T                               |
| 0.98777  | 0.9879 | K.YGVK[325.13]VGLTNYAAAYC[160.03]TGLLLAR.R           |
| 0.98777  | 0.9962 | R.TLK[325.13]TLLHTLC[160.03]K.L                      |
| 0.987765 | 0.9936 | K.RPLEDGDQPDAK[325.13]K.V                            |
| 0.98773  | 0.9959 | R.YSASKPLK[325.13]GAR.I                              |
| 0.987729 | 0.5217 | K.ADK[325.13]DYHFKVDNDENEHQLSLR.T                    |
| 0.987711 | 0.9976 | K.ELQENQDEIENMMNAIFK[325.13]GVFVHR.Y                 |
| 0.9877   | 0.9981 | R.ELFSNLQEFAGPSGK[325.13]LSLLEVGC[160.03]GTGANF      |
| 0.98769  | 0.9947 | K.IAFAITAIK[325.13]GVGR.R                            |
| 0.987679 | 0.9716 | R.GANLK[325.13]DYYSR.K                               |
| 0.987672 | 0.9982 | R.IQFAC[160.03]SVC[160.03]K[325.13]FR.S              |
| 0.987635 | 0.9353 | R.YTILIK[325.13]YGGDEIPFSPYR.V                       |
| 0.987626 | 0.9603 | K.KNPIAK[325.13]IHSDLAER.G                           |

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| 0.98762  | 0.998 K.LAK[325.13]EWC[160.03]FKPC[160.03]EIR.E          |
| 0.987603 | 0.9899 R.AIK[325.13]FLSTK.L                              |
| 0.987602 | 0.9982 K.YPWGPK[325.13]LR.I                              |
| 0.987593 | 0.9972 R.TK[325.13]FSASQFWDDC[160.03]RK.Y                |
| 0.98758  | 0.8528 K.EIK[325.13]ILNIFGVK.G                           |
| 0.987574 | 0.9295 K.IGKPHTVPC[160.03]K[325.13]VTGR.C                |
| 0.987567 | 0.989 K.HALIIYDDLK[325.13]QAVAYR.Q                       |
| 0.987564 | 0.8784 K.GIYQSLEGAVQAGQK[325.13]VPPGYHPLDVEKEWGK.L       |
| 0.98756  | 0.8636 R.K[325.13]MFTLLDVVNR.K                           |
| 0.987544 | 0.9369 R.LGDK[325.13]HATLQK.S                            |
| 0.987541 | 0.9979 K.FK[325.13]LPVWETIVC[160.03]TMR.E                |
| 0.987525 | 0.9759 K.GHLPK[325.13]LQMPSFK.V                          |
| 0.98752  | 0.914 R.LLLNNGAK[325.13]MPILGLGTWK.S                     |
| 0.987516 | 0.9969 R.LGQMVLSGVDTVLGK[325.13]SEEWADNHLPLTDAELAR.      |
| 0.987514 | 0.9739 R.K[325.13]QFGAQANVIGPWQTK.M                      |
| 0.987512 | 0.9733 R.HM[147.04]YHSLYLK[325.13]VK.G                   |
| 0.987512 | 0.4016 R.VTGALQFGELQK[325.13]QGAGGVEGAEWATQAFHQF         |
| 0.98751  | 0.9938 R.TLTGTVIDSGDGVTHVIPVAEGYVIGSC[160.03]IK[325.13]  |
| 0.987503 | 0.9472 K.FK[325.13]MPDLHLK.A                             |
| 0.987502 | 0.9938 R.VM[147.04]TIAPGLFGTPLLTSLEPK[325.13]VC[160.03]N |
| 0.987493 | 0.998 K.GNLK[325.13]MIHILLYK.A                           |
| 0.987493 | 0.9251 R.IYC[160.03]KPHFNQLFK[325.13]SK.G                |
| 0.987488 | 0.9904 K.LNNLVLFDK[325.13]ATYDK.L                        |
| 0.987482 | 0.9199 K.TLHPDLGTDKDK[325.13]EQWK.E                      |
| 0.98748  | 0.998 R.AFK[325.13]SSHNLAVHR.M                           |
| 0.98748  | 0.9973 K.KLPK[325.13]NEPQNATGAPGR.N                      |
| 0.987467 | 0.8595 R.IAK[325.13]AVNEK.S                              |
| 0.987454 | 0.9964 R.GGLGLSGAK[325.13]ANYR.G                         |
| 0.987448 | 0.9915 K.TIYTAPLDMLQVTQAK[325.13]KSQAIASDVDYK.H          |
| 0.987444 | 0.9648 R.GLPFGC[160.03]SK[325.13]EEIVQFFSGLEIVPNGITLPVDI |
| 0.987437 | 0.9935 K.VLSVC[160.03]PSNKPAIVEAGGMQALGK[325.13]HLTSN    |
| 0.987425 | 0.9012 R.K[325.13]LLEGEESR.I                             |
| 0.987421 | 0.9964 R.NYGFQGGQNK[325.13]YVGTGGIDQKPR.T                |
| 0.987418 | 0.9497 R.IK[325.13]AAVPSIK.F                             |
| 0.987408 | 0.9749 R.K[325.13]ITINPGC[160.03]VVVDGMPPGVSK.A          |
| 0.987407 | 0.7047 R.TLSDYNIQK[325.13]ESTLHLVLR.L                    |
| 0.987399 | 0.9853 K.LVLPMIK[325.13]EHIMQMLQNPDWK.Y                  |
| 0.987397 | 0.9461 R.EK[325.13]LQEEMLQREEAENTLQSFR.Q                 |
| 0.98739  | 0.7941 K.EGKPLLK[325.13]AVMR.R                           |
| 0.987376 | 0.9966 R.HQLVHTGEK[325.13]PFQC[160.03]TFEGC[160.03]GK.R  |
| 0.987375 | 0.9933 K.LHVGNISPTC[160.03]TNK[325.13]ELR.A              |
| 0.987341 | 0.9831 K.GK[325.13]GSPRPQAPK.A                           |
| 0.987332 | 0.9905 K.K[325.13]YHNVGLSK.C                             |
| 0.987326 | 0.9984 K.LDFLRPYTPNK[325.13]K.G                          |
| 0.987325 | 0.8441 R.GAVGALLVYDIAK[325.13]HLTYENVER.W                |
| 0.987319 | 0.9955 R.TDLK[325.13]THIVSIPLR.G                         |
| 0.987314 | 0.6364 R.VSFELFADKVPK[325.13]TAENFR.A                    |

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| 0.987309 | 0.9446 R.FVPAEMGHTHTVSVK[325.13]YK.G                      |
| 0.987308 | 0.9951 R.WLSTRPEVASIEPLGLDEQQC[160.03]SQK[325.13]AVVQ     |
| 0.987303 | 0.9946 K.HLTHAQSTLDAK[325.13]ATK.A                        |
| 0.987303 | 0.9973 K.LHK[325.13]PPADSGVDLR.E                          |
| 0.987302 | 0.9644 R.LPFK[325.13]ATTPVIM[147.04]VGPGTGVAPFIGFIQER.A   |
| 0.987301 | 0.9801 R.C[160.03]LTPPK[325.13]C[160.03]HTPPLYR.M         |
| 0.987295 | 0.998 R.SPGLPMSDLK[325.13]THNVHVEIEQR.W                   |
| 0.987294 | 0.9977 K.EPESILQVLSQMEK[325.13]IVR.I                      |
| 0.987266 | 0.9912 R.IFYHPETTQLMILSASEATVK[325.13]R.V                 |
| 0.987256 | 0.9558 K.YHTINGHNC[160.03]EVK[325.13]K.A                  |
| 0.987244 | 0.9872 R.LQHYAK[325.13]IAADFR.N                           |
| 0.987243 | 0.9858 K.FHEK[325.13]VIAALLQTMEDQGNQR.V                   |
| 0.987223 | 0.9955 R.LKDK[325.13]WDELK.E                              |
| 0.987198 | 0.9257 K.LAQSHHVK[325.13]QVLVAPGNAGTAC[160.03]SEK.I       |
| 0.987186 | 0.9933 R.AVPEDAK[325.13]QLASFLHGNASLLFR.R                 |
| 0.987182 | 0.966 K.RTDEAAAFQK[325.13]LMSNLDSNR.D                     |
| 0.987172 | 0.9474 R.K[325.13]PVTVHSR.A                               |
| 0.987171 | 0.9645 R.EK[325.13]QTVHSVFR.K                             |
| 0.987171 | 0.9088 K.K[325.13]LRPLYDIPYMFEAR.E                        |
| 0.98717  | 0.8431 R.VVDLMAHMASK[325.13]E.-                           |
| 0.987157 | 0.9983 R.LKVDK[325.13]EDVMTTC[160.03]LIK.G                |
| 0.98715  | 0.9947 R.GPFSEISAFK[325.13]TC[160.03]LPGFPGAPC[160.03]AIK |
| 0.987149 | 0.9927 R.IFGSNK[325.13]WTTEQQQR.F                         |
| 0.987141 | 0.9973 K.LALK[325.13]FHPDK.N                              |
| 0.987122 | 0.9677 R.ELTGLK[325.13]ALYETELADAR.R                      |
| 0.987117 | 0.9263 R.EAGSQK[325.13]DENLALYVENQFR.E                    |
| 0.987102 | 0.9482 K.KVEELEGEITTLNHK[325.13]LQDASAEVER.L              |
| 0.987095 | 0.9922 R.VLGVPIIVQASQAEK[325.13]NR.A                      |
| 0.987092 | 0.9944 R.THVDSHGHNVEFK[325.13]ER.I                        |
| 0.987088 | 0.9463 R.AGQK[325.13]GYHHR.T                              |
| 0.987083 | 0.973 R.SGEPQTFTLK[325.13]FK.R                            |
| 0.98707  | 0.8525 K.TVTAM[147.04]DVVYALK[325.13]R.Q                  |
| 0.987058 | 0.9935 R.LSDGSLK[325.13]LYPFQC[160.03]FLAHDQAVR.T         |
| 0.987054 | 0.7909 R.TK[325.13]TEISEMNR.N                             |
| 0.987035 | 0.9971 K.WKDEDISQK[325.13]DMYNIIR.I                       |
| 0.987019 | 0.8492 R.VLADPSDDTK[325.13]GFFDPNTHENLTYR.Q               |
| 0.987012 | 0.9982 R.LSAKPAPPKPEPK[325.13]PR.K                        |
| 0.987008 | 0.6189 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                 |
| 0.987006 | 0.9973 R.LGVLHVGQK[325.13]LEEQDEFEK.I                     |
| 0.987003 | 0.9874 K.NADPILISLK[325.13]HGYPGK.N                       |
| 0.986999 | 0.9955 R.KTPC[160.03]GEGSK[325.13]TWDR.F                  |
| 0.986997 | 0.9641 R.VK[325.13]ILFNKK.E                               |
| 0.986969 | 0.8872 R.HGK[325.13]YM[147.04]AC[160.03]C[160.03]LLYR.G   |
| 0.986954 | 0.8718 K.K[325.13]C[160.03]GHTNNLRPK.K                    |
| 0.986948 | 0.8606 K.AVTK[325.13]YTSSK.-                              |
| 0.986942 | 0.9397 R.GAAKEAAGK[325.13]SSGPTSLFAVTVAPPGAR.Q            |
| 0.986941 | 0.9512 K.VTNVK[325.13]DGTTHQTSLELFMYLNEVAGK.H             |

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| 0.986934 | 0.9973 K.SGLGSGPK[325.13]C[160.03]C[160.03]H.-            |
| 0.986931 | 0.7739 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I          |
| 0.986928 | 0.9808 R.K[325.13]NNFSDTGNGFGIQEHIDLGK.Y                  |
| 0.986924 | 0.9976 R.WFK[325.13]DHYQDPVPGITPSSSSR.T                   |
| 0.986917 | 0.9949 R.YHPK[325.13]SQPFVDHVFTFTILDNR.I                  |
| 0.986915 | 0.9625 K.EKPGPEDK[325.13]LHEQC[160.03]RPWR.K              |
| 0.9869   | 0.9462 K.MFLGDNAHLSIINEYLSQSYQK[325.13]FR.R               |
| 0.986893 | 0.9268 R.DLFEDELVPLFEK[325.13]AGPIWDLR.L                  |
| 0.986884 | 0.9214 R.GFPTIYFSPANK[325.13]K.L                          |
| 0.986881 | 0.998 K.IQHSITAQDHQPTPDSC[160.03]IISMVVGQLK[325.13]AC     |
| 0.986863 | 0.967 R.HGESGSMVAFHQQTGPSYSESK[325.13]R.L                 |
| 0.98685  | 0.5556 R.GTK[325.13]VILHLK.E                              |
| 0.986847 | 0.9627 K.K[325.13]EM[147.04]QPTHPIR.L                     |
| 0.986843 | 0.9869 K.KYGGLK[325.13]TPTQLEGATR.G                       |
| 0.98684  | 0.9914 K.K[325.13]PMVLGHEASGTVEK.V                        |
| 0.986838 | 0.7409 K.YDNSLK[325.13]IISNASC[160.03]TTNC[160.03]LAPLAK. |
| 0.986836 | 0.9944 K.NLVLAGIK[325.13]AVTIHDTEK.C                      |
| 0.986835 | 0.9554 R.SYSK[325.13]LLC[160.03]GLLAER.L                  |
| 0.98682  | 0.9946 R.TSK[325.13]LLSDPNYGVHLPVK.L                      |
| 0.986813 | 0.9962 R.EISYAIK[325.13]NIHGVR.T                          |
| 0.986805 | 0.9677 R.FHMYEGYPLWK[325.13]VTFPVR.V                      |
| 0.986794 | 0.9878 R.GVEVTVGHEQEEGGK[325.13]WPYAGTAEAIK.A             |
| 0.986791 | 0.943 R.ANQK[325.13]HQGLK.L                               |
| 0.98679  | 0.9679 R.KENPLQFK[325.13]FR.A                             |
| 0.986776 | 0.9944 R.HLK[325.13]TSGGQGYK.F                            |
| 0.986771 | 0.994 R.MHFSK[325.13]TK.H                                 |
| 0.986769 | 0.854 R.WQLK[325.13]ANEALR.L                              |
| 0.986766 | 0.9634 R.EK[325.13]QTVHSVFR.K                             |
| 0.986742 | 0.9777 R.LSYNTASNK[325.13]TR.L                            |
| 0.986714 | 0.9982 R.INAGMLAQFIDK[325.13]PVC[160.03]FVGR.L            |
| 0.986707 | 0.9898 K.VRDK[325.13]LNNLVLFDK.A                          |
| 0.986704 | 0.7321 R.LNSASLK[325.13]QPYITQNYFPVGTVEYEC[160.03]RPG     |
| 0.986694 | 0.9964 R.IK[325.13]IQHMELQLIK.K                           |
| 0.986692 | 0.9974 R.TKDIEDVFYK[325.13]YGAIR.D                        |
| 0.986681 | 0.9957 K.KVGDDIAK[325.13]ATGDWK.G                         |
| 0.986674 | 0.9973 K.VK[325.13]LEGHELPADLPPHLVPPSK.R                  |
| 0.986657 | 0.9739 K.GEHSIVYLK[325.13]PSYAFGSVGK.E                    |
| 0.986652 | 0.9969 R.VAGC[160.03]SVHK[325.13]GYAFVQYSNER.H            |
| 0.98665  | 0.9183 K.LITEDVQGK[325.13]NC[160.03]LTNFHGM DLTR.D        |
| 0.98663  | 0.9906 R.ARPPSGSSK[325.13]ATDLGGTSQAGTSQR.F               |
| 0.986627 | 0.9876 R.K[325.13]FLPLFDR.V                               |
| 0.986626 | 0.9977 R.IVEK[325.13]YGYTHLSAGELLR.D                      |
| 0.986621 | 0.9451 R.AGLGEEFEK[325.13]EIR.T                           |
| 0.986599 | 0.9948 K.TAHETDKSEGGK[325.13]R.K                          |
| 0.986598 | 0.9785 R.IALSVHK[325.13]K.N                               |
| 0.986595 | 0.9219 K.IVADK[325.13]DYSVTANSK.I                         |
| 0.986589 | 0.9421 K.NNIK[325.13]LYVR.R                               |

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| 0.986589 | 0.9152 K.EGVHGGLINK[325.13]K.C                           |
| 0.986584 | 0.9737 K.IC[160.03]DQWDNLGALTQK[325.13]R.R               |
| 0.986572 | 0.9744 K.AAYLQETGK[325.13]PLDETLKK.A                     |
| 0.986562 | 0.9774 R.LSYNTASNK[325.13]TR.L                           |
| 0.986558 | 0.8515 K.KPAAATVTK[325.13]K.V                            |
| 0.986542 | 0.5123 K.KAK[325.13]VAKPK.K                              |
| 0.986524 | 0.8809 K.GSFK[325.13]TLTLPSLPLNSADEIYELR.V               |
| 0.986522 | 0.9769 R.DFKPGDLIFAK[325.13]MK.G                         |
| 0.98652  | 0.9379 K.TVLSSHK[325.13]VLPLEALVTDAGEVTEAGK.A            |
| 0.986514 | 0.873 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.   |
| 0.986507 | 0.9543 R.SYSK[325.13]LLC[160.03]GLLAER.L                 |
| 0.986501 | 0.9935 K.NAK[325.13]FYPVTR.E                             |
| 0.986498 | 0.9775 K.EISLWFK[325.13]PEELVDYK.S                       |
| 0.986491 | 0.9976 K.VVMEFLHEC[160.03]MVNK[325.13]FK.K               |
| 0.986486 | 0.9982 K.K[325.13]FLPGMAIGYSSSK.L                        |
| 0.986485 | 0.9155 R.AAAEK[325.13]LFGNM[147.04]EGDC[160.03]PSDWK.T   |
| 0.986479 | 0.9556 K.LLEPVLLLGK[325.13]ER.F                          |
| 0.986478 | 0.9927 R.RDTALETALNAK[325.13]AYK.R                       |
| 0.986477 | 0.9575 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q                |
| 0.986467 | 0.7334 R.VIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I           |
| 0.986427 | 0.9953 R.KTPC[160.03]GEGSK[325.13]TWDR.F                 |
| 0.986426 | 0.9811 R.LNRLPAAGVGDMVMATVK[325.13]K.G                   |
| 0.986421 | 0.8543 K.HVSLNK[325.13]AK.K                              |
| 0.986395 | 0.9365 K.APLK[325.13]IFAQDGEGQR.I                        |
| 0.986388 | 0.9693 R.TAK[325.13]LWALPQC[160.03]QLLGVFSGHR.R          |
| 0.986387 | 0.9968 K.FLHK[325.13]HDLDLIC[160.03]R.A                  |
| 0.986375 | 0.8552 K.AVTK[325.13]YTSSK.-                             |
| 0.986375 | 0.9314 R.MIAGQVLDINLAAEPK[325.13]VNR.G                   |
| 0.986362 | 0.9975 K.EK[325.13]LNLLHEFLQTEIK.N                       |
| 0.986353 | 0.92 R.EHFEEK[325.13]WGTLTDC[160.03]VVMR.D               |
| 0.986347 | 0.9958 R.TDLVSPK[325.13]HALMVFR.V                        |
| 0.986335 | 0.9981 K.FLIHLSK[325.13]K.S                              |
| 0.986332 | 0.9743 R.K[325.13]LSDQC[160.03]TGLQGFLVFHSGGGTSGSGFTSI   |
| 0.986317 | 0.8346 K.TVDGPSGK[325.13]LWR.D                           |
| 0.986314 | 0.9796 R.ELLTLDEK[325.13]DPRR.L                          |
| 0.986302 | 0.855 R.GGK[325.13]NSTWSGESK.T                           |
| 0.986297 | 0.965 R.TDITYAGFM[147.04]DVISIDK[325.13]TGENFR.L         |
| 0.986291 | 0.9933 R.TGIIVTTSEAVLLQLVADK[325.13]DHPK.F               |
| 0.986289 | 0.945 K.IHLAQSLHK[325.13]LSTAC[160.03]PGR.V              |
| 0.986288 | 0.9737 K.VHVIFNYK[325.13]GK.N                            |
| 0.986286 | 0.9825 R.VAILK[325.13]ANLR.K                             |
| 0.986276 | 0.9738 K.HALK[325.13]GAGTNEK.V                           |
| 0.986259 | 0.9832 R.SYSDPPLK[325.13]FMSVQRPGPYDRPGTAR.R             |
| 0.986258 | 0.9222 R.FDDAVVQSDMK[325.13]HWPFMVVNDAGRPK.V             |
| 0.986256 | 0.7181 R.GC[160.03]GPEK[325.13]DHVYLQLHHLPEQLATR.L       |
| 0.98625  | 0.8339 K.TVDGPSGK[325.13]LWR.D                           |
| 0.98625  | 0.9455 R.C[160.03]PEALFQPSFLGMESC[160.03]GIHETTFNSIMK[:] |

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| 0.986249 | 0.9354 R.LLAAGK[325.13]VPQR.A                           |
| 0.986247 | 0.8323 K.EAAGK[325.13]SSGPTSLFAVTVAPPGAR.Q              |
| 0.986218 | 0.862 R.K[325.13]AC[160.03]QIFVR.N                      |
| 0.986206 | 0.9314 K.RDELTLEGIK[325.13]QFFVAVER.E                   |
| 0.986182 | 0.9397 R.MPSLPSYK[325.13]VGDK.I                         |
| 0.986181 | 0.975 K.WGTDEEK[325.13]FITIFGTR.S                       |
| 0.986166 | 0.6318 R.HNGTGGK[325.13]SIYGEK.F                        |
| 0.986153 | 0.983 R.YHPDK[325.13]NKEPGAEEK.F                        |
| 0.986135 | 0.9975 K.FGDLDEQEFVYKEPAITK[325.13]LAEISHR.L            |
| 0.986135 | 0.0907 K.WGDAGA EYVVESTGVFTTMEK[325.13]AGAH LQGGAK.R    |
| 0.986129 | 0.8405 K.INQVFHGSC[160.03]ITEGNETLK[325.13]TLIK.L       |
| 0.986124 | 0.9784 K.K[325.13]EGHWDC[160.03]SIC[160.03]LVR.N        |
| 0.986103 | 0.9931 R.VM[147.04]TIAPGLFGTPLLTSLEK[325.13]VC[160.03]N |
| 0.986095 | 0.9455 K.LRK[325.13]EAEQEAAR.R                          |
| 0.986084 | 0.4953 R.TVSLGAGAKDELHIVEAEAMNYEGSPIK[325.13]VTLATLK.   |
| 0.986041 | 0.9922 K.FLDASGAK[325.13]LDYR.R                         |
| 0.986029 | 0.9968 R.LIAEK[325.13]VQAERPDTMLGVVC[160.03]GALHVADV    |
| 0.986021 | 0.9942 R.DQLASIFLAC[160.03]TSHK[325.13]VR.R             |
| 0.98602  | 0.9012 K.GIVEFSGK[325.13]PAAR.K                         |
| 0.986017 | 0.8953 K.NK[325.13]GLWVPEGQR.A                          |
| 0.986013 | 0.9862 R.LK[325.13]VFDGIPPPYDK.K                        |
| 0.986005 | 0.9231 R.GGNRFEPYANPTK[325.13]R.Y                       |
| 0.985992 | 0.986 R.K[325.13]HIC[160.03]PYR.T                       |
| 0.98599  | 0.9978 R.NSDPTYGQQGHPNTWK[325.13]R.E                    |
| 0.985962 | 0.9506 K.YGK[325.13]IVGC[160.03]SVHK.G                  |
| 0.985961 | 0.6844 R.HIADLAGNSEVILPVPAFNVINGGSHAGNK[325.13]LAMQ     |
| 0.985956 | 0.9199 R.LPSGNHM[147.04]K[325.13]ESR.E                  |
| 0.985938 | 0.853 R.WQLK[325.13]ANEALR.L                            |
| 0.985934 | 0.9736 R.AYGLK[325.13]SGLK.K                            |
| 0.985926 | 0.9187 R.GFGFVTFDDHDPVVK[325.13]IVLQK.Y                 |
| 0.985916 | 0.9306 K.AGVENGKPTHFTVYTK[325.13]GAGK.A                 |
| 0.9859   | 0.9272 R.VK[325.13]ILFNK.K                              |
| 0.985865 | 0.9947 K.LTEK[325.13]QAAQYLGMSK[160.03]DGPFPKPDHYR.Y    |
| 0.985862 | 0.9968 K.LYSILQGDSPK[325.13]WR.T                        |
| 0.985849 | 0.0889 K.WGDAGA EYVVESTGVFTTMEK[325.13]AGAH LQGGAK.R    |
| 0.985845 | 0.9674 R.YIEIFK[325.13]SSR.A                            |
| 0.985842 | 0.9929 R.SQNP HGLK[325.13]QIGLDQIWDDL.R.A               |
| 0.985841 | 0.9942 R.ARVQAQSTNDGLDFQESQLVK[325.13]K.L               |
| 0.985825 | 0.9827 K.SNLMDAISFVLGEK[325.13]TSNLR.V                  |
| 0.985824 | 0.998 K.DVGLHIK[325.13]AVR.S                            |
| 0.985811 | 0.978 K.EGLPVALDK[325.13]HILGFDTGDAVLNEAAQILR.L         |
| 0.98581  | 0.9901 K.DGPLNM[147.04]ILDDGGDLTNLIHTK[325.13]YPQLLPGI  |
| 0.985799 | 0.9838 K.VEAQVYILSK[325.13]EEGGR.H                      |
| 0.985798 | 0.9982 R.FVADSK[325.13]DKEPEVVFIGDSLVLQMHQC[160.03]EIN  |
| 0.985798 | 0.9982 K.WLPVQESSTDDK[325.13]KPGER.K                    |
| 0.985797 | 0.9637 K.KIYK[325.13]IGQGYLIK.D                         |
| 0.985779 | 0.9418 R.WTDENIDTVALK[325.13]HFPNIDR.E                  |

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| 0.985776 | 0.8277 | K.GLGILSLK[325.13]QQEMMAALTDAIQDKK.N           |
| 0.985775 | 0.9843 | K.HIVK[325.13]TVDFQTQDSNYLLTGGQDK.L            |
| 0.985775 | 0.9938 | R.LLM[147.04]TEVAWTK[325.13]DELKEALDDVTLPR.L   |
| 0.985773 | 0.9915 | R.VWNEEGEDGLPRPK[325.13]DPVPSIQLFPGLR.E        |
| 0.985764 | 0.9921 | R.FAYKDPEK[325.13]NWN.R                        |
| 0.985764 | 0.9896 | R.EDSARPGAHAK[325.13]VK.K                      |
| 0.985759 | 0.9267 | K.HQPTAIIAK[325.13]TFK.G                       |
| 0.985749 | 0.9491 | K.C[160.03]SRAEAEAWYQTK[325.13]FETLQAQAGK.H    |
| 0.985743 | 0.4628 | K.HTGPGILSMANAGPNTNGSQFFIC[160.03]TAK[325.13]T |
| 0.985736 | 0.9957 | R.YLASGSFDK[325.13]C[160.03]VHIWNTQTGALVHSYR.G |
| 0.985711 | 0.9796 | R.SVDETTQAMAFDGIIFQGQSLK[325.13]IR.R           |
| 0.985705 | 0.9905 | K.KASAIK[325.13]LGSSKPK.E                      |
| 0.985666 | 0.9748 | R.GGGVGGFLPAMK[325.13]QIGNVAALPGIVHR.S         |
| 0.985664 | 0.9901 | K.NEK[325.13]GQYISPFHDIPYADKDVFMVVEVPR.W       |
| 0.985658 | 0.8265 | K.NGVK[325.13]ITLPVDFVTADKFDENAK.T             |
| 0.985604 | 0.9848 | R.ELAILLGMMLDPAEK[325.13]DEK.G                 |
| 0.985604 | 0.9976 | K.FTLFK[325.13]GVITRPDLPSK.K                   |
| 0.985594 | 0.9942 | K.SELPLDPLVPTEEGNPLLK[325.13]HYR.G             |
| 0.985591 | 0.9034 | K.SNYNFEK[325.13]PFLWLR.K                      |
| 0.985583 | 0.9679 | R.EK[325.13]LC[160.03]FLDKVEPHATIAEIK.N        |
| 0.985582 | 0.4882 | R.LLLPGELAKHAVSEGK[325.13]AVTK.Y               |
| 0.985549 | 0.8918 | R.LLGWIQNK[325.13]LPQLPITNFSR.D                |
| 0.98554  | 0.9746 | K.RDLVLSGDLGSLYAMTQDK[325.13]VFR.L             |
| 0.985534 | 0.9705 | R.DMHSAYK[325.13]HADGK.K                       |
| 0.985503 | 0.9888 | R.C[160.03]IESLIAVFQK[325.13]YAGK.D            |
| 0.985498 | 0.9909 | R.AWAGSPK[325.13]GTIQVITQGTSLK.N               |
| 0.985487 | 0.9695 | K.TGNAWHSK[325.13]NFTK.Y                       |
| 0.98548  | 0.9771 | R.ITALK[325.13]SQYEGR.I                        |
| 0.985468 | 0.9651 | R.ALK[325.13]M[147.04]IVDPVEPHGEMK.F           |
| 0.985463 | 0.945  | R.EKETK[325.13]ALSLAR.A                        |
| 0.985451 | 0.8616 | K.FASFIDK[325.13]VR.F                          |
| 0.98544  | 0.8367 | R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V            |
| 0.985437 | 0.9977 | K.KVEQK[325.13]IANDNSLNHEYLPILGLAEFR.S         |
| 0.985435 | 0.6514 | R.LIPDGC[160.03]GVK[325.13]YIPNR.G             |
| 0.985422 | 0.9976 | K.DKQNK[325.13]PTGFALGSIEGR.V                  |
| 0.985418 | 0.9959 | K.LKDWQEGGYTINDK[325.13]PNPR.G                 |
| 0.985406 | 0.9771 | R.EVC[160.03]DEVK[325.13]AHLLADMAHISGLVAAK.V   |
| 0.985404 | 0.9504 | K.MK[325.13]IMVIK.D                            |
| 0.98537  | 0.9928 | R.GLPFQANAQDIINFFAPLK[325.13]PVR.I             |
| 0.985361 | 0.9293 | R.QLLHNFPDQLTSSGAPFWSGPK[325.13]R.C            |
| 0.98536  | 0.9385 | K.GIVEFASK[325.13]PAAR.K                       |
| 0.98535  | 0.9362 | R.ASLSLWQAMEK[325.13]GLVPQNEGLPLLQVQLATGGVV    |
| 0.985348 | 0.9941 | K.SELPLDPLVPTEEGNPLLK[325.13]HYR.G             |
| 0.985347 | 0.9856 | K.GFTPIPGTIEMLHPWNNNEGAPPEDK[325.13]VVPSFLPVDI |
| 0.985343 | 0.4065 | K.ALESPERPFLAILGGAK[325.13]VADK.I              |
| 0.985328 | 0.9969 | K.LNSTMK[325.13]LVSHLTAQLNELK.E                |
| 0.985301 | 0.9565 | R.KTVTAM[147.04]DVVYALK[325.13]R.Q             |



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| 0.985296 | 0.9676 K.K[325.13]VTHAVVTPAYFNDAQR.Q                   |
| 0.985287 | 0.9405 R.K[325.13]YAYSAASGGR.R                         |
| 0.985279 | 0.3411 R.DWSHYFK[325.13]IIEDLR.A                       |
| 0.985276 | 0.9922 R.RVQATK[325.13]PQASR.H                         |
| 0.985274 | 0.9142 K.K[325.13]VHVIFNYK.G                           |
| 0.985258 | 0.998 R.DIAK[325.13]HLPDGC[160.03]PAMLVLPLYASLPYAQQLF  |
| 0.985251 | 0.9389 R.IEEELGSKAK[325.13]FAGR.N                      |
| 0.98525  | 0.9289 R.LSK[325.13]VSFR.G                             |
| 0.985248 | 0.9978 R.RPSAAPASQQQLQSLESK[325.13]LTSVR.F             |
| 0.985244 | 0.996 R.VK[325.13]VFGWVHR.L                            |
| 0.985241 | 0.7496 R.KQSLGELIGTLNAAK[325.13]VPADTEVVC[160.03]APPTA |
| 0.985208 | 0.9685 R.VK[325.13]ATPMPSRPSTTPFIDK.K                  |
| 0.985205 | 0.9927 R.HGK[325.13]HYFIEVNSR.L                        |
| 0.985192 | 0.9035 R.TFIAIK[325.13]PDGVQR.G                        |
| 0.985179 | 0.9174 R.INLAQK[325.13]AFC[160.03]GFEDPR.T             |
| 0.98517  | 0.9981 K.K[325.13]DLHDANTDLIGR.H                       |
| 0.985167 | 0.8138 R.GELAIK[325.13]DANAK.L                         |
| 0.985149 | 0.9975 R.VEENFLK[325.13]LTHVQR.Q                       |
| 0.985145 | 0.9622 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T       |
| 0.985144 | 0.9969 R.LC[160.03]QK[325.13]FGEYHKDDPSSFR.F           |
| 0.985134 | 0.9777 K.MGAK[325.13]AMNWMSGK.I                        |
| 0.985105 | 0.8642 R.GVLK[325.13]VFLENVIR.D                        |
| 0.985096 | 0.9888 K.TEISFRPNDPK[325.13]SYEAYVLNIVR.F              |
| 0.985093 | 0.9423 R.ADAVWNK[325.13]IQEENVIPR.E                    |
| 0.985089 | 0.8303 K.GIQSLEGAVQAGQLK[325.13]VPPGYHPLDVEKEWGK.L     |
| 0.985086 | 0.9933 R.HC[160.03]NMVLENVK[325.13]EMWTEVPK.S          |
| 0.985068 | 0.9841 R.NGNPAPK[325.13]ITWYR.N                        |
| 0.985049 | 0.9283 K.SHLAK[325.13]EGLYQYK.N                        |
| 0.985036 | 0.9765 R.VVIIGAGKPAAVVLQTK[325.13]GSPEsr.L             |
| 0.985027 | 0.974 K.NLATAYDNFVELVANLK[325.13]EGTK.F                |
| 0.985019 | 0.9981 R.VPAK[325.13]STLLQVLQHQR.Y                     |
| 0.985006 | 0.9826 R.VVFNLNITYK[325.13]TK.E                        |
| 0.984999 | 0.8902 R.FEPYANPTK[325.13]R.Y                          |
| 0.984991 | 0.9969 R.TVQK[325.13]QGFHHLWLQR.D                      |
| 0.984991 | 0.998 R.EK[325.13]LTPEQLHSMR.Q                         |
| 0.984977 | 0.9115 K.HGEVC[160.03]PAGWKPGSDTIK[325.13]PDVQK.S      |
| 0.984975 | 0.9835 R.K[325.13]IGLETVGVK.I                          |
| 0.984965 | 0.8978 R.VHK[325.13]ISNVNK.A                           |
| 0.984951 | 0.9721 K.K[325.13]SADTLWGIQK.E                         |
| 0.984935 | 0.997 R.FLENHEK[325.13]MTSTTR.Y                        |
| 0.984927 | 0.9745 R.QFLFRPWDVTK[325.13]LK.S                       |
| 0.984925 | 0.9713 K.LNC[160.03]QVIGASVDSHFC[160.03]HLAWVNTPK[325. |
| 0.984904 | 0.9974 R.IVEK[325.13]YGYTHLSAGELLR.D                   |
| 0.984894 | 0.9659 R.LK[325.13]LSPSPSSR.V                          |
| 0.984891 | 0.993 K.FDEC[160.03]VLDK[325.13]LGWVRPDLGELSK.V        |
| 0.984887 | 0.9936 R.K[325.13]SDLHPTLPAGR.Y                        |
| 0.984879 | 0.9978 R.LLGEK[325.13]TTTAAGSSHSRPGVPVEGSPGR.N         |

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| 0.984875 | 0.9869 R.VTIK[325.13]AGIHAR.L                             |
| 0.984858 | 0.9973 R.DVPIDHSDLVADLLK[325.13]ELSNHNER.V                |
| 0.984854 | 0.8616 R.K[325.13]ESYSVYVYK.V                             |
| 0.984846 | 0.9592 K.ILHIK[325.13]QDER.V                              |
| 0.984842 | 0.8615 R.K[325.13]ESYSVYVYK.V                             |
| 0.98484  | 0.9941 K.YK[325.13]YGYEIPVDM[147.04]LC[160.03]K.R         |
| 0.984817 | 0.9956 R.GGGPTSSEQIMK[325.13]TGALLLQGFIQDR.A              |
| 0.984803 | 0.756 R.SSFDWLTGSSTDPLVDHTSPSSDSSLFAHK[325.13]R.S         |
| 0.984798 | 0.9714 K.NPNGPYPYTLK[325.13]LC[160.03]FSTAQHAS.-          |
| 0.984782 | 0.9661 K.K[325.13]IADDKYNDTFWK.E                          |
| 0.984743 | 0.9337 K.FK[325.13]IPEMHLK.A                              |
| 0.984724 | 0.979 R.MPEK[325.13]VTWMR.R                               |
| 0.984697 | 0.8169 K.TIAPALVSK[325.13]K.L                             |
| 0.984677 | 0.9971 R.LTRPGSSYFNLNPFVQLQIDPEVTDEEIKK[325.13]R.F        |
| 0.984672 | 0.998 K.LDDFLDLNHK[325.13]YWER.Y                          |
| 0.984668 | 0.9694 R.LATNTSAPDLK[325.13]NVR.S                         |
| 0.984663 | 0.9757 K.K[325.13]YEDIC[160.03]PSTHNMDVPMK.R              |
| 0.984658 | 0.8978 R.VIFGLFGK[325.13]TVPK.T                           |
| 0.98463  | 0.9375 K.VDINAPDVEVHGPDWHLK[325.13]MPK.V                  |
| 0.984622 | 0.933 R.VHFK[325.13]NTR.E                                 |
| 0.984616 | 0.926 R.LSK[325.13]VSFR.G                                 |
| 0.984615 | 0.9271 K.LLLQVQHASK[325.13]QIAADK.Q                       |
| 0.984612 | 0.9962 R.K[325.13]LVGFISAIPANIHIYDTEK.K                   |
| 0.984611 | 0.9967 K.FLDDLGNK[325.13]SHLMSLYSAC[160.03]SSEVPHGPVI     |
| 0.984598 | 0.9372 R.TLINELVK[325.13]GILPR.S                          |
| 0.984594 | 0.9906 K.TVNVVQFEPK[325.13]GAIGK.A                        |
| 0.984592 | 0.9859 R.THMQNIK[325.13]DITSSIHFEAYR.V                    |
| 0.984575 | 0.9947 K.NKDNVK[325.13]FK.V                               |
| 0.984573 | 0.9364 R.KEPLFGISTGNLITGLAAGAK[325.13]TYK.M               |
| 0.984566 | 0.9963 K.EIPAK[325.13]IIFEDDR.C                           |
| 0.984557 | 0.9819 K.VK[325.13]C[160.03]YRC[160.03]GETGHVAINC[160.03] |
| 0.984549 | 0.9771 K.KPYC[160.03]NAHYPK[325.13]QSFTMVADTPENLR.L       |
| 0.98452  | 0.7396 R.QLFHPEQLITGK[325.13]EDAANNYAR.G                  |
| 0.984514 | 0.9553 R.TFK[325.13]TVFAEHISDEC[160.03]K.R                |
| 0.984511 | 0.9643 R.EVDRPGSK[325.13]VNK.K                            |
| 0.984504 | 0.8194 K.IK[325.13]IIAPPER.K                              |
| 0.984498 | 0.997 R.LK[325.13]IDFGEAAR.A                              |
| 0.984491 | 0.808 R.LQAEIEGLK[325.13]GQR.A                            |
| 0.984488 | 0.9971 K.HKENVK[325.13]DYYQK.W                            |
| 0.984483 | 0.8373 R.AGK[325.13]ITFAEK.V                              |
| 0.984483 | 0.9808 R.EGAPIEDPPVSHWK[325.13]PEAVQYYEDGAR.I             |
| 0.984473 | 0.9832 R.VRPK[325.13]ALQTTGTAK.S                          |
| 0.984469 | 0.9401 K.ESPLLFK[325.13]FR.A                              |
| 0.984465 | 0.9909 R.YGEGDSLTLQQLK[325.13]ALLNHLDVGVGR.G              |
| 0.984421 | 0.9886 R.YELLEHK[325.13]K.R                               |
| 0.9844   | 0.9924 R.ASGGK[325.13]LIFYDLR.G                           |
| 0.984385 | 0.985 K.QDLPNAMNAEITDK[325.13]LGLHSLR.H                   |

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| 0.984376 | 0.9978 K.ALNRPPPTYPTK[325.13]YFGC[160.03]ELGAQTQFDVK.N   |
| 0.984375 | 0.9 R.TAQSTPSAPPQK[325.13]VMC[160.03]VSM[147.04]GST      |
| 0.98436  | 0.9754 R.TLQIQK[325.13]AHGDHMASSR.N                      |
| 0.984359 | 0.8978 K.LLETK[325.13]WTLLQEQK.S                         |
| 0.984349 | 0.8958 K.TVWDWELMNDIK[325.13]PIWQRPSK.E                  |
| 0.984331 | 0.9979 K.KPK[325.13]GFFGYK.S                             |
| 0.984323 | 0.9574 K.AK[325.13]EALNMLTWR.A                           |
| 0.984307 | 0.9326 K.EFDK[325.13]HFGK.G                              |
| 0.984289 | 0.936 R.FQEHLLQLQNLGINPANIGFSTLTMESDK[325.13]FIC[160.03] |
| 0.984278 | 0.9318 K.SIDNK[325.13]ALYDTFSAFGNILSC[160.03]K.V         |
| 0.984253 | 0.9211 R.REEAAVDAQQK[325.13]R.S                          |
| 0.984239 | 0.9894 K.VLK[325.13]NHELSGLNKEELAVLLQSDPFFMPEIC[160.03]  |
| 0.984236 | 0.9968 R.GFTAAGILSAHK[325.13]IIASSPEM[147.04]NLPTVSALR.I |
| 0.984235 | 0.9931 R.LIDGIVLTK[325.13]FDTIDDK.V                      |
| 0.984226 | 0.9786 R.NGNPAPK[325.13]ITWYR.N                          |
| 0.984213 | 0.4221 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVL.R   |
| 0.984212 | 0.964 R.LIK[325.13]VHLDK.A                               |
| 0.9842   | 0.8367 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                |
| 0.984196 | 0.9976 R.K[325.13]APQHTAVGFK.Q                           |
| 0.984196 | 0.9949 R.HQGVMMVGMGQK[325.13]DC[160.03]YVGDEAQSK.R       |
| 0.984165 | 0.9964 K.EFNPTKPLLSVNK[325.13]STSTPTSPGPR.T              |
| 0.984154 | 0.9962 K.EIPAK[325.13]IIFEDDR.C                          |
| 0.984149 | 0.9933 K.DTHPK[325.13]FPAGGK.M                           |
| 0.984114 | 0.9707 K.K[325.13]C[160.03]YEMASHLR.R                    |
| 0.984112 | 0.9533 R.EFLDFFWDIAK[325.13]PEQETR.L                     |
| 0.984112 | 0.9896 K.KPMVLGHEASGTVEK[325.13]VGSSVK.H                 |
| 0.984111 | 0.972 R.ILQEHEQIK[325.13]K.K                             |
| 0.984094 | 0.9254 R.INEILSNALK[325.13]R.G                           |
| 0.984094 | 0.8999 K.HVVFGK[325.13]VK.E                              |
| 0.984088 | 0.7754 K.K[325.13]GIIRPGTAFELLEQAATGYVIDPIK.G            |
| 0.984087 | 0.7253 R.VETGVLK[325.13]PGMVVTFAPVNVTTVEVK.S             |
| 0.984067 | 0.9949 R.YLYTLVITDK[325.13]EK.A                          |
| 0.984065 | 0.9345 K.HAAENPGK[325.13]YNILGTNTIMDK.M                  |
| 0.98405  | 0.8978 K.K[325.13]HPDASVNFSEFSK.K                        |
| 0.984048 | 0.9689 K.LPEGQVPEGAGLK[325.13]GHLPKVDM[147.04]PSFK.M     |
| 0.984042 | 0.8266 R.IAK[325.13]AVNEK.S                              |
| 0.984033 | 0.1226 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S         |
| 0.98403  | 0.9973 K.FK[325.13]LPVWETIVC[160.03]TMR.E                |
| 0.984028 | 0.0789 K.WGDAGAEEYVVESTGVFTTMEK[325.13]AGAHLLQGGAK.R     |
| 0.984026 | 0.9888 K.IKDIAWTEDSK[325.13]R.I                          |
| 0.984005 | 0.9314 K.ELLYK[325.13]FIC[160.03]TTSIQNR.F               |
| 0.983981 | 0.9978 R.LYQTDPSGTYHAWK[325.13]ANAIGR.G                  |
| 0.98398  | 0.9063 R.K[325.13]FLVYVANFDEKDPR.T                       |
| 0.983973 | 0.8935 K.TVWDWELMNDIK[325.13]PIWQRPSK.E                  |
| 0.98397  | 0.9923 R.SEHK[325.13]LSTDHIPILYR.T                       |
| 0.983962 | 0.9537 K.YDLHQVK[325.13]K.A                              |
| 0.983961 | 0.997 K.HKENVK[325.13]DYYQK.W                            |

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| 0.983959 | 0.993 R.LLM[147.04]TEVAWTK[325.13]DELKEALDDVTLPR.L  |
| 0.983958 | 0.9728 K.GFVVINQK[325.13]GIDPFSLDALSK.E             |
| 0.983942 | 0.9937 K.VTSLGK[325.13]DWHRPC[160.03]LR.C           |
| 0.983934 | 0.7926 R.FANYIDK[325.13]VR.F                        |
| 0.983885 | 0.9951 R.SLK[325.13]SDMMSHLVK.I                     |
| 0.983884 | 0.9969 R.DKQPNAQPQYLHGSK[325.13]ALNLAYSSIIYGSYR.N   |
| 0.983881 | 0.99 K.NKPK[325.13]WLLQGIFSTTVLC[160.03]QK.L        |
| 0.983878 | 0.4645 R.TLSDYNIQK[325.13]ESTLHLVLR.L               |
| 0.983875 | 0.9344 K.VK[325.13]QLPLVKPYLR.S                     |
| 0.983838 | 0.9926 R.KADIDLTk[325.13]R.A                        |
| 0.983835 | 0.973 K.TFPQNPVELK[325.13]ALYNQYIHFk.E              |
| 0.983795 | 0.9911 R.FIK[325.13]PLSNAYHELAQVYSTNNPSEL.R.N       |
| 0.98379  | 0.9109 R.TVVTGIEM[147.04]FHK[325.13]SLER.A          |
| 0.983785 | 0.9676 R.IYC[160.03]K[325.13]PHFNQLFK.S             |
| 0.983782 | 0.9915 K.GSIQK[325.13]FVPYLIAGIQHGC[160.03]QDIGAR.S |
| 0.98377  | 0.9876 K.DK[325.13]M[147.04]MNGGHYTYSEN.R.V         |
| 0.98374  | 0.9527 K.GK[325.13]ILFIFIDSDHTDNQR.I                |
| 0.983729 | 0.9717 K.FGK[325.13]GGQAHR.C                        |
| 0.983722 | 0.9958 K.GK[325.13]VAAQC[160.03]SHAAVSAYK.Q         |
| 0.983685 | 0.9831 R.GSSIFGLAPGK[325.13]AR.D                    |
| 0.983676 | 0.9823 R.LHGK[325.13]DSASPR.Y                       |
| 0.983675 | 0.9974 R.LSAKPAPPK[325.13]PEPKPK.K                  |
| 0.983659 | 0.9956 R.IEHLIGK[325.13]K.L                         |
| 0.983653 | 0.9511 R.GLK[325.13]M[147.04]AVTFIGNSTAIQELFK.R     |
| 0.983639 | 0.9284 R.SGKPAELLK[325.13]MFGIDR.D                  |
| 0.983635 | 0.9696 K.TLVLLMGK[325.13]EGVHGGLINKK.C              |
| 0.983632 | 0.9688 R.VIK[325.13]DFM[147.04]IQGGDFTR.G           |
| 0.983629 | 0.9674 R.ELAFQISK[325.13]EYER.F                     |
| 0.983607 | 0.855 R.AK[325.13]VTLNGVPAQPLGPR.A                  |
| 0.983594 | 0.8063 K.K[325.13]LGEMWNNNTAADDKQPYEK.K             |
| 0.983594 | 0.9591 R.QIEYEEK[325.13]LAQALHEMR.E                 |
| 0.983582 | 0.8859 R.TLTIVDTGIGMTK[325.13]ADLINNLGTIAK.S        |
| 0.983576 | 0.9883 R.NALQQENHIIDGVK[325.13]VQVHTR.R             |
| 0.983572 | 0.9707 R.LAADVGK[325.13]AGAER.E                     |
| 0.983571 | 0.9727 R.VVFLK[325.13]QLASGLLLVTGPLVLNR.V           |
| 0.983543 | 0.8123 K.FASFIDK[325.13]VR.F                        |
| 0.983538 | 0.9288 K.K[325.13]AAVTPGKK.A                        |
| 0.983536 | 0.8834 R.IDFSK[325.13]LTSLNVK.Y                     |
| 0.983525 | 0.8638 R.DTPAK[325.13]NAQK.S                        |
| 0.983515 | 0.9665 R.SGK[325.13]APILIATDVASR.G                  |
| 0.983502 | 0.8051 R.LK[325.13]STC[160.03]IYGGAPK.G             |
| 0.983501 | 0.9641 R.LC[160.03]K[325.13]TVGATALPR.L             |
| 0.983498 | 0.9716 K.ANIPWK[325.13]VPGLPTPIENMILR.Y             |
| 0.983489 | 0.9961 K.K[325.13]PHIIIATPGR.L                      |
| 0.983481 | 0.8251 R.K[325.13]MFTLLDVVNR.K                      |
| 0.983451 | 0.9153 R.VK[325.13]ILFNK.K                          |
| 0.983451 | 0.9683 R.KPGEK[325.13]TFTQR.S                       |

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| 0.983438 | 0.9841 K.VEQIK[325.13]TFSGQTHGFVHR.K                     |
| 0.983438 | 0.9847 R.AGK[325.13]IVVNLTR.L                            |
| 0.983433 | 0.8951 K.GIVEFSGK[325.13]PAAR.K                          |
| 0.983431 | 0.9137 R.INSGGK[325.13]LPNFGFVVDSEPVQK.V                 |
| 0.983425 | 0.9252 K.LK[325.13]GTVGEPTYDAEFQHFLR.G                   |
| 0.983417 | 0.9972 R.SFLHGPELTK[325.13]GQLR.I                        |
| 0.983414 | 0.9024 R.IYC[160.03]KPHFNQLFK[325.13]SK.G                |
| 0.983408 | 0.9926 K.VK[325.13]SLSVYHPQLAYC[160.03]VVQFLEK.E         |
| 0.983407 | 0.9918 R.IVGC[160.03]IC[160.03]EEDNTSVVWFWLHK[325.13]GI  |
| 0.983404 | 0.9955 K.K[325.13]ALLALNHGLDK.A                          |
| 0.983391 | 0.9703 K.VYVQHLLK[325.13]QDR.E                           |
| 0.983359 | 0.9898 R.SSPK[325.13]ALNFGGIGVVVGHELTAFDDQGR.E           |
| 0.98335  | 0.7491 R.TLLIK[325.13]TVETR.D                            |
| 0.983326 | 0.9043 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF |
| 0.983317 | 0.8692 K.APEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]VG   |
| 0.983307 | 0.8039 K.AAKPK[325.13]VVKPK.K                            |
| 0.983289 | 0.9743 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT   |
| 0.983274 | 0.9752 K.LHIFNAK[325.13]K.A                              |
| 0.983261 | 0.9862 K.TFNQVEIKPEMIGHYLGESITYK[325.13]PVK.H            |
| 0.983249 | 0.9974 R.IVAAHNK[325.13]C[160.03]PR.D                    |
| 0.983247 | 0.9971 K.LLEHK[325.13]EIDGR.L                            |
| 0.983246 | 0.9865 K.FMQASEDLLK[325.13]EHYVDLK.D                     |
| 0.983206 | 0.9942 R.SDKVPDNK[325.13]NTHTLLAGVFR.G                   |
| 0.9832   | 0.9635 R.ALYK[325.13]AISVPR.V                            |
| 0.983191 | 0.988 R.VLFHLK[325.13]GQDWPPGSGSLPC[160.03]AR.L          |
| 0.98319  | 0.9373 K.HKDAIYLVTSLASK[325.13]AQTQK.H                   |
| 0.983183 | 0.7792 K.LGLVGVNLTLDGVK[325.13]SWLKPR.L                  |
| 0.98318  | 0.9941 R.K[325.13]QMVIDVLHPGK.A                          |
| 0.983175 | 0.9887 K.QLDDLK[325.13]VELSQLR.V                         |
| 0.98316  | 0.9357 K.GEGERPAQNEK[325.13]R.K                          |
| 0.983149 | 0.9922 K.EPPLLGLVHPNPK[325.13]LR.Q                       |
| 0.983133 | 0.9087 R.HDSPEDVK[325.13]R.R                             |
| 0.983104 | 0.9644 R.K[325.13]LDALC[160.03]NIHENIR.V                 |
| 0.983089 | 0.9929 R.WYNHIK[325.13]SYEK.E                            |
| 0.983088 | 0.9661 K.DASIVGFFDDSFSEAHSEFLK[325.13]AASNLR.D           |
| 0.983081 | 0.9935 R.KASGPPK[325.13]GPSR.A                           |
| 0.983065 | 0.9319 R.VIDQK[325.13]TLHTLR.V                           |
| 0.983055 | 0.9708 K.SSGEIVYC[160.03]GQVFEK[325.13]SPLR.V            |
| 0.983048 | 0.7742 R.IAAYLFK[325.13]GNNR.W                           |
| 0.983036 | 0.8799 R.DLQQYQSQAK[325.13]QLFR.K                        |
| 0.983034 | 0.9498 R.K[325.13]M[147.04]FTLLDVVNR.K                   |
| 0.983033 | 0.9957 K.LQHINPLLPAC[160.03]LNK[325.13]EESK.T            |
| 0.983029 | 0.9736 K.LNLKPRSTPK[325.13]EDDSSASTSQSTR.A               |
| 0.983024 | 0.9948 K.LVLSK[325.13]LYEEGSNKR.L                        |
| 0.983019 | 0.9311 K.TLFVK[325.13]GLSEDTEETLK.E                      |
| 0.982997 | 0.9949 K.FNFVGK[325.13]ILGPQGNTIK.R                      |
| 0.982996 | 0.7639 R.LK[325.13]LLLPWLEAR.I                           |

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| 0.982989 | 0.8942 R.TAQSTPSAPPQK[325.13]VM[147.04]C[160.03]VSMGST   |
| 0.98298  | 0.9283 K.ARDDYK[325.13]TLINAEDPPMVVVR.K                  |
| 0.982978 | 0.9959 K.AM[147.04]TAK[325.13]GGDISVC[160.03]EWYQR.V     |
| 0.982944 | 0.7107 K.TM[147.04]QNVK[325.13]HPVTGQFLYQDSNWASK.V       |
| 0.982941 | 0.9502 R.K[325.13]TVTAM[147.04]DVVYALK.R                 |
| 0.982914 | 0.9816 R.DKLC[160.03]GPYEK[325.13]FIC[160.03]EQDHQNFLR.L |
| 0.982912 | 0.9964 K.EVEVIGGADK[325.13]YHSVC[160.03]R.L              |
| 0.982901 | 0.9821 K.AAFHK[325.13]SIR.S                              |
| 0.982884 | 0.8919 K.GIVEFSGK[325.13]PAAR.K                          |
| 0.98288  | 0.9978 R.LVIGK[325.13]LPAQLAWEALEQR.V                    |
| 0.982866 | 0.9926 K.KGEPGPPDADGPLYLPYK[325.13]TLVSTVGSMVFNEGEA      |
| 0.982842 | 0.9676 R.VASATK[325.13]IALYETPTGWK.F                     |
| 0.982842 | 0.9907 R.SAFK[325.13]LIQLNR.R                            |
| 0.982809 | 0.9933 K.YK[325.13]YGYEIPVDM[147.04]LC[160.03]K.R        |
| 0.982794 | 0.773 K.VSASPLLYTLIEK[325.13]TMQNVK.H                    |
| 0.982784 | 0.9652 K.K[325.13]PVGEVHSQFSTGHANSPC[160.03]TIIGK.A      |
| 0.982775 | 0.966 K.AK[325.13]SIVFHR.K                               |
| 0.982769 | 0.978 K.GFGFGLVK[325.13]LDVK.T                           |
| 0.982751 | 0.8847 K.LYEEK[325.13]TGNAWHSK.N                         |
| 0.982719 | 0.994 R.KTPC[160.03]GEGSK[325.13]TWDR.F                  |
| 0.982715 | 0.8935 R.TFIAIK[325.13]PDGVQR.G                          |
| 0.982715 | 0.7922 K.FYEAFSK[325.13]NLK.L                            |
| 0.982699 | 0.9957 R.TLNHQYDYTFDWTMLK[325.13]QK.A                    |
| 0.982698 | 0.1055 R.K[325.13]DGNASGTTLLEALDC[160.03]ILPPTRPTDKPLR.  |
| 0.982634 | 0.7999 K.VHSPSGAVEEC[160.03]HVSELEPDK[325.13]YAVR.F      |
| 0.982625 | 0.9595 K.RLK[325.13]VPPAINQFTQALDR.Q                     |
| 0.982591 | 0.9967 R.K[325.13]PALELLHYLK.N                           |
| 0.982587 | 0.9929 R.VQLIK[325.13]ALLALPIRPATR.R                     |
| 0.982583 | 0.8913 R.K[325.13]ESYSIYVYK.V                            |
| 0.982574 | 0.7322 K.FHGTVK[325.13]AENGK.L                           |
| 0.982562 | 0.9793 R.LVQAFQYTDKHGEVC[160.03]PAGWK[325.13]PGSETIPI    |
| 0.982546 | 0.9837 R.LIHPK[325.13]SGR.S                              |
| 0.982536 | 0.9517 R.K[325.13]LTWFFVNEGLVDGWDDPR.F                   |
| 0.982528 | 0.9652 R.NQSFC[160.03]PTVNLDK[325.13]LWTLVSEQTR.V        |
| 0.982516 | 0.9942 K.TFGK[325.13]AAGPSLSHTSGGTQSK.V                  |
| 0.982498 | 0.9901 R.K[325.13]VAQVPLGPEC[160.03]SR.A                 |
| 0.982495 | 0.9329 R.RGVM[147.04]LAVDAVIAELK[325.13]K.Q              |
| 0.982492 | 0.9465 K.SLKDEDVLQK[325.13]LPVGTATLYFR.D                 |
| 0.982469 | 0.9001 R.K[325.13]SQVLFSVTR.G                            |
| 0.982452 | 0.9717 K.ALSK[325.13]HLPSSDSMSLK.V                       |
| 0.982448 | 0.8628 K.DQVDIAVQELLQK[325.13]AQYK.S                     |
| 0.982437 | 0.9524 K.VM[147.04]TK[325.13]DGQWFTDWDVPHSR.H            |
| 0.98243  | 0.9964 K.IK[325.13]SVALC[160.03]VAAC[160.03]PR.Q         |
| 0.982422 | 0.9057 R.K[325.13]LMVALAK.G                              |
| 0.98242  | 0.9117 R.K[325.13]AMKGLGTDEESILTLLTSR.S                  |
| 0.982369 | 0.9024 R.TK[325.13]TEISEM[147.04]NR.N                    |
| 0.982339 | 0.6859 K.EITALAPSTMK[325.13]IK.I                         |

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| 0.982315 | 0.9809 | K.VADWTGATYQDK[325.13]R.Y                            |
| 0.982313 | 0.9919 | R.K[325.13]FIC[160.03]HVVGITYQHIDR.W                 |
| 0.982313 | 0.9972 | R.TMPIILSPGNTQTLTELELK[325.13]WQHWHEEC[160.03]E      |
| 0.982307 | 0.9904 | R.GLAVNMVDSK[325.13]HSMNILNR.I                       |
| 0.982296 | 0.8366 | K.AVTK[325.13]YTSAK.-                                |
| 0.982273 | 0.9236 | K.K[325.13]QIPAITC[160.03]IQSQWR.G                   |
| 0.98227  | 0.2955 | R.DWSHYFK[325.13]IIEDLR.A                            |
| 0.982262 | 0.9282 | K.KISLK[325.13]YTAAR.L                               |
| 0.982247 | 0.9883 | R.VVVSGLPPSGSWQDLK[325.13]DHMR.E                     |
| 0.982221 | 0.9791 | R.FGIAAK[325.13]YQLDPTASISAK.V                       |
| 0.982216 | 0.9953 | R.NQK[325.13]LLQAGEENQVLELLIHR.D                     |
| 0.982215 | 0.9956 | R.K[325.13]LVGFISAIPANIHIYDTEKK.M                    |
| 0.982211 | 0.926  | K.VKAEPK[325.13]IEAFR.A                              |
| 0.982201 | 0.9972 | R.DAK[325.13]HTNFVEFR.N                              |
| 0.982197 | 0.9695 | R.VLPGK[325.13]YLEEIATQMR.T                          |
| 0.982191 | 0.983  | K.ARPFFNEFQGADSEIK[325.13]FAK.T                      |
| 0.982178 | 0.8948 | R.ADHPPAEVTSHAASGAK[325.13]ADQEEQIHPR.S              |
| 0.982173 | 0.6422 | K.MLETK[325.13]WSLLQQQK.T                            |
| 0.982158 | 0.9278 | R.ETVSEESNVLC[160.03]LSK[325.13]SPNK.H               |
| 0.98215  | 0.9511 | R.RPGEK[325.13]TYTQR.C                               |
| 0.982148 | 0.995  | R.KLSYAEVC[160.03]QK[325.13]PPKEPSSVLVQPLR.E         |
| 0.982106 | 0.9972 | K.ALLQHK[325.13]NAEYQR.K                             |
| 0.9821   | 0.984  | R.HLK[325.13]IVYR.R                                  |
| 0.982079 | 0.9275 | K.IPWSALK[325.13]TLMAQSIYGGR.V                       |
| 0.982066 | 0.9669 | K.K[325.13]HPFPC[160.03]PTSYP.T                      |
| 0.98206  | 0.9241 | R.DLPWMK[325.13]FLHGK.L                              |
| 0.982028 | 0.9908 | K.SQGK[325.13]VLQATVVAVGSGSK.G                       |
| 0.981985 | 0.9841 | K.LLGPHVEGLK[325.13]AEER.H                           |
| 0.981975 | 0.9971 | K.HLLK[325.13]NLFK.I                                 |
| 0.981966 | 0.9437 | K.YGIIC[160.03]MEDLIHEIYTVGK[325.13]R.F              |
| 0.981951 | 0.8906 | K.TIGGGDDSFTHFFC[160.03]ETGAGK[325.13]HVPR.A         |
| 0.981951 | 0.9788 | K.LALK[325.13]YHPDKNPNEGEK.F                         |
| 0.981924 | 0.9281 | R.TIEK[325.13]FEK.E                                  |
| 0.981917 | 0.9426 | K.IAVMELFRPK[325.13]GESK.D                           |
| 0.981914 | 0.9141 | R.NLATTVTEEILEK[325.13]SFSEFGK.L                     |
| 0.981904 | 0.7721 | K.EDLYLK[325.13]PIQR.T                               |
| 0.981879 | 0.9704 | R.EYSLQVLK[325.13]NAR.A                              |
| 0.981871 | 0.9956 | R.SSWVMTC[160.03]AYAPSGNYVAC[160.03]GGLDNIC[160.03]E |
| 0.98187  | 0.9637 | K.DPNIVIAK[325.13]MDATANDVPSPYEV.R                   |
| 0.981867 | 0.9396 | R.K[325.13]VGLIAR.R                                  |
| 0.981861 | 0.063  | K.EITALAPSTMKIK[325.13]IIAPPER.K                     |
| 0.981847 | 0.8912 | R.LK[325.13]LYLPK.E                                  |
| 0.981846 | 0.7358 | R.K[325.13]VSQPIEGHAASFAQFK.M                        |
| 0.981821 | 0.8883 | R.SLVEIIEHGLVDEQQK[325.13]VR.T                       |
| 0.981819 | 0.9971 | K.LSQNNFALGYK[325.13]AADFQLHTHVNDGTEFGGSYQK          |
| 0.981795 | 0.9713 | K.KWGVPIEK[325.13]IYNK.T                             |
| 0.981765 | 0.9971 | R.K[325.13]GASVEHVC[160.03]HR.I                      |

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| 0.98176  | 0.9911 R.ASGGK[325.13]LIFYDLR.G                         |
| 0.98175  | 0.9445 K.SMTEAEQQQLIDHFLFDK[325.13]PVSPLLASGMAR.D       |
| 0.981746 | 0.9247 R.AYILNLVK[325.13]QIK.K                          |
| 0.981745 | 0.7304 R.TLLIK[325.13]TVETR.D                           |
| 0.981732 | 0.9857 R.K[325.13]KQDPPVTHDLR.V                         |
| 0.981712 | 0.9261 K.LPVLAGC[160.03]LK[325.13]GLSSLLC[160.03]NFTK.S |
| 0.981704 | 0.9729 R.NGYGAK[325.13]LC[160.03]NIFSTK.F               |
| 0.9817   | 0.9214 R.IK[325.13]NPFLSLAAC[160.03]VMPSR.L             |
| 0.9817   | 0.9969 R.NYLLSLPHK[325.13]NK.V                          |
| 0.98168  | 0.9968 R.LQHLEK[325.13]SNIYSK.F                         |
| 0.981669 | 0.7767 R.TK[325.13]TEISEMNR.N                           |
| 0.981666 | 0.9448 R.TDDVHAK[325.13]DNTRPGANSPBMWSEAIK.I            |
| 0.981654 | 0.7783 R.GELAIKDANAK[325.13]LSELEAALQR.A                |
| 0.981649 | 0.9557 R.YTASGVHK[325.13]GATYVFR.L                      |
| 0.98163  | 0.9975 R.SVIRPPFK[325.13]K.F                            |
| 0.981616 | 0.9874 K.AIHYNLC[160.03]C[160.03]GLAGGVEQFISDIC[160.03] |
| 0.981609 | 0.7981 R.FHVEEEGK[325.13]GKDASGNK.V                     |
| 0.981597 | 0.8468 K.LDK[325.13]AQIHDLVLVGGSTR.I                    |
| 0.981587 | 0.8834 K.K[325.13]SAEFLHMLK.N                           |
| 0.981533 | 0.9293 K.LTFDTTFSPNTGK[325.13]K.S                       |
| 0.98151  | 0.996 R.FGEVDC[160.03]TIK[325.13]TDPVTGR.S              |
| 0.981474 | 0.9614 R.FGTK[325.13]GLAITFVSDENDAK.I                   |
| 0.981473 | 0.9387 R.EKIK[325.13]SDHPGISITLSK.K                     |
| 0.98146  | 0.9877 R.SIFYVPDMK[325.13]PSMFDVSR.E                    |
| 0.981456 | 0.9642 R.NYEQWGK[325.13]LTDC[160.03]VVMRDPASK.R         |
| 0.981439 | 0.9922 K.GPLK[325.13]TPIAAGHPSMNLLLR.K                  |
| 0.981416 | 0.9654 R.SDTPLIYK[325.13]AVPSWFVR.V                     |
| 0.981411 | 0.8933 R.TK[325.13]IDC[160.03]DNLEQYFIQQGGPDKK.G        |
| 0.981391 | 0.9943 R.SK[325.13]LAAAILGGVDQIHIKPGAK.V                |
| 0.981362 | 0.8344 R.SIQFVDWC[160.03]PTGFK[325.13]VGINYQPPTVPPGGC   |
| 0.981357 | 0.1464 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y            |
| 0.981356 | 0.9959 K.GLK[325.13]YNQATQTFHQWR.D                      |
| 0.981354 | 0.9954 R.NPQQQESLK[325.13]HATR.I                        |
| 0.981351 | 0.7724 K.SK[325.13]GIAYIEFK.T                           |
| 0.981347 | 0.9137 R.K[325.13]TAPYKNVNVQNFHISWK.D                   |
| 0.981334 | 0.8099 K.AVTK[325.13]YTSSK.-                            |
| 0.981323 | 0.9904 R.NEK[325.13]IAVHC[160.03]TVR.G                  |
| 0.981318 | 0.9961 R.GGGIAHK[325.13]DLDR.V                          |
| 0.981313 | 0.9966 K.EPESILQVLSQMEK[325.13]IVR.I                    |
| 0.981311 | 0.9079 R.M[147.04]IAGQVLDINLAAEPK[325.13]VNR.G          |
| 0.981278 | 0.9705 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K               |
| 0.981277 | 0.9823 K.K[325.13]AHAAIR.E                              |
| 0.981276 | 0.9955 K.FALLK[325.13]GSFSEQGINEFLR.E                   |
| 0.98127  | 0.9633 R.DKTIIMWK[325.13]LTR.D                          |
| 0.981261 | 0.9451 K.VLVGK[325.13]NFEDVAFDEK.K                      |
| 0.98125  | 0.9653 K.GYISHQHQBK[325.13]LVVSK.Q                      |
| 0.98125  | 0.8918 R.KQLATK[325.13]AAR.K                            |



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| 0.981241 | 0.5997 R.AK[325.13]HHAISAK.L                            |
| 0.981241 | 0.9969 R.SFAQWDQLVAHK[325.13]R.V                        |
| 0.98122  | 0.9822 K.VYLGDIPLK[325.13]TK.E                          |
| 0.981213 | 0.9242 K.LTK[325.13]DFSALSQLQDTQELLQEENR.Q              |
| 0.981182 | 0.9542 R.FHMYEGYPLWK[325.13]VTFPVR.V                    |
| 0.981161 | 0.9258 K.LLK[325.13]ELHK.E                              |
| 0.981161 | 0.9198 K.EFDK[325.13]HFGK.G                             |
| 0.981159 | 0.992 K.IHLFDIDVPGK[325.13]ITFQESK.T                    |
| 0.981151 | 0.7501 K.SK[325.13]GIAYIEFK.T                           |
| 0.981116 | 0.9904 R.RPLYK[325.13]NIVLSGGSTMFR.D                    |
| 0.981109 | 0.9975 R.K[325.13]YGGISTASVDFEQPTR.D                    |
| 0.981077 | 0.9739 R.GNYCY[160.03]VVSATWK[325.13]QR.N               |
| 0.981077 | 0.9926 K.YGLFAPVHK[325.13]VTK.I                         |
| 0.981059 | 0.9637 K.KK[325.13]VVDPFSK.K                            |
| 0.981038 | 0.8813 K.LIPDSIGK[325.13]DIEKAC[160.03]QSIYPLHDVFVR.K   |
| 0.981002 | 0.959 R.SLGNK[325.13]FIGELFK.L                          |
| 0.980979 | 0.9516 R.LSM[147.04]QK[325.13]SMQNHAAVFR.V              |
| 0.980973 | 0.8617 K.NFGIGQDIQPK[325.13]R.D                         |
| 0.980932 | 0.9864 R.IC[160.03]HGK[325.13]PVTQVTHGR.G               |
| 0.980921 | 0.966 R.AASGYPVK[325.13]VPLEVQEADK.L                    |
| 0.980891 | 0.99 R.DK[325.13]FYHLAK.E                               |
| 0.980885 | 0.9901 R.VVIIGAGK[325.13]PAAVVLQTK.G                    |
| 0.980867 | 0.9615 K.TKPYIQVDIGGGQTK[325.13]TFAPEEISAMVLTK.M        |
| 0.980862 | 0.8607 K.NK[325.13]GLWVPEGQR.A                          |
| 0.980862 | 0.994 K.AM[147.04]K[325.13]GLGTDEDTIIDITHR.S            |
| 0.98086  | 0.8458 R.LK[325.13]VGLQVAVK.A                           |
| 0.980809 | 0.8799 R.WYHPGC[160.03]FVK[325.13]NR.E                  |
| 0.9808   | 0.8496 K.TDK[325.13]TLVLLMGK.E                          |
| 0.9808   | 0.8298 K.WKPPMIDNPSYQGIWK[325.13]PR.K                   |
| 0.980796 | 0.7928 K.K[325.13]ADQKGVTIIPATVGGIKPGC[160.03]FK.I      |
| 0.980772 | 0.912 R.GQKPTLWALLNSEYVTEEK[325.13]K.L                  |
| 0.980758 | 0.9974 R.VPTAPAATSK[325.13]PGLRPR.T                     |
| 0.980739 | 0.947 K.TDK[325.13]TLVLLM[147.04]GK.E                   |
| 0.980712 | 0.9918 R.HLK[325.13]TSGGQGYK.F                          |
| 0.980712 | 0.9652 K.MAILQIMK[325.13]ELNKR.G                        |
| 0.980711 | 0.9803 K.SVGK[325.13]IEHSFWR.S                          |
| 0.980704 | 0.9559 -.M[147.04]QIFVK[325.13]TLTGK.T                  |
| 0.980701 | 0.8847 R.HIVK[325.13]EFK.R                              |
| 0.980693 | 0.7148 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y       |
| 0.980667 | 0.4008 K.KTESHHK[325.13]AK.G                            |
| 0.980561 | 0.7647 K.EK[325.13]PYFPIPEEYTFIQNVPLEDR.V               |
| 0.980541 | 0.9893 R.TSFDK[325.13]ILLR.W                            |
| 0.98054  | 0.9644 R.K[325.13]YEMFAQTLQQSR.G                        |
| 0.980539 | 0.9255 R.DFLK[325.13]PELLR.A                            |
| 0.980525 | 0.9902 R.LSAFFEEHISVLSDYK[325.13]SALR.F                 |
| 0.980524 | 0.9973 K.VKDGPBGK[325.13]EATWVVDVK.N                    |
| 0.980521 | 0.9145 K.GYLGPEQLPDC[160.03]LK[325.13]GC[160.03]DVVVIPA |

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| 0.980513 | 0.1996 R.HQGVMMVGM[147.04]GQKDSYVGDEAQSK[325.13]R.G |
| 0.980507 | 0.9485 K.K[325.13]ALWFQGR.C                         |
| 0.980506 | 0.9805 R.K[325.13]HIC[160.03]PYR.T                  |
| 0.980491 | 0.8686 K.GHLSGLAK[325.13]R.A                        |
| 0.98049  | 0.9868 K.IC[160.03]QFK[325.13]LVLLGESAVGK.S         |
| 0.980455 | 0.9969 R.EEIDHAEYYLYK[325.13]FR.H                   |
| 0.980455 | 0.9969 K.IADMGHLLK[325.13]YYLAPK.I                  |
| 0.980452 | 0.9123 K.SAEFLHMLK[325.13]NAESNAELK.G               |
| 0.980429 | 0.9665 R.VLPGK[325.13]YLEEIATQMR.T                  |
| 0.980419 | 0.1412 R.K[325.13]DLYANTVLSGGTMYPGIADR.M            |
| 0.980408 | 0.7674 K.IITFTK[325.13]NNQFQALLQYADPVSAQHAK.L       |
| 0.980407 | 0.936 R.LQLETEIEALKEELFM[147.04]K[325.13]K.N        |
| 0.9804   | 0.9187 K.GTGASGSFK[325.13]LNKK.A                    |
| 0.980396 | 0.9902 K.LHGVNINVEASK[325.13]NK.S                   |
| 0.980381 | 0.9191 R.YLSPK[325.13]YIK.M                         |
| 0.980376 | 0.9897 R.AVPEDAK[325.13]QLASFLHGNASLLFR.R           |
| 0.98037  | 0.9975 R.K[325.13]C[160.03]IGKPGGSLDNSEQK.C         |
| 0.980366 | 0.9801 R.IHLEIK[325.13]QLNR.Q                       |
| 0.980356 | 0.9363 R.YIEVFK[325.13]SHR.T                        |
| 0.980344 | 0.9605 K.SGVGNIFIK[325.13]NLDK.S                    |
| 0.980343 | 0.994 R.LVSLIGSK[325.13]TQIPTQR.Y                   |
| 0.980336 | 0.9846 R.K[325.13]KQDPPVTHDLR.V                     |
| 0.980332 | 0.9596 R.K[325.13]YDEVLHMR.N                        |
| 0.980327 | 0.8933 R.TVVTGIEM[147.04]FHK[325.13]SLER.A          |
| 0.980282 | 0.9604 K.K[325.13]SQIFSTASDNQPTVTIK.V               |
| 0.980275 | 0.9742 R.NFLGEK[325.13]YIR.R                        |
| 0.980269 | 0.9954 R.IQDTIEITGTFK[325.13]HR.K                   |
| 0.980264 | 0.9216 K.YFDK[325.13]ASYR.V                         |
| 0.980252 | 0.9909 K.ILLDHEK[325.13]EWK.L                       |
| 0.980244 | 0.8212 R.MFAPTK[325.13]TWR.R                        |
| 0.980226 | 0.989 K.K[325.13]GTPWEGGLFK.L                       |
| 0.980225 | 0.9955 K.IVIGYQSHADTATK[325.13]SGSTTK.N             |
| 0.980219 | 0.9967 R.VK[325.13]LQIWDTAGQER.F                    |
| 0.980216 | 0.995 R.SPPVQFSLHLSK[325.13]FHLC[160.03]SVATR.A     |
| 0.980207 | 0.9166 K.FK[325.13]MPEMHFR.A                        |
| 0.980188 | 0.747 K.LAGANPAVITC[160.03]DELLLGHEK[325.13]APAFR.D |
| 0.980161 | 0.9925 R.TM[147.04]GVMFTPLTVK[325.13]YAYYDTER.I     |
| 0.980127 | 0.9837 K.LEHAK[325.13]SVASR.A                       |
| 0.980124 | 0.997 R.AVMYLYK[325.13]HPK.E                        |
| 0.980106 | 0.969 R.K[325.13]KVHPAVVIR.Q                        |
| 0.980099 | 0.8883 K.TLQIFNIEM[147.04]K[325.13]SK.M             |
| 0.980093 | 0.8404 R.LK[325.13]VGLQVVAVK.A                      |
| 0.980078 | 0.9199 K.FKMPPEMNIK[325.13]APK.I                    |
| 0.980045 | 0.9894 R.LYWVDSK[325.13]LHQLSSIDFSGGNR.K            |
| 0.980039 | 0.9912 R.SVLISLK[325.13]QAPLVH.-                    |
| 0.979998 | 0.967 K.KPPK[325.13]PQLMANYYNK.V                    |
| 0.979989 | 0.974 R.SAK[325.13]AGVIFPVGR.M                      |

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| 0.979973 | 0.7687 K.K[325.13]GWLYYEAGQR.F                           |
| 0.979963 | 0.9972 R.IHAK[325.13]GSYESAR.I                           |
| 0.97995  | 0.9715 R.GQHTK[325.13]TTGR.R                             |
| 0.979936 | 0.9971 R.VIVC[160.03]NTK[325.13]LDNNWGR.E                |
| 0.979933 | 0.8906 R.VDFNVPM[147.04]K[325.13]NNQITNNQR.I             |
| 0.979932 | 0.9812 K.TFNQVEIK[325.13]PEMIGHYLGEFSITYKPKV.H           |
| 0.979911 | 0.8594 K.LWNTLGVC[160.03]K[325.13]YTVQDESHSEWVSC[160.03] |
| 0.979902 | 0.9972 R.AAGGFTHDELLK[325.13]VWK.G                       |
| 0.979886 | 0.9706 K.TPGYVVTPTHMNLK[325.13]QHLEITGGQVR.T             |
| 0.979883 | 0.8996 K.LLQK[325.13]GIHPTIISFQK.A                       |
| 0.979858 | 0.9605 R.GVPDAK[325.13]JIR.I                             |
| 0.979854 | 0.9923 K.SGNLTEDDKHNNAK[325.13]YAVSMAR.R                 |
| 0.979828 | 0.8799 R.FGWDC[160.03]HGLPVEYEIDK[325.13]TLGIR.G         |
| 0.979793 | 0.9966 K.VAGQDGSVVQFK[325.13]JK.R                        |
| 0.979788 | 0.9139 R.ETWHK[325.13]LSELEPGTGDLR.F                     |
| 0.979777 | 0.9133 K.AK[325.13]LGDSHDLQR.F                           |
| 0.97977  | 0.8747 R.GQPIYIQFSNHK[325.13]ELK.T                       |
| 0.979751 | 0.777 K.MKEIAEAYLGK[325.13]TVTNAVVTVPAYFNDSQR.Q          |
| 0.979736 | 0.979 R.GSSIFGLAPGK[325.13]AR.D                          |
| 0.979732 | 0.98 K.TSFFQALGITTK[325.13]ISR.G                         |
| 0.979717 | 0.9965 K.IDQLQEELLHTQLK[325.13]YQR.I                     |
| 0.979707 | 0.9918 R.FK[325.13]AADLNGDLTATR.E                        |
| 0.979697 | 0.8455 R.AEVQK[325.13]LQMEAPHIIVGTPGR.V                  |
| 0.979684 | 0.9121 R.SGKPAELLK[325.13]MFGIDR.D                       |
| 0.979659 | 0.9513 R.KSLLVQTK[325.13]R.R                             |
| 0.979641 | 0.9963 R.GFAFVYFENVDDAK[325.13]EAK.E                     |
| 0.979626 | 0.9182 K.HVGNQQYNVTYVVK[325.13]ER.G                      |
| 0.97956  | 0.8264 K.KAVTK[325.13]AQK.K                              |
| 0.979552 | 0.9615 R.GLVGEIHK[325.13]R.F                             |
| 0.979524 | 0.0642 R.HQGVMMVGM[147.04]GQK[325.13]DSYVGDEAQSK.R       |
| 0.979521 | 0.9962 R.HQASSSVFSWQKEK[325.13]TPSHLSSNSQR.T             |
| 0.979512 | 0.853 R.MPK[325.13]VQQTVQDLFGR.A                         |
| 0.9795   | 0.9973 R.HTLTGHSGK[325.13]VLSAK.F                        |
| 0.979492 | 0.9911 R.ATNWAK[325.13]FTATASLGVIHK.G                    |
| 0.979478 | 0.8607 R.KQLATK[325.13]AAR.K                             |
| 0.979452 | 0.9918 K.DLLHPSPEEEK[325.13]RK.H                         |
| 0.979449 | 0.8823 R.KQLATK[325.13]AAR.K                             |
| 0.979447 | 0.8799 R.FPGAYLK[325.13]GK.K                             |
| 0.979446 | 0.9633 K.GNYDEGFGRPHK[325.13]DLWASK.N                    |
| 0.979418 | 0.8706 K.TYSAK[325.13]LDNAR.Q                            |
| 0.979409 | 0.9749 R.VITYLDHSTQK[325.13]PLIAC[160.03]VEK.Q           |
| 0.979403 | 0.9925 R.C[160.03]K[325.13]ELGITALHIK.L                  |
| 0.979384 | 0.9422 K.GETKAFYPEEISSMVLTK[325.13]M[147.04]K.E          |
| 0.979376 | 0.9961 R.DGEDQTQDTELVEPTRPAGDGTQK[325.13]WAAVVVPSC       |
| 0.97937  | 0.7406 R.LGQSDPAPLQHQMIDIYQK[325.13]R.C                  |
| 0.97937  | 0.7181 R.EAPHVK[325.13]NNAIISLR.K                        |
| 0.979369 | 0.9925 R.VQEK[325.13]QHPVPPPAQNQNQVR.S                   |

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| 0.979362 | 0.978 R.KIGLETVGVK[325.13]INEK.T                         |
| 0.979349 | 0.731 K.WSLLQQQK[325.13]TAR.S                            |
| 0.979333 | 0.9552 R.LC[160.03]K[325.13]TVGATALPR.L                  |
| 0.97932  | 0.9557 R.GPLDK[325.13]WR.A                               |
| 0.979317 | 0.9784 K.GILAADESTGSIK[325.13]R.L                        |
| 0.979314 | 0.9962 K.AHPPELK[325.13]K.F                              |
| 0.979306 | 0.9322 K.GVVEVTHDLQK[325.13]HLAGLGLTEAIDK.N              |
| 0.979295 | 0.9968 R.NK[325.13]DHAPAFPLYFPMELHR.K                    |
| 0.97929  | 0.989 R.YPM[147.04]AVGLNK[325.13]GHK.V                   |
| 0.979281 | 0.9169 R.KLVPLLEDGGEAPAALEAALEEK[325.13]SALEQMR.K        |
| 0.979243 | 0.7575 R.YAIC[160.03]SALAASALPALVM[147.04]SK[325.13]GHR. |
| 0.979241 | 0.9806 R.LIHPK[325.13]SGR.S                              |
| 0.979218 | 0.8423 K.VM[147.04]IGENVDEK[325.13]HLPDLDHPIIPADYVAIK.A  |
| 0.9792   | 0.9958 K.SLPAPVAQRPDSPGGGLQAPGQK[325.13]RTPR.R           |
| 0.979191 | 0.9897 R.GQGSSPVAMQK[325.13]AQQVSQGLDVLTA.V              |
| 0.979184 | 0.7351 K.VEAK[325.13]FINYVK.N                            |
| 0.979178 | 0.9462 R.VGSHITGGDIYGIVSENSLIK[325.13]HK.I               |
| 0.979155 | 0.7297 K.SK[325.13]GIAYIEFK.T                            |
| 0.979133 | 0.9964 R.K[325.13]EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR.G   |
| 0.979132 | 0.9675 R.KK[325.13]VHPAVVIR.Q                            |
| 0.979128 | 0.9907 R.TK[325.13]TPGPGAQSALR.A                         |
| 0.979108 | 0.819 R.LQLETEIEALKEELFMK[325.13]K.N                     |
| 0.979104 | 0.7715 K.EIK[325.13]ILNIFGVIK.G                          |
| 0.979092 | 0.9601 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V             |
| 0.979088 | 0.9957 R.GRDPALPTLLNPK[325.13]TLPSGLDDYPR.A              |
| 0.979078 | 0.8489 R.RAPFDLFENK[325.13]K.K                           |
| 0.979046 | 0.87 K.GIVEFSGK[325.13]PAAR.K                            |
| 0.979045 | 0.967 R.YVASYLLAALGGNSSPSAK[325.13]DIK.K                 |
| 0.979041 | 0.916 R.K[325.13]KLEMDLK.D                               |
| 0.979018 | 0.8978 K.VQK[325.13]HQAFAELSANQSR.I                      |
| 0.979015 | 0.9898 R.MLEILEGK[325.13]GLSFLFPLK.L                     |
| 0.978997 | 0.9512 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI |
| 0.97899  | 0.9958 R.LQEALNLFK[325.13]SIWNNR.W                       |
| 0.978974 | 0.9959 R.K[325.13]YAVLYQPLFDKR.F                         |
| 0.97895  | 0.9916 R.LAAC[160.03]VNLIPQITSYEWK[325.13]GK.I           |
| 0.978946 | 0.9913 K.ITFHGEGDQEPGLEPGDIIIVLDQK[325.13]DHAVFTR.R      |
| 0.978918 | 0.9125 K.KVEK[325.13]VVVSNR.L                            |
| 0.978917 | 0.8573 R.KQLATK[325.13]AAR.K                             |
| 0.978905 | 0.9406 R.QTATQLLK[325.13]LAHK.Y                          |
| 0.978899 | 0.9742 R.NGFPK[325.13]QTAAQLILK.A                        |
| 0.978896 | 0.9965 R.FIIQSEK[325.13]PPHYLES.R                        |
| 0.97889  | 0.917 K.VK[325.13]WGDIEFPFGR.E                           |
| 0.978857 | 0.8792 K.AVPYQK[325.13]FEAHPNDLYVEGLPENIPFR.S            |
| 0.978843 | 0.7623 K.THINIVVIGHVDSGK[325.13]STTTGHLYK.C              |
| 0.97884  | 0.907 R.LNVLEK[325.13]SSPGHR.A                           |
| 0.978833 | 0.7448 K.TVDGPSGK[325.13]LWR.D                           |
| 0.978828 | 0.9973 R.LNHSVAK[325.13]ETAR.R                           |

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| 0.97881  | 0.9908 R.ATNWAK[325.13]FTATASLGVIHK.G                     |
| 0.978801 | 0.9151 K.NTC[160.03]TSVYTK[325.13]DR.A                    |
| 0.978797 | 0.9964 -.MK[325.13]PLVVFLGGPGAGK.G                        |
| 0.978786 | 0.3364 R.IHFPLATYAPVISA EK[325.13]AYHEQLSVAEITNAC[160.03] |
| 0.978779 | 0.981 R.GGGNQVSLNVMMDLK[325.13]K.C                        |
| 0.978767 | 0.8654 R.NVNIFK[325.13]FIIPNVVK.Y                         |
| 0.978739 | 0.9591 K.AVDALLTHC[160.03]K[325.13]SR.K                   |
| 0.978736 | 0.9791 K.FGFAIGSQTTK[325.13]K.A                           |
| 0.97871  | 0.9955 R.LC[160.03]VHC[160.03]LQAVFPFK[325.13]PPQR.I      |
| 0.978705 | 0.9834 R.AQLLLK[325.13]ATPEDNGR.S                         |
| 0.978702 | 0.9274 K.YHTINGHNC[160.03]EVK[325.13]K.A                  |
| 0.978695 | 0.9084 R.AFLGELK[325.13]TQMTSAVR.E                        |
| 0.978691 | 0.8656 K.K[325.13]VNVTVDYIRPASPATETVPAFSER.T              |
| 0.978671 | 0.9967 K.IK[325.13]STNPGISIGDVAK.K                        |
| 0.978661 | 0.8698 K.EGVHGGLINK[325.13]K.C                            |
| 0.978657 | 0.7726 K.DSYVGDEAQSK[325.13]R.G                           |
| 0.978654 | 0.9916 R.ESYEVSLTQK[325.13]TDPSVRPMHER.V                  |
| 0.978646 | 0.9101 K.VWNLANC[160.03]K[325.13]LK.T                     |
| 0.97864  | 0.9145 R.NLLESYHVPELIK[325.13]DAHLLVESK.N                 |
| 0.978636 | 0.8891 R.GAFGK[325.13]PQGTVAR.V                           |
| 0.978627 | 0.8658 R.DAVTYTEHAK[325.13]R.K                            |
| 0.978604 | 0.9892 R.LGAQALLGAAK[325.13]M[147.04]LLHSEQHPGQLK.D       |
| 0.978598 | 0.9966 R.K[325.13]KGTHFNFAIVFTDVK.R                       |
| 0.97859  | 0.9659 K.FHHTFSTEIAK[325.13]FLK.V                         |
| 0.978587 | 0.9556 R.HIYAK[325.13]VSGGPSLEQR.F                        |
| 0.978585 | 0.9951 R.KC[160.03]PK[325.13]C[160.03]NAAFGANDFHR.I       |
| 0.978584 | 0.9109 K.LLSISGK[325.13]R.S                               |
| 0.97857  | 0.9605 K.K[325.13]GFVLHK.S                                |
| 0.978558 | 0.9698 K.NKPGPYSSVPPPSAPPPK[325.13]K.S                    |
| 0.978534 | 0.9961 K.KSQEGKPK[325.13]EHTEPK.S                         |
| 0.978533 | 0.9141 R.GGEPQGPPFIK[325.13]YSTR.Q                        |
| 0.978524 | 0.7705 R.MVTSESKNVK[325.13]LTVSNVLK.E                     |
| 0.978515 | 0.9184 R.YESLTDPSKLD SGK[325.13]ELK.I                     |
| 0.978458 | 0.8591 R.DFTVSAMHGDM DQK[325.13]ER.D                      |
| 0.978433 | 0.9621 K.HK[325.13]TGP NLHGLFGR.K                         |
| 0.97843  | 0.9956 R.GFTAAGILSAHK[325.13]IIASSPEM[147.04]NLPTVSALR.I  |
| 0.978417 | 0.9792 R.AFTELFQVAC[160.03]AK[325.13]PPPLGLC[160.03]DYP:  |
| 0.978417 | 0.7705 K.LMPEIVATASK[325.13]VDIAPHVR.D                    |
| 0.9784   | 0.9882 R.K[325.13]M[147.04]DADGFLPITLIASFHR.V             |
| 0.978385 | 0.9622 K.GFQQILAGEYDHLPEQAFY MVGPIEEAVAK[325.13]ADK.L     |
| 0.978326 | 0.7618 K.IK[325.13]IIAPPER.K                              |
| 0.978316 | 0.9713 R.AGGK[325.13]ILTFDQLALDSPK.G                      |
| 0.978271 | 0.985 R.RPTFVPQWYVQQMK[325.13]R.G                         |
| 0.978244 | 0.9872 R.SHISDQSPLSSK[325.13]R.K                          |
| 0.978231 | 0.994 K.HQK[325.13]PVL TGQR.F                             |
| 0.978216 | 0.9929 R.NLLSVAYK[325.13]NVVGGQR.A                        |
| 0.978202 | 0.9923 R.AMELLK[325.13]VSK.D                              |

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| 0.978197 | 0.9703 K.LHPESK[325.13]DDKHGSYEDAVHSGALND.-             |
| 0.978197 | 0.9601 R.IPLSLDLTHQISK[325.13]DYGVYLED SGHTLR.G         |
| 0.978172 | 0.9956 R.K[325.13]LLC[160.03]TVFETLSDFESGLK.Y           |
| 0.978167 | 0.9661 K.SPPYTAFLGNLPYDVTEESIK[325.13]EFFR.G            |
| 0.97815  | 0.8777 K.NLHSEISGK[325.13]R.D                           |
| 0.978133 | 0.9784 R.LK[325.13]VFDGIPPPYDK.K                        |
| 0.978133 | 0.8429 R.RAPFDLFENK[325.13]K.K                          |
| 0.978084 | 0.9966 K.HGGGTESLFFDK[325.13]VR.K                       |
| 0.978067 | 0.8618 R.TFIAIK[325.13]PDGVQR.G                         |
| 0.978065 | 0.8751 R.KQLATK[325.13]AAR.K                            |
| 0.97806  | 0.8823 R.NLANTVTEEILEK[325.13]AFSQFGK.L                 |
| 0.978059 | 0.9972 R.LALHK[325.13]QFASLEHGIVPVTSDC[160.03]QYLFPK.V  |
| 0.97803  | 0.9972 R.SLETDSLILDVPLGVISRIEK[325.13]M[147.04]GGATSR.C |
| 0.978014 | 0.3785 R.TLSDYNIQK[325.13]ESTLHLVLR.L                   |
| 0.978012 | 0.8542 R.VNFAMNVGK[325.13]AR.G                          |
| 0.978009 | 0.8566 R.DIM[147.04]LATGK[325.13]LSPDAIPGK.W            |
| 0.977992 | 0.997 R.SQFSPAVFVYK[325.13]GGR.E                        |
| 0.977971 | 0.912 R.GVQK[325.13]LVLTSR.S                            |
| 0.977925 | 0.9873 R.ADLIAYLK[325.13]K.A                            |
| 0.977912 | 0.9922 K.AVYTQDC[160.03]PLAAAK[325.13]AIQGLR.A          |
| 0.97789  | 0.9556 K.AK[325.13]KDDTDDEIAK.Y                         |
| 0.977878 | 0.9664 K.LK[325.13]PTDVGLLAVIANNIITINK.D                |
| 0.977871 | 0.995 R.K[325.13]AIQISQQTPYWHC[160.03]R.L               |
| 0.977859 | 0.997 R.K[325.13]TYFAHDALQQC[160.03]TVGDIVLLR.A         |
| 0.977833 | 0.7461 K.FYEAFSK[325.13]NLK.L                           |
| 0.977831 | 0.9636 K.VPSPPPGHK[325.13]WK.E                          |
| 0.977819 | 0.8507 R.KQLATK[325.13]AAR.K                            |
| 0.977785 | 0.8614 K.TYSAK[325.13]LDNAR.Q                           |
| 0.977779 | 0.6786 K.FHGTVK[325.13]AENGK.L                          |
| 0.977769 | 0.9954 R.FQVDK[325.13]VNFHMFVDVGGQR.D                   |
| 0.977761 | 0.9316 R.LSFFGLEK[325.13]LLTNLGLGER.K                   |
| 0.977756 | 0.9882 R.RLSQPESA EK[325.13]HVTQR.L                     |
| 0.977754 | 0.8389 R.TLK[325.13]IPAMTIAK.N                          |
| 0.977746 | 0.7646 R.K[325.13]VESLQEEIAFLK.K                        |
| 0.97773  | 0.8599 R.TFIAIK[325.13]PDGVQR.G                         |
| 0.977723 | 0.9055 K.KELNYFAK[325.13]ALESERPFLAILGGAK.V             |
| 0.977712 | 0.9515 K.IQASTMAFK[325.13]QMEQISQFLQAAER.Y              |
| 0.977675 | 0.9109 K.GLK[325.13]AELMER.L                            |
| 0.977669 | 0.9682 R.NK[325.13]LDHYAIK.F                            |
| 0.977669 | 0.9553 R.ELAILLGMLDPAEKDEK[325.13]GM[147.04]PVTAR.V     |
| 0.977647 | 0.8602 K.ESYSIYVYK[325.13]VLK.Q                         |
| 0.977633 | 0.9605 R.TK[325.13]STGGAPT FNVTVT.K.T                   |
| 0.977629 | 0.9658 K.ISDSEGFK[325.13]ANLSLLR.R                      |
| 0.977626 | 0.9531 R.M[147.04]HAPGK[325.13]GLSQSALPYR.R             |
| 0.977608 | 0.7143 R.RFDDAVVQSDM[147.04]K[325.13]HWPFMVVNDAGRP      |
| 0.97759  | 0.8859 R.GC[160.03]TATLGNFAK[325.13]ATFDAISK.T          |
| 0.97759  | 0.9685 K.VNC[160.03]LDK[325.13]FWHK.A                   |

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| 0.977588 | 0.8603 K.TYSAK[325.13]LDNAR.Q                            |
| 0.977567 | 0.9105 R.TIEK[325.13]FEKEAAEMGK.G                        |
| 0.977541 | 0.7783 K.AVTK[325.13]YTSSK.-                             |
| 0.977531 | 0.9953 R.K[325.13]EVVHTVSLHEIDVINSR.T                    |
| 0.97753  | 0.9035 K.KIGYNPDTVAFVPISGWNGDNMLEPSANMPWFK[325.13]       |
| 0.977525 | 0.9556 K.GIIWGEDTLMEYLENPK[325.13]K.Y                    |
| 0.977519 | 0.9964 R.LSAKPAPPK[325.13]PEPKPK.K                       |
| 0.977511 | 0.9969 R.RENK[325.13]GATAAPQR.K                          |
| 0.977504 | 0.9754 R.K[325.13]FLDGIYVSEK.G                           |
| 0.977488 | 0.7676 R.IPELNK[325.13]VAR.A                             |
| 0.977486 | 0.9828 R.LYPWGVVEVENPEHNDFLK[325.13]LR.T                 |
| 0.977452 | 0.8764 K.SIYGKEKFEDENFILK[325.13]HTGPGILSMANAGPNTNGSQ    |
| 0.977442 | 0.9768 K.DINAYNC[160.03]EEPTEK[325.13]LPFPIIDDR.N        |
| 0.977437 | 0.9963 K.MK[325.13]QEPVKPEEGR.D                          |
| 0.97743  | 0.8176 K.KAVTK[325.13]AQK.K                              |
| 0.97741  | 0.9615 K.EMNPALGIDC[160.03]LHK[325.13]GTNDMK.Q           |
| 0.977393 | 0.9962 R.DHQALAK[325.13]AVQVHQDTLR.T                     |
| 0.977376 | 0.8654 R.FK[325.13]IPGSPPEMGR.G                          |
| 0.977364 | 0.9711 R.LHETLK[325.13]QC[160.03]QDLK.T                  |
| 0.977344 | 0.8586 R.EIAQDFK[325.13]TDLR.F                           |
| 0.977338 | 0.8764 K.IGKPHTVPC[160.03]K[325.13]VTGR.C                |
| 0.977308 | 0.8927 K.GNK[325.13]PWISLPR.G                            |
| 0.977305 | 0.7764 K.AVTK[325.13]YTSSK.-                             |
| 0.977298 | 0.9095 K.HGLEVIYMIPEIDCYC[160.03]VQQLK[325.13]EFEGK.T    |
| 0.977291 | 0.9971 K.LIPFLEK[325.13]LVELNEDVRPHIR.D                  |
| 0.977291 | 0.9971 R.SGTVDQPQLQK[325.13]ALTTMGFR.L                   |
| 0.977281 | 0.9195 R.HIQQVDC[160.03]SGNDLEQLHIK[325.13]VTSLC[160.03] |
| 0.977281 | 0.9851 R.LGVQDLFNSSK[325.13]ADLSGMSGAR.D                 |
| 0.977281 | 0.8677 R.VAPEEHPVLLTEAPLNPK[325.13]ANREK.M               |
| 0.977232 | 0.9948 R.AIK[325.13]AAIWESQHEGPEGAR.S                    |
| 0.977199 | 0.8704 R.K[325.13]FLVYVANFDEKDPR.T                       |
| 0.977185 | 0.9965 K.VPFIHVGNQVVSELGPIVQFVK[325.13]AK.G              |
| 0.977179 | 0.8566 R.AEAESM[147.04]YQIK[325.13]YEELQSLAGK.H          |
| 0.977174 | 0.8866 R.ERHPGSFDVVHVK[325.13]DANGNSFATR.L               |
| 0.977168 | 0.9915 R.SIC[160.03]TTVLELLDK[325.13]YLIANATNPESK.V      |
| 0.977139 | 0.9965 R.FSEFK[325.13]SHSGEFR.Q                          |
| 0.977133 | 0.5161 K.ANEVISK[325.13]LYAVHQEGNK.N                     |
| 0.977124 | 0.9643 K.LNNC[160.03]GMGIGGGK[325.13]ILAAALTEC[160.03]F  |
| 0.977123 | 0.9908 K.DILADLIPK[325.13]EQAR.I                         |
| 0.977106 | 0.8681 R.GAFGK[325.13]PQGTVAR.V                          |
| 0.977085 | 0.8616 K.GATLK[325.13]ITLDNAYM[147.04]EK.C               |
| 0.977077 | 0.8607 R.VTIPK[325.13]DIQLAR.R                           |
| 0.977061 | 0.995 R.TC[160.03]GPEHSK[325.13]GGGR.V                   |
| 0.977056 | 0.8821 R.DMVGIAQTGSGK[325.13]TLAYLLPAIVHINHQPYLER.G      |
| 0.977052 | 0.9961 K.VQK[325.13]VMVQPINLIFR.Y                        |
| 0.977026 | 0.976 K.LFPK[325.13]VSVPSNLSYGEWLHGFEK.K                 |
| 0.977019 | 0.9969 K.GHQC[160.03]SLK[325.13]SVAFSK.F                 |

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| 0.977016 | 0.7457 K.MPK[325.13]FSMPGFK.A                                 |
| 0.977007 | 0.9908 K.AQITQK[325.13]IGVHAFQQR.L                            |
| 0.976988 | 0.9612 R.VLPEK[325.13]LGVDLDAQTWR.I                           |
| 0.976964 | 0.9959 R.TLFGFLGK[325.13]IDELR.L                              |
| 0.976917 | 0.9023 R.K[325.13]LIADLQPNTEYSFVLMNR.G                        |
| 0.976865 | 0.9955 R.AASHEQAAAALK[325.13]NAGQAVTIVAQYRPEEYSR.F            |
| 0.976857 | 0.9449 K.K[325.13]TQEQLALEMAELTAR.I                           |
| 0.976855 | 0.9961 K.K[325.13]GNFNIEFTR.I                                 |
| 0.976851 | 0.8354 K.LTLHGLQQYYVK[325.13]LK.D                             |
| 0.976836 | 0.9758 K.ENEVQSLHSK[325.13]LTDTLVSK.Q                         |
| 0.976834 | 0.8677 R.YQK[325.13]STELLIR.K                                 |
| 0.97683  | 0.771 K.KPAGATPK[325.13]K.A                                   |
| 0.97682  | 0.6786 K.EITALAPSTM[147.04]K[325.13]IK.I                      |
| 0.97681  | 0.9462 R.LQAEIDNIK[325.13]NQR.A                               |
| 0.976761 | 0.9907 R.NVFHC[160.03]EPANILYIC[160.03]ENQPLK[325.13]K.L      |
| 0.976724 | 0.5664 R.GILTLK[325.13]YPIEHGIVTNWDDMEK.I                     |
| 0.976721 | 0.9934 R.NFIGDYIGMEEHPELQQFVGK[325.13]R.E                     |
| 0.976693 | 0.6994 R.NDNDTFTVK[325.13]YTPR.G                              |
| 0.976674 | 0.9702 R.SIRPDNMSEYSK[325.13]QMQR.F                           |
| 0.976673 | 0.9496 K.K[325.13]EVPIHR.V                                    |
| 0.97667  | 0.8613 R.VK[325.13]VFQSSANYAENFIQSIISTVEPAQR.Q                |
| 0.97667  | 0.9903 R.VYC[160.03]GPSPSC[160.03]LVQSSSLNAHIDYTTK[325.13]K.L |
| 0.976662 | 0.8192 R.GYPTIK[325.13]FFR.N                                  |
| 0.976625 | 0.5 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF              |
| 0.976615 | 0.6755 R.GC[160.03]GPEK[325.13]DHVYLQLHHLPEQLATR.L            |
| 0.976596 | 0.9346 K.K[325.13]EM[147.04]QPTHPIR.L                         |
| 0.97658  | 0.9947 R.VLSHSSK[325.13]IIIVNR.N                              |
| 0.976572 | 0.9934 K.GVK[325.13]IDKTDYMGVSYGPR.A                          |
| 0.976555 | 0.7639 K.LVINGNPITIFQERDPSK[325.13]IK.W                       |
| 0.976554 | 0.9555 R.FSPNSSNPIIVSC[160.03]GWDK[325.13]LVK.V               |
| 0.976524 | 0.997 K.STVAALLQNLYQPTGGQLLLDGK[325.13]PLPQYEHR.Y             |
| 0.976491 | 0.9862 K.HLSASQK[325.13]ALK.E                                 |
| 0.976479 | 0.7946 K.ESYSVYVYK[325.13]VLK.Q                               |
| 0.976456 | 0.994 R.K[325.13]LVIIEGDLER.T                                 |
| 0.976445 | 0.9959 R.K[325.13]AIHEVFVGVTSR.S                              |
| 0.97641  | 0.7705 R.TM[147.04]PVEQVFAK[325.13]NFR.V                      |
| 0.976394 | 0.443 R.TQLVNVAIFGPPWMAFK[325.13]ER.K                         |
| 0.976368 | 0.9094 K.IVIQK[325.13]YHTVNGHNC[160.03]EVR.K                  |
| 0.976366 | 0.993 R.K[325.13]PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPF            |
| 0.976354 | 0.8605 R.TVPQYK[325.13]YAAGVR.N                               |
| 0.976336 | 0.9309 K.THILLFLPK[325.13]SVSDYDGK.L                          |
| 0.976326 | 0.8647 R.K[325.13]TSYAQHQQVR.Q                                |
| 0.976321 | 0.8606 R.VHK[325.13]ISNVNK.A                                  |
| 0.976316 | 0.9881 R.VK[325.13]TTGIVETHFTFK.D                             |
| 0.976315 | 0.8616 K.HK[325.13]PGGGDVK.I                                  |
| 0.976286 | 0.5559 K.IAPSFAVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S        |
| 0.976245 | 0.9957 K.EK[325.13]IYVLLR.R                                   |



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| 0.976236 | 0.995 R.GYHK[325.13]VSLQVHPDR.V                           |
| 0.976232 | 0.8593 R.FK[325.13]IPGSPPESMGR.G                          |
| 0.976218 | 0.9361 K.VM[147.04]TK[325.13]DGQWFTDWDVPHSR.H             |
| 0.976202 | 0.7422 R.GELAIKDANAK[325.13]LSELEAALQR.A                  |
| 0.9762   | 0.8859 R.VLAEK[325.13]LAAIGEATR.L                         |
| 0.976199 | 0.9434 R.YTLHYK[325.13]TDAPLNIR.S                         |
| 0.976198 | 0.9606 K.EK[325.13]VLATVTKPVGGDK.N                        |
| 0.976195 | 0.9774 R.VKHEVSGETVVVFQGGALGK[325.13]TPDGQGLSTYK.E        |
| 0.976176 | 0.8854 R.SFVGK[325.13]QFSANDK.V                           |
| 0.976171 | 0.9612 K.TFDYK[325.13]IPYTTVLR.L                          |
| 0.976155 | 0.9619 R.IALSVHK[325.13]K.N                               |
| 0.976153 | 0.9746 R.VTSLGK[325.13]DWHRPC[160.03]LK.C                 |
| 0.976141 | 0.9745 K.KFHTVSGSK[325.13]C[160.03]EIK.V                  |
| 0.976127 | 0.8484 K.NTHC[160.03]SSLPHYQK[325.13]LK.K                 |
| 0.976124 | 0.8505 R.NVNIFK[325.13]FIIPNVVK.Y                         |
| 0.976078 | 0.2667 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K           |
| 0.976073 | 0.8634 R.K[325.13]TSYAQHQQVR.Q                            |
| 0.976037 | 0.8352 K.NIC[160.03]K[325.13]VVEVGSK.I                    |
| 0.976009 | 0.6306 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I          |
| 0.976006 | 0.9594 K.LEHEYIQNFK[325.13]ILQAGFK.R                      |
| 0.976003 | 0.9947 R.VVPDSC[160.03]C[160.03]K[325.13]TVVALC[160.03]GC |
| 0.975996 | 0.9624 R.LIYDTK[325.13]GR.F                               |
| 0.975982 | 0.7946 R.DTPAK[325.13]NAQK.S                              |
| 0.975981 | 0.7235 K.GVSK[325.13]AVEHINK.T                            |
| 0.97597  | 0.9958 K.INEVQTDVGVDTK[325.13]HQTQGVAFPISR.E              |
| 0.975965 | 0.982 R.VK[325.13]IQDAHR.L                                |
| 0.975943 | 0.9905 R.ESYEVSLTQK[325.13]TDPSVRPMHER.V                  |
| 0.975919 | 0.8677 R.LPSGNHM[147.04]K[325.13]ESR.E                    |
| 0.975896 | 0.9909 K.LTEK[325.13]QAQYLGMSC[160.03]DGPFPKPDHYR.Y       |
| 0.975889 | 0.7474 K.VHSFPTLK[325.13]FFPASADR.T                       |
| 0.975875 | 0.9967 R.GLTAHGINIK[325.13]DR.S                           |
| 0.975838 | 0.8294 R.GRPSGKGIVEFSGK[325.13]PAAR.K                     |
| 0.975807 | 0.6686 K.EITALAPSTM[147.04]K[325.13]IK.I                  |
| 0.975805 | 0.9001 K.LLSISGK[325.13]R.S                               |
| 0.975804 | 0.9953 R.VAIHYINPPNPAK[325.13]DNFTFK.C                    |
| 0.975769 | 0.722 R.C[160.03]QK[325.13]IC[160.03]DQWDALGSLTHSR.R      |
| 0.975761 | 0.9886 R.LTHQIQELTDTPTYFK[325.13]IQAR.N                   |
| 0.975742 | 0.9817 R.YTC[160.03]HVQHEGLPK[325.13]PLTLR.W              |
| 0.975725 | 0.8653 R.K[325.13]SQVLFSVTR.G                             |
| 0.975716 | 0.8453 R.KSEIEYYAMLAK[325.13]TGVHHYSGNNIELGTAC[160.03]    |
| 0.975712 | 0.9881 K.STAVK[325.13]ALTGGIAHLFK.Q                       |
| 0.975684 | 0.8654 K.LQNK[325.13]EHVIEALR.R                           |
| 0.975665 | 0.8454 K.TLHPDLGTDKDK[325.13]EQWK.E                       |
| 0.975664 | 0.4423 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                 |
| 0.975659 | 0.9084 K.AEPAK[325.13]IEAFR.A                             |
| 0.975658 | 0.9966 R.LGTQEYLQQLESHMK[325.13]SR.K                      |
| 0.975653 | 0.966 R.K[325.13]VVVSHSTHR.T                              |

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| 0.975642 | 0.9934 R.IEHLIGK[325.13]K.L                            |
| 0.97564  | 0.9807 K.GATYGKPVHHGVNQLK[325.13]FAR.S                 |
| 0.975603 | 0.0643 K.EITALAPSTMKIK[325.13]IIAPPER.K                |
| 0.975589 | 0.6593 R.LESGM[147.04]QNMSIHTK[325.13]TTSGYAGGLSSAYGC  |
| 0.975588 | 0.6813 R.NTDQASM[147.04]PDNTAAQK[325.13]VSHLLGINVTDF   |
| 0.975575 | 0.8682 K.GKWKPPMIDNPSYQGIWK[325.13]PRK.I               |
| 0.975568 | 0.9959 K.ASGANYSFHK[325.13]ESGR.F                      |
| 0.975562 | 0.9968 K.HLNSK[325.13]TVGQC[160.03]LETTAQR.V           |
| 0.975562 | 0.8989 K.MPEMHFK[325.13]APK.I                          |
| 0.975556 | 0.9387 R.HK[325.13]NM[147.04]SVHLSPC[160.03]FR.D       |
| 0.975527 | 0.8992 K.VIQYLAYVASSHK[325.13]SK.K                     |
| 0.975513 | 0.8607 R.K[325.13]VIDDTNITR.L                          |
| 0.97549  | 0.862 R.K[325.13]ESYSIYVYK.V                           |
| 0.975473 | 0.9362 R.IPENNPVK[325.13]LSC[160.03]AYSGFSSPR.V        |
| 0.975459 | 0.9908 K.GVSPEPIHLK[325.13]IFSPNVNLTLDLPGMTK.V         |
| 0.975441 | 0.9556 K.GVLFGVPGAFTPGC[160.03]SK[325.13]THLPGFVEQAEA  |
| 0.975425 | 0.9904 R.DSK[325.13]HIVVYHR.G                          |
| 0.975392 | 0.7132 K.TVDGPSGK[325.13]LWR.D                         |
| 0.975385 | 0.8554 R.TVPQYK[325.13]YAAGVR.N                        |
| 0.975332 | 0.7181 R.EIFNFVLK[325.13]AIRPQIDLK.R                   |
| 0.975331 | 0.9131 K.NLFTK[325.13]THPQWYPAR.Q                      |
| 0.975291 | 0.9955 R.FHINQPALK[325.13]QR.E                         |
| 0.975245 | 0.9966 R.VANPK[325.13]DIIHFFR.H                        |
| 0.975237 | 0.8811 R.TPC[160.03]EEILVK[325.13]HVGSR.L              |
| 0.975234 | 0.7528 K.K[325.13]LLEAQSHFR.K                          |
| 0.975229 | 0.9703 R.WGEDNHWIC[160.03]K[325.13]PWNLAR.S            |
| 0.975226 | 0.9903 K.LTK[325.13]QQLILAR.D                          |
| 0.975226 | 0.5394 R.GILTLK[325.13]YPIEHGIVTNWDDMEK.I              |
| 0.975224 | 0.99 R.DM[147.04]HSAYK[325.13]HADGK.K                  |
| 0.975213 | 0.9899 R.LC[160.03]HDKETYK[325.13]LQR.R                |
| 0.975201 | 0.8611 K.VK[325.13]LEAEIATYR.R                         |
| 0.975197 | 0.9924 R.LVSLIGSK[325.13]TQIPTQR.Y                     |
| 0.975195 | 0.6519 R.RYQK[325.13]STELLIR.K                         |
| 0.975176 | 0.9906 K.IK[325.13]EWVDKYDPGALVIPFSGALELK.L            |
| 0.975171 | 0.9524 R.AK[325.13]ELLGQGILLR.S                        |
| 0.97516  | 0.9966 K.DKLEFAPK[325.13]AVLNR.N                       |
| 0.975133 | 0.9769 R.MVVPAALK[325.13]VVR.L                         |
| 0.975111 | 0.9306 K.K[325.13]EM[147.04]QPTHPIR.L                  |
| 0.975101 | 0.9918 R.LRPESALAQAQK[325.13]C[160.03]FALYR.Q          |
| 0.975099 | 0.9603 K.SLNLK[325.13]HIK.H                            |
| 0.97508  | 0.8809 R.DAVTYTEHAK[325.13]RK.T                        |
| 0.975032 | 0.5558 K.MLETK[325.13]WSLLQQQK.T                       |
| 0.975    | 0.9256 K.AK[325.13]ISKPAPYWEGTAVIDGEFK.E               |
| 0.974994 | 0.9047 K.ITLDNAYMEK[325.13]C[160.03]DENILWLDYK.N       |
| 0.974994 | 0.9968 K.TVLELQYVLDK[325.13]LGDDEV.R.T                 |
| 0.974978 | 0.9912 K.LAAK[325.13]LIHTLDDR.T                        |
| 0.97497  | 0.9711 K.AGLQVYNK[325.13]C[160.03]WKFEHC[160.03]NFNDVT |

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| 0.974969 | 0.7427 K.ARPFPDGLAEDIDK[325.13]GEVSAR.Q                   |
| 0.974945 | 0.9917 K.TPALK[325.13]YQQLFEDIR.G                         |
| 0.974927 | 0.5217 K.SIYGEEK[325.13]FEDENFILK.H                       |
| 0.974914 | 0.966 K.LLGLGQK[325.13]HLVMGDIPA AVNAFQEAASLLGK.K         |
| 0.974901 | 0.9566 K.KAGEIWK[325.13]GMSK.E                            |
| 0.974897 | 0.9619 K.IHHS GAK[325.13]VVLSK.L                          |
| 0.974884 | 0.9843 K.KPLKPC[160.03]C[160.03]AC[160.03]PETK[325.13]K.A |
| 0.974815 | 0.9937 K.HC[160.03]VDPTSFLKPIAK[325.13]LFSVIK.N           |
| 0.974795 | 0.8946 R.K[325.13]QITMEELVR.S                             |
| 0.974794 | 0.8713 -.MQIFVK[325.13]TLTGK.T                            |
| 0.974775 | 0.9505 K.AK[325.13]SIVFHR.K                               |
| 0.974764 | 0.9547 R.ISEVLQK[325.13]LQNEILK.D                         |
| 0.974749 | 0.8189 R.MHAPGK[325.13]GLSQSALPYR.R                       |
| 0.974741 | 0.9871 R.LSDGSLK[325.13]LYPFQC[160.03]FLAHDQAVR.T         |
| 0.97468  | 0.9559 K.VIMVTGDHPITAK[325.13]AIAK.G                      |
| 0.974671 | 0.9835 R.K[325.13]VLISDSLDPK[160.03]C[160.03]R.K          |
| 0.97467  | 0.8578 R.KQLATK[325.13]AAR.K                              |
| 0.974667 | 0.8564 R.K[325.13]VIDDTNITR.L                             |
| 0.974647 | 0.9813 R.LDPNK[325.13]YPVPENWLHK.E                        |
| 0.974625 | 0.9741 K.IDGSANLK[325.13]SQDDRDK.F                        |
| 0.974611 | 0.9735 R.ELPSFLGK[325.13]R.T                              |
| 0.974608 | 0.9958 K.RSPYAGLQLGAAK[325.13]KPPVTFAEK.G                 |
| 0.974601 | 0.8954 K.MK[325.13]LPQFGISTPGSDLHVNAK.G                   |
| 0.974599 | 0.8574 K.EGVHGGLINK[325.13]K.C                            |
| 0.974577 | 0.8596 K.DK[325.13]GFGFIR.L                               |
| 0.974574 | 0.8902 K.K[325.13]WTTLNSLQLHGLQLR.I                       |
| 0.97457  | 0.9956 K.IETWHK[325.13]PDLGTLENVHGLDPNTWK.T               |
| 0.974562 | 0.9113 K.ITGEAFVQFASQELAEK[325.13]ALGK.H                  |
| 0.974548 | 0.9706 K.LAK[325.13]TQGNVFATDAILATLMSC[160.03]TR.S        |
| 0.974543 | 0.9824 K.K[325.13]VNAVFEWHITK.G                           |
| 0.974532 | 0.9957 K.K[325.13]GNFNIEFTR.I                             |
| 0.974525 | 0.9963 R.VIVC[160.03]NTK[325.13]LDNNWGR.E                 |
| 0.974511 | 0.3121 K.GIIRPGTAFELLEQAATGYVIDPIK[325.13]GLK.L           |
| 0.974505 | 0.9764 K.IDGSANLK[325.13]SQDDRDK.F                        |
| 0.974486 | 0.9962 K.TPQQLWYTHEK[325.13]K.V                           |
| 0.974465 | 0.9864 K.VEELEGEITTLNHK[325.13]LQDASAEVER.L               |
| 0.974444 | 0.9965 K.HTWQK[325.13]ANDQFLESQR.L                        |
| 0.974417 | 0.9928 R.KGLYMANDLK[325.13]LLR.H                          |
| 0.974404 | 0.9958 R.TWLLK[325.13]THWTLDK.Y                           |
| 0.974399 | 0.9615 K.LMC[160.03]SLC[160.03]HC[160.03]PGATIGC[160.03]C |
| 0.974399 | 0.8358 R.K[325.13]PYIWEYSR.L                              |
| 0.974377 | 0.5997 K.SVVLM SHLGRPDGVPM[147.04]PDK[325.13]YSLEPVAVI    |
| 0.974375 | 0.9956 R.IVG YFVSGC[160.03]DPSIMGIGVPVPAISGALK[325.13]K.A |
| 0.974357 | 0.2439 K.EAHLPPGAMAAVGLSWEEC[160.03]K[325.13]QR.C         |
| 0.974287 | 0.9959 K.SC[160.03]LLLQFTDK[325.13]R.F                    |
| 0.974279 | 0.8496 K.LYEEK[325.13]TGNAWHSK.N                          |
| 0.974273 | 0.8966 R.VRGPK[325.13]GPEEK.K                             |

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| 0.974264 | 0.955 R.INSGGKLPNFGFVVFDDSEPVQK[325.13]VLSNRPIM[147.   |
| 0.974255 | 0.8429 R.YK[325.13]LLGGLAVR.R                          |
| 0.974214 | 0.9012 K.K[325.13]TESHHK.A                             |
| 0.974202 | 0.9172 K.LLEPVLLLKG[325.13]ER.F                        |
| 0.974199 | 0.8872 R.AK[325.13]AVVQLKPR.H                          |
| 0.974187 | 0.834 K.VNQIGSVTESLQAC[160.03]K[325.13]LAQANGWGMV.     |
| 0.974159 | 0.9416 R.DLANDIMTLMSHTK[325.13]PYIR.K                  |
| 0.974153 | 0.8119 R.K[325.13]LLEGEESR.I                           |
| 0.974136 | 0.9642 K.KLQK[325.13]AALLK.A                           |
| 0.97413  | 0.9573 R.TKAPK[325.13]IQR.L                            |
| 0.974126 | 0.9267 R.HYAHTDC[160.03]PGHADYVK[325.13]NMITGTAPLDGC   |
| 0.974091 | 0.9417 K.AK[325.13]DPFAHLPK.S                          |
| 0.974085 | 0.9731 R.AWVWNTHADFADEC[160.03]PK[325.13]PELLAIR.F     |
| 0.974062 | 0.9853 K.TTWAIK[325.13]HAASNPSK.K                      |
| 0.974042 | 0.9962 R.TDLVK[325.13]SELLHIESQVELLR.F                 |
| 0.974036 | 0.9847 R.NK[325.13]THTLC[160.03]R.R                    |
| 0.974021 | 0.9682 R.RAPKK[325.13]PLTR.A                           |
| 0.97402  | 0.9832 R.NIVDK[325.13]TASFVAR.N                        |
| 0.974014 | 0.8918 R.ANQK[325.13]HQGLK.L                           |
| 0.973995 | 0.8437 K.HVVFGK[325.13]VK.E                            |
| 0.97398  | 0.9556 R.VLPGK[325.13]YLEEIATQMR.T                     |
| 0.973974 | 0.9962 R.K[325.13]HGGPKDEER.H                          |
| 0.973936 | 0.9587 K.GPVFAPPYEPLPENVK[325.13]FYYDGK.V              |
| 0.973933 | 0.9386 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V           |
| 0.973905 | 0.9591 R.ELNITAAK[325.13]EIEVGGGR.K                    |
| 0.9739   | 0.6901 R.VPLAIVNK[325.13]AHQANQLYPFAISLIESVR.T         |
| 0.973874 | 0.9558 R.DFRPLK[325.13]DSR.F                           |
| 0.973848 | 0.8904 R.GFYNRPLSPDLSYQC[160.03]FVLASLK[325.13]EPMQDKI |
| 0.973843 | 0.9318 K.NAK[325.13]GSNYWR.N                           |
| 0.973842 | 0.8573 R.LLFNDVQTLK[325.13]DGRHPQGEQM[147.04]YR.R      |
| 0.973836 | 0.8576 K.AVLFC[160.03]LSEDK[325.13]K.N                 |
| 0.973832 | 0.8542 R.DAVTYTEHAK[325.13]RK.T                        |
| 0.973814 | 0.9803 K.HK[325.13]SIEEIVR.R                           |
| 0.973812 | 0.2289 K.TVTAMDVVYALK[325.13]R.Q                       |
| 0.973772 | 0.9868 R.VLVSGLPPSGSWQDLK[325.13]DHMR.E                |
| 0.973766 | 0.9468 K.EVIQEWNLNLIK[325.13]R.W                       |
| 0.973764 | 0.9934 R.FHMDSETHDPIDLQTK[325.13]ELR.E                 |
| 0.973727 | 0.981 R.HLGK[325.13]PEEYK.M                            |
| 0.973696 | 0.9779 K.K[325.13]ELLLPGNNR.K                          |
| 0.97366  | 0.1337 R.FLEQQNK[325.13]ILLAELEQLK.G                   |
| 0.973653 | 0.9873 K.KTESHK[325.13]AK.S                            |
| 0.973646 | 0.7043 R.TAPDLLPHK[325.13]PLPASAYIEDGR.F               |
| 0.973644 | 0.8755 K.K[325.13]SADTLWDIQLK.D                        |
| 0.973609 | 0.9626 R.HVFGESDELIGQK[325.13]VAHALAEGLGVIAC[160.03]IG |
| 0.973607 | 0.8682 R.HNGTGGK[325.13]SIYGEK.F                       |
| 0.973606 | 0.8547 R.AK[325.13]FEELNMDLFR.S                        |
| 0.973584 | 0.8698 K.KPVVGK[325.13]K.G                             |

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| 0.973567 | 0.7296 R.LAHYNK[325.13]R.S                              |
| 0.973555 | 0.7046 R.LK[325.13]STC[160.03]IYGGAPK.G                 |
| 0.973552 | 0.8895 R.TNEK[325.13]VELQELNDR.F                        |
| 0.973487 | 0.9101 R.VLSGEFQIVNPHELLK[325.13]DLTER.G                |
| 0.973467 | 0.9966 R.VTPK[325.13]EWR.N                              |
| 0.973467 | 0.8569 K.ALSVGNIDDALQC[160.03]YSEAIK[325.13]LDPHNHVLYS  |
| 0.973463 | 0.8593 R.HGYIK[325.13]GIVK.D                            |
| 0.973457 | 0.9928 R.WK[325.13]QLSLPQQEAQK.I                        |
| 0.973454 | 0.8553 K.SDFGK[325.13]FVLSSGK.F                         |
| 0.973453 | 0.8954 K.DATNVGDEGGFAPNILENK[325.13]EGLELLK.T           |
| 0.973443 | 0.9537 R.ANGLK[325.13]SC[160.03]VIVLR.I                 |
| 0.973433 | 0.9658 R.IAK[325.13]ASGATILSTLANLEGEETFEAAMLGQAEEVVQI   |
| 0.973429 | 0.8614 R.HDSPEDVK[325.13]R.R                            |
| 0.973425 | 0.8815 K.K[325.13]SFFQAAATEHLLPMGTALPLLEAQAATHTLVDPITC  |
| 0.973398 | 0.9058 K.FVGDPALVLNDIHK[325.13]K.I                      |
| 0.973392 | 0.8613 K.VMTK[325.13]DGQWFTDWDVAPHSR.H                  |
| 0.973375 | 0.6905 R.C[160.03]FASNK[325.13]LGTAMSHEIR.L             |
| 0.973314 | 0.4423 R.VSFELFADKVPK[325.13]TAENFR.A                   |
| 0.973294 | 0.7461 R.TM[147.04]PVEQVFAK[325.13]NFR.V                |
| 0.973283 | 0.9884 R.ISQHEAK[325.13]IK.S                            |
| 0.973258 | 0.8655 R.YQHLK[325.13]GK.N                              |
| 0.973236 | 0.6994 R.LDYLSSLKVK[325.13]GLVLGPIHK.N                  |
| 0.973232 | 0.8582 R.HGYIK[325.13]GIVK.D                            |
| 0.973184 | 0.9957 R.GVSAFSTWEK[325.13]ELHK.I                       |
| 0.973182 | 0.2397 R.M[147.04]VNHFAIEFK[325.13]R.K                  |
| 0.973146 | 0.8584 R.VK[325.13]ILFNK.K                              |
| 0.973127 | 0.9951 R.ITFTGEADQAPGVEPGDIVLLLQEK[325.13]EHEVFQR.D     |
| 0.973121 | 0.8942 K.HLIK[325.13]AQR.H                              |
| 0.973121 | 0.8942 K.WVVK[325.13]HLIK.A                             |
| 0.973085 | 0.9773 R.LVC[160.03]YNNK[325.13]ITASYEDR.V              |
| 0.973064 | 0.991 K.FSPGAPGGSGSQPNQK[325.13]LGHPALSAGTGSPQPPS       |
| 0.973057 | 0.9954 R.K[325.13]SFYSSHYAR.E                           |
| 0.97302  | 0.974 R.ENFC[160.03]NIHVSLVPQPSSTGEQK[325.13]TKPTQNSV   |
| 0.972959 | 0.9665 K.K[325.13]TDKQPLQKPSHC[160.03]TIYVAK.N          |
| 0.972949 | 0.9552 K.MYGISLC[160.03]QAILDETK[325.13]GDYEK.I         |
| 0.972928 | 0.8935 K.K[325.13]GLLSAEVAR.L                           |
| 0.97292  | 0.9281 K.LHQAM[147.04]K[325.13]GVGTR.H                  |
| 0.972912 | 0.9924 R.ENPHDAVVFHVK[325.13]FVGK.T                     |
| 0.972901 | 0.9955 R.LGIGTK[325.13]MLNHVLNIC[160.03]EK.D            |
| 0.972876 | 0.9953 K.LMYK[325.13]ESGVFEGIPTYR.F                     |
| 0.972865 | 0.9956 R.ELAKVEEIQTLISQVLAAC[325.13]EK.H                |
| 0.972865 | 0.3287 K.KAK[325.13]KPAAAAGAK.K                         |
| 0.972842 | 0.7107 R.DGSIDLVINLPNNNTK[325.13]FVHDNYVIR.R            |
| 0.972804 | 0.9098 R.DVQIGDIVTVGEC[160.03]RPLSK[325.13]TVR.F        |
| 0.972804 | 0.7844 R.HGK[325.13]YM[147.04]AC[160.03]C[160.03]LLYR.G |
| 0.972799 | 0.8427 K.TIGGGDDSFSTFFC[160.03]ETGAGK[325.13]HVPR.A     |
| 0.972779 | 0.9868 K.SWHK[325.13]AC[160.03]FR.C                     |

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| 0.97276  | 0.7162 K.LTPK[325.13]IGFPWSEIR.N                           |
| 0.972732 | 0.9933 R.HPQLLYESK[325.13]LYK.I                            |
| 0.972727 | 0.8618 -.MQIFVK[325.13]TLTGK.T                             |
| 0.972727 | 0.9943 K.HPEK[325.13]LATVLSGAC[160.03]DGEVR.I              |
| 0.972718 | 0.985 K.GSIQK[325.13]FVPYLIAGIQHGC[160.03]QDIGAR.S         |
| 0.972712 | 0.9938 R.SENKNEGQDATM[147.04]YC[160.03]K[325.13]SVGYPH     |
| 0.972705 | 0.8446 K.NQQFHK[325.13]ER.E                                |
| 0.972705 | 0.9965 K.GQK[325.13]ISIFNEHK.S                             |
| 0.972682 | 0.9493 R.AK[325.13]LQIELGK.C                               |
| 0.972663 | 0.838 K.KAPK[325.13]SPAK.A                                 |
| 0.972658 | 0.8859 K.AAKPKK[325.13]APK.S                               |
| 0.972654 | 0.8641 K.VIPSPFK[325.13]HADIVTTTHK.T                       |
| 0.972618 | 0.8595 R.FPGAYLK[325.13]GK.K                               |
| 0.972598 | 0.9877 R.LGC[160.03]FNLTIK[325.13]GHAK.C                   |
| 0.972595 | 0.9816 R.LNKHEENLK[325.13]TK.K                             |
| 0.97249  | 0.8598 R.KVLRDNIQGITK[325.13]PAIR.R                        |
| 0.972477 | 0.9953 R.NYLLSLPHK[325.13]NK.V                             |
| 0.972468 | 0.6871 K.FINYVK[325.13]NC[160.03]FR.M                      |
| 0.972465 | 0.9375 R.GANLK[325.13]DYYSR.K                              |
| 0.972465 | 0.876 R.IAEDDGKPRPAFSNALEPDFK[325.13]ATSITVTGSGSC[160.03]G |
| 0.972462 | 0.8359 R.K[325.13]ESYSIYVK.V                               |
| 0.972445 | 0.9925 K.AAIISAEGDSK[325.13]AAELIANSLATAGDGLIELR.K         |
| 0.972444 | 0.993 R.AVGNIIVGTDEQTQVVLNC[160.03]DALSHFPALLTHPK[325.13]K |
| 0.972434 | 0.9531 R.ANTFVAELK[325.13]GLDPAR.V                         |
| 0.972421 | 0.7035 K.K[325.13]GWLYYEAGQR.F                             |
| 0.972351 | 0.8563 R.GDGTGGK[325.13]SIYGER.F                           |
| 0.972343 | 0.9359 K.TVM[147.04]PYISTTPAK[325.13]LR.N                  |
| 0.972336 | 0.994 R.TDC[160.03]NHIFLNFVPTVIMDPSK[325.13]IEESVR.S       |
| 0.972322 | 0.8421 K.DVNAAIATIK[325.13]TK.R                            |
| 0.972254 | 0.9851 K.FNK[325.13]IVHSSM[147.04]TR.A                     |
| 0.972228 | 0.9882 R.YPPWPGK[325.13]IVNPPK.D                           |
| 0.97215  | 0.8918 R.ALDTM[147.04]NFDVIK[325.13]GKPVR.I                |
| 0.972137 | 0.9846 R.WK[325.13]YMIVDEGHR.M                             |
| 0.972123 | 0.8906 K.VK[325.13]VYGPGVAK.T                              |
| 0.972105 | 0.9716 R.FSYVLPLVHSLEPTMGPK[325.13]AGGTR.I                 |
| 0.972095 | 0.722 R.VQAQGPGLK[325.13]EAFTNKPNVFTVVTR.G                 |
| 0.972071 | 0.9949 R.FLDK[325.13]ALELNMLSLK.G                          |
| 0.972055 | 0.8935 K.K[325.13]TESHHK.A                                 |
| 0.972039 | 0.9172 K.YQLDK[325.13]DGVVLFK.K                            |
| 0.972001 | 0.98 R.AQLGGPEAAK[325.13]SDETA.AK.-                        |
| 0.971986 | 0.8774 R.NFGTK[325.13]ISAR.A                               |
| 0.971981 | 0.9682 K.SINAGGHK[325.13]VGLALELEA.-                       |
| 0.97198  | 0.9884 R.TVDATGK[325.13]EIELTHR.M                          |
| 0.971949 | 0.4023 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T                  |
| 0.971949 | 0.9513 K.LSGLPK[325.13]HR.V                                |
| 0.971944 | 0.9964 R.K[325.13]WQAQDLATPLAFAHNPSR.V                     |
| 0.971939 | 0.9953 R.LK[325.13]GSGVTTYSVHPGTVQSELVR.H                  |

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| 0.971899 | 0.4989 R.TYTWLK[325.13]GHQK.S                            |
| 0.971877 | 0.9176 R.LAAIVAK[325.13]QVLLGR.K                         |
| 0.971876 | 0.7831 K.KPAGATPK[325.13]K.A                             |
| 0.971868 | 0.9918 R.DALAK[325.13]ALHAR.V                            |
| 0.971865 | 0.9887 R.NAYVWTLK[325.13]GR.T                            |
| 0.971861 | 0.8789 K.VWNLANC[160.03]K[325.13]LK.T                    |
| 0.971856 | 0.9799 R.GGRPNEIEPPPEMPPWQK[325.13]R.Q                   |
| 0.971838 | 0.9795 R.FSLVPHNYGLVLYENK[325.13]AAYER.Q                 |
| 0.971827 | 0.98 K.NFSEIHPGMLLIGFVK[325.13]SIK.D                     |
| 0.97182  | 0.6895 R.GITGVEDK[325.13]ESWHGKPLPK.N                    |
| 0.971813 | 0.9743 K.DFTPGKPLK[325.13]C[160.03]IHK.H                 |
| 0.971793 | 0.9588 K.IAHLAGVK[325.13]DQLTK.E                         |
| 0.971767 | 0.9914 K.ALGA[K[325.13]HC[160.03]VK.E                    |
| 0.971761 | 0.8049 K.NFGIGQDIQPK[325.13]R.D                          |
| 0.971734 | 0.9942 K.VK[325.13]LEGHELPADLPPHLVPPSK.R                 |
| 0.971713 | 0.8597 R.HNGTGGK[325.13]SIYGEK.F                         |
| 0.971708 | 0.8347 R.FLQDYFDGNLK[325.13]R.Y                          |
| 0.971708 | 0.8556 K.VIRPLDQPSSFDPATPYIK[325.13]DLFTC[160.03]TIK.R   |
| 0.971639 | 0.9427 R.DMHSAVK[325.13]HADGK.K                          |
| 0.971593 | 0.8424 R.YQK[325.13]STELLIR.K                            |
| 0.971583 | 0.8602 R.IDKPILK[325.13]AGR.A                            |
| 0.971576 | 0.9865 R.GILQK[325.13]NVPILYTASQAC[160.03]LQHPDVAAYK.A   |
| 0.971573 | 0.9835 K.DGPVGFADFVYK[325.13]HIVPAC[160.03]FLAPLK.Q      |
| 0.971547 | 0.9961 R.VVNSETPVVVDFHAQWC[160.03]GPC[160.03]K[325.13]   |
| 0.971528 | 0.9788 R.ASC[160.03]ILQLVK[325.13]HIQK.L                 |
| 0.971429 | 0.9718 R.K[325.13]AGNFYVPAEPK.L                          |
| 0.971425 | 0.8329 R.VIFGLFGK[325.13]TVPK.T                          |
| 0.971415 | 0.996 K.AINQIAAALFTIHK[325.13]GSIEDR.L                   |
| 0.971409 | 0.9914 K.LHREFHHGPDPTDTAPGEQAQDVASSPPESSFQK[325.13]      |
| 0.971348 | 0.8633 R.K[325.13]YAYSAASGGR.R                           |
| 0.971333 | 0.9816 R.GNWEQPQNQNQTQHK[325.13]QRPQATAEQIR.L            |
| 0.971321 | 0.9954 R.AVSNNLSTQLTFQAIHK[325.13]PR.V                   |
| 0.971306 | 0.8869 R.K[325.13]PVTVHSR.A                              |
| 0.971287 | 0.6051 K.EITALAPSTMK[325.13]IK.I                         |
| 0.971286 | 0.6626 R.IAAYLFK[325.13]GNNR.W                           |
| 0.971274 | 0.9183 K.AMK[325.13]GLGTDEESILTLLTSR.S                   |
| 0.971269 | 0.9405 R.GLK[325.13]MSATFIGNSTAIQELFK.R                  |
| 0.971268 | 0.9513 R.IHAEIK[325.13]NSLK.I                            |
| 0.971245 | 0.9244 R.RMPQAPPSLC[160.03]VTPYPEPSEC[160.03]SWK[325.13] |
| 0.971244 | 0.9765 R.FLTAVNLEHPEMLEK[325.13]ASR.E                    |
| 0.971191 | 0.9954 R.SPGLPMSDLK[325.13]THNVHVEIEQR.W                 |
| 0.971191 | 0.6859 K.AVGK[325.13]VIPELNGK.L                          |
| 0.971189 | 0.9837 R.SPSDEYKDNLHQVSK[325.13]R.L                      |
| 0.971175 | 0.8872 K.APK[325.13]ISMPDIDLNLK.G                        |
| 0.971175 | 0.8872 K.LK[325.13]MPEMHFK.A                             |
| 0.971173 | 0.9397 K.TGFYC[160.03]K[325.13]LC[160.03]SLFYTNEEVAK.N   |
| 0.97116  | 0.996 K.FFK[325.13]SKPELPPGLSPEATAPVTPSRPEGGEPLSK.T      |

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| 0.971152 | 0.8751 K.QFAEMYVAK[325.13]FAAK.G                         |
| 0.971147 | 0.9951 R.AIAYLFPSGLFEK[325.13]R.A                        |
| 0.971126 | 0.971 K.TYGLWK[325.13]C[160.03]VLPEEDSGELAKPK.I          |
| 0.971112 | 0.962 R.SSPSFSSLHYQDAGNYVC[160.03]ETALQEVEGLK[325.13]    |
| 0.971107 | 0.7202 K.K[325.13]AASGEAKPK.A                            |
| 0.971089 | 0.8451 R.K[325.13]FVADGIFK.A                             |
| 0.971082 | 0.9954 K.HVVFGQVIK[325.13]GIGVAR.I                       |
| 0.970997 | 0.9936 R.VLISSLK[325.13]DC[160.03]LHGIEAK.S              |
| 0.97099  | 0.8441 R.EAGSQK[325.13]DENLALYVENQFR.E                   |
| 0.970985 | 0.989 K.GQLGHGDTK[325.13]R.V                             |
| 0.970984 | 0.8883 K.ISLK[325.13]YTAAR.L                             |
| 0.970969 | 0.6985 K.VSYFPTVPGVYIVSTK[325.13]FADEHVPGPSFTVK.I        |
| 0.970967 | 0.8872 R.AGK[325.13]DLVSSLTSGLLTIGDR.F                   |
| 0.970925 | 0.7258 K.TAIGK[325.13]AGYTDK.V                           |
| 0.970922 | 0.2435 R.LAHYNK[325.13]R.S                               |
| 0.970914 | 0.9816 K.LPK[325.13]GTVSFHSHSDHR.F                       |
| 0.970892 | 0.9699 K.LC[160.03]FLDK[325.13]VEPHATIAEIK.N             |
| 0.970891 | 0.9953 R.GFALYNAANLK[325.13]SIDFHR.R                     |
| 0.97088  | 0.9562 K.GLAPDLPEDLYHLIK[325.13]K.A                      |
| 0.970877 | 0.9509 K.LK[325.13]HEC[160.03]GAAFTSK.L                  |
| 0.970875 | 0.9191 R.MRGETTLWNPGC[160.03]DHAGIATQVVVEK[325.13]K.I    |
| 0.970838 | 0.6083 R.K[325.13]LAVNMVFPFR.L                           |
| 0.970837 | 0.9962 R.VLETASSLHTLK[325.13]FR.H                        |
| 0.970791 | 0.8906 R.HPFIVNHPK[325.13]VGR.V                          |
| 0.970787 | 0.9734 K.WLDLKDNPDLPLAK[325.13]VAGDC[160.03]LDEK.Q       |
| 0.970761 | 0.9615 R.TAHSLFK[325.13]R.Y                              |
| 0.970726 | 0.995 R.IEGC[160.03]IIGFDEYMNVLDDAEEIHSK[325.13]TK.S     |
| 0.970723 | 0.9876 R.LAAC[160.03]VNLIPQITSYEWK[325.13]GK.I           |
| 0.970708 | 0.8216 R.K[325.13]ISNQFDWALMR.L                          |
| 0.970694 | 0.9024 K.GDYQK[325.13]ALLYLC[160.03]GGDD.-               |
| 0.970684 | 0.994 R.GQAFVIFK[325.13]EVSSATNALR.S                     |
| 0.97067  | 0.9821 K.SLPK[325.13]GPFTYISPSNTELTLMIQER.G              |
| 0.970657 | 0.9885 K.TAHETDK[325.13]SEGGKR.K                         |
| 0.970606 | 0.8897 R.YIGIVK[325.13]QAGLER.M                          |
| 0.970596 | 0.9648 R.LTFSVTLK[325.13]NKR.E                           |
| 0.97059  | 0.8405 R.VVVLMGSTSDLGHC[160.03]EK[325.13]IKK.A           |
| 0.970588 | 0.9914 R.FGAGTLK[325.13]SLHYD.-                          |
| 0.970559 | 0.9792 K.EHLLK[325.13]YEYQPFAGK.I                        |
| 0.970541 | 0.9933 R.VLSHSSK[325.13]IIIVNR.N                         |
| 0.97053  | 0.8637 K.GNK[325.13]PWISLPR.G                            |
| 0.970506 | 0.9512 R.FFK[325.13]LHQEDQAC[160.03]ATC[160.03]LILAC[160 |
| 0.970505 | 0.9385 R.M[147.04]HAPGK[325.13]GLSQSALPYR.R              |
| 0.970503 | 0.8591 K.AENGK[325.13]LVINGNPITIFQER.D                   |
| 0.970498 | 0.9682 R.DKLC[160.03]GPYEK[325.13]FIC[160.03]EQDHQNFLR.L |
| 0.970454 | 0.9673 R.IVYLYTK[325.13]K.V                              |
| 0.970443 | 0.9735 R.HLK[325.13]IVYR.R                               |
| 0.970424 | 0.9874 K.NGFVVLK[325.13]GRPC[160.03]K.I                  |



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| 0.970418 | 0.7107 K.AVKPK[325.13]AAKPK.A                           |
| 0.970391 | 0.981 K.LPNLTHLNLSGNK[325.13]LK.D                       |
| 0.970307 | 0.9601 R.DTLFC[160.03]YHK[325.13]ASEVFLQR.L             |
| 0.970289 | 0.2608 K.VTLATLK[325.13]M[147.04]SVQPTVSLGGFEITPPVVLR.L |
| 0.970251 | 0.765 R.LPSGNHMK[325.13]ESR.E                           |
| 0.970224 | 0.9848 R.TAAAPK[325.13]AGPGVVR.K                        |
| 0.970205 | 0.9949 K.NIDHMLWLEQPENIATC[160.03]IALRPYPK[325.13]EEVC  |
| 0.970204 | 0.9949 R.VISK[325.13]HDLGHFMLR.C                        |
| 0.970203 | 0.9846 R.K[325.13]SDLHPTLPAGR.Y                         |
| 0.970194 | 0.9268 R.QIEYKYK[325.13]LAQALHEMR.E                     |
| 0.970171 | 0.8751 R.VHFK[325.13]NTR.E                              |
| 0.970155 | 0.973 R.LC[160.03]IEHFDK[325.13]LLVEDINKDK.N            |
| 0.970155 | 0.9959 R.VSPTGEK[325.13]VTHTGQVYDDKDYR.R                |
| 0.97015  | 0.8872 R.C[160.03]FASNK[325.13]LGTAM[147.04]SHEIR.L     |
| 0.970144 | 0.9155 K.TESHHK[325.13]AK.G                             |
| 0.970093 | 0.5994 R.DLTDYLM[147.04]K[325.13]ILTER.G                |
| 0.970079 | 0.5187 R.VTYK[325.13]NVPNWHR.D                          |
| 0.970064 | 0.0596 R.HQGVMM[147.04]VGM[147.04]GQK[325.13]DSYVGDEA   |
| 0.970051 | 0.8617 K.GNK[325.13]PWISLPR.G                           |
| 0.970046 | 0.0505 R.KDGNASGTTLEALDC[160.03]ILPPTTRPTDK[325.13]PLR. |
| 0.970026 | 0.9587 K.DK[325.13]YPNLQVIGGNVVTAAQAK.N                 |
| 0.970019 | 0.9525 R.VVIIGAGKPAAVVLQTK[325.13]GSPESR.L              |
| 0.970008 | 0.6975 K.FASFIDK[325.13]VR.F                            |
| 0.97     | 0.97 R.AIQTLGYFPVGDGDFPHQK[325.13]LLLQGLMDSVEAK.Q       |
| 0.969996 | 0.9944 R.HWFFK[325.13]GQLHVDGQK.L                       |
| 0.969978 | 0.8371 R.K[325.13]SQVLFSVTR.G                           |
| 0.969936 | 0.8311 R.HAK[325.13]WFQAR.A                             |
| 0.969927 | 0.8692 R.NFGTK[325.13]ISAR.A                            |
| 0.96992  | 0.8895 R.QATK[325.13]DAGTIAGLNVLR.I                     |
| 0.969918 | 0.9815 R.LATALQK[325.13]LEEAEEK.A                       |
| 0.969897 | 0.9949 R.LK[325.13]PPTLIHGQAPSAGLPSQKPK.E               |
| 0.969893 | 0.9765 K.IC[160.03]QFK[325.13]LVLLGESAVGK.S             |
| 0.969862 | 0.9856 K.K[325.13]LSELSNSQQSVQTLWLIIHR.K                |
| 0.969842 | 0.9926 R.K[325.13]GDSWAYIQYESLDAHAATHMR.G               |
| 0.969839 | 0.834 K.EVAGAKPHITAAEGK[325.13]LHNMIVDLDNVVK.K          |
| 0.969831 | 0.9902 K.LVALHK[325.13]QVLM[147.04]GPYNPDTC[160.03]PEV  |
| 0.969827 | 0.9622 K.LVDQSGPPHEPK[325.13]FVYQAK.V                   |
| 0.969814 | 0.8764 K.FK[325.13]MPEMHFR.A                            |
| 0.969793 | 0.9478 R.GKQGGK[325.13]AR.A                             |
| 0.969791 | 0.911 R.IYWMNSKILHIK[325.13]QDER.V                      |
| 0.969768 | 0.8751 K.NVNAGGHK[325.13]LGLGLEFQA.-                    |
| 0.969749 | 0.9133 R.HYAHTDC[160.03]PGHADYVK[325.13]NMITGTAPLDGC    |
| 0.969748 | 0.9176 R.NRPLSDEELDAM[147.04]FPEGYK[325.13]VLPPPAGYVP   |
| 0.969716 | 0.9585 R.MPEK[325.13]VTWMR.R                            |
| 0.969714 | 0.9891 R.KPQAILEEK[325.13]LK.Q                          |
| 0.969687 | 0.8113 K.HK[325.13]SDFGK.F                              |
| 0.969686 | 0.9776 R.GGAGVGSMK[325.13]IYGGR.Q                       |

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| 0.969684 | 0.9854 K.FAQK[325.13]IGGSER.C                           |
| 0.969667 | 0.8394 K.K[325.13]VHVIFNYK.G                            |
| 0.969647 | 0.944 R.GK[325.13]IGLDFC[160.03]K.Y                     |
| 0.969644 | 0.9456 R.AHQLVLPPC[160.03]DVVIK[325.13]AVADYVR.N        |
| 0.969604 | 0.8973 R.ALANSLAC[160.03]QGK[325.13]YTPSGQAGAAASESLFV:  |
| 0.969558 | 0.0718 R.VAPEEHPVLLTEAPLNPK[325.13]ANR.E                |
| 0.969556 | 0.8301 R.GAFGK[325.13]PQGTVAR.V                         |
| 0.969472 | 0.9938 R.IQHYAGK[325.13]VLYQVEGFVDKNNDLLYR.D            |
| 0.969432 | 0.2329 R.LVYLVENPGGYVAYSK[325.13]AATVTGK.L              |
| 0.969428 | 0.8677 K.LK[325.13]GTVGEPTYDAEFQHFLR.G                  |
| 0.969424 | 0.6075 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I          |
| 0.969402 | 0.8726 K.AK[325.13]LGDSHDLQR.F                          |
| 0.969377 | 0.9892 K.K[325.13]QVAPEKPVKK.Q                          |
| 0.969375 | 0.6761 K.FYEAFSK[325.13]NLK.L                           |
| 0.969335 | 0.7113 K.ADK[325.13]DYHFK.V                             |
| 0.969294 | 0.8505 R.VK[325.13]ILFNK.K                              |
| 0.969257 | 0.7096 K.KPAAAGVK[325.13]K.V                            |
| 0.969251 | 0.8612 R.AYILNLVK[325.13]QIK.K                          |
| 0.969242 | 0.6674 R.LDYLSSLKVK[325.13]GLVLGPIHK.N                  |
| 0.96921  | 0.9012 K.GRPC[160.03]K[325.13]IVEMSTSK.T                |
| 0.969148 | 0.8918 R.IFLC[160.03]QGK[325.13]RPR.S                   |
| 0.969148 | 0.9909 R.GWVLGPNNYYSFASQQKPEDTTIPSTELAK[325.13]QVIE     |
| 0.969141 | 0.9801 R.LNK[325.13]C[160.03]GVISPR.F                   |
| 0.969137 | 0.961 K.IC[160.03]DYLFNVSDSSALNLAK[325.13]NIGLTK.A      |
| 0.969041 | 0.9055 K.LNLSTRPEK[325.13]FLGDIEVWDQAEK.Q               |
| 0.969033 | 0.9018 K.TESHHK[325.13]AK.G                             |
| 0.969031 | 0.8739 K.AFNQGK[325.13]IFK.-                            |
| 0.96901  | 0.9696 K.VGK[325.13]APKSAC[160.03]GVC[160.03]PGR.L      |
| 0.969004 | 0.5306 R.IHPVSTMVK[325.13]GMYGIENEVFLSLPC[160.03]ILNAR  |
| 0.968991 | 0.6883 K.IK[325.13]IIAPPER.K                            |
| 0.968981 | 0.949 R.YLPPATQVVLISATLPHEILEMTNK[325.13]FM[147.04]TD   |
| 0.968979 | 0.9034 K.K[325.13]LVGSVNLFSDENVPR.L                     |
| 0.96893  | 0.988 R.IPDIVLWPTC[160.03]HDDVVK[325.13]IVNLAC[160.03]I |
| 0.968917 | 0.9904 R.QLAQYHAK[325.13]DPNNLFMVR.L                    |
| 0.968896 | 0.8466 R.GAPLAK[325.13]VVFR.D                           |
| 0.968873 | 0.936 R.VINHK[325.13]LYK.N                              |
| 0.968836 | 0.9856 R.AQK[325.13]LHFLQR.G                            |
| 0.968813 | 0.9733 K.IITFTK[325.13]NNQFQALLQYADPVNAHYAK.M           |
| 0.96878  | 0.8787 K.ISMPDLHLK[325.13]SPK.A                         |
| 0.968776 | 0.7959 K.LAQM[147.04]FSDMVLK[325.13]DGFQPSR.S           |
| 0.968756 | 0.815 R.TLK[325.13]IPAMTIK.N                            |
| 0.968728 | 0.9504 R.K[325.13]PLLESGTLGKGNVQVVIPFLTESYSSSQDPPEK.S   |
| 0.968724 | 0.8654 K.FC[160.03]LDNGAK[325.13]SVVLMShLGRPDGVPMPDK    |
| 0.96872  | 0.8176 R.TAQSTPSAPPQK[325.13]VM[147.04]C[160.03]VSMGST  |
| 0.968718 | 0.9267 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V            |
| 0.968718 | 0.8278 K.M[147.04]QASIEK[325.13]GGSLPK.V                |
| 0.968699 | 0.9365 R.LLELGPK[325.13]PEVAQQTR.K                      |

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| 0.968696 | 0.9141 R.RM[147.04]EELHNQEVQK[325.13]R.K               |
| 0.968659 | 0.8545 K.GFK[325.13]EQIYDVYR.Y                         |
| 0.96865  | 0.9408 K.FVLSSGK[325.13]FYGDEEKDK.G                    |
| 0.968626 | 0.8518 R.NLLSVAYK[325.13]NVVGAR.R                      |
| 0.96862  | 0.9373 K.KFK[325.13]GDSR.S                             |
| 0.968606 | 0.9733 K.AIK[325.13]VEQATKPSFESGR.R                    |
| 0.968559 | 0.9948 K.VFLISASSK[325.13]DTGQLYAALHHR.I               |
| 0.968514 | 0.8415 R.GAPLAK[325.13]VVFR.D                          |
| 0.968512 | 0.9166 K.IK[325.13]LYWSK.V                             |
| 0.968501 | 0.9218 R.EITLK[325.13]GFR.E                            |
| 0.968496 | 0.9496 K.K[325.13]GEKDIPGLTDTTVPR.R                    |
| 0.968484 | 0.9059 K.ALYKPK[325.13]QEVK.F                          |
| 0.968476 | 0.8315 R.LPSGNHM[147.04]K[325.13]ESR.E                 |
| 0.968455 | 0.8714 K.AAKPK[325.13]TAKPK.A                          |
| 0.968439 | 0.9849 R.ILNFLMHPKPSGK[325.13]PLPK.S                   |
| 0.968422 | 0.9361 K.AGLQVYNK[325.13]C[160.03]WK.F                 |
| 0.968413 | 0.9737 R.K[325.13]ALVTGYFM[147.04]QVAHLER.T            |
| 0.968396 | 0.9363 K.VIK[325.13]HGPQR.S                            |
| 0.968382 | 0.8732 R.KVEDLFLTFK[325.13]K.A                         |
| 0.968371 | 0.8811 K.RIAK[325.13]AVNEK.S                           |
| 0.968365 | 0.0682 K.LHIEVGTPPTGNQPFPK[325.13]K.A                  |
| 0.968363 | 0.8063 R.KSEIEYYAMLAK[325.13]TGVHHYSGNNIELGTAC[160.03] |
| 0.968302 | 0.941 K.DHWQK[325.13]YGR.N                             |
| 0.968296 | 0.8622 K.GIVEFASK[325.13]PAAR.K                        |
| 0.96824  | 0.9818 R.IFGSNK[325.13]WTTEQQQR.F                      |
| 0.968144 | 0.9925 R.FGPLASVK[325.13]IMWPR.T                       |
| 0.968129 | 0.8603 R.QLMWSATWPK[325.13]EVR.Q                       |
| 0.968077 | 0.9469 K.SQLDIIHSLK[325.13]K.C                         |
| 0.968046 | 0.9592 R.NHAAPFSK[325.13]VLTFLR.R                      |
| 0.968038 | 0.99 R.LIK[325.13]HAVQER.L                             |
| 0.968037 | 0.8799 R.LAEVEAALEK[325.13]QR.Q                        |
| 0.96803  | 0.9562 K.YTEGVQSLNWTk[325.13]IMK.T                     |
| 0.968019 | 0.9821 K.KGVLFVPGAFTPGC[160.03]SK[325.13]THLPGFVEQAE.  |
| 0.96798  | 0.9533 R.IVSRPEELREDDVGTGAGLLEIK[325.13]K.I            |
| 0.967974 | 0.9921 K.TGRPAGK[325.13]GSITISAEIKNR.V                 |
| 0.96796  | 0.8192 R.LK[325.13]LYLPK.E                             |
| 0.967929 | 0.9254 R.LAK[325.13]AAFDDAIAELDTLSEESYK.D              |
| 0.967927 | 0.5925 R.DGVVRPLK[325.13]C[160.03]TVFHGAQVEDAFR.Y      |
| 0.967901 | 0.9959 K.K[325.13]AHENWLK.A                            |
| 0.967883 | 0.8479 K.AENGK[325.13]LVINGNPITIFQER.D                 |
| 0.967872 | 0.9735 R.LHNQK[325.13]TGQEVVFAEPDNK.N                  |
| 0.967866 | 0.9955 R.EQFYHSC[160.03]K[325.13]QYGITGENVR.G          |
| 0.967851 | 0.9455 K.SLK[325.13]FATEAAITILR.I                      |
| 0.967784 | 0.7187 K.WQSLK[325.13]DLVK.E                           |
| 0.967755 | 0.8751 K.LQDAINILK[325.13]EMK.E                        |
| 0.967746 | 0.8701 K.DLILPTIQK[325.13]SLLR.S                       |
| 0.96774  | 0.9921 R.GLC[160.03]GAIHSSIAK[325.13]QMK.S             |

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| 0.967731 | 0.9601 R.ASNIK[325.13]APGEQTVPALNLQNAFR.I                  |
| 0.967726 | 0.9949 R.REPAVK[325.13]LQYAVSGLEPLAWSEDHR.V                |
| 0.967699 | 0.9667 K.LK[325.13]LSILYPATTGR.N                           |
| 0.967691 | 0.8278 R.LPSGNHM[147.04]K[325.13]ESR.E                     |
| 0.96769  | 0.9837 K.TSTK[325.13]LHVGNISPTC[160.03]TNK.E               |
| 0.967683 | 0.9365 K.DNIK[325.13]HVPGGGNVQIQNK.K                       |
| 0.967664 | 0.8603 R.NFGTK[325.13]ISAR.A                               |
| 0.967658 | 0.9795 K.INFVIDNNK[325.13]HTGAVSAR.N                       |
| 0.967653 | 0.878 R.SSK[325.13]GQIIGNFQAFDEDTGLPAHAR.Y                 |
| 0.967597 | 0.9204 K.TC[160.03]TTVAFTQVNSEDK[325.13]GALAK.L            |
| 0.967597 | 0.8726 K.NGQDLGVAFK[325.13]ISK.E                           |
| 0.967595 | 0.8606 K.KAAK[325.13]SAAK.A                                |
| 0.967577 | 0.9948 R.YYDPK[325.13]TC[160.03]GFDFTGAVEDISK.I            |
| 0.967519 | 0.9952 R.LLGEK[325.13]TTTAAGSSHSRPGVPVEGSPGR.N             |
| 0.967514 | 0.985 R.IAPELYHK[325.13]MLVVGGIDR.V                        |
| 0.967507 | 0.8666 R.GC[160.03]ITIIGGGDTATC[160.03]C[160.03]AK[325.13] |
| 0.967444 | 0.9067 R.K[325.13]LDELYGTWR.K                              |
| 0.967424 | 0.9817 K.K[325.13]GVLFGVPGAFTPGC[160.03]SK.T               |
| 0.96742  | 0.9827 K.YHPDKNPNEGEK[325.13]FK.Q                          |
| 0.967414 | 0.6603 K.AAKPKAAK[325.13]PK.A                              |
| 0.967404 | 0.8666 K.NNIK[325.13]LYVR.R                                |
| 0.967397 | 0.6939 K.IK[325.13]IIAPPERK.Y                              |
| 0.967384 | 0.8738 R.KK[325.13]LEMDLK.D                                |
| 0.967381 | 0.8842 R.K[325.13]PVTVHSR.A                                |
| 0.967352 | 0.9955 R.ILPHPK[325.13]FDPR.T                              |
| 0.967342 | 0.6874 R.LANQFAIYK[325.13]PVTDFFLQLVDAGK.V                 |
| 0.96733  | 0.6699 R.ALM[147.04]LQGVDLLADAVAVTMGPK[325.13]GR.T         |
| 0.967318 | 0.8429 K.GETK[325.13]SFYPEEVSSMVLTK.M                      |
| 0.96724  | 0.0868 R.K[325.13]DLYANTVLSGGTTMYPGIADR.M                  |
| 0.967155 | 0.8654 K.SPVTTLLEC[160.03]MHK[325.13]LGNSC[160.03]EFR.L    |
| 0.967146 | 0.6397 R.IMK[325.13]AQALR.D                                |
| 0.967126 | 0.8729 K.VSASPLLYTLIEK[325.13]TMQNVKHPVTGQFLYQDSNWA        |
| 0.9671   | 0.9594 R.ASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGG          |
| 0.967092 | 0.521 K.KAKK[325.13]PAAAAGAK.K                             |
| 0.96707  | 0.9833 K.K[325.13]YAWQGVALLPFVDER.R                        |
| 0.967049 | 0.9326 R.LPAAGVGDMVM[147.04]ATVK[325.13]K.G                |
| 0.967045 | 0.9955 K.IFVLGPK[325.13]YSPLEFLR.R                         |
| 0.967021 | 0.995 R.AAHVFFTDSC[160.03]PDALFNELVK[325.13]SR.A           |
| 0.967004 | 0.793 K.VYGK[325.13]GNPTK.V                                |
| 0.967001 | 0.9425 K.YVIGPK[325.13]GNSLQEILER.T                        |
| 0.966983 | 0.8728 R.DVFTK[325.13]GYGFGLIK.L                           |
| 0.966962 | 0.8646 K.ILES DRK[325.13]EPLFGISTGNLITGLAAGAK.T            |
| 0.966937 | 0.4623 R.RQQEGFK[325.13]GTFPDAR.E                          |
| 0.966923 | 0.9954 R.C[160.03]HQGPIK[325.13]PYQQGR.Q                   |
| 0.966911 | 0.8764 K.FTGLSK[325.13]EELLK.V                             |
| 0.966839 | 0.9394 K.LSGFPK[325.13]NR.V                                |
| 0.966831 | 0.9691 R.K[325.13]FLPLFDR.V                                |

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| 0.96683  | 0.9792 R.QYK[325.13]IPDWFLNR.Q                              |
| 0.966819 | 0.8726 K.LLVGVDEK[325.13]LNPEDIKK.H                         |
| 0.966818 | 0.9887 R.FGALTAEK[325.13]LR.S                               |
| 0.966789 | 0.4271 R.GFGFVYATVEEVDAAMNARPHK[325.13]VDGR.V               |
| 0.966768 | 0.9941 K.YK[325.13]GIFNGFSVTLK.E                            |
| 0.966768 | 0.9892 R.DGISC[160.03]EASNPHGNK[325.13]R.H                  |
| 0.966748 | 0.9555 K.DATSK[325.13]VALVYQGMNEPPGAR.A                     |
| 0.966741 | 0.9839 R.TSGSVYITLK[325.13]K.Y                              |
| 0.966701 | 0.9594 R.THINYGVK[325.13]GDVAVVR.I                          |
| 0.966695 | 0.8714 R.MQK[325.13]EITALAPSTM[147.04]K.I                   |
| 0.966689 | 0.865 R.GWPLELLC[160.03]EK[325.13]SIGTANRPMGAGEALR.R        |
| 0.966682 | 0.7945 K.DKYK[325.13]NIGAK.L                                |
| 0.96668  | 0.6858 R.IPELNK[325.13]VAR.A                                |
| 0.966674 | 0.994 K.K[325.13]NISHDTFGTTYGR.I                            |
| 0.96666  | 0.3139 R.LLLPGELAKHAVSEGTK[325.13]AVTK.Y                    |
| 0.966649 | 0.9425 K.STGGAPT FNVTVK[325.13]TDK.T                        |
| 0.966633 | 0.5886 K.LSPDAIPGK[325.13]WTSQDSLLGMEFSGR.D                 |
| 0.966615 | 0.787 K.AAGAGK[325.13]VTK.S                                 |
| 0.96661  | 0.9313 R.EAVEK[325.13]EFEPLLNWMK.D                          |
| 0.966607 | 0.4683 K.GFGYK[325.13]GSC[160.03]FHR.I                      |
| 0.966579 | 0.9954 K.APTIVGK[325.13]SSLNPILFR.G                         |
| 0.966563 | 0.9956 R.IK[325.13]QLHHEAQQSEGEQNYR.K                       |
| 0.966507 | 0.9578 R.IYDLNKPEAEPK[325.13]EISGHTSGIKK.A                  |
| 0.966461 | 0.6674 K.DKGEYTLVVK[325.13]WGDEHIPGSPYR.V                   |
| 0.966456 | 0.8667 R.HPALFKAIGVK[325.13]PPR.G                           |
| 0.966442 | 0.8738 K.KHVSLNK[325.13]AK.K                                |
| 0.96644  | 0.963 R.FSVLPPTFHPGDQK[325.13]QYGGFDNR.G                    |
| 0.966415 | 0.8628 K.FK[325.13]MPDMHFK.A                                |
| 0.9664   | 0.8573 K.SAEFLLHMLK[325.13]NAESNAELK.G                      |
| 0.966398 | 0.8463 R.SYDVPPPPMEPDHPFYSNISK[325.13]DR.R                  |
| 0.966373 | 0.2826 K.K[325.13]AKKPAAATVTK.K                             |
| 0.966367 | 0.4986 R.AK[325.13]VTLNGVPAQPLGPR.A                         |
| 0.966321 | 0.5903 K.K[325.13]HSQFIGYPITLFVEK.K                         |
| 0.966285 | 0.9929 R.LNYEHDNISLK[325.13]R.V                             |
| 0.966284 | 0.9364 K.GNK[325.13]ALSVGNIDDALQC[160.03]YSEAIK.L           |
| 0.966279 | 0.9928 K.MLA AK[325.13]SADGSAPAGEGEGVTLQR.N                 |
| 0.966241 | 0.9766 R.EQC[160.03]C[160.03]YNC[160.03]GK[325.13]PGHLAR    |
| 0.966231 | 0.8063 R.LYKEELEQTYHAK[325.13]LENAR.L                       |
| 0.966214 | 0.9831 K.LFGYEPTIYYPKRPNK[325.13]PLFTALVTQC[160.03]QK.M     |
| 0.966186 | 0.9372 K.AVLEC[160.03]KPLGIK[325.13]TALK.A                  |
| 0.96614  | 0.8616 K.VDGHK[325.13]DIQMPDGIR.R                           |
| 0.966136 | 0.9746 K.LYNNITFEELGALLEIPAAK[325.13]AEK.I                  |
| 0.966129 | 0.6476 R.AL GALVDSC[160.03]APGLC[160.03]PDWDSWDASK[325.13]D |
| 0.966102 | 0.983 K.K[325.13]DILLPFQQLDSIPVSNPSC[160.03]PM[147.04]P     |
| 0.966025 | 0.8436 R.IAAYK[325.13]SILQER.V                              |
| 0.965986 | 0.8751 R.DLAALGDK[325.13]VNSLGETAER.L                       |
| 0.965976 | 0.8689 R.LPKDDVHAK[325.13]ESK.I                             |

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| 0.965941 | 0.9942 K.VTLPC[160.03]HHQLGLPEK[325.13]DTLDIEWLLTDNEGI   |
| 0.965934 | 0.9438 R.NSQFAGGPLGNPNTTAK[325.13]VQQR.L                 |
| 0.965878 | 0.9472 K.C[160.03]VAC[160.03]DASK[325.13]PTHKPIAEAPSAFTL |
| 0.965872 | 0.9593 K.LLTQGFTNWNK[325.13]R.D                          |
| 0.965871 | 0.973 R.HIITVDGK[325.13]PPTWSEFPK.G                      |
| 0.965842 | 0.9774 R.WLK[325.13]GGVVLKEDALPGQK.T                     |
| 0.965839 | 0.9132 K.FVADGIFK[325.13]AELNEFLTR.E                     |
| 0.96583  | 0.8255 K.GFVLHK[325.13]SK.S                              |
| 0.965817 | 0.9941 R.FC[160.03]LIC[160.03]NYLSK[325.13]IIPALQSR.C    |
| 0.965802 | 0.9683 K.LVTLPVSFAQLK[325.13]NLK.W                       |
| 0.965777 | 0.9937 K.LPHSVLLEIQK[325.13]ELLDYK.G                     |
| 0.965772 | 0.8087 K.SAPATGGVK[325.13]KPHR.Y                         |
| 0.96576  | 0.9945 R.AYSQEEITQGFETGDTLYAPYSTHFQLQNQPPQK[325.13]      |
| 0.965743 | 0.9436 K.VVSQYSSLLSPMSVNAVMMK[325.13]VIDPATATSVDLR.D     |
| 0.965739 | 0.9362 R.ASPSK[325.13]PASAPASR.S                         |
| 0.965702 | 0.9937 R.ALK[325.13]SC[160.03]SPELQK.F                   |
| 0.9657   | 0.9012 R.ALQASALK[325.13]AWGGK.K                         |
| 0.965699 | 0.993 R.LEDTHFVQC[160.03]PSVPSHK[325.13]FC[160.03]FPC[1  |
| 0.96569  | 0.8138 K.DKYK[325.13]NIGAK.L                             |
| 0.965687 | 0.9947 R.VPIWDQDIQFLPGSQK[325.13]LVTC[160.03]TGYHQVR.1   |
| 0.965656 | 0.8666 K.KVEK[325.13]VTISNR.L                            |
| 0.965645 | 0.4656 R.DALSDLALHFLNK[325.13]M[147.04]K.I               |
| 0.965629 | 0.8677 R.ELISNASDALDK[325.13]IR.Y                        |
| 0.965621 | 0.7487 R.M[147.04]KENQK[325.13]HIYYITGETK.D              |
| 0.9656   | 0.8603 R.FKLPK[325.13]FNFSGSK.V                          |
| 0.965593 | 0.9584 K.M[147.04]LGEALSK[325.13]NPGYIK.L                |
| 0.96559  | 0.8509 R.VGTVIGSNK[325.13]LEQMPSKEDAIEHFMK.L             |
| 0.965559 | 0.785 R.FK[325.13]KPGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V     |
| 0.965546 | 0.8738 R.NFGTK[325.13]ISAR.A                             |
| 0.965521 | 0.9946 R.ITTTFGEHLNAVQASAEHQK[325.13]R.L                 |
| 0.965514 | 0.8159 R.VVLIGGK[325.13]PDR.V                            |
| 0.965501 | 0.7119 R.IPELNK[325.13]VAR.A                             |
| 0.965473 | 0.829 R.IAESNHIK[325.13]LSGSNPYTTVTPQIINSK.W             |
| 0.965465 | 0.8912 K.TESHHK[325.13]AK.G                              |
| 0.965439 | 0.9893 R.VK[325.13]VAAC[160.03]NVHSTC[160.03]GDC[160.03] |
| 0.965437 | 0.7071 R.VIISAPSADAPM[147.04]FVMGVNHEK[325.13]YDNSLK.I   |
| 0.965436 | 0.8603 R.DLPWWMK[325.13]FLHGK.L                          |
| 0.965329 | 0.8654 R.RGPPEK[325.13]EWR.R                             |
| 0.965319 | 0.94 K.LSGLPK[325.13]HR.V                                |
| 0.965305 | 0.8492 R.QLMWSATWPK[325.13]EVR.Q                         |
| 0.965273 | 0.9299 K.KAVLFC[160.03]LSEDK[325.13]K.N                  |
| 0.965272 | 0.9379 R.KAVDALLTHC[160.03]K[325.13]SR.K                 |
| 0.965269 | 0.9944 R.IHFGQITSNQMLVPVIEK[325.13]LR.E                  |
| 0.965229 | 0.9942 K.K[325.13]LGVNNISGIEEVMFTNQGTVIHFNNPK.V          |
| 0.965227 | 0.6981 K.GTIQVITQGTSLK[325.13]NAGNC[160.03]LSPAVIVGLLK.  |
| 0.965208 | 0.9591 R.RYIGIVK[325.13]QAGLER.M                         |
| 0.965206 | 0.9403 K.LSDFFK[325.13]THYR.L                            |

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| 0.965197 | 0.9813 K.ATIAGGGVIPHIHK[325.13]SLIGK.K                   |
| 0.965197 | 0.828 K.K[325.13]GDVVIVLTGWRPGSGFTNTM[147.04]R.V         |
| 0.965194 | 0.9553 R.EQQLVGEK[325.13]SWVQFNSNSQLMYGLPDSSHVVGK.H      |
| 0.96519  | 0.6189 R.LQAEIEGLK[325.13]GQR.A                          |
| 0.9651   | 0.9702 R.KAEPMQWASLELPAAK[325.13]K.Q                     |
| 0.965087 | 0.9838 R.LAQQPHQNQAK[325.13]LVVALSR.T                    |
| 0.96508  | 0.8578 K.GFGFVDFNSEEDAK[325.13]AAK.E                     |
| 0.965057 | 0.9668 R.NK[325.13]GVLC[160.03]SGHGEC[160.03]HC[160.03]G |
| 0.965035 | 0.9577 K.MLGEALSK[325.13]NPGYIK.L                        |
| 0.965007 | 0.7128 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                |
| 0.965004 | 0.9883 K.EITIHTK[325.13]LPAK.D                           |
| 0.964985 | 0.754 R.TGNK[325.13]YINVYPTYDFAC[160.03]PIVDSIEGVTHALR   |
| 0.964984 | 0.8366 R.ASEEHLK[325.13]QHYIDLK.D                        |
| 0.964963 | 0.8654 R.LFK[325.13]TALQEEIK.S                           |
| 0.96495  | 0.8768 R.HLTGEFEK[325.13]K.Y                             |
| 0.964919 | 0.9814 R.RLSQPESA EK[325.13]HVTQR.L                      |
| 0.964919 | 0.8598 R.VHFK[325.13]NTR.E                               |
| 0.9649   | 0.9272 R.GAGM[147.04]PGQHGGQITQQELDTVVK[325.13]TQHEIL    |
| 0.96488  | 0.9272 R.IK[325.13]KPEGKPDQK.F                           |
| 0.964873 | 0.9954 R.IMLLNHPDK[325.13]GGSPYIAAK.I                    |
| 0.96487  | 0.8505 K.FC[160.03]LDNGAK[325.13]SVVLMMSHLGRPDGVPMPDK    |
| 0.964843 | 0.9658 R.HGK[325.13]QVLDGNSNPYDIFLK.D                    |
| 0.964836 | 0.9953 R.K[325.13]LAQLQVAYHQLFQEYDNHIK.S                 |
| 0.964771 | 0.9933 R.ALVSTK[325.13]WLAESIR.T                         |
| 0.964767 | 0.8679 R.AM[147.04]LAQQYQEGTLSVEKLA AK[325.13]LSATLEQA   |
| 0.96475  | 0.8051 R.LIDFLEC[160.03]GK[325.13]TNLR.R                 |
| 0.964728 | 0.9344 R.K[325.13]SDIYVC[160.03]MISFAHNVA AQGK.Y         |
| 0.964699 | 0.9929 K.DC[160.03]TSALALVPFSIK[325.13]PLLR.R            |
| 0.964659 | 0.4573 R.DALSDLALHFLNK[325.13]M[147.04]K.I               |
| 0.964644 | 0.9434 K.ALSK[325.13]HLPSSDSMSLK.V                       |
| 0.964622 | 0.7649 R.GRPSGKGIVEFSGK[325.13]PAAR.K                    |
| 0.964585 | 0.8641 R.MK[325.13]IDPEAFITR.H                           |
| 0.964584 | 0.9951 R.LNDH GK[325.13]NWR.H                            |
| 0.964581 | 0.918 R.NALLSLAK[325.13]GDR.S                            |
| 0.96456  | 0.8566 K.EQLAK[325.13]LMATLR.N                           |
| 0.964537 | 0.9951 R.DNSGMIDKNELK[325.13]QALSGFGYR.L                 |
| 0.964453 | 0.9928 K.ISFK[325.13]FDHLR.K                             |
| 0.964442 | 0.8427 K.FLK[325.13]HWDH LTQVK.K                         |
| 0.964396 | 0.9801 R.AVLLGPPGAGK[325.13]GTQAPR.L                     |
| 0.964394 | 0.9954 K.GLVTLK[325.13]HSATPFLK.V                        |
| 0.964386 | 0.8594 R.TLTAAAVSGAQPILSK[325.13]LEPQIASASEY AHR.G       |
| 0.964347 | 0.9829 K.LNK[325.13]QQTDIAVNWAGGLHHAK.K                  |
| 0.964336 | 0.862 K.K[325.13]TESHHK.A                                |
| 0.964312 | 0.9751 K.LWALQDFSC[160.03]LK[325.13]TFEGHDASVLK.V        |
| 0.96427  | 0.9649 R.AFLIEEQK[325.13]IVVK.V                          |
| 0.964207 | 0.8628 K.GLILK[325.13]DHGIR.L                            |
| 0.964181 | 0.6201 R.TLLAK[325.13]NLPYK.V                            |

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| 0.964177 | 0.6502 R.SGK[325.13]YDLDFK.S                            |
| 0.964172 | 0.9882 R.NLLSVAYK[325.13]NVVGGQR.A                      |
| 0.964146 | 0.9892 R.RTNSTFNQVVLK[325.13]R.L                        |
| 0.964123 | 0.995 R.TPFLSGTSYK[325.13]DLMPHDLAR.A                   |
| 0.964099 | 0.8542 K.LFGNMEGDC[160.03]PSDWK[325.13]TDSTC[160.03]R.I |
| 0.964095 | 0.9939 K.FTLFK[325.13]GVITRPDLPSK.K                     |
| 0.964087 | 0.9942 R.LAK[325.13]DVLAEIPEQFLSYMR.A                   |
| 0.964079 | 0.9628 K.KSDVEAIFSK[325.13]YGK.I                        |
| 0.964023 | 0.9938 R.SEWGSLEELVAEGK[325.13]ISETTAR.T                |
| 0.963934 | 0.8641 R.VC[160.03]K[325.13]ILGSGISSSVLHGMVFK.K         |
| 0.963881 | 0.8597 K.SK[325.13]IAHLAGVK.D                           |
| 0.963845 | 0.9932 R.HQASSVFSWQKEK[325.13]TPSHLSSNSQR.T             |
| 0.963844 | 0.933 R.VIEK[325.13]YYTR.L                              |
| 0.963843 | 0.5015 R.ILGLLDAYLK[325.13]TR.T                         |
| 0.963841 | 0.9437 R.NIIHGSDSVK[325.13]SAEK.E                       |
| 0.963834 | 0.9951 R.ESLVLPIYEGIPVLNC[160.03]WGALPLGGK[325.13]ALHK. |
| 0.963805 | 0.8011 R.K[325.13]SNFAEALAAHK.Y                         |
| 0.963798 | 0.8614 K.K[325.13]AAGAGK.V                              |
| 0.963763 | 0.9922 R.NK[325.13]IADLC[160.03]HTFIK.D                 |
| 0.963695 | 0.8125 K.K[325.13]KDQVTAQEIQDNHEDGPTAK.K                |
| 0.963675 | 0.9862 K.LEEHFK[325.13]NQELR.Q                          |
| 0.963654 | 0.9735 K.GLIK[325.13]LVSK.H                             |
| 0.963642 | 0.9842 K.VATHEK[325.13]EWK.C                            |
| 0.963639 | 0.9743 R.LYQVEYAFK[325.13]AINQGGLTSVAVR.G               |
| 0.963621 | 0.9281 K.RNPGVK[325.13]EGYK.F                           |
| 0.963551 | 0.8211 R.MVLAAAGGVEHQQLDLAQK[325.13]HLGGIPWTYAEDA       |
| 0.963519 | 0.994 K.HDDPALTLVAGLTSNKPTDK[325.13]LR.A                |
| 0.963503 | 0.9936 K.RLTDLDK[325.13]AQLLEIAK.A                      |
| 0.96346  | 0.6296 R.GIFPVLC[160.03]K[325.13]DPVQEAWAEDVDLR.V       |
| 0.963456 | 0.9935 R.YPHLGQK[325.13]PGGSDFLR.K                      |
| 0.963444 | 0.8787 R.LQAAYAGDK[325.13]ADDIQK.R                      |
| 0.963431 | 0.8603 K.SAPAPK[325.13]K.G                              |
| 0.963426 | 0.9791 R.K[325.13]VAQVPLGPEC[160.03]SR.A                |
| 0.963425 | 0.8155 K.VLEEANQAINPK[325.13]LMQLVDHR.G                 |
| 0.96342  | 0.8518 R.GAGIGGLGITVEGPSESK[325.13]INC[160.03]R.D       |
| 0.963416 | 0.1652 R.VEYHFLSPYVSPK[325.13]ESPFR.H                   |
| 0.9634   | 0.8654 R.LGEDLNK[325.13]WQALLVQIR.K                     |
| 0.963387 | 0.9712 K.K[325.13]TGKPMINLYTDKDTGKPK.G                  |
| 0.963383 | 0.9597 K.ANGTTVHVGIHPSK[325.13]VVITR.L                  |
| 0.96338  | 0.9487 K.VNC[160.03]LDK[325.13]FWHK.A                   |
| 0.963354 | 0.9855 K.TYNVDK[325.13]HVPDSGATATAYLC[160.03]GVK.G      |
| 0.963328 | 0.9819 K.IGIMPGHIHK[325.13]K.G                          |
| 0.963273 | 0.856 R.EQSHK[325.13]VYVQHLLK.Q                         |
| 0.963268 | 0.5961 K.M[147.04]LK[325.13]DKFNEC[160.03]GHVLYADIK.M   |
| 0.963268 | 0.9863 K.KDDEENYDLFSHK[325.13]NMK.L                     |
| 0.963265 | 0.9954 R.LKAHLMSQPLAYHTPDC[160.03]NK[325.13]QGFIDLPEFI  |
| 0.963262 | 0.4026 R.ETAQAIK[325.13]GMHIR.K                         |



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| 0.963261 | 0.978 K.K[325.13]DILLPFQQLDSIPVSNPSC[160.03]PMIPLYR.N |
| 0.963242 | 0.9625 R.K[325.13]PHTESLELQVR.G                       |
| 0.963229 | 0.9866 R.TLSEAGK[325.13]STSIQSFK.D                    |
| 0.96318  | 0.9354 K.RLK[325.13]AADIDQEVK.E                       |
| 0.963178 | 0.9827 K.LEQIDGHIAEHNSK[325.13]IK.Y                   |
| 0.963169 | 0.8579 K.K[325.13]TESHHK.A                            |
| 0.963167 | 0.9603 K.LIDIFYPGDQQSVTFGTK[325.13]SR.V               |
| 0.9631   | 0.8119 R.IINEPTAAAIAYGLDK[325.13]R.E                  |
| 0.963091 | 0.9951 R.VAEGQTLDLK[325.13]C[160.03]VVPGQAHQVTHWK.R   |
| 0.963059 | 0.9943 K.K[325.13]KNAINTEMYHEIMR.A                    |
| 0.962928 | 0.921 K.FLAAGTHLGGTNLDFQMEQYIYK[325.13]R.K            |
| 0.962917 | 0.9854 R.YFILPDSLPLDTLLVDVEPK[325.13]VK.S             |
| 0.962894 | 0.9418 R.K[325.13]NGGLGHMNIALLSDLTK.Q                 |
| 0.962892 | 0.5886 K.DLLLTSSYLSDSGSTGEHTK[325.13]SLVTQYLNATGNR.W  |
| 0.962874 | 0.9887 K.ALANVNIGSLIC[160.03]NVGAGGPAPAAGAAPAGGPAPS   |
| 0.962858 | 0.9916 R.LYELK[325.13]AAVDGLSK.M                      |
| 0.962835 | 0.7884 K.NQQFHK[325.13]ER.E                           |
| 0.962798 | 0.9882 R.K[325.13]SSTVATLQGTPDHGDPR.T                 |
| 0.962797 | 0.9619 K.NPTLFIFAENDVVIPLK[325.13]DVSLLTQK.L          |
| 0.962792 | 0.9024 R.YQQFK[325.13]DFQR.R                          |
| 0.962765 | 0.9937 R.HVTMIPGDGIGPELMLHVK[325.13]SVFR.H            |
| 0.96276  | 0.9699 R.LHTLEEEK[325.13]EELAQYQK.W                   |
| 0.962743 | 0.8578 R.QYFHQLEK[325.13]MNVK.I                       |
| 0.962741 | 0.9163 -.M[147.04]QIFVK[325.13]TLTGK.T                |
| 0.962736 | 0.6765 R.AK[325.13]VTLNGVPAQPLGPR.A                   |
| 0.962727 | 0.9829 K.VIGAGK[325.13]SWHK.A                         |
| 0.962696 | 0.9429 K.KLDSLTTSGFPVGAATLVDEVGVDVAK[325.13]HVAEDLC   |
| 0.962648 | 0.9682 R.IGK[325.13]VTSEELHYFVQNHFTSAR.M              |
| 0.962645 | 0.913 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V           |
| 0.96263  | 0.8492 R.IYTTK[325.13]IKPR.L                          |
| 0.962614 | 0.8036 R.VGTVIGSNK[325.13]LEQMPSKEDAIEHFMK.L          |
| 0.962569 | 0.9171 K.AQAK[325.13]VGSLDNVGHLPAGGAVK.T              |
| 0.962509 | 0.8841 K.APK[325.13]PDGPGGGPGGSHM[147.04]GGNYGDDR.R   |
| 0.962506 | 0.6399 R.LLFNDVQTLK[325.13]DGR.H                      |
| 0.962501 | 0.8161 R.EESGKPGAHVTVK[325.13]K.L                     |
| 0.962488 | 0.9197 R.DGWPAMC[160.03]IHGDK[325.13]SQPER.D          |
| 0.96243  | 0.8228 K.GKWKPPM[147.04]IDNPSYQGIWK[325.13]PRK.I      |
| 0.962423 | 0.6053 K.AAKPK[325.13]AAKPK.A                         |
| 0.962421 | 0.9301 K.ASGGEIK[325.13]IHK.M                         |
| 0.962419 | 0.9936 R.LGK[325.13]HDVTC[160.03]TVSGGGR.S            |
| 0.96236  | 0.8065 K.TVWDWELMNDIK[325.13]PIWQRPSK.E               |
| 0.962359 | 0.9903 R.NLGFTAIPLHGQMSQSK[325.13]R.L                 |
| 0.962327 | 0.9346 R.EANFTVSSMHGDMPPQK[325.13]ER.E                |
| 0.962293 | 0.4873 K.KAK[325.13]KPAAAAGAK.K                       |
| 0.962291 | 0.9496 K.VNNSSLIGLYTQTLK[325.13]PGIK.L                |
| 0.962206 | 0.8333 R.YLSPK[325.13]YIK.M                           |
| 0.962195 | 0.2857 R.LLLPGELAKHAVSEGTK[325.13]AVTK.Y              |

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| 0.962145 | 0.9939 K.GVHC[160.03]VMSLGVPGPATLAK[325.13]ALLQTHPEAC        |
| 0.962132 | 0.9723 R.NQLSQNRGLGGIMVK[325.13]R.A                          |
| 0.962128 | 0.8138 R.GSK[325.13]DHNIR.A                                  |
| 0.962079 | 0.9281 R.K[325.13]ILGQEGDASYLASEISTWDGVIVTPSEK.A             |
| 0.962023 | 0.8539 K.HQIK[325.13]QAVK.K                                  |
| 0.961969 | 0.834 R.IAEDDGKPRPAFSNALEPDFK[325.13]ATSITVTGSGSC[160.03]R.A |
| 0.961955 | 0.7272 K.NIC[160.03]K[325.13]VVEVGSK.I                       |
| 0.961951 | 0.2391 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K              |
| 0.961913 | 0.8605 K.AIRPQIDLK[325.13]R.Y                                |
| 0.961896 | 0.9217 R.GLK[325.13]MSATFIGNSTAIQELFK.R                      |
| 0.961856 | 0.9556 K.ESK[325.13]ALMGLYHGQVLC[160.03]K.K                  |
| 0.961848 | 0.9719 R.GFGFVYFQNHDAADK[325.13]AAVVK.F                      |
| 0.961841 | 0.9937 R.DPNSPLYSVK[325.13]SFEELR.L                          |
| 0.961782 | 0.7831 R.HKNPK[325.13]TGIYEEK.H                              |
| 0.961765 | 0.8945 R.GGMGSGGLATGIAGGLAGM[147.04]GGIQNEK[325.13]I         |
| 0.96174  | 0.9947 R.ERPQIGGTIK[325.13]QPPSNPPPRPPAEAR.K                 |
| 0.96174  | 0.9947 K.HVTSEQEWDK[325.13]YC[160.03]HYVAGLVGIGLSR.L         |
| 0.961735 | 0.5321 R.SRAEAESMYQIK[325.13]YEELQSLAGK.H                    |
| 0.961713 | 0.8906 R.INK[325.13]M[147.04]LSC[160.03]AGADR.L              |
| 0.961671 | 0.9317 K.IFVGGIK[325.13]EDTEEYNLR.D                          |
| 0.961645 | 0.6358 K.IK[325.13]IIAPPER.K                                 |
| 0.961639 | 0.9876 K.K[325.13]FMDQHPEMDFSK.A                             |
| 0.961636 | 0.9121 K.TVM[147.04]PYISTTPAK[325.13]LR.N                    |
| 0.96157  | 0.7538 R.DLQQYQSQAK[325.13]QLFR.K                            |
| 0.961523 | 0.98 R.THIFK[325.13]IHAR.S                                   |
| 0.961515 | 0.8359 K.FTASAGIQVVGDDLTVTNPK[325.13]R.I                     |
| 0.961514 | 0.6377 K.SK[325.13]FADLSEAANR.N                              |
| 0.96144  | 0.9318 K.IK[325.13]AIPQLQGYLR.S                              |
| 0.961419 | 0.8751 R.RIPWTAASSQLK[325.13]EHFAQFGHVR.R                    |
| 0.961413 | 0.9543 R.LGFFTTYFLPLANTLK[325.13]SK.A                        |
| 0.961387 | 0.1872 R.LAHYNK[325.13]R.S                                   |
| 0.961375 | 0.945 K.GQIK[325.13]EIGWTDVGGWTGQGSILGTK.R                   |
| 0.961374 | 0.9481 R.SLVEQHK[325.13]R.E                                  |
| 0.961358 | 0.9449 K.DVTLQK[325.13]QC[160.03]VPFR.R                      |
| 0.961357 | 0.8567 K.VINTGIK[325.13]VWC[160.03]R.N                       |
| 0.961257 | 0.9352 R.QFLFRPWDVTK[325.13]LK.S                             |
| 0.961209 | 0.9931 R.SEIK[325.13]GFYDPPRR.L                              |
| 0.961187 | 0.7972 R.VVVLMGSTSDLGHC[160.03]EK[325.13]IKK.A               |
| 0.961186 | 0.8873 K.EAAENSLVAYK[325.13]AASDIAMTELPPTHPIR.L              |
| 0.961171 | 0.928 K.YIAIVSTTVETK[325.13]EPEKEIRPALELLEPIEQK.F            |
| 0.961157 | 0.8674 R.AK[325.13]GKPDAAK.K                                 |
| 0.96115  | 0.9916 K.GVHQK[325.13]EGWPSSAYGVTK.I                         |
| 0.96113  | 0.8508 K.HQIK[325.13]QAVK.K                                  |
| 0.961064 | 0.9116 R.GELALK[325.13]DAR.A                                 |
| 0.961047 | 0.9937 R.YLDLHDC[160.03]YLK[325.13]YINLK.A                   |
| 0.960996 | 0.8176 R.EQSHK[325.13]VYVQHLLK.Q                             |
| 0.960983 | 0.9917 R.EDVLWFK[325.13]PVELR.T                              |

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| 0.960978 | 0.801 R.GFK[325.13]DQIYDIFQK.L                              |
| 0.960969 | 0.8518 R.DVLK[325.13]QLILVLC[160.03]SEENMQK.A               |
| 0.96093  | 0.7059 K.NSSYFVEWIPNNVK[325.13]TAVC[160.03]DIPPR.G          |
| 0.960924 | 0.9923 R.AHAYGDPNAGLNSQLHYK[325.13]R.Q                      |
| 0.960894 | 0.9289 K.K[325.13]C[160.03]YEMASHLR.R                       |
| 0.960855 | 0.6844 R.LLGWIQNK[325.13]LPQLPITNFSR.D                      |
| 0.960818 | 0.9291 R.KVMSQNFNTNC[160.03]HTK[325.13]IR.H                 |
| 0.960779 | 0.8933 K.TC[160.03]SLPGTALK[325.13]VSC[160.03]FNVR.F        |
| 0.96077  | 0.9937 R.NSDPTYGQQGHPNTWK[325.13]R.E                        |
| 0.960756 | 0.9813 R.K[325.13]WC[160.03]ELIPGAEFR.C                     |
| 0.960739 | 0.9907 R.GFGHIGIAVPDVYSAC[160.03]K[325.13]R.F               |
| 0.960727 | 0.9708 R.SALSC[160.03]VISK[325.13]TAR.L                     |
| 0.960699 | 0.8542 K.TLNNKFASFIDK[325.13]VR.F                           |
| 0.960697 | 0.9846 R.SHLEK[325.13]AWLISQQIPQFEDVK.F                     |
| 0.960657 | 0.9949 R.EPSFPDVQHGVLIHK[325.13]VILGSPAHR.A                 |
| 0.960657 | 0.9949 R.SSTFLSHSISNQANVHQSVISSWLSTDPAK[325.13]DR.I         |
| 0.960651 | 0.9326 K.GPKADVM[147.04]TPVVEVSLPSMEVDVEAPGAK[325.13]       |
| 0.960624 | 0.8629 R.HLTGEFEK[325.13]K.Y                                |
| 0.960597 | 0.9306 K.IPQALEK[325.13]ILQLK.E                             |
| 0.960585 | 0.9944 K.EIGELTQLK[325.13]ELHIQGNR.L                        |
| 0.960583 | 0.9932 R.VPLHQVPYAVK[325.13]GC[160.03]FR.F                  |
| 0.960572 | 0.9922 R.AGLIPK[325.13]FVSFLGR.T                            |
| 0.960561 | 0.9524 K.THK[325.13]NPALK.A                                 |
| 0.960553 | 0.6943 R.K[325.13]AC[160.03]QIFVR.N                         |
| 0.960496 | 0.1979 R.GALQNIIPASTGAAK[325.13]AVGK.V                      |
| 0.960477 | 0.8125 K.IGQGYLIK[325.13]DGK.L                              |
| 0.960446 | 0.702 K.NSSYFVEWIPNNVK[325.13]TAVC[160.03]DIPPR.G           |
| 0.960435 | 0.9771 R.TC[160.03]TDIKPEWLVK[325.13]IAPQYYDMSNFPQC[160.03] |
| 0.960434 | 0.957 R.LHGGK[325.13]DSASPR.Y                               |
| 0.960429 | 0.9313 K.YVIGPK[325.13]GNSLQEILER.T                         |
| 0.960396 | 0.5416 R.AEAESMYQIK[325.13]YEELQSLAGK.H                     |
| 0.960394 | 0.8496 K.LDVGK[325.13]VLQASVLDDWFPLQGGQGQVHLR.L             |
| 0.960362 | 0.944 K.RGTK[325.13]LMC[160.03]SLC[160.03]HC[160.03]PGA     |
| 0.960351 | 0.585 R.LQAEIEGLK[325.13]GQR.A                              |
| 0.960322 | 0.9787 R.IHFFLSK[325.13]K.K                                 |
| 0.960265 | 0.9945 R.VGAYQAK[325.13]VLQLLLEAFHC[160.03]AEPSSR.Q         |
| 0.960262 | 0.9922 R.DKQPNAQPQYLHGSK[325.13]ALNLAYSSYGSYR.N             |
| 0.960253 | 0.938 R.EYFSWEGAFQHVGK[325.13]AFNQGK.I                      |
| 0.960185 | 0.7461 R.VLEQHK[325.13]LNKDQWEER.I                          |
| 0.960178 | 0.8475 K.K[325.13]TESHHK.A                                  |
| 0.960094 | 0.9087 R.EESGK[325.13]PGAHVTVK.K                            |
| 0.960091 | 0.9847 R.TM[147.04]GVMFTPLTVK[325.13]YAYYDTER.I             |
| 0.960025 | 0.9946 R.ELVHIK[325.13]PDQSNVR.R                            |
| 0.960024 | 0.9741 K.ASHGYGGK[325.13]FGVEQDR.M                          |
| 0.959978 | 0.9531 K.VSVYLQNWSHVLSYVSK[325.13]AESTPEIAEQR.G             |
| 0.95997  | 0.9794 R.RPLYK[325.13]NIVLSGGSTMFR.D                        |
| 0.959916 | 0.9771 R.VK[325.13]DLESFHR.S                                |

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| 0.959912 | 0.9893 K.AFK[325.13]VALLDVFR.E                         |
| 0.959879 | 0.9819 R.TK[325.13]TPGPGAQSALR.A                       |
| 0.959875 | 0.9468 K.VLQHM[147.04]K[325.13]AVQADQER.E              |
| 0.959859 | 0.7623 K.TVWDWELMNDIK[325.13]PIWQRPSK.E                |
| 0.959796 | 0.9098 R.YIEIFK[325.13]SSR.A                           |
| 0.959761 | 0.8624 K.KPRPTRAEGSDVANAVLDGADC[160.03]IMLSGETAK[325   |
| 0.959712 | 0.861 K.DISLSDYK[325.13]GK.Y                           |
| 0.959706 | 0.9295 K.IIPLVVK[325.13]FC[160.03]NVDDDEL.R.E          |
| 0.959651 | 0.9911 K.AHHAAC[160.03]K[325.13]EEK.L                  |
| 0.959648 | 0.1601 R.VIHLSNLP HSGYSDSAVLK[325.13]LAEPY GK.I        |
| 0.959521 | 0.9946 R.EVLDVAAGMIK[325.13]PGVTTEEIDHAVHLAC[160.03]IA |
| 0.959516 | 0.8751 R.DQK[325.13]WHDK.Q                             |
| 0.959463 | 0.7062 R.K[325.13]ESYSVYVYK.V                          |
| 0.959417 | 0.9408 K.KIESFGSPK[325.13]GSVC[160.03]R.R              |
| 0.959405 | 0.6364 R.SHKDEVVK[325.13]IQSLAR.M                      |
| 0.959361 | 0.8505 K.IVIQK[325.13]YHTVNGHNC[160.03]EVR.K           |
| 0.959355 | 0.9717 R.QMSGAIK[325.13]IANPVEGSSGR.Q                  |
| 0.959355 | 0.9705 R.FPLEK[325.13]ALEAFETFKK.G                     |
| 0.95932  | 0.8225 R.K[325.13]SQVLFSVTR.G                          |
| 0.959307 | 0.9864 K.IGSLIDVNQSK[325.13]DPEGLR.V                   |
| 0.959246 | 0.9905 R.ILVGSLEK[325.13]NEFITLAHVNPQSFPAPK.E          |
| 0.959224 | 0.9153 R.WC[160.03]DK[325.13]SDEDDWSKPLPPSER.L         |
| 0.959221 | 0.9656 K.K[325.13]ELLLPGNNR.K                          |
| 0.959152 | 0.9258 K.KIIP TLEGLQLPSPTATSQLPLESDAVEC[160.03]LNYQHYK |
| 0.959128 | 0.9931 R.VPLHK[325.13]PTDWQK.K                         |
| 0.959118 | 0.7742 R.NLK[325.13]ASLENSLR.E                         |
| 0.959055 | 0.4601 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I      |
| 0.959039 | 0.9504 R.GGHI AK[325.13]DC[160.03]KEPK.R               |
| 0.959017 | 0.9778 R.LHSVC[160.03]TL SK[325.13]MLEILEQQK.K         |
| 0.958994 | 0.829 R.FKK[325.13]PGSK.N                              |
| 0.958967 | 0.838 K.MK[325.13]LPQFGISTPGSDLHVNAK.G                 |
| 0.958965 | 0.9181 R.K[325.13]GTDVNVFNTILTTR.S                     |
| 0.958944 | 0.7538 R.VHK[325.13]ISNVNK.A                           |
| 0.958939 | 0.8913 R.IDAM[147.04]HGVVGPYVK[325.13]K.I              |
| 0.958931 | 0.8859 R.TFK[325.13]TVFAEHISDEC[160.03]K.R             |
| 0.958927 | 0.0596 R.DLTDYLMK[325.13]ILTER.G                       |
| 0.958858 | 0.9873 K.VYVGNLGTGAGK[325.13]GELER.A                   |
| 0.958838 | 0.9484 R.K[325.13]HFGAGGNQR.I                          |
| 0.958836 | 0.9338 K.LSEGV TISYK[325.13]SYC[160.03]K.N             |
| 0.958826 | 0.8918 R.GLK[325.13]MAVTFIGNSTAIQELFK.R                |
| 0.958805 | 0.9839 R.K[325.13]LVILEGELER.A                         |
| 0.958803 | 0.9688 R.VLTVINQTQK[325.13]ENLR.K                      |
| 0.958786 | 0.9945 R.AAEPVTFHVPWK[325.13]R.L                       |
| 0.958754 | 0.6268 R.LAHY NK[325.13]R.S                            |
| 0.958699 | 0.9819 K.HGEK[325.13]VSLSSK.C                          |
| 0.958666 | 0.8441 K.LDVQFSGLTK[325.13]GDAVR.D                     |
| 0.958666 | 0.8441 R.AHSSMVGVNLPQK[325.13]AGGFLMK.K                |

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| 0.958597 | 0.8835 K.MDSTANEVEAVK[325.13]VHSFPTLK.F                   |
| 0.958583 | 0.7259 R.MHAPGK[325.13]GLSQSALPYR.R                       |
| 0.958559 | 0.9 R.AK[325.13]FYPEDVSEELIQDITQR.L                       |
| 0.958543 | 0.9933 R.QK[325.13]TLEHLQLSHDQLLEV.K.R                    |
| 0.958519 | 0.9414 K.AMK[325.13]QYNGVPLDGRPMNIQLVTSQIDAQR.R           |
| 0.958511 | 0.9337 R.QIYGAK[325.13]GFSLSDPQAEISGEHLR.I                |
| 0.958495 | 0.7959 R.RTK[325.13]TEISEM[147.04]NR.N                    |
| 0.958483 | 0.8266 R.AK[325.13]AVVQLKPR.H                             |
| 0.958482 | 0.8417 K.HQIK[325.13]QAVK.K                               |
| 0.958465 | 0.5183 K.LLGK[325.13]VTIAQGGVLPNIQAVLLPK.K                |
| 0.958398 | 0.959 R.HISVLVPC[160.03]FLTFRPK[325.13]QC[160.03]R.M      |
| 0.958353 | 0.8121 K.LGLAK[325.13]SIHHAR.V                            |
| 0.958326 | 0.4098 K.GFGYK[325.13]GSC[160.03]FHR.I                    |
| 0.958322 | 0.8697 R.YIEVFK[325.13]SHR.T                              |
| 0.958273 | 0.756 K.IGQGYLIK[325.13]DGK.L                             |
| 0.958273 | 0.8479 R.YIGIVK[325.13]QAGLER.M                           |
| 0.958264 | 0.9163 R.AK[325.13]QEELEAALQR.G                           |
| 0.958263 | 0.9383 K.GSAITGPVAK[325.13]EC[160.03]ADLWPR.I             |
| 0.958254 | 0.9877 K.SLGHGLINK[325.13]K.R                             |
| 0.958244 | 0.5735 R.VIISAPSADAPM[147.04]FVMGVNHEK[325.13]YDNSLK.I    |
| 0.958218 | 0.9106 K.TAK[325.13]LHVAVK.V                              |
| 0.958212 | 0.8262 R.RGPPEK[325.13]EWR.R                              |
| 0.958209 | 0.9356 K.K[325.13]EGHWDC[160.03]SIC[160.03]LVR.N          |
| 0.95817  | 0.9104 K.KSDYIK[325.13]LYVR.R                             |
| 0.958132 | 0.9759 K.TGK[325.13]PM[147.04]INLYTDKDTGPK.G              |
| 0.958127 | 0.9721 R.GFGGITHGPPEK[325.13]K.M                          |
| 0.958083 | 0.7809 K.VK[325.13]LEAEIATYR.R                            |
| 0.958068 | 0.9926 K.DK[325.13]FSPFPVQDRPESSLVFK.D                    |
| 0.958052 | 0.2722 R.KPAGAAK[325.13]KPK.K                             |
| 0.958036 | 0.961 K.TLTSGGHAHEGK[325.13]PYC[160.03]NHPC[160.03]YA     |
| 0.958018 | 0.9845 K.ELGITALHIK[325.13]LR.A                           |
| 0.957998 | 0.927 R.DNIQGITK[325.13]PAIR.R                            |
| 0.957994 | 0.8003 R.DVQNTFYDIVAELGAMEHAQAVDYIK[325.13]K.L            |
| 0.957975 | 0.9696 R.EEFWEMFDGSLYHK[325.13]LR.E                       |
| 0.957964 | 0.919 R.LAVYIDK[325.13]VR.S                               |
| 0.957937 | 0.9059 K.NVHELEKSK[325.13]R.A                             |
| 0.957931 | 0.9807 R.VGK[325.13]VLC[160.03]SPVESEYISAEQIVC[160.03]EIG |
| 0.957826 | 0.9414 K.VGDK[325.13]VLLPEYGGTK.V                         |
| 0.957821 | 0.9771 R.GLVLGK[325.13]LGK.A                              |
| 0.957752 | 0.7873 R.LLSDATVEKDESHAGK[325.13]VVLR.S                   |
| 0.957691 | 0.991 R.K[325.13]EVVHTVSLHEIDVINSR.T                      |
| 0.957677 | 0.9748 R.K[325.13]LYGKSPLFGQYFVLENPGTIK.V                 |
| 0.957674 | 0.7937 K.GSIHK[325.13]FVPYLIAGIQHSC[160.03]QDIGAK.S       |
| 0.957664 | 0.9332 K.WGVPIEK[325.13]IYNK.T                            |
| 0.957659 | 0.6234 K.VYGERPLTK[325.13]DNHLLGTDFLTGIPPAPR.G            |
| 0.957651 | 0.9391 K.EAISDLQQLWK[325.13]QNP.K.D                       |
| 0.957648 | 0.9916 K.DK[325.13]LLHIYYQNSIDDR.L                        |

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| 0.957646 | 0.9718 K.FLIPNASQAESK[325.13]VFYLK.M                   |
| 0.95756  | 0.9935 R.WTPK[325.13]AAHVLR.K                          |
| 0.957545 | 0.9941 R.VSPTGEK[325.13]VTHTGQVYDDKDYS.R               |
| 0.957512 | 0.9679 K.YHNVGLSK[325.13]C[160.03]EIK.V                |
| 0.957508 | 0.859 K.YGK[325.13]IVGC[160.03]SVHK.G                  |
| 0.957491 | 0.9746 R.K[325.13]YLLGVQPAWGSAAVDIDR.S                 |
| 0.957491 | 0.5258 R.K[325.13]VSQPIEGHAASFAQFK.M                   |
| 0.957372 | 0.8189 K.SRLDQELK[325.13]LIGEYGLR.N                    |
| 0.957367 | 0.9088 R.THQK[325.13]FVIATSTK.I                        |
| 0.957349 | 0.8731 R.YHVK[325.13]DSSR.H                            |
| 0.957311 | 0.8328 K.DLILPTIQK[325.13]SLLR.S                       |
| 0.95729  | 0.8076 K.DK[325.13]GFGFIR.L                            |
| 0.95725  | 0.9907 K.AK[325.13]GVVLSGAESLLEHSR.K                   |
| 0.957231 | 0.8597 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTSGSGFTS |
| 0.957214 | 0.8393 K.MPK[325.13]ISMPGFK.G                          |
| 0.957208 | 0.8441 K.LKGPK[325.13]FK.M                             |
| 0.957151 | 0.9438 R.LSPEPWTPETGLVTDFAK[325.13]LK.R                |
| 0.957149 | 0.9926 K.AGGSASAMLQPLLDNQVGFK[325.13]NMQNVHVPLSLC      |
| 0.957136 | 0.925 K.VLLPEYGGTK[325.13]VVLDDKDYFLFR.D               |
| 0.957127 | 0.8155 K.ALANVNIGSLIC[160.03]NVGAGGPAPAAGAAPAGGPAPS    |
| 0.957123 | 0.6073 K.KAASGEAKPK[325.13]AK.K                        |
| 0.957068 | 0.8689 R.GTNLNK[325.13]AMTLQEAEAFVGAER.C               |
| 0.957067 | 0.9321 K.ITGC[160.03]ASPGK[325.13]TVTIVVR.G            |
| 0.957025 | 0.8341 R.VHKPPK[325.13]VQEK.C                          |
| 0.956984 | 0.9123 R.VK[325.13]LLLQVQHASK.Q                        |
| 0.956924 | 0.9905 K.HGKPTDSTPATWK[325.13]QEYVDYSESAK.K            |
| 0.956922 | 0.9904 K.MDPTDAK[325.13]YHMQR.C                        |
| 0.95691  | 0.8383 R.DHALLEEQSK[325.13]QQSNEHLR.R                  |
| 0.956907 | 0.7575 R.K[325.13]M[147.04]C[160.03]LFAGFQR.K          |
| 0.956904 | 0.6075 K.IK[325.13]IIAPPER.K                           |
| 0.956892 | 0.8954 R.EVDRPGSK[325.13]VNKK.E                        |
| 0.956887 | 0.5348 K.K[325.13]GDVVIVLTGWRPGSGFTNTMR.V              |
| 0.956861 | 0.9839 R.HAGGLGK[325.13]EFSR.S                         |
| 0.956773 | 0.9922 K.AFELMHSGK[325.13]SIR.T                        |
| 0.956749 | 0.9912 R.EVFSK[325.13]YGPIADVSIYDQQSR.R                |
| 0.956742 | 0.8904 K.VFSATLGLVDIVK[325.13]GTNSYYK.L                |
| 0.95671  | 0.9811 R.LVVPASQC[160.03]GSLIGK[325.13]GGC[160.03]K.I  |
| 0.956673 | 0.9533 K.FASYLTFSPSEVK[325.13]SLR.T                    |
| 0.956613 | 0.6146 K.FDLMYAK[325.13]R.A                            |
| 0.956597 | 0.5262 R.RVEHNQSYSQAGITETEWTSKGSSK[325.13]GGPLQALTR.E  |
| 0.95659  | 0.9904 K.AHHAAC[160.03]K[325.13]EEK.L                  |
| 0.956553 | 0.9862 R.LGEK[325.13]DTSLYRPALEELRR.Q                  |
| 0.956552 | 0.9816 R.LALHELK[325.13]NLTQYSWLLDGFPR.T               |
| 0.956528 | 0.9721 R.K[325.13]DVGRPQPGR.E                          |
| 0.9565   | 0.7431 K.VNQIGSVTESLQAC[160.03]K[325.13]LAQANGWGMV     |
| 0.956494 | 0.9877 K.IHLVVLVK[325.13]PSGAR.C                       |
| 0.95649  | 0.6446 R.LPSGNHMK[325.13]ESR.E                         |

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|----------|--------------------------------------------------------|
| 0.95649  | 0.966 K.LLGHEVEDVLIK[325.13]C[160.03]QLPK.R            |
| 0.956486 | 0.7212 K.NK[325.13]GLWVPEGQR.A                         |
| 0.956423 | 0.8367 K.DVDEAYMNK[325.13]VELES.R                      |
| 0.9564   | 0.8417 K.YIQAAC[160.03]K[325.13]TGQIK.E                |
| 0.956361 | 0.9821 R.TK[325.13]YWELIYEDSMDLIAK.L                   |
| 0.956343 | 0.9933 R.LATDNIGYIDWDPYVPK[325.13]IFTR.I               |
| 0.956299 | 0.9895 R.IASHSHVK[325.13]GLGLDESLAK.Q                  |
| 0.956267 | 0.7144 R.YM[147.04]AQGK[325.13]HIGK.V                  |
| 0.95626  | 0.9436 K.LALK[325.13]YHPDKNPNEGEK.F                    |
| 0.956253 | 0.9193 K.GTGNK[325.13]NKITITNDQNR.L                    |
| 0.956226 | 0.823 K.KIGYNPDTVAFVPISGWNGDNMLEPSANMPWFK[325.13]      |
| 0.956206 | 0.9943 R.SVFDIPIFTEEFLNHSK[325.13]AR.E                 |
| 0.956184 | 0.8265 K.AK[325.13]LKPGAPLRPK.L                        |
| 0.956154 | 0.9865 R.RIK[325.13]ETQR.L                             |
| 0.956101 | 0.9939 R.SC[160.03]HYGVIDK[325.13]FR.L                 |
| 0.956051 | 0.8112 R.YLYTLVITDKEK[325.13]AEK.L                     |
| 0.956004 | 0.8635 K.KITAASK[325.13]K.A                            |
| 0.95597  | 0.8617 R.K[325.13]AHLTNQYM[147.04]QR.V                 |
| 0.955917 | 0.9683 R.LDDFFK[325.13]VTGSLSSAK.R                     |
| 0.955883 | 0.6476 R.FEPYANPTK[325.13]R.Y                          |
| 0.955791 | 0.9928 R.GVSAFSTWEK[325.13]ELHK.I                      |
| 0.955776 | 0.9322 K.IVKPNGEKPDEFESGISQALLELEMNSDLK[325.13]AQLR.E  |
| 0.955688 | 0.9727 R.SK[325.13]SYSFHQSQHR.K                        |
| 0.95568  | 0.8683 R.AGAIAPC[160.03]EVTVPAQNTGLGPEK[325.13]TSFFQAI |
| 0.955672 | 0.9832 R.VNHVTLSQLK[325.13]IVK.W                       |
| 0.955602 | 0.7586 R.VK[325.13]VFQSSANYAENFIQSIISTVEPAQR.Q         |
| 0.955581 | 0.8498 K.LLEPVLLLGK[325.13]ER.F                        |
| 0.955558 | 0.9237 R.FFMGNQVLK[325.13]VFAAR.D                      |
| 0.955522 | 0.8908 R.NGMVLKPHFHK[325.13]DWQR.R                     |
| 0.955522 | 0.6761 K.NSSYFVEWIPNNVK[325.13]TAVC[160.03]DIPPR.G     |
| 0.955481 | 0.773 R.LPSGNHM[147.04]K[325.13]ESR.E                  |
| 0.955389 | 0.9658 K.VGAVDADK[325.13]HHS LGGQYGVQGFPTIK.I          |
| 0.955335 | 0.8379 R.VYYTMEPEHPVGNWQK[325.13]HNVDDSLTTVGSLLEDI     |
| 0.955332 | 0.7654 K.NM[147.04]AEQIIQEISQIQSK[325.13]K.K           |
| 0.955307 | 0.8961 K.SFPK[325.13]DDPSKPVHLTAFLGYK.A                |
| 0.955273 | 0.9092 K.FIQENIFGIC[160.03]PHMTEDNK[325.13]DLIQGK.D    |
| 0.955229 | 0.8328 K.ADLINNLGTIAK[325.13]SGTK.A                    |
| 0.955181 | 0.7857 K.GKWKPPMIDNPSYQGIWK[325.13]PR.K                |
| 0.955157 | 0.6221 K.EK[325.13]LC[160.03]YVALDFEQEMATAASSSSLEK.S   |
| 0.955119 | 0.8376 R.YIGIVK[325.13]QAGLER.M                        |
| 0.955109 | 0.9235 R.TPSNELYK[325.13]PLR.A                         |
| 0.955038 | 0.3482 R.GFGFVTYATVEEVDAAMNARPHK[325.13]VDGR.V         |
| 0.955034 | 0.8512 K.LK[325.13]SIAFPSIGSGR.N                       |
| 0.95502  | 0.8063 K.SAAK[325.13]AVKPK.A                           |
| 0.954966 | 0.5994 R.SKGQESFK[325.13]K.Q                           |
| 0.95495  | 0.8419 R.HYPVFENPK[325.13]QGK.L                        |
| 0.954922 | 0.9907 K.TGVIEHEHPVVK[325.13]ISFIAR.D                  |

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| 0.954892 | 0.8847 R.FNVLK[325.13]VTK.A                               |
| 0.954872 | 0.9756 R.YLK[325.13]GDHAGVLK.A                            |
| 0.954862 | 0.8228 K.GFNK[325.13]VVLK.H                               |
| 0.954847 | 0.9829 R.TELLNVC[160.03]MNAK[325.13]HHK.E                 |
| 0.954797 | 0.9121 K.IHNAENIQPGEQK[325.13]YEYK.S                      |
| 0.954771 | 0.5455 R.IYDLNKPEAEPK[325.13]EISGHTSGIK.K                 |
| 0.95474  | 0.779 R.ELDSITPEVLPGWK[325.13]GMSVSDLADKLSTDDLNSLIAI      |
| 0.95465  | 0.9242 R.LLADPTGAFGK[325.13]ETDLLLDDSLVSIFGNR.R           |
| 0.95461  | 0.9933 R.VDGSKPIWK[325.13]YETGPGGTSR.G                    |
| 0.954606 | 0.8598 K.TESHHK[325.13]AK.G                               |
| 0.954583 | 0.7609 K.SSEHINEGETAM[147.04]LVC[160.03]K[325.13]SESVPPV  |
| 0.954571 | 0.9889 K.M[147.04]HLAGK[325.13]TEQAK.A                    |
| 0.954548 | 0.8617 R.VFIGNLNTLVVK[325.13]K.S                          |
| 0.954528 | 0.9929 K.ILK[325.13]HEGLGAFYK.G                           |
| 0.954522 | 0.5886 R.RYQK[325.13]STELLIR.K                            |
| 0.954516 | 0.9092 K.EDLVFIFWAPESAPLK[325.13]SK.M                     |
| 0.954506 | 0.8745 K.YLAIAPPIIK[325.13]QSTIVC[160.03]HNR.V            |
| 0.954485 | 0.5925 R.NPDDITQEEYGEFYK[325.13]SLTNDWEDHLAVK.H           |
| 0.954465 | 0.8343 R.VYYTMEPEHPVGNWQK[325.13]HNVDDSLTTVGSLLEDI        |
| 0.954443 | 0.828 K.K[325.13]TESHHK.A                                 |
| 0.954422 | 0.9935 R.VK[325.13]IRPMEHC[160.03]C[160.03]C[160.03]SVR.I |
| 0.954404 | 0.9727 R.GKPAVAALGDLTDLPTYEHIQTALSSK[325.13]DGR.L         |
| 0.954387 | 0.9504 R.LHGGK[325.13]DSASPR.Y                            |
| 0.95436  | 0.5425 K.FAAK[325.13]GEGQLGPAER.A                         |
| 0.954358 | 0.9928 R.LEC[160.03]VAFSHQNLK[325.13]LK.W                 |
| 0.95431  | 0.6126 K.VTLDWAK[325.13]PK.G                              |
| 0.95428  | 0.9199 R.VDSTAK[325.13]VAEIEHAEKEK.M                      |
| 0.954266 | 0.9704 R.ELFVQSEIFLETPAFAIK[325.13]EQGFR.A                |
| 0.954246 | 0.9822 K.TVTQNGTHVASVPTAVHGVNNAAASPLHMLATHASASA           |
| 0.954241 | 0.9939 R.VAFTLLEK[325.13]VLDEFSK.Q                        |
| 0.95424  | 0.9932 R.HVVLGAIENK[325.13]VESK.G                         |
| 0.954183 | 0.6877 K.IGHPAPNFK[325.13]ATAVM[147.04]PDGQFK.D           |
| 0.954168 | 0.9759 R.VVIIGAGK[325.13]PAAVVLQTK.G                      |
| 0.954159 | 0.9787 K.YEK[325.13]PDGSPVFIAFR.S                         |
| 0.954156 | 0.952 K.GILAADESTGSIK[325.13]R.L                          |
| 0.954113 | 0.9936 K.TYGEIFEK[325.13]FHPIR.-                          |
| 0.954023 | 0.9606 K.K[325.13]LLDIEGLYSK.V                            |
| 0.954005 | 0.9568 R.LIHPK[325.13]SGR.S                               |
| 0.954005 | 0.8689 R.GLK[325.13]M[147.04]AVTFIGNSTAIQELFK.R           |
| 0.953957 | 0.9596 R.HISPSAK[325.13]PFENGQYLDIYGITR.D                 |
| 0.953932 | 0.9899 R.SIYFQPPSFYVSAQDLPHIENGGVAVLTGK[325.13]K.V        |
| 0.953915 | 0.9832 K.KHELK[325.13]ITQQGTDPVLVLAVQSK.E                 |
| 0.95386  | 0.5732 K.FYEAFSK[325.13]NLK.L                             |
| 0.953811 | 0.7131 R.FEPYANPTK[325.13]R.Y                             |
| 0.953804 | 0.9683 K.K[325.13]YKPLDLRPK.K                             |
| 0.95376  | 0.7483 R.EGQEDQGLTK[325.13]DYGNSPLHR.F                    |
| 0.953745 | 0.9913 R.LHQLK[325.13]VPTK.R                              |



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| 0.953742 | 0.8125 | K.LIEK[325.13]LDIK.L                           |
| 0.953694 | 0.6355 | R.K[325.13]AC[160.03]QIFVR.N                   |
| 0.953681 | 0.9838 | K.LTPLK[325.13]LIDSWMGK.G                      |
| 0.953592 | 0.8076 | K.SAEFLHMLK[325.13]NAESNAELK.G                 |
| 0.953556 | 0.4846 | R.RYQK[325.13]STELLIR.K                        |
| 0.953541 | 0.9547 | K.MFVGGLSWDTSK[325.13]K.D                      |
| 0.95344  | 0.9836 | R.EYTINIHK[325.13]R.I                          |
| 0.953397 | 0.7769 | R.FPGAYLK[325.13]GK.K                          |
| 0.953311 | 0.8872 | R.EVDRPGSK[325.13]VNKK.E                       |
| 0.953293 | 0.9088 | R.IYC[160.03]K[325.13]PHFNQLFK.S               |
| 0.953284 | 0.8265 | K.ILGFMKTK[325.13]DLPVTEAVFSALVTGHAR.A         |
| 0.953255 | 0.6088 | R.K[325.13]MFTLLDVVNR.K                        |
| 0.953245 | 0.8454 | R.SYSK[325.13]LLC[160.03]GLLAER.L              |
| 0.953244 | 0.8615 | R.IGK[325.13]PAPDFK.A                          |
| 0.95322  | 0.5537 | K.FINYVK[325.13]NC[160.03]FR.M                 |
| 0.953144 | 0.8554 | K.KITAASK[325.13]K.A                           |
| 0.953004 | 0.8726 | R.NFK[325.13]VSNTQDASVSIVDYEPR.R               |
| 0.952983 | 0.754  | R.FDASFFGVHPK[325.13]QAHTM[147.04]DPQLR.L      |
| 0.952927 | 0.9608 | R.KEAAENSLVAYK[325.13]AASDIAMTELPPTHPIR.L      |
| 0.952916 | 0.9497 | R.KIGLETVGVK[325.13]INEK.T                     |
| 0.952818 | 0.9098 | K.YVK[325.13]NTHATTHNAYDLEVIDIFK.I             |
| 0.952777 | 0.9663 | K.IGPLGLSPK[325.13]K.V                         |
| 0.952765 | 0.7526 | R.GLK[325.13]YELISETGGSHDKR.F                  |
| 0.952761 | 0.9228 | R.YAPVAK[325.13]DLASR.D                        |
| 0.95276  | 0.9749 | K.GAGAFGYFEVTHDITK[325.13]YSK.A                |
| 0.952757 | 0.9909 | R.HYQTGQPLPK[325.13]NMVSR.L                    |
| 0.9527   | 0.8872 | R.GKGGK[325.13]GLGK.G                          |
| 0.952686 | 0.801  | R.GWPLELLC[160.03]EK[325.13]SIGTANRPMGAGEALR.R |
| 0.952666 | 0.9139 | R.ILAK[325.13]LPIEPR.F                         |
| 0.952648 | 0.9112 | R.ALK[325.13]AVSDWIDEQEK.G                     |
| 0.952606 | 0.9811 | R.NRPEGK[325.13]VLETVGVFEVVK.Q                 |
| 0.952581 | 0.9127 | R.SPSTLLPKK[325.13]PTAIK.T                     |
| 0.952579 | 0.9698 | R.HISPSAK[325.13]PFENGQYLDIYGITR.D             |
| 0.952561 | 0.7035 | K.NFGIGQDIQPK[325.13]R.D                       |
| 0.952557 | 0.7513 | K.VTQQGLK[325.13]M[147.04]VVPGLDGAQIPR.D       |
| 0.952552 | 0.7019 | K.NK[325.13]GLWVPEGQR.A                        |
| 0.952537 | 0.8241 | R.ELISNSSDALDK[325.13]IR.Y                     |
| 0.952524 | 0.9938 | R.ISHLVLPVQPENALK[325.13]R.G                   |
| 0.95251  | 0.9908 | K.K[325.13]GYFYIPPLATH TIC[160.03]DR.N         |
| 0.952484 | 0.9089 | K.LK[325.13]MLTEAIMHDC[160.03]VVK.L            |
| 0.95244  | 0.9501 | R.VYNVTQHAVGIVVNK[325.13]QVK.G                 |
| 0.952413 | 0.8454 | K.NQTLQK[325.13]EIQGHQPR.I                     |
| 0.952394 | 0.9696 | R.ESC[160.03]LEAYTGIVQGLK[325.13]GDQENVHPDVMLV |
| 0.952375 | 0.909  | K.YHPK[325.13]IIGR.K                           |
| 0.952361 | 0.81   | R.IMEFTTTLLNTSPEGWK[325.13]LLK.K               |
| 0.95232  | 0.8492 | R.VINEEYK[325.13]IWK.K                         |
| 0.952287 | 0.8589 | R.IGK[325.13]PAPDFK.A                          |

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| 0.952251 | 0.3892 R.RYQK[325.13]STELLIR.K                           |
| 0.952214 | 0.8151 K.VIQYLAYVASSHK[325.13]SK.K                       |
| 0.952198 | 0.785 R.VDEVPDGA VKPPTNK[325.13]LPIFFFGTHETAFLGPK.D      |
| 0.952175 | 0.3671 K.TVDLKP DWGK[325.13]GYSR.K                       |
| 0.952171 | 0.9101 R.K[325.13]GSEHQAI VQHLEK.S                       |
| 0.952141 | 0.956 R.DGMLDDEEFALASHLIEAK[325.13]LEGHGLPANLPR.R        |
| 0.952102 | 0.7867 R.K[325.13]AYGQALAK.L                             |
| 0.952055 | 0.5074 R.EAPHVK[325.13]NNAIISLR.K                        |
| 0.952049 | 0.9932 R.K[325.13]DFQQLQGISEDVPHR.L                      |
| 0.952045 | 0.8125 K.AASGEAKPK[325.13]AK.K                           |
| 0.95202  | 0.9844 K.LK[325.13]QFVFDLHSGK.L                          |
| 0.951949 | 0.9498 K.TVDFTQDSNYLLTGGQDK[325.13]LLR.I                 |
| 0.951927 | 0.9172 R.ANGLK[325.13]SC[160.03]VIVLR.I                  |
| 0.951888 | 0.9679 K.EDALPGQKTEFK[325.13]VDSDDQWGEYSC[160.03]VFLF    |
| 0.951886 | 0.6926 K.VAVATPAK[325.13]KAAVTPGK.K                      |
| 0.951779 | 0.6454 R.GEIIAK[325.13]QGGGGGGGSGVPGIER.M                |
| 0.95175  | 0.9829 K.AALSSFQK[325.13]VLELEGEKGEWGFK.A                |
| 0.951712 | 0.9047 K.GEVIK[325.13]AWDIAIATMK.V                       |
| 0.95168  | 0.9556 R.M[147.04]ISK[325.13]QFHHQLR.V                   |
| 0.951618 | 0.979 K.EILTLK[325.13]EVFQIASNDHDAAINR.Y                 |
| 0.951605 | 0.9771 K.LEQIDGHIAEHNSK[325.13]JK.Y                      |
| 0.951602 | 0.7522 R.YQK[325.13]STELLIR.K                            |
| 0.951588 | 0.9815 R.RPLILQLVHVSQEDK[325.13]R.K                      |
| 0.951588 | 0.8847 R.GKGGK[325.13]GLGK.G                             |
| 0.951574 | 0.9753 R.VK[325.13]TTGIVETHFTFK.D                        |
| 0.951568 | 0.8566 K.HK[325.13]FMVQTI FAPPNTSDMEAVWK.E               |
| 0.951566 | 0.9917 R.VFDK[325.13]DGNGYISAAELR.H                      |
| 0.951445 | 0.9854 R.EIVSGMK[325.13]YIQHTYR.K                        |
| 0.951393 | 0.9893 R.LEWVGLVESK[325.13]IR.I                          |
| 0.951375 | 0.9618 K.IC[160.03]QFK[325.13]LVLLGESAVGK.S              |
| 0.951368 | 0.9932 R.GPGGSSLLIEALSNSHK[325.13]C[160.03]QADIR.H       |
| 0.951295 | 0.8227 R.SLHDALC[160.03]VVK[325.13]R.V                   |
| 0.95124  | 0.8063 K.FWHK[325.13]AC[160.03]FHC[160.03]ETC[160.03]K.M |
| 0.95116  | 0.7742 R.VTGNFK[325.13]HASPILPITEFSDIPR.R                |
| 0.951153 | 0.974 R.K[325.13]GLEFPMTDLMLSPIHTPQR.T                   |
| 0.951146 | 0.9724 R.GHFK[325.13]VVDSR.M                             |
| 0.951117 | 0.9467 K.TIAEC[160.03]LADELINAAK[325.13]GSSNSYAIK.K      |
| 0.951094 | 0.9392 K.NLNGK[325.13]SYSMIVNNLLKPISVEGSSK.K             |
| 0.951077 | 0.7894 K.SHLAK[325.13]EGLYQYK.N                          |
| 0.951043 | 0.8165 R.K[325.13]DALHLLVFTTDDVPHIALDGK.L                |
| 0.951042 | 0.9685 R.K[325.13]DVGRPQPGR.E                            |
| 0.951029 | 0.8614 R.EK[325.13]QTVHSVFR.K                            |
| 0.951    | 0.9506 R.LQHYAK[325.13]IAADFR.N                          |
| 0.950976 | 0.6337 R.TLTIVDTGIGMTK[325.13]ADLINNLGTIAK.S             |
| 0.950966 | 0.4584 R.HVMQPYK[325.13]DILPC[160.03]LDGYLK.T            |
| 0.950965 | 0.9786 K.NKGDSHLNVQVS NFK[325.13]SGK.G                   |
| 0.950963 | 0.5569 K.FYEAFSK[325.13]NLK.L                            |

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| 0.950922 | 0.76   | K.HLNMK[325.13]LTR.A                             |
| 0.950903 | 0.5847 | K.VYEGERPLTK[325.13]DNHLLGTFDLTGIPPAPR.G         |
| 0.950855 | 0.8239 | R.NDLMEYAK[325.13]QHGIPIPVTPK.N                  |
| 0.950747 | 0.9873 | K.EAHLTPYSLQAIK[325.13]ASR.H                     |
| 0.950707 | 0.4301 | R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M       |
| 0.950657 | 0.9571 | K.EAPPM EKPEVVK[325.13]THLR.D                    |
| 0.950587 | 0.7919 | K.DWHRPC[160.03]LK[325.13]C[160.03]EK.C          |
| 0.950582 | 0.8036 | R.AFLGELK[325.13]TQMTSAVR.E                      |
| 0.950348 | 0.8076 | K.WVK[325.13]HWVK.G                              |
| 0.950326 | 0.9935 | K.FNDK[325.13]HITTLQASFLTK.K                     |
| 0.950316 | 0.476  | R.TK[325.13]TEISEMNR.N                           |
| 0.950257 | 0.8969 | R.K[325.13]SLVMHTPPVLK.K                         |
| 0.950227 | 0.9801 | K.RNEIDAEPK[325.13]R.H                           |
| 0.950219 | 0.8146 | K.YQLDPTASISAK[325.13]VNNSSLIGVGYTQTLRPGVK.L     |
| 0.950188 | 0.9509 | K.K[325.13]ELSDIAHR.I                            |
| 0.950185 | 0.8056 | K.ANPFGGASHAK[325.13]GIVLEK.V                    |
| 0.950094 | 0.8989 | R.LKDLFGK[325.13]FGPALSVK.V                      |
| 0.950065 | 0.9666 | R.VLQALEGLK[325.13]MVEK.D                        |
| 0.95005  | 0.9643 | R.IWDTTQK[325.13]EHLLK.Y                         |
| 0.950045 | 0.8427 | K.ENDAVTIQVLNQLIQK[325.13]IR.E                   |
| 0.949983 | 0.9636 | K.DGNLASTLGQHK[325.13]GPIFALK.W                  |
| 0.949977 | 0.9646 | R.YVAQAHDK[325.13]PR.Y                           |
| 0.949956 | 0.9855 | K.VMNLISK[325.13]LSAK.F                          |
| 0.949849 | 0.7941 | R.FAK[325.13]QYINAIKDYELQLVTYK.A                 |
| 0.949844 | 0.9741 | R.FKEK[325.13]LPAPILEFFAVVMGTGISAGFNLK.E         |
| 0.949844 | 0.8479 | R.VFITDDFHDM[147.04]MPK[325.13]YLNFBVK.G         |
| 0.949822 | 0.9746 | K.IGIMPGHIHK[325.13]K.G                          |
| 0.949759 | 0.912  | R.KWQQLQAK[325.13]R.Y                            |
| 0.949745 | 0.9547 | R.HLK[325.13]IVYR.R                              |
| 0.94971  | 0.9214 | R.YVASYLLAALGGNSSPSAK[325.13]DIK.K               |
| 0.949687 | 0.829  | K.ALANVNIGSLIC[160.03]NVGAGGPAPAAGAAPAGGPAPS     |
| 0.949677 | 0.5486 | R.IHPVSTMVK[325.13]GMYGIENEVFLSLPC[160.03]ILNAR  |
| 0.949671 | 0.8662 | K.LWK[325.13]TFTDC[160.03]FNC[160.03]LPAAIVDEK.I |
| 0.949657 | 0.9918 | K.VPPNHVGK[325.13]PLLK.K                         |
| 0.949639 | 0.9374 | K.NLNGK[325.13]SYSMIVNNLLKPISVEGSSK.K            |
| 0.949639 | 0.9414 | K.IFSGPSSEQFGYAVQQFINPK[325.13]GNWLLVGSPWSGFI    |
| 0.949541 | 0.9918 | R.EDDSIRPFK[325.13]VETSDEEIHDLHQR.I              |
| 0.949534 | 0.8341 | K.VVLSK[325.13]LPIGDVATQYFADR.D                  |
| 0.949533 | 0.9401 | K.GVTIPYRPK[325.13]PSSSPVIFAGGQDR.Y              |
| 0.949488 | 0.9382 | K.GKLEAIITPPPAK[325.13]K.A                       |
| 0.949459 | 0.9367 | R.K[325.13]HFGAGGNQR.I                           |
| 0.949454 | 0.8071 | R.TYHYHC[160.03]ALHDK[325.13]AQIR.E              |
| 0.949429 | 0.9817 | R.LKDK[325.13]WDELK.E                            |
| 0.949268 | 0.9929 | K.LYPAAVDTIVAIMAEGK[325.13]QHALC[160.03]VGVMK.   |
| 0.9492   | 0.9815 | K.APPARPVK[325.13]GAYR.E                         |
| 0.949165 | 0.602  | R.AGK[325.13]ITFAEK.V                            |
| 0.949153 | 0.6627 | R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E        |

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| 0.949107 | 0.9011 K.LSKDPNIVIAK[325.13]MDATANDVSPPYEVR.G           |
| 0.9491   | 0.989 K.VLPGDYEILATHPTWALK[325.13]EASTTVR.V             |
| 0.949099 | 0.5994 K.AAGAGK[325.13]VTK.S                            |
| 0.948944 | 0.923 R.HPAENGK[325.13]SNFLNC[160.03]YVSGFHPSDIEVDLLK   |
| 0.948942 | 0.9081 R.YGDGPRPPK[325.13]MAR.Y                         |
| 0.948927 | 0.8427 R.LQLETEIEALKEELFM[147.04]K[325.13]K.N           |
| 0.948912 | 0.9739 R.VK[325.13]TTGIVETHFTFK.D                       |
| 0.94889  | 0.5622 K.IK[325.13]IIAPPER.K                            |
| 0.948871 | 0.9626 R.SGYIAIDDIQVLSYPC[160.03]DK[325.13]SPHFLR.L     |
| 0.948866 | 0.9933 K.K[325.13]EIPVFNFTIHEIHC[160.03]QR.N            |
| 0.948823 | 0.9928 R.DPNLLSVSK[325.13]DHALR.L                       |
| 0.948809 | 0.9882 K.DKNFMLHYEFPPYATNEIGK[325.13]VTGLNR.R           |
| 0.948791 | 0.9788 R.VVRPDELGERPPEDNQSFDHEAFLGK[325.13]EDSK.T       |
| 0.948769 | 0.5886 R.GIFPVLC[160.03]K[325.13]DPVQEAWAEDVDLR.V       |
| 0.948752 | 0.9703 R.IVQK[325.13]HPHTGDTK.E                         |
| 0.948683 | 0.989 R.EGDKHTLSK[325.13]K.E                            |
| 0.948625 | 0.3764 R.AK[325.13]VTLNGVPAQPLGPR.A                     |
| 0.948605 | 0.9674 R.M[147.04]GVVEC[160.03]AK[325.13]HELLQPFNVLYEK. |
| 0.948592 | 0.7013 K.KPVVGK[325.13]K.G                              |
| 0.948586 | 0.9928 K.LYPAAVDTIVAIMAEGK[325.13]QHALC[160.03]VGVMK.   |
| 0.948548 | 0.9931 R.K[325.13]ALLHAPTGTC[160.03]SDGQAHSISLVR.N      |
| 0.948543 | 0.9912 R.LK[325.13]GSGVTTVSVHPGTVQSELVR.H               |
| 0.9485   | 0.8023 K.ARDDYK[325.13]TLINAEDPPMVVVR.K                 |
| 0.948482 | 0.8677 K.LHQAM[147.04]K[325.13]GVGTR.H                  |
| 0.94843  | 0.752 R.VK[325.13]ILFNK.K                               |
| 0.948397 | 0.9908 K.TK[325.13]PSDEEMLFYGHYK.Q                      |
| 0.948394 | 0.9714 R.RLIELYK[325.13]EAGISK.D                        |
| 0.948354 | 0.9697 R.ILDWHVANTDK[325.13]K.S                         |
| 0.948348 | 0.6705 K.KPAEK[325.13]KPTTEEK.K                         |
| 0.948346 | 0.9483 K.KYGGLK[325.13]TPTQLEGATR.G                     |
| 0.948332 | 0.7882 K.GIVEFASK[325.13]PAAR.K                         |
| 0.948321 | 0.8422 K.TESHHK[325.13]AK.G                             |
| 0.94826  | 0.7021 R.FK[325.13]KPGSKNFQNIFFPSATLHLSNIPPSVSEEDLK.V   |
| 0.94825  | 0.9674 R.DAVSGMGVIVHIEK[325.13]DK.I                     |
| 0.948216 | 0.1952 R.AEGSDVANAVLDGADC[160.03]IMLSGETAK[325.13]GD'   |
| 0.948199 | 0.972 K.LLAHEIFEK[325.13]SNAAGVPC[160.03]DLVTGEER.V     |
| 0.948185 | 0.4774 R.GC[160.03]GPEK[325.13]DHVYLQLHHLPEQLATR.L      |
| 0.948183 | 0.9385 K.IIDINYYPVPEAC[160.03]LSNK[325.13]R.H           |
| 0.948173 | 0.5475 R.LQLETEIEALK[325.13]EELLFMK.K                   |
| 0.948143 | 0.9354 K.FPVKPGDLK[325.13]K.R                           |
| 0.948138 | 0.9932 R.ALLSHQFK[325.13]R.R                            |
| 0.948118 | 0.9904 K.LYQHEINLFK[325.13]SK.T                         |
| 0.948103 | 0.2544 R.HNGTGGK[325.13]SIYGEK.F                        |
| 0.948082 | 0.7328 K.NQQFHK[325.13]ER.E                             |
| 0.948069 | 0.8482 R.YYK[325.13]NIGLGFK.T                           |
| 0.948046 | 0.7692 K.AENGK[325.13]LVINGNPITIFQER.D                  |
| 0.948031 | 0.7321 K.AIADTGANVVVTGGK[325.13]VADMALHYANK.Y           |

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| 0.948028 | 0.9145 R.AFREEAIK[325.13]FSEEQR.F                        |
| 0.948025 | 0.8466 R.NYYEQWGK[325.13]LTDC[160.03]VVMR.D              |
| 0.947998 | 0.6346 K.K[325.13]C[160.03]GHTNNLRPK.K                   |
| 0.947908 | 0.6471 K.LDK[325.13]AQIHDLVLVGGSTR.I                     |
| 0.947851 | 0.5501 K.TVDGPSGK[325.13]LWR.D                           |
| 0.947847 | 0.9296 R.NGNPAPK[325.13]ITWYR.N                          |
| 0.947823 | 0.9909 K.DIHDDQDYLHSLGK[325.13]AR.T                      |
| 0.947806 | 0.9791 R.IEK[325.13]VEHSDLSFSK.D                         |
| 0.947767 | 0.7394 R.K[325.13]SQVLFSVTR.G                            |
| 0.947713 | 0.9274 K.K[325.13]KVLDPNETNEIANANSR.Q                    |
| 0.947623 | 0.6788 K.NK[325.13]GLWVPEGQR.A                           |
| 0.947612 | 0.859 R.LSFFGLEK[325.13]LLTNLGLGER.K                     |
| 0.947536 | 0.7526 R.FQLQATTK[325.13]EGPGEAIVR.E                     |
| 0.947508 | 0.9921 R.LLGEK[325.13]TTTAAGSSHSRPGVPVEGSPGR.N           |
| 0.947487 | 0.7285 R.RGEEGHDPK[325.13]EPEQLR.K                       |
| 0.947447 | 0.8088 K.AQK[325.13]LLVGVDEK.L                           |
| 0.947419 | 0.9911 R.IVGWYHTGPK[325.13]LHK.N                         |
| 0.94741  | 0.9931 R.GNEFFC[160.03]EVEDEDIQDK[325.13]FNLTGLNEQVPH    |
| 0.947317 | 0.1856 K.SVHELEKSK[325.13]R.A                            |
| 0.947266 | 0.9926 R.NGVSEENLAK[325.13]LIQHANVQAHSSLIR.N             |
| 0.947257 | 0.8965 R.FNIKLWK[325.13]TFTDC[160.03]FNC[160.03]LPIAAIVD |
| 0.947213 | 0.9076 R.VYK[325.13]APEEPNIQVNPLGIPVNSK.E                |
| 0.94719  | 0.9583 R.GYVK[325.13]EQFAWR.H                            |
| 0.947179 | 0.7259 K.VAVATPAK[325.13]KAAVTPGK.K                      |
| 0.947178 | 0.7538 K.GETK[325.13]SFYPEEVSSM[147.04]VLTK.M            |
| 0.947175 | 0.9908 K.IHQETFGK[325.13]SGC[160.03]R.R                  |
| 0.947114 | 0.8989 R.LAVYIDK[325.13]VR.S                             |
| 0.947056 | 0.8744 K.LHGK[325.13]PIR.I                               |
| 0.947028 | 0.0751 R.K[325.13]DLYANTVLSGGTTM[147.04]YPGIADR.M        |
| 0.947019 | 0.8738 K.YGK[325.13]AGEVFIHK.D                           |
| 0.947018 | 0.6957 R.WVESLK[325.13]GILADEDSSRPVWLK.A                 |
| 0.946986 | 0.0508 R.AAAEVAGQFVIK[325.13]LTHDVELNLDYER.Y             |
| 0.946892 | 0.5483 R.SGK[325.13]YDLDFK.S                             |
| 0.946886 | 0.9484 K.NADPILISLK[325.13]HGYPGK.N                      |
| 0.946784 | 0.841 K.AK[325.13]ISKPAPYWEGTAVIDGEFK.E                  |
| 0.94675  | 0.8733 K.HK[325.13]FM[147.04]VQTIFAPPNTSDMEAVWK.E        |
| 0.946724 | 0.9145 R.IYPTFLHLHGK[325.13]TFDYK.I                      |
| 0.946698 | 0.6507 R.VTQKSYK[325.13]VSTSGPR.A                        |
| 0.946665 | 0.7474 R.HPDSHQLFIGNLPHEVDK[325.13]SELK.D                |
| 0.946627 | 0.9314 K.APRPPK[325.13]QPNVQDFQFFPR.L                    |
| 0.946607 | 0.9871 R.TAVFGFETSEAK[325.13]GPDGMALPRPR.D               |
| 0.94658  | 0.8542 K.TESHHK[325.13]AK.G                              |
| 0.946562 | 0.7844 K.QFAEMYVAK[325.13]FAAK.G                         |
| 0.94652  | 0.9276 K.LHPESK[325.13]DDKHGSYEDAVHSGALND.-              |
| 0.946499 | 0.9916 R.IAAHPNVQK[325.13]VVLVSSASDIPVQSHR.T             |
| 0.946475 | 0.9659 R.VLHK[325.13]LTTLHVYEEDPR.E                      |
| 0.946458 | 0.8215 R.KQLLEK[325.13]WLK.E                             |

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| 0.946445 | 0.8049 K.GATPGK[325.13]ALVATPGKK.G                      |
| 0.946398 | 0.9902 R.TLFGFLGK[325.13]IDELR.L                        |
| 0.946384 | 0.6811 R.HAK[325.13]WFQAR.A                             |
| 0.946203 | 0.2294 R.LIPDGC[160.03]GVK[325.13]YIPNR.G               |
| 0.9462   | 0.7346 R.LPSGNHM[147.04]K[325.13]ESR.E                  |
| 0.94616  | 0.6273 K.VNQIGSVTESLQAC[160.03]K[325.13]LAQANGWGMV      |
| 0.946136 | 0.9919 K.DGLALGMGQGLK[325.13]AWPR.Y                     |
| 0.946092 | 0.7636 K.AGGFLM[147.04]K[325.13]K.E                     |
| 0.946067 | 0.9844 K.AHTLILQPPSEK[325.13]GR.Q                       |
| 0.946025 | 0.9024 K.AGEVFIHK[325.13]DK.G                           |
| 0.946009 | 0.9157 R.YVASYLALGNGSSPSAK[325.13]DIK.K                 |
| 0.945992 | 0.8035 K.K[325.13]SFYGSTLFLC[160.03]R.R                 |
| 0.945972 | 0.9873 K.ILSVNGQDLK[325.13]NLLHQDAVDLFR.N               |
| 0.945913 | 0.4573 R.AEAESMYQIK[325.13]YEELQSLAGK.H                 |
| 0.945905 | 0.8933 K.K[325.13]LISPESTVMLLEAQAATGGIIDPHRNEK.L        |
| 0.945838 | 0.9169 R.DHWK[325.13]ESDRK.D                            |
| 0.945823 | 0.6786 R.HAK[325.13]WFQAR.A                             |
| 0.945819 | 0.7083 K.EGKPLLK[325.13]AVM[147.04]R.R                  |
| 0.945795 | 0.9676 R.K[325.13]HFALER.G                              |
| 0.94579  | 0.1322 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K         |
| 0.945744 | 0.9816 K.EITIHTK[325.13]LPAK.D                          |
| 0.945722 | 0.8076 K.LKGPK[325.13]FK.M                              |
| 0.945713 | 0.8775 K.SGYLAGDK[325.13]LLPQR.V                        |
| 0.945696 | 0.4636 R.AWTSK[325.13]GSGPLSPSIQSR.T                    |
| 0.945684 | 0.795 R.K[325.13]LLEGEER.L                              |
| 0.945639 | 0.5994 R.VNFAMNVGK[325.13]AR.G                          |
| 0.945613 | 0.9636 K.LSK[325.13]HC[160.03]SQVDSVR.G                 |
| 0.945604 | 0.8023 K.AALSALESFLK[325.13]QVSNMVAK.N                  |
| 0.945604 | 0.8023 K.GLAGHLK[325.13]SNSPR.L                         |
| 0.945603 | 0.8418 K.KITAASK[325.13]K.A                             |
| 0.945588 | 0.5594 K.FSK[325.13]SATSPEGK.K                          |
| 0.945578 | 0.4947 R.GILTLK[325.13]YPIEHGIITNWDDM[147.04]EK.I       |
| 0.945567 | 0.9911 R.INLNLIYDHNPK[325.13]VFLGNVETFIK.Q              |
| 0.945525 | 0.9524 K.NVPNLHVMK[325.13]AMQSLK.S                      |
| 0.945502 | 0.9699 R.IIK[325.13]PC[160.03]NHVLSLSFPIR.R             |
| 0.945479 | 0.7599 R.YISPDQLADLYKSEK[325.13]DYPVVSIEDPFDQDDWGAM     |
| 0.945439 | 0.6483 R.DAVTYTEHAK[325.13]R.K                          |
| 0.945385 | 0.39 K.FSGK[325.13]HVVFIAQR.R                           |
| 0.945356 | 0.9882 R.IQDALSTVLQYAEDVLSGK[325.13]VSADNTVGR.F         |
| 0.945334 | 0.8953 K.DSYLK[325.13]QLPHFTSEHIK.R                     |
| 0.945315 | 0.9917 K.AYSELIVHPVLDSPNAVHEVEK[325.13]WLPR.L           |
| 0.945242 | 0.9538 R.NPGGQMEGPWC[160.03]FTQNK[325.13]NVR.M          |
| 0.945233 | 0.9928 K.ILPFQYVLC[160.03]AATSPAVK[325.13]LHDETLTYLNQGI |
| 0.945223 | 0.9475 R.ILK[325.13]LPSFELLHK.E                         |
| 0.945191 | 0.9597 K.LK[325.13]VPEWVDTVK.L                          |
| 0.945127 | 0.8456 R.GLFIDGK[325.13]GVLR.Q                          |
| 0.945117 | 0.9904 K.KLLVPGK[325.13]IQHILC[160.03]TGNLC[160.03]TK.E |

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| 0.945037 | 0.8454 R.SVPTWLK[325.13]LTSDDVK.E                           |
| 0.945018 | 0.7959 K.QAADAEMEK[325.13]HKK.F                             |
| 0.944953 | 0.7007 K.EK[325.13]LLLWSQR.M                                |
| 0.944944 | 0.6982 R.KFLDGNELTLADC[160.03]NLLPK[325.13]LHIVQVVC[160.03] |
| 0.944923 | 0.6834 R.KQLATK[325.13]AAR.K                                |
| 0.944917 | 0.9467 R.AK[325.13]DINQEVYNFLATAGAK.Y                       |
| 0.944832 | 0.992 R.HVLDNSGEWSVTK[325.13]R.Q                            |
| 0.944817 | 0.7916 K.VYIYHSSSK[325.13]GLLR.Q                            |
| 0.944799 | 0.9592 K.GFGGK[325.13]FGVQTDR.Q                             |
| 0.944794 | 0.9729 K.K[325.13]LSELSNSQQSVQTLWLIIHR.K                    |
| 0.944794 | 0.9517 R.VTIK[325.13]AGIHAR.L                               |
| 0.944751 | 0.7757 K.LTFDSSFSPNTGK[325.13]K.N                           |
| 0.944731 | 0.8076 R.SVETLK[325.13]EMIK.S                               |
| 0.944659 | 0.5405 K.IK[325.13]IIAPPER.K                                |
| 0.944598 | 0.533 K.MPK[325.13]FSMPGFK.A                                |
| 0.944559 | 0.9278 K.AVLK[325.13]GVHSHK.K                               |
| 0.944535 | 0.8315 R.YIEVFK[325.13]SHR.T                                |
| 0.944507 | 0.5064 K.TVDGPSGK[325.13]LWR.D                              |
| 0.944404 | 0.9863 K.M[147.04]HLAGK[325.13]TEQAK.A                      |
| 0.944398 | 0.8978 K.KPK[325.13]FELGK.L                                 |
| 0.944393 | 0.7427 R.VYKAPEEPNIQVNPLGIPVNSK[325.13]EPEEVATC[160.03]     |
| 0.944383 | 0.8215 R.M[147.04]FAPTK[325.13]TWR.R                        |
| 0.944379 | 0.8859 R.KSTGGK[325.13]APR.K                                |
| 0.944373 | 0.9891 R.K[325.13]LVEALC[160.03]AAGHR.A                     |
| 0.944272 | 0.9888 R.LGPLK[325.13]LTLEQGQQLVAEGHPGASQASAR.A             |
| 0.944243 | 0.9667 K.SAHLTNPWNEHKPVK[325.13]IGR.D                       |
| 0.944223 | 0.7071 K.GATLK[325.13]ITLDNAYM[147.04]EK.C                  |
| 0.944207 | 0.955 K.DKTTGQSK[325.13]GFAFISFHR.R                         |
| 0.944189 | 0.956 K.NRPGSALEK[325.13]EVESMGAHLNAYSTR.E                  |
| 0.944184 | 0.8924 K.GIIWGEDTLMEYLENPK[325.13]K.Y                       |
| 0.944175 | 0.9623 K.IVHAFDM[147.04]EDLGDK[325.13]AVYC[160.03]R.C       |
| 0.944091 | 0.1144 K.TVTAMDVVYALK[325.13]R.Q                            |
| 0.944088 | 0.8996 K.GK[325.13]HYEYVSC[160.03]HDQGLC[160.03]R.V         |
| 0.944087 | 0.9078 K.HK[325.13]SETDTSILR.G                              |
| 0.944056 | 0.992 R.K[325.13]IGDLAC[160.03]ANIQHLSSR.S                  |
| 0.944005 | 0.8941 R.FYGK[325.13]NSSYVHGGLDSNGKPADAVYGQK.E              |
| 0.944001 | 0.9622 K.EFSGNPIK[325.13]VSFATR.R                           |
| 0.943956 | 0.7487 K.SKEYFSK[325.13]QK.-                                |
| 0.943928 | 0.9687 K.NHAAPFSK[325.13]VLTIFYR.K                          |
| 0.943872 | 0.9145 K.AGLQVYNKC[160.03]WK[325.13]FEHC[160.03]NFNDVT      |
| 0.94379  | 0.9823 R.K[325.13]GC[160.03]VITISGR.M                       |
| 0.943785 | 0.5753 K.SYK[325.13]VSTSGPR.A                               |
| 0.943774 | 0.8543 R.KAASLK[325.13]SNYNLPMHK.M                          |
| 0.943697 | 0.9918 K.IADLGAC[160.03]WVHK[325.13]HFTEDIQTR.Q             |
| 0.943642 | 0.9316 R.DDGYSTK[325.13]DSYSSR.D                            |
| 0.943622 | 0.9349 K.VDDKWEK[325.13]K.C                                 |
| 0.943606 | 0.9059 R.DFRPLK[325.13]DSR.F                                |

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| 0.943602 | 0.8354 R.EM[147.04]AGDNK[325.13]LLGQFTLIGIPPAPR.G      |
| 0.943567 | 0.9019 R.K[325.13]MDADGFLPITLIASFHR.V                  |
| 0.943549 | 0.9409 R.ELPSFLGK[325.13]R.T                           |
| 0.94349  | 0.9187 R.SRLPK[325.13]SPPYTAFLGNLPYDVTEESIK.E          |
| 0.943454 | 0.52 K.IPQK[325.13]GILIGIQSFRPR.F                      |
| 0.943454 | 0.7946 R.RQVDQLTNDK[325.13]AR.V                        |
| 0.943403 | 0.9745 R.LIAGC[160.03]IGK[325.13]PLGEQFR.K             |
| 0.943337 | 0.6352 R.VTQKSYK[325.13]VSTSGPR.A                      |
| 0.943308 | 0.9531 K.GKTPALK[325.13]YQQLFEDIR.G                    |
| 0.943305 | 0.8811 R.SK[325.13]LILFPR.K                            |
| 0.943249 | 0.195 R.EIVHIQAGQC[160.03]GNQIGAK[325.13]FWEVISDEHGII  |
| 0.943209 | 0.7465 R.TLK[325.13]LTTPTYGDLNHLVSATM[147.04]SGVTTC[16 |
| 0.943203 | 0.8677 R.ETAQAIK[325.13]GM[147.04]HIR.K                |
| 0.9432   | 0.9464 R.DMLLANK[325.13]VPAAAR.A                       |
| 0.943109 | 0.9844 R.TTHYTPLAC[160.03]GSNPLK[325.13]R.E            |
| 0.943101 | 0.9526 R.LASQANIAQVLAELK[325.13]EYATEVDVDFVR.K         |
| 0.943006 | 0.9579 R.QIHK[325.13]FEELNR.T                          |
| 0.94296  | 0.8988 K.LIQYC[160.03]QSK[325.13]GIVVTAYSPLGSPDRPWAKPE |
| 0.942929 | 0.992 K.TTLHK[325.13]TGIASSILDAISQGSSEQHALEK.C         |
| 0.942922 | 0.7273 R.K[325.13]GNLQLQGTR.L                          |
| 0.94285  | 0.9736 R.FYQHK[325.13]FPEVEDVVMVNV.R.S                 |
| 0.942744 | 0.9895 R.LHLPIGDSASNLLFK[325.13]WR.N                   |
| 0.942725 | 0.8738 -.M[147.04]QIFVK[325.13]TLTGK.T                 |
| 0.942723 | 0.9851 R.KVPELMEMFLPATK[325.13]NLLNEK.N                |
| 0.942698 | 0.8666 R.ETAQAIK[325.13]GM[147.04]HIR.K                |
| 0.942683 | 0.8981 R.GRDPVNPEK[325.13]LLVITVATAETEGYLR.F           |
| 0.942658 | 0.853 K.FSDSYASVIK[325.13]ALEHSALAINHK.L               |
| 0.942557 | 0.1252 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K        |
| 0.942484 | 0.974 K.AK[325.13]LTHPGK.A                             |
| 0.942474 | 0.5711 K.AVTK[325.13]YTSSK.-                           |
| 0.942359 | 0.9928 R.AK[325.13]IDNYIPIF.-                          |
| 0.942323 | 0.988 K.FQDTDGK[325.13]HLLPK.I                         |
| 0.942307 | 0.9898 K.AALSAGK[325.13]VSPETVDSVIMGNVLQSSSDAIYLAR.H   |
| 0.942295 | 0.6273 K.VYGK[325.13]GNPTK.V                           |
| 0.942215 | 0.9776 K.K[325.13]PIPDEHLILK.T                         |
| 0.942194 | 0.9187 R.LNYGIPAIVK[325.13]LLNQPNQWPLVK.A              |
| 0.942131 | 0.7083 R.VAPEEHPVLLTEAPLNPK[325.13]ANREK.M             |
| 0.942052 | 0.857 R.K[325.13]ASVHSSGR.G                            |
| 0.941987 | 0.988 R.IYHEQQVK[325.13]TR.G                           |
| 0.941889 | 0.238 R.AEAEAWYQTK[325.13]FETLQAQAGK.H                 |
| 0.941844 | 0.9851 K.FGQK[325.13]SHVEC[160.03]AR.F                 |
| 0.941843 | 0.9453 K.TLTSGGHAHEGK[325.13]PYC[160.03]NHPC[160.03]YA |
| 0.941669 | 0.7007 R.LREK[325.13]LQEEM[147.04]LQR.E                |
| 0.941494 | 0.8835 R.TEK[325.13]LLETIDQLYLEYAK.R                   |
| 0.941471 | 0.7897 K.ITLPVDFVTADK[325.13]FDENAK.T                  |
| 0.941437 | 0.932 K.GVTIPYRPK[325.13]PSSSPVIFAGGQDR.Y              |
| 0.941421 | 0.7013 R.FLQDYFDGNLK[325.13]R.Y                        |



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| 0.941314 | 0.9602 R.SNLPAK[325.13]AIGHR.I                           |
| 0.94126  | 0.7665 K.QFAEMYVAK[325.13]FAAK.G                         |
| 0.941239 | 0.6311 R.K[325.13]SNFAEALAAHK.Y                          |
| 0.941231 | 0.7805 R.KVEDLFLTFAK[325.13]K.A                          |
| 0.941228 | 0.5382 K.K[325.13]KAEGGGGGGRPGAPAAGDGK.T                 |
| 0.941213 | 0.0623 K.LDSTDFTGTIK[325.13]LLNENSYVPR.E                 |
| 0.941188 | 0.5963 K.DFLAGGIAAAISK[325.13]TAVAPIER.V                 |
| 0.941184 | 0.7844 K.LMSAISK[325.13]TFC[160.03]PAHK.S                |
| 0.94116  | 0.9231 K.VPAQK[325.13]ATGQK.A                            |
| 0.94113  | 0.517 K.TVDGPSGK[325.13]LWR.D                            |
| 0.941128 | 0.1645 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K          |
| 0.94108  | 0.7718 R.AFLGELK[325.13]TQMTSAVR.E                       |
| 0.941049 | 0.7144 R.LPSGNHM[147.04]K[325.13]ESR.E                   |
| 0.941042 | 0.626 K.IGHPAPNFK[325.13]ATAVM[147.04]PDGQFK.D           |
| 0.940959 | 0.9654 R.IEINFPAEYPFKPPK[325.13]ITFK.T                   |
| 0.940954 | 0.8229 K.K[325.13]SNAHYNLQNAFNLAEQHLGLTK.L               |
| 0.940949 | 0.7448 R.LIFAGK[325.13]QLEDGR.T                          |
| 0.940904 | 0.7148 R.VTYTPM[147.04]APGSYLISIK[325.13]YGGPYHIGGSPFK.. |
| 0.940869 | 0.8872 K.LLGK[325.13]GNIIISTPEK.W                        |
| 0.940858 | 0.8823 R.AHWK[325.13]FLK.T                               |
| 0.940822 | 0.8481 R.YTASGVHK[325.13]GATYVFR.L                       |
| 0.940791 | 0.4744 K.VSASPLLYTLIEK[325.13]TMQNVK.H                   |
| 0.940706 | 0.9866 R.IC[160.03]LDILK[325.13]DKWSPALQIR.T             |
| 0.940634 | 0.9809 R.K[325.13]QM[147.04]VIDVLHPGK.A                  |
| 0.940615 | 0.4136 R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTTEVK.S     |
| 0.9406   | 0.9117 R.DHWK[325.13]ESDR.K                              |
| 0.940591 | 0.8764 R.SLGNIK[325.13]FIGELFK.L                         |
| 0.940563 | 0.9514 R.NK[325.13]LLQC[160.03]LHAK.R                    |
| 0.940539 | 0.9853 K.M[147.04]HLAGK[325.13]TEQAK.A                   |
| 0.940516 | 0.9447 K.SITHDIEEK[325.13]GVR.M                          |
| 0.940426 | 0.9556 R.GISTKPVYIPEVELNHK[325.13]LIK.G                  |
| 0.940366 | 0.3927 R.K[325.13]MC[160.03]LFAGFQR.K                    |
| 0.940359 | 0.987 R.ISVYYNEASSHK[325.13]YVPR.A                       |
| 0.940259 | 0.8315 K.SVSDYDGK[325.13]LSNFK.T                         |
| 0.940228 | 0.8869 K.GEHSIVYLK[325.13]PSYAFGSVGK.E                   |
| 0.940211 | 0.9594 K.WHYK[325.13]LTK.A                               |
| 0.940138 | 0.9442 R.YAK[325.13]LGDTGR.Y                             |
| 0.940133 | 0.9752 K.TAHETDK[325.13]SEGGKR.K                         |
| 0.940047 | 0.4825 R.FANYIDK[325.13]VR.F                             |
| 0.940037 | 0.7456 R.GLVMVKPGSIK[325.13]PHQK.V                       |
| 0.940017 | 0.9854 K.TLVPHYC[160.03]ELVGANPK[325.13]VRPNPAR.F        |
| 0.939982 | 0.838 K.M[147.04]K[325.13]GYPHWPAR.V                     |
| 0.939835 | 0.7879 K.K[325.13]TESHHK.A                               |
| 0.939754 | 0.1611 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K          |
| 0.939694 | 0.9728 R.EELEALFLPYDLK[325.13]R.L                        |
| 0.939667 | 0.8542 R.LSM[147.04]QK[325.13]SMQNHA AVFR.V              |
| 0.939631 | 0.815 R.GGK[325.13]LMITYTR.K                             |

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| 0.939584 | 0.7824 K.KVEELEGEITTLNHK[325.13]LQDASAEVER.L          |
| 0.939524 | 0.8795 R.WLK[325.13]GGVVLK.E                          |
| 0.939505 | 0.1605 K.EITALAPSTM[147.04]KIK[325.13]HAPPER.K        |
| 0.93949  | 0.5538 R.K[325.13]LLEGEESR.I                          |
| 0.93949  | 0.7322 R.TIPWLEDVPPQK[325.13]TIQEMQQK.L               |
| 0.939383 | 0.981 R.IWTK[325.13]DGNLASTLGQHK.G                    |
| 0.939258 | 0.9867 K.HAQTFGAK[325.13]QPTHQGGPAQDR.G               |
| 0.939247 | 0.9914 R.GSTK[325.13]WVHQAC[160.03]LQR.W              |
| 0.939238 | 0.6166 R.K[325.13]LMVALAK.G                           |
| 0.93917  | 0.5331 R.FLEQQNK[325.13]ILLAELEQLKGQK.S               |
| 0.939158 | 0.9093 K.EQWWLK[325.13]LRPLMK.I                       |
| 0.939155 | 0.5847 R.VLGEAQTK[325.13]AQHQQALSSLELLNVLF.R.T        |
| 0.939045 | 0.8547 R.RPIK[325.13]GAAGRPLELSDFR.M                  |
| 0.939026 | 0.9015 R.K[325.13]HGVVPLATYMR.I                       |
| 0.939008 | 0.9789 R.HGNQYIQVNEPWK[325.13]R.I                     |
| 0.939002 | 0.7658 K.MK[325.13]IMVIK.D                            |
| 0.938982 | 0.6224 K.KPAEK[325.13]KPTTEEK.K                       |
| 0.938895 | 0.8764 K.IQASTMAFK[325.13]QMEQISQFLQAAER.Y            |
| 0.938784 | 0.1252 K.AVELAANTK[325.13]GIC[160.03]FIR.T            |
| 0.938782 | 0.9722 K.GVTFNVTTVDTK[325.13]R.R                      |
| 0.938766 | 0.8881 R.VYYTM[147.04]EPEHPVGNWQK[325.13]HNVDDSLLTTV  |
| 0.938754 | 0.9919 K.QALGK[325.13]SSVNSAVLKDR.V                   |
| 0.938685 | 0.8893 K.FVIK[325.13]RPELLTHSTTEVTQPR.T               |
| 0.938668 | 0.8835 K.TVPK[325.13]TVDNFVALATGEK.G                  |
| 0.938647 | 0.9776 K.SFSEDVISHK[325.13]GDLR.Y                     |
| 0.938646 | 0.9807 R.SPLTQK[325.13]HGLGYSLLER.L                   |
| 0.938628 | 0.778 K.VIPELNGK[325.13]LTGMAFR.V                     |
| 0.938613 | 0.4483 R.NDNDTFTVK[325.13]YTPR.G                      |
| 0.938604 | 0.9365 R.RTEITIVK[325.13]PQESAHR.R                    |
| 0.938576 | 0.9422 R.KAGNFYVPAEPK[325.13]LAFVIR.I                 |
| 0.93849  | 0.819 K.FEDENFILK[325.13]HTGPGILSM[147.04]ANAGPNTNGSI |
| 0.938467 | 0.9322 K.ANGTTVHVGIHPSK[325.13]VVITR.L                |
| 0.938442 | 0.9896 K.GLMLVHNK[325.13]LVDPLYSIK.E                  |
| 0.938416 | 0.9813 R.QQFLSLEQANK[325.13]GAPHSSPAR.G               |
| 0.938397 | 0.9334 R.YHPDK[325.13]NKEPGAEEK.F                     |
| 0.938341 | 0.9681 K.ALTGGIAHLFK[325.13]QNK.V                     |
| 0.938327 | 0.9238 K.K[325.13]TDKQPLQKPSHC[160.03]TIYVAK.N        |
| 0.938315 | 0.9725 K.RKPK[325.13]SQETPATK.K                       |
| 0.938158 | 0.6434 R.WVESLK[325.13]GILADESSRPVWLK.A               |
| 0.93813  | 0.9521 R.DTAYPETNDAIPMISK[325.13]LR.Y                 |
| 0.938119 | 0.9804 R.ANSLK[325.13]NSGVPDDIFKLDDLSVLDLSHNQLTEC[160 |
| 0.938088 | 0.9859 R.SYDSLHRPK[325.13]STPLSQPSANGVQTEGLDYDR.L     |
| 0.938077 | 0.6746 K.K[325.13]SAEFLHMLK.N                         |
| 0.938052 | 0.9891 K.YPHYFPLLK[325.13]K.C                         |
| 0.938042 | 0.9321 R.IK[325.13]LQLWDTAGQER.F                      |
| 0.938037 | 0.3482 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S      |
| 0.938031 | 0.6606 K.HKLDELYPQGYPESVIQHLGYLFLK[325.13]MSPEDIR.K   |

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| 0.93799  | 0.4774 R.LDYLSSLKVK[325.13]GLVLGPIHK.N                   |
| 0.93797  | 0.8614 R.EESGK[325.13]PGAHVTVK.K                         |
| 0.937922 | 0.6956 K.LC[160.03]YVALDFENEM[147.04]ATAASSSSLEK[325.13] |
| 0.937901 | 0.8978 R.LK[325.13]YALTGDEVKK.I                          |
| 0.937857 | 0.6811 R.MPK[325.13]VQQTVQDLFGR.A                        |
| 0.937819 | 0.9887 R.VGTHGGTLSSYIVK[325.13]NIALDK.T                  |
| 0.937787 | 0.7132 R.WK[325.13]AGLYGLPR.R                            |
| 0.937778 | 0.9821 R.K[325.13]WRPIASDEIVPGDIVSIGR.S                  |
| 0.937755 | 0.8289 K.K[325.13]GLTPSQIGVILR.D                         |
| 0.937754 | 0.8565 R.SSSGLLEWESK[325.13]SDALETGLFLNHYQM[147.04]K.N   |
| 0.937751 | 0.6698 R.K[325.13]IPNPDDFFEDLEPFR.M                      |
| 0.937713 | 0.1201 R.GENSWFSTQVDTVATK[325.13]VK.D                    |
| 0.9377   | 0.9778 R.EYTINIHK[325.13]R.I                             |
| 0.937643 | 0.5258 K.AAK[325.13]PKAAKPK.A                            |
| 0.937604 | 0.9471 R.YVASYLLAALGGNSSPSAK[325.13]DIKK.I               |
| 0.93758  | 0.2553 R.LK[325.13]VPPAINQFTQALDR.Q                      |
| 0.937538 | 0.8823 K.GC[160.03]EVVVSGK[325.13]LR.G                   |
| 0.937529 | 0.9798 R.K[325.13]SSTVATLQGTPDHGDPR.T                    |
| 0.937497 | 0.9611 R.VTDPVGDIVSFMHSFEK[325.13]YGR.A                  |
| 0.937485 | 0.9644 K.EAK[325.13]HIAEEADRK.Y                          |
| 0.937433 | 0.9563 K.VK[325.13]FTQQNYHDR.L                           |
| 0.937431 | 0.7156 R.TPK[325.13]LSSIIDC[160.03]TGTASYHGFLPVLVR.N     |
| 0.937417 | 0.2639 R.AVVEK[325.13]GQGTVLLHNSVPVADGQPHEVSVHINAHF      |
| 0.937368 | 0.962 K.K[325.13]DILLPFQQLDSIPVSNPSC[160.03]PMIPLYR.N    |
| 0.937343 | 0.9552 R.SLNYK[325.13]STSSGHR.E                          |
| 0.937298 | 0.934 R.DLLVQQASQC[160.03]LSK[325.13]LVQIASR.T           |
| 0.937224 | 0.7059 R.INLAQK[325.13]AFC[160.03]GFEDPR.T               |
| 0.937221 | 0.9721 R.ISQHEAK[325.13]IK.S                             |
| 0.937151 | 0.8835 R.NAK[325.13]LVGQSIAYLQK.K                        |
| 0.937142 | 0.9528 R.RVLQALEGLK[325.13]MVEK.D                        |
| 0.937111 | 0.9516 K.GQYISPFHDIPIYADK[325.13]DVFHMOVVEVPR.W          |
| 0.937077 | 0.9896 R.YLDLHDC[160.03]YLK[325.13]YINLK.A               |
| 0.937048 | 0.972 K.TTWAIK[325.13]HAASNPSKK.Y                        |
| 0.937014 | 0.8738 R.LKDLEFGK[325.13]FGPALSVK.V                      |
| 0.936992 | 0.7071 R.IM[147.04]K[325.13]AQALR.D                      |
| 0.936915 | 0.9564 K.K[325.13]YKPLDLRPK.K                            |
| 0.936787 | 0.9829 R.AVAHC[160.03]PK[325.13]AEVLWLMGAK.S             |
| 0.936754 | 0.6296 R.IPK[325.13]EQGVLSFWR.G                          |
| 0.936728 | 0.8958 K.K[325.13]DNDFIYHDR.V                            |
| 0.936726 | 0.9148 R.GK[325.13]LHIFNAK.K                             |
| 0.936711 | 0.6591 R.VLEQHK[325.13]LNK.D                             |
| 0.936699 | 0.9045 K.LK[325.13]PEDITQIQPQLVLR.L                      |
| 0.93669  | 0.7303 K.SYENQKPPFDAK[325.13]NPFLAAVTTNR.K               |
| 0.936641 | 0.5183 R.TSFPEDTVITYK[325.13]C[160.03]EESFVK.I           |
| 0.936636 | 0.9802 R.MNYFQVAK[325.13]TVAQR.L                         |
| 0.936567 | 0.9883 R.TLFGFLGK[325.13]IDELR.L                         |
| 0.936554 | 0.8944 R.FQSSAVM[147.04]ALQEASEAYLVGLFEDTNLC[160.03]A    |

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| 0.936536 | 0.778 R.GVLK[325.13]EYGVK.V                           |
| 0.936514 | 0.3421 R.SLDM[147.04]DSIIAEVK[325.13]AQYEDIANR.S      |
| 0.936514 | 0.0614 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I |
| 0.936471 | 0.0532 R.HQGVMMVGM[147.04]GQK[325.13]DSYVGDEAQSKR.G   |
| 0.936424 | 0.7747 K.VDINTPDVDVHGPDWHLK[325.13]MPK.V              |
| 0.936419 | 0.7137 K.DLAGSIIGK[325.13]GGQR.I                      |
| 0.936377 | 0.8496 R.LFK[325.13]QLHPQLLLPDDYLDC[160.03]LGK.Q      |
| 0.936374 | 0.9 R.NMLK[325.13]GQHEK.E                             |
| 0.936341 | 0.988 K.KIK[325.13]LQIWDTAGQER.F                      |
| 0.936328 | 0.9514 R.NELHNLLDK[325.13]PQLQGIPVLVLGNK.R            |
| 0.9363   | 0.854 K.SFPKDDPSKPVHLTAFLGYK[325.13]AGMTHIVR.E        |
| 0.936265 | 0.8823 K.HALK[325.13]GAGTNEK.V                        |
| 0.936208 | 0.7678 R.AVVVK[325.13]KIETR.D                         |
| 0.93608  | 0.9526 K.GFGGK[325.13]FGVQTDR.Q                       |
| 0.935932 | 0.3743 R.QLFHPEQLITGK[325.13]EDAANNYAR.G              |
| 0.935922 | 0.9635 K.K[325.13]GTPWEGGLFK.L                        |
| 0.935921 | 0.7985 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTSGSFTS |
| 0.935915 | 0.9335 K.LC[160.03]FLDK[325.13]VEPHATIAEIK.N          |
| 0.935877 | 0.7718 R.LNHQEFK[325.13]SC[160.03]LR.S                |
| 0.935842 | 0.9903 R.K[325.13]HGGPKDEER.H                         |
| 0.935831 | 0.953 R.FPLEK[325.13]ALEAFETFKK.G                     |
| 0.935654 | 0.991 R.EVK[325.13]YFSFPGELLMR.M                      |
| 0.935631 | 0.8582 R.SK[325.13]LILFPR.K                           |
| 0.935616 | 0.7151 R.EDSVKPGAHLTVK[325.13]K.I                     |
| 0.935552 | 0.9567 K.YGLVK[325.13]SIEIPRPVDGVEVPGC[160.03]GK.I    |
| 0.935535 | 0.8202 K.AK[325.13]ISKPAPYWEGTAVIDGEFK.E              |
| 0.935535 | 0.7721 R.ALQAAIQLAEAQPEATAK[325.13]NLLHSLQSSGIGSK.A   |
| 0.935529 | 0.7718 K.VK[325.13]VGVNGFGR.I                         |
| 0.935506 | 0.8393 R.FNVLK[325.13]VTK.A                           |
| 0.935472 | 0.9902 K.DGLALGMGQGLK[325.13]AWPR.Y                   |
| 0.935416 | 0.8602 K.KYHNVGLSK[325.13]C[160.03]EIK.V              |
| 0.935356 | 0.7652 R.AVVVK[325.13]KIETR.D                         |
| 0.935242 | 0.9729 K.SDLFFHDYSIAPLFVQENYIHVK[325.13]PVAAGGDM[147. |
| 0.935231 | 0.7132 R.KSAPATGGVK[325.13]KPHR.Y                     |
| 0.935229 | 0.9757 R.GDPGYPK[325.13]PISVWQGIPASPK.G               |
| 0.935198 | 0.2067 R.HNGTGK[325.13]SIYGEK.F                       |
| 0.935191 | 0.9916 R.SEARAPPLDAQGNIQPPASF[325.13]K.Y              |
| 0.935185 | 0.7708 K.IKWGDAGAEYVVESTGVFTTMEK[325.13]AG AHLQGGAK   |
| 0.935179 | 0.8447 R.HK[325.13]NM[147.04]SVHLSPC[160.03]FR.D      |
| 0.935165 | 0.5785 K.VNQIGSVTESLQAC[160.03]K[325.13]LAQANGWGVMMV  |
| 0.935142 | 0.944 K.ELFSEK[325.13]HASLQNSQR.T                     |
| 0.935139 | 0.3184 R.VTYK[325.13]NVPNWHR.D                        |
| 0.935137 | 0.7334 R.GGEPNQRPELK[325.13]NHIDR.V                   |
| 0.935126 | 0.9899 R.YSLRDEFLLTTK[325.13]R.V                      |
| 0.935092 | 0.6773 R.YFPTQALNFAFK[325.13]DKYK.Q                   |
| 0.935089 | 0.39 R.VETGVLK[325.13]PGM[147.04]VVTFAPVNVTTTEVK.S    |
| 0.935088 | 0.939 R.SLGTK[325.13]LAEEMR.K                         |

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| 0.935037 | 0.521 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                    |
| 0.935036 | 0.9624 R.IQQESGC[160.03]K[325.13]IQIAPDSGGLPER.S            |
| 0.935025 | 0.9438 K.DK[325.13]MM[147.04]NGGHYTYSENVRVEK.D              |
| 0.935006 | 0.8664 K.K[325.13]YSQFINFPIYVWSSK.T                         |
| 0.93499  | 0.5229 R.TM[147.04]PVEQVFAK[325.13]NFR.V                    |
| 0.934931 | 0.973 R.TRPWLQELSMGSPGPVTNK[325.13]ATK.I                    |
| 0.934931 | 0.9511 R.RVLQALEGLK[325.13]MVEK.D                           |
| 0.934901 | 0.9099 R.K[325.13]VVVSHSTHR.T                               |
| 0.934857 | 0.9825 R.LSMSLMEQLLK[325.13]TLR.Y                           |
| 0.934826 | 0.9081 R.GQHTK[325.13]TTGR.R                                |
| 0.934754 | 0.7652 K.TDLLLEPYNK[325.13]YR.F                             |
| 0.93468  | 0.5145 K.AEISC[160.03]TDNQDGTG[160.03]SVSYLPVLPDYSILVK      |
| 0.934615 | 0.8872 R.FLVTVIK[325.13]DLLGLC[160.03]EQK.R                 |
| 0.934614 | 0.9849 R.HTPLSK[325.13]LMK.A                                |
| 0.934608 | 0.9765 K.K[325.13]LGEWVGLC[160.03]K.I                       |
| 0.934604 | 0.8654 R.GPLDK[325.13]WR.A                                  |
| 0.9346   | 0.9579 K.INFVIDNNK[325.13]HTGAVSAR.N                        |
| 0.934576 | 0.8978 R.YDGQVAVFGSDLQEK[325.13]LGK.Q                       |
| 0.934575 | 0.8935 K.EISLWFK[325.13]PEELVDYK.S                          |
| 0.934564 | 0.9567 R.DISILQC[160.03]HGDC[160.03]DPLVPLMFGSLTVEK[325.13] |
| 0.934561 | 0.5258 K.AVTK[325.13]YTSSK.-                                |
| 0.934561 | 0.5666 R.VSFELFADK[325.13]VPK.T                             |
| 0.934471 | 0.693 R.VEAVNMAEGIIHDTETK[325.13]MEEFKDQLPADEC[160.03]      |
| 0.934456 | 0.7843 R.LFC[160.03]VGFTK[325.13]K.R                        |
| 0.934453 | 0.8513 R.K[325.13]AHLTNQYMQR.V                              |
| 0.934401 | 0.9807 R.NYAQVFNK[325.13]LIR.R                              |
| 0.93439  | 0.9499 K.DLIGFGLQVAK[325.13]GMK.Y                           |
| 0.934384 | 0.2991 K.VELC[160.03]SFSGYK[325.13]IYPGHGR.R                |
| 0.934373 | 0.7897 K.C[160.03]SRAEAEAWYQTK[325.13]FETLQAQAGK.H          |
| 0.934363 | 0.9214 K.ATISNDGATILK[325.13]LLDVVHPAAK.T                   |
| 0.934357 | 0.5314 R.K[325.13]ISNQFDWALMR.L                             |
| 0.934348 | 0.7844 R.LAHEVGWK[325.13]YQAVTATLEEK.R                      |
| 0.934289 | 0.9668 R.DVPRPILLGASAPLK[325.13]IK.C                        |
| 0.934259 | 0.9884 R.IEGC[160.03]IIGFDEYMNVLDDAEIHSK[325.13]TK.S        |
| 0.934252 | 0.9735 K.YK[325.13]YGEIPVDM[147.04]LC[160.03]K.R            |
| 0.934178 | 0.979 K.ISELGAGNGGVVFK[325.13]VSHKPSGLVMAR.K                |
| 0.934145 | 0.2032 K.QVHPDTGISSK[325.13]AM[147.04]GIMNSFVNDIFER.I       |
| 0.934114 | 0.9898 K.FTNSK[325.13]LTSLNEEYTK.N                          |
| 0.9341   | 0.9553 K.IVHAFDM[147.04]EDLGDK[325.13]AVYC[160.03]R.C       |
| 0.934036 | 0.97 R.VWELGGC[160.03]ANK[325.13]EVLDYSTPTTNGTPEAAL         |
| 0.934022 | 0.9588 R.RTDIFGVEETAIGK[325.13]K.I                          |
| 0.933984 | 0.8607 R.DHC[160.03]VAHK[325.13]LFNNLK.-                    |
| 0.933981 | 0.831 R.IVTLFSDFK[325.13]PYK.T                              |
| 0.933955 | 0.9911 K.VVVPIYC[160.03]TSFLAVEEDK[325.13]QQKIAR.L          |
| 0.933946 | 0.8286 R.GLPFGC[160.03]SK[325.13]EEIVQFFSGLEIVPNGITLPVDI    |
| 0.933893 | 0.1208 R.VIISAPSADAPMFVMGVNHEK[325.13]YDNSLK.I              |
| 0.933878 | 0.9059 K.FSAYIK[325.13]NSNPALNDNLEK.G                       |

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| 0.933829 | 0.6376 K.HK[325.13]SDFGK.F                             |
| 0.933815 | 0.9266 K.VIASELGSMPELK[325.13]K.Y                      |
| 0.933774 | 0.7678 K.YLYVDK[325.13]NFINNPLAQADWAAK.K               |
| 0.933763 | 0.9862 R.IYHEQQVK[325.13]TR.G                          |
| 0.933757 | 0.7792 K.VVK[325.13]QASEGPLK.G                         |
| 0.933695 | 0.9891 K.LGVVFEK[325.13]EKDR.T                         |
| 0.933684 | 0.7194 R.LRENELTYYC[160.03]C[160.03]K[325.13]K.D       |
| 0.933673 | 0.9403 R.YVWLVEQDRPLK[325.13]C[160.03]DEPILSNR.S       |
| 0.933609 | 0.8895 K.LKK[325.13]DTYIENEK.L                         |
| 0.93354  | 0.9874 R.LTRPGSSYFNLNPFEVLQIDPEVTDEEIK[325.13]K.R      |
| 0.933517 | 0.8811 R.EFSFEAWNNAK[325.13]ITDLK.Q                    |
| 0.933493 | 0.9379 K.INALIK[325.13]AAGVNVEPFWPGLFAK.A              |
| 0.933423 | 0.9626 R.LHSVC[160.03]TLISK[325.13]MLEILEQQK.K         |
| 0.933418 | 0.9564 R.HIITVDGKPPTWSEFPK[325.13]GIIVHTMAAVEALGAK.A   |
| 0.933382 | 0.9194 R.GGENVK[325.13]AINQQTGAFVEISR.Q                |
| 0.933321 | 0.8429 R.QIEYEEK[325.13]LAQALHEMR.E                    |
| 0.933315 | 0.8738 R.TQNVLGEK[325.13]GR.R                          |
| 0.93324  | 0.9638 R.SQAASILTK[325.13]FQELK.D                      |
| 0.933151 | 0.9827 R.TLNHQDYTFDWTMLK[325.13]QK.A                   |
| 0.933071 | 0.9724 R.NAYVWTLK[325.13]GR.T                          |
| 0.933022 | 0.9549 R.AGGPLGLSIVGGS DHSSHPFGVQEPGVFISK[325.13]VLPR. |
| 0.932996 | 0.8796 K.K[325.13]SLEGDLEDLKDQIAQLEASLAAK.K            |
| 0.932895 | 0.8454 K.VFYLK[325.13]MK.G                             |
| 0.932878 | 0.4909 R.IAAYLFK[325.13]GNNR.W                         |
| 0.932855 | 0.7661 R.SLHDALC[160.03]VVK[325.13]R.V                 |
| 0.93283  | 0.9873 R.FHINQPALK[325.13]QR.E                         |
| 0.932816 | 0.1279 R.LEK[325.13]PAKYDDIKK.V                        |
| 0.932788 | 0.9887 R.DC[160.03]LFRPLNK[325.13]QVTNAVVK.L           |
| 0.93278  | 0.6411 R.VHK[325.13]ISNVNK.A                           |
| 0.932665 | 0.8935 R.AITGASLADIMAK[325.13]R.N                      |
| 0.932612 | 0.9504 R.SGYIAIDDIQVLSYPC[160.03]DK[325.13]SPHFLR.L    |
| 0.932605 | 0.9856 R.FAGVFHVEK[325.13]NGR.Y                        |
| 0.932575 | 0.9495 R.MSSFGDFVALSDVC[160.03]DVPTAK[325.13]IISR.E    |
| 0.932574 | 0.7011 R.KVLRDNIQGITK[325.13]PAIR.R                    |
| 0.932563 | 0.5241 R.K[325.13]LLEGEESR.I                           |
| 0.932544 | 0.8663 R.VEWK[325.13]FDQGDTR.L                         |
| 0.932542 | 0.8429 R.GKGGK[325.13]GLGK.G                           |
| 0.932495 | 0.4322 K.EGKPLLK[325.13]AVMR.R                         |
| 0.932482 | 0.9713 R.TVDATGK[325.13]EIELTHR.M                      |
| 0.93248  | 0.9585 R.SPEEQC[160.03]LDVVTHWIEGEEGRPK[325.13]DDR.H   |
| 0.932432 | 0.9389 R.VGVM[147.04]KPPEMPQK[325.13]R.R               |
| 0.932418 | 0.9047 K.YITK[325.13]SGTR.V                            |
| 0.932399 | 0.5425 R.IPELNK[325.13]VAR.A                           |
| 0.932353 | 0.7636 K.GVTIIGPATVGGIK[325.13]PGC[160.03]FKIGNTGGMLDN |
| 0.932327 | 0.9518 R.THFGGGK[325.13]TTGFGM[147.04]IYDSL DYAK.K     |
| 0.932322 | 0.985 R.ATSLAWHPHTPSTVAVGSK[325.13]GGDIMLWNFGIK.D      |
| 0.932257 | 0.5183 R.VTQKSYK[325.13]VSTSGPR.A                      |

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| 0.932207 | 0.6523 K.GTGASGSFK[325.13]LNK.K                          |
| 0.932203 | 0.6138 R.K[325.13]TFSHELSDFGLESTAGEIPVVAIR.T             |
| 0.932173 | 0.8328 K.AFFK[325.13]GAWSNVLR.G                          |
| 0.932158 | 0.2795 R.DALSDLALHFLNK[325.13]M[147.04]K.I               |
| 0.932139 | 0.7208 R.K[325.13]YSNEDTLSVALPYFWEHFDK.D                 |
| 0.932054 | 0.7419 R.IIAQK[325.13]IYGADDIELLPEAQHK.A                 |
| 0.932034 | 0.8127 R.FNVLK[325.13]VTK.A                              |
| 0.931996 | 0.9172 R.GHPDPK[325.13]LSWSQLGGSPAEPGR.Q                 |
| 0.931981 | 0.7705 K.KNNIK[325.13]LYVR.R                             |
| 0.93196  | 0.8764 K.QEWPk[325.13]HWPTFISDIVGASR.T                   |
| 0.931928 | 0.971 R.YSIK[325.13]DLLNHAFQEETGVR.V                     |
| 0.931796 | 0.7613 K.GAGLSK[325.13]AFVGQK.S                          |
| 0.931796 | 0.8787 K.LSEK[325.13]IMHFPTWVDLK.G                       |
| 0.931788 | 0.4828 K.AAKPK[325.13]VVKPK.K                            |
| 0.931757 | 0.9903 R.IIHGAGYSEEDK[325.13]R.G                         |
| 0.931755 | 0.9469 K.LPGIPIK[325.13]IVMEAIQQASVAK.K                  |
| 0.931747 | 0.9892 R.ELDLVFLDHSYAK[325.13]PWSAHPDASSARPTRM[147.0     |
| 0.931733 | 0.8799 R.NLVVIPK[325.13]SVTPER.I                         |
| 0.931733 | 0.9873 R.LHNLAQFEGGESK[325.13]VNTLVAAANSLDNLC[160.03]    |
| 0.931724 | 0.093 R.TNIQVTVTGPSSPSPVK[325.13]FLIDTHNR.L              |
| 0.931721 | 0.6955 R.K[325.13]LMVALAK.G                              |
| 0.931711 | 0.9835 R.AVGNIVTGDDIQTQVILNC[160.03]SALPC[160.03]LLHLLS  |
| 0.931671 | 0.9827 R.IHGVGFK[325.13]K.R                              |
| 0.931622 | 0.9802 R.NIK[325.13]TIAEC[160.03]LADELINAAK.G            |
| 0.931562 | 0.9322 R.TMGVMFTPLTVK[325.13]YAYYDTER.I                  |
| 0.931469 | 0.9346 K.SLTGVVNAQALTSASFSPHTK[325.13]PWIGLAEALGTLM[1    |
| 0.931466 | 0.8689 R.NTKK[325.13]EGDLIAAQAR.L                        |
| 0.931448 | 0.8197 R.SPVFLYEDHTGK[325.13]PGPEDYPLFR.G                |
| 0.931426 | 0.8745 R.LAYINPDLALEEK[325.13]NKGNEC[160.03]FQK.G        |
| 0.931412 | 0.9669 R.K[325.13]AHDEAVR.S                              |
| 0.931387 | 0.9647 K.SIAK[325.13]FFDHSGTLVMDAYEPEISR.L               |
| 0.931364 | 0.7903 R.YAHWVVSQPPDTYLK[325.13]PLMTELLK.R               |
| 0.931316 | 0.6126 K.NFGIGQDIQPK[325.13]R.D                          |
| 0.931275 | 0.8949 R.DFRPLK[325.13]DSR.F                             |
| 0.931256 | 0.5925 K.K[325.13]AASGEAKPK.A                            |
| 0.931242 | 0.685 R.DFLK[325.13]PELLR.A                              |
| 0.931179 | 0.7096 R.IFLC[160.03]QGK[325.13]RPR.S                    |
| 0.931171 | 0.9786 K.SQDDRDK[325.13]FLGR.V                           |
| 0.931102 | 0.9319 K.K[325.13]ELSDIAHR.I                             |
| 0.931053 | 0.6618 R.GLKPSC[160.03]TIIPLM[147.04]K[325.13]K.D        |
| 0.930993 | 0.6519 R.TLK[325.13]IPAMTIAK.N                           |
| 0.930952 | 0.9883 K.GLK[325.13]GLPGPAGPPGPRGDLGSTGNPGEPLR.G         |
| 0.930937 | 0.9899 R.AIIAPHAGYTYC[160.03]GSC[160.03]AAHAYK[325.13]Q' |
| 0.930915 | 0.6544 K.VIHDNFGIVEGLM[147.04]TTVHAITATQK[325.13]TVDGI   |
| 0.93091  | 0.1108 R.LVYLVENPGGYVAYSK[325.13]AATVTGK.L               |
| 0.93091  | 0.4087 R.K[325.13]LAVNM[147.04]VPFPR.L                   |
| 0.930835 | 0.7652 R.LSVDYGK[325.13]KSK.L                            |

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| 0.930832 | 0.9496 R.LK[325.13]GLLQSGQIPGR.E                         |
| 0.930831 | 0.9813 R.FGHGSAK[325.13]LAR.Q                            |
| 0.930779 | 0.9904 K.EAVILPIK[325.13]FPHLFTGK.R                      |
| 0.930754 | 0.4989 K.DLAPYLPSVTPGLK[325.13]ASLLDPVPEVR.T             |
| 0.93073  | 0.5155 K.GHLSGLAK[325.13]R.A                             |
| 0.930708 | 0.9387 K.SELK[325.13]ELLTR.E                             |
| 0.930696 | 0.9623 K.VGEFSGANK[325.13]EK.L                           |
| 0.93069  | 0.5817 R.VTQKSYK[325.13]VSTSGPR.A                        |
| 0.930645 | 0.887 K.K[325.13]ASFEEASNQLINHIEQFLDTNETPYFMK.S          |
| 0.930601 | 0.8996 K.KKPEDSPSDDDLIVYELTPTAEQK[325.13]ALATK.L         |
| 0.93058  | 0.6918 R.LLLSK[325.13]GHSC[160.03]YRPR.R                 |
| 0.930547 | 0.9864 R.HLISGAEDGLIC[160.03]IWDK[325.13]K.W             |
| 0.930335 | 0.9899 R.EQFYHSC[160.03]K[325.13]QYGITGENVR.G            |
| 0.930313 | 0.8115 R.FK[325.13]EANNFLWPFK.L                          |
| 0.930257 | 0.8621 R.WLK[325.13]GGVVLK.E                             |
| 0.930234 | 0.9907 R.ASK[325.13]FAAQLHQNLR.K                         |
| 0.930187 | 0.1538 R.SSFDWLTGSSTDPLVDHTSPSSDLSLLFAHK[325.13]R.S      |
| 0.93017  | 0.9726 R.VQLIK[325.13]ALLALPIRPATR.R                     |
| 0.930153 | 0.975 K.GLLQLQWK[325.13]QDLDR.G                          |
| 0.930145 | 0.7322 K.KDIK[325.13]GSYVSIHSSGFR.D                      |
| 0.930142 | 0.4628 K.K[325.13]LGEMWNNTAADDKQPYEK.K                   |
| 0.930141 | 0.7575 K.KLK[325.13]EVFSMAGVVVR.A                        |
| 0.930131 | 0.5795 R.VTQKSYK[325.13]VSTSGPR.A                        |
| 0.930088 | 0.9896 K.IIPLLTDPK[325.13]NHGLSDEHVFEVIC[160.03]PSIPGYGF |
| 0.929961 | 0.9799 R.SDHLSK[325.13]HIK.T                             |
| 0.929768 | 0.8883 K.HLK[325.13]TFDR.G                               |
| 0.929755 | 0.7946 R.DQK[325.13]WHDK.Q                               |
| 0.929648 | 0.9832 R.IEQLSPFPDLLLLK[325.13]EVQK.Y                    |
| 0.929471 | 0.9824 K.M[147.04]HLAGK[325.13]TEQAK.A                   |
| 0.929366 | 0.9298 K.TSFFQALGITTK[325.13]ISR.G                       |
| 0.929354 | 0.8935 K.K[325.13]SSGEIVYC[160.03]GQVFEK.S               |
| 0.929322 | 0.9067 K.K[325.13]NIFLLFK.K                              |
| 0.929271 | 0.6674 R.KQLATK[325.13]AAR.K                             |
| 0.929232 | 0.9047 K.AEVHESYK[325.13]HLK.S                           |
| 0.929211 | 0.9836 K.EK[325.13]LNLSC[160.03]IHSPVVNELMR.G            |
| 0.929183 | 0.0531 R.LVQAFQFTDK[325.13]HGEVC[160.03]PAGWKPGSDTIK     |
| 0.929164 | 0.3479 K.K[325.13]THIQDNHDGTYTVAYVPDVTGR.Y               |
| 0.929155 | 0.9629 R.TGLK[325.13]ITSLTEVVC[160.03]GLDLC[160.03]NQGN  |
| 0.929145 | 0.9335 K.ENLK[325.13]AAQEEYVKR.A                         |
| 0.929091 | 0.8024 K.SMTEAEQQQLIDHFLFDK[325.13]PVSPLLLASGMAR.D       |
| 0.929054 | 0.9328 R.TTTGNK[325.13]VFGALK.G                          |
| 0.929033 | 0.4928 R.RLYWDDLK[325.13]R.K                             |
| 0.929032 | 0.7501 R.NLPFDFTWK[325.13]MLK.D                          |
| 0.929022 | 0.8061 R.EK[325.13]QTVHSVFR.K                            |
| 0.929012 | 0.1577 R.VLAFTAVGDGPPSPTIQVK[325.13]TQQGVPAQPADFQAE      |
| 0.928985 | 0.2963 K.VYEGERPLTK[325.13]DNHLLGTFDLTGIPPAPR.G          |
| 0.928978 | 0.9756 R.SLDTHVTK[325.13]SLHSIIR.H                       |



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| 0.928961 | 0.8603 R.AK[325.13]ELLGQGLLLR.S                        |
| 0.928913 | 0.3878 R.M[147.04]KENQK[325.13]HIYYITGETK.D            |
| 0.92883  | 0.7425 K.KAAGGATPK[325.13]K.S                          |
| 0.928812 | 0.9651 R.K[325.13]LHELTVMQDR.R                         |
| 0.928806 | 0.4175 R.RAPFDLFENK[325.13]K.K                         |
| 0.928794 | 0.8764 K.LGEMWNNTAADDKQPYEK[325.13]K.A                 |
| 0.928793 | 0.5994 R.TLK[325.13]IPAMTIAK.N                         |
| 0.928741 | 0.943 R.TYVGPMTESLFPGYHTK[325.13]AR.A                  |
| 0.928579 | 0.9583 K.STVTLSWKPVQK[325.13]VEIGQK.R                  |
| 0.928546 | 0.8847 K.IK[325.13]ELVVTQLGYDTR.V                      |
| 0.928546 | 0.8847 K.IK[325.13]ELVVTQLGYDTR.V                      |
| 0.9285   | 0.6213 K.GTGASGSFK[325.13]LNK.K                        |
| 0.928497 | 0.6425 R.K[325.13]M[147.04]C[160.03]LFAGFQR.K          |
| 0.92836  | 0.5149 K.RGEIIAK[325.13]QGGGGGGGSPGIER.M               |
| 0.928319 | 0.6557 K.FNVWDTAGQEK[325.13]FGGLR.D                    |
| 0.928301 | 0.7253 R.LPVEVAYK[325.13]R.G                           |
| 0.928285 | 0.9462 K.K[325.13]GIHYWEVELQK.N                        |
| 0.928205 | 0.8946 R.K[325.13]FHEAQLSEK.I                          |
| 0.928199 | 0.4779 R.LAHYNK[325.13]R.S                             |
| 0.928196 | 0.7487 K.AFNQ GK[325.13]IFK.-                          |
| 0.928183 | 0.975 K.VYGK[325.13]TSHLR.A                            |
| 0.928164 | 0.6731 K.SMK[325.13]FVDGLMIHSGDPVNYVDTAVR.H            |
| 0.928162 | 0.8756 R.K[325.13]GVAINFK.N                            |
| 0.928143 | 0.9624 R.FKEK[325.13]LPAPILEFFAVVMGTGISAGFNLK.E        |
| 0.92811  | 0.7082 R.VC[160.03]K[325.13]ILGSGISSSSVLHGMVFK.K       |
| 0.928069 | 0.989 K.DGLALGMGQGLK[325.13]AWPR.Y                     |
| 0.928057 | 0.8726 R.IKKPEGK[325.13]PDQK.F                         |
| 0.928025 | 0.7087 K.GKWKPPM[147.04]IDNPSYQGIWK[325.13]PRK.I       |
| 0.928001 | 0.747 K.NLYIISVK[325.13]GIK.G                          |
| 0.927946 | 0.913 R.HK[325.13]PAFTEEDVLNIFPVVK.H                   |
| 0.927874 | 0.6883 K.ISDSVLVDIKDTEPLIQ TAK[325.13]TTLGSK.V         |
| 0.927855 | 0.1427 K.ADK[325.13]DYHFKVDNDENEHQLSLR.T               |
| 0.927845 | 0.8251 R.HGESGSMVAFHQ TQGPSYSESK[325.13]R.L            |
| 0.927787 | 0.9899 K.HVVFGK[325.13]IIDGLLVMR.K                     |
| 0.927751 | 0.9116 K.KGGK[325.13]EFVEAVLELR.K                      |
| 0.927725 | 0.9319 K.LLLLQK[325.13]MLK.N                           |
| 0.927664 | 0.9098 K.EWAHATIIPK[325.13]VLAMSGDPNYLHR.M             |
| 0.927635 | 0.9692 K.AK[325.13]WDAWNEK.G                           |
| 0.927575 | 0.8453 K.SYIYSGSHDGHINYWDSETGENDSFAGK[325.13]GHTNQV    |
| 0.927473 | 0.6998 K.SYENQKPPFDAK[325.13]NPFLAAVTTNR.K             |
| 0.927439 | 0.9833 K.GLK[325.13]YNQATQTFHQWR.D                     |
| 0.927382 | 0.9868 R.EGISFHFTPVLVC[160.03]K[325.13]DPIR.T          |
| 0.927307 | 0.9454 K.WK[325.13]ALFEEVPELLTEAEK.K                   |
| 0.927247 | 0.6458 R.AAAEK[325.13]LFGNM[147.04]EGDC[160.03]PSDWK.T |
| 0.927198 | 0.4685 R.C[160.03]RPDQLTGLSLLPLSEK[325.13]AAR.A        |
| 0.927178 | 0.9365 R.K[325.13]GAAPAPPR.K                           |
| 0.927065 | 0.9458 R.QIHK[325.13]FEELNR.T                          |

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| 0.927053 | 0.6835 K.GKWKPPMIDNPSYQGIWK[325.13]PR.K                  |
| 0.926996 | 0.6583 K.EAHLPPGAM[147.04]AAVGLSWEEC[160.03]K[325.13]C   |
| 0.926898 | 0.8429 R.K[325.13]GVAINMVTEEDKR.T                        |
| 0.926875 | 0.9147 R.GFGGK[325.13]FGVQMDR.V                          |
| 0.926873 | 0.7698 R.DLYDAGVK[325.13]R.K                             |
| 0.926847 | 0.7633 K.ALANVNIGSLIC[160.03]NVGAGGPAPAAGAAPAGGPAPS      |
| 0.926845 | 0.9696 R.LC[160.03]HDKETYK[325.13]LQR.R                  |
| 0.926815 | 0.7177 K.GIVEFASK[325.13]PAAR.K                          |
| 0.926757 | 0.7692 K.VMSQNFTNC[160.03]HTK[325.13]IR.H                |
| 0.926688 | 0.9035 R.AGGK[325.13]ILTFDQLALDSPK.G                     |
| 0.926681 | 0.7334 R.EK[325.13]LQEEMLQR.E                            |
| 0.926663 | 0.1466 K.KAK[325.13]VAKPK.K                              |
| 0.926643 | 0.8847 R.ALVFQPVAELK[325.13]DQTDFEHR.I                   |
| 0.926553 | 0.6932 R.INSGGK[325.13]LPNFGFVVFDSEPVQK.V                |
| 0.926538 | 0.4844 K.KPAAATVTK[325.13]K.V                            |
| 0.926345 | 0.9555 R.SHISDQSPLSSK[325.13]R.K                         |
| 0.926341 | 0.9635 K.STVVVK[325.13]AISGVHTVR.F                       |
| 0.926297 | 0.7462 K.AK[325.13]KPAGAAK.K                             |
| 0.926294 | 0.8616 K.AGISFIIK[325.13]RPFLEPK.K                       |
| 0.926281 | 0.9745 R.EISLLK[325.13]ELNHPNIVK.L                       |
| 0.926271 | 0.88 R.NFLGEK[325.13]YIR.R                               |
| 0.926212 | 0.8764 R.INK[325.13]GVATNWL.R.A                          |
| 0.926125 | 0.9368 R.TTSLNNGGC[160.03]QYLC[160.03]LPAPQINPHSPK[325.1 |
| 0.926106 | 0.5795 K.IVSGK[325.13]DYNVTANSK.L                        |
| 0.926025 | 0.9901 K.AVLLLQEK[325.13]C[160.03]PHVTEHIPR.E            |
| 0.925891 | 0.8717 K.K[325.13]VGFGVGNWALDPAKM[147.04]NR.G            |
| 0.92587  | 0.9577 K.TIQTIALITYLMEHK[325.13]R.L                      |
| 0.925855 | 0.7339 K.K[325.13]HLLVHAPEDKK.E                          |
| 0.925812 | 0.9874 K.FIHDQTSPNPK[325.13]YR.G                         |
| 0.925786 | 0.9881 R.AEHIPAGK[325.13]R.T                             |
| 0.925771 | 0.7003 K.K[325.13]SADTLWDIQQ.D                           |
| 0.925732 | 0.6861 R.LK[325.13]GSGNLEAIHIIK.K                        |
| 0.925656 | 0.5952 K.EK[325.13]LLLWSQR.M                             |
| 0.925625 | 0.9756 R.LVLPVEK[325.13]ASLLLC[160.03]GSDLPLHK.M         |
| 0.925601 | 0.8725 R.NEC[160.03]NQC[160.03]K[325.13]APKPDGPGGGPGG:   |
| 0.925551 | 0.9696 K.VTSLGK[325.13]DWHRPC[160.03]LR.C                |
| 0.92555  | 0.4628 K.SFIK[325.13]DYPVVSIEDPFDQDDWGAWQK.F             |
| 0.925542 | 0.9864 R.DSK[325.13]LTHLFK.N                             |
| 0.925532 | 0.1323 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K          |
| 0.925519 | 0.9521 R.C[160.03]LAK[325.13]AYVR.G                      |
| 0.925466 | 0.7435 R.RQK[325.13]LEDSYR.F                             |
| 0.925424 | 0.7113 R.VINEEYK[325.13]IWK.K                            |
| 0.925384 | 0.9899 R.IFK[325.13]QHFMDSR.I                            |
| 0.92536  | 0.9334 R.ASVFVK[325.13]LQKPNAAIR.D                       |
| 0.925353 | 0.88 K.AKDPFAHLPK[325.13]STFVLDEFK.R                     |
| 0.925328 | 0.9689 K.IINEVSK[325.13]PLAHHIPVEK.I                     |
| 0.925309 | 0.7682 R.FELSC[160.03]YSLAPQIK[325.13]VIAPWR.M           |

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| 0.925264 | 0.4458 R.DGSIDLVINLPNNNTK[325.13]FVHDNYVIR.R            |
| 0.925251 | 0.5978 R.K[325.13]QVVNIPSFIVR.L                         |
| 0.925061 | 0.9891 R.K[325.13]HIQDLNWQR.K                           |
| 0.925032 | 0.9531 R.SK[325.13]SYSFHQSQHR.K                         |
| 0.925018 | 0.9769 K.K[325.13]MFHATVATENEVFR.V                      |
| 0.924981 | 0.9815 K.TK[325.13]AAAAAAAAAPAAAATAPTTAATTAATAAQ.-      |
| 0.924966 | 0.443 R.MSHLK[325.13]VGSAADIPINISETDLSLLTATVVPPSGR.E    |
| 0.924963 | 0.7406 R.FLSNGHVTIPGQQDK[325.13]DMFQETMEAMR.I           |
| 0.924944 | 0.9086 R.SYSDPPLK[325.13]FMSVQRP GPYDRPGTAR.R           |
| 0.924943 | 0.6403 R.GLKPSC[160.03]TIIPLM[147.04]K[325.13]K.D       |
| 0.924927 | 0.8635 K.K[325.13]YDAFLASESLIK.Q                        |
| 0.924913 | 0.7167 R.IMGLDLPDGGHLTHGYMSDVK[325.13]R.I               |
| 0.92491  | 0.9791 R.TTHYTPLAC[160.03]GSNPLK[325.13]R.E             |
| 0.924812 | 0.8221 K.ALEAVFGK[325.13]YGR.I                          |
| 0.92476  | 0.9832 K.HANAK[325.13]PFEVPFLK.F                        |
| 0.924704 | 0.7818 R.DQK[325.13]WHDK.Q                              |
| 0.924635 | 0.694 K.KEQTPEHGK[325.13]K.K                            |
| 0.92463  | 0.9098 K.ATISNDGATILK[325.13]LLDVVHPAAK.T               |
| 0.924534 | 0.9892 R.IIHGAGYSEEDK[325.13]R.G                        |
| 0.924528 | 0.9877 R.LDILK[325.13]IHSR.K                            |
| 0.924516 | 0.5154 K.DSYVGDEAQSK[325.13]R.G                         |
| 0.924501 | 0.9318 K.LKTK[325.13]DEPQR.E                            |
| 0.924483 | 0.8341 R.KESPLLFK[325.13]FR.A                           |
| 0.924438 | 0.9833 R.WQAIYK[325.13]QFDTDR.S                         |
| 0.924387 | 0.8835 K.KWGVPIEK[325.13]IYNK.T                         |
| 0.924347 | 0.6969 R.K[325.13]QVVNIPSFIVR.L                         |
| 0.924257 | 0.8881 R.EHGAFDAVK[325.13]C[160.03]THWAEGGK.G           |
| 0.924235 | 0.9568 K.VVGAK[325.13]VVTNAR.S                          |
| 0.924117 | 0.9874 K.EIDKNDHLYILLSTLEPTDAGILGTTK[325.13]DSPK.L      |
| 0.924044 | 0.959 K.ALIGK[325.13]GHPEFSTNR.Q                        |
| 0.924037 | 0.8628 K.AVLEC[160.03]KPLGIK[325.13]TALK.A              |
| 0.923948 | 0.6127 K.AGGFLMK[325.13]K.E                             |
| 0.923807 | 0.8726 K.SSGEIVYC[160.03]GQVF EK[325.13]SPLR.V          |
| 0.923796 | 0.9862 R.MPILISK[325.13]IFPGLAADQSR.A                   |
| 0.923793 | 0.856 K.TFPQNPVELK[325.13]ALYNQYIHF.K                   |
| 0.923788 | 0.5394 R.HGK[325.13]YM[147.04]AC[160.03]C[160.03]LLYR.G |
| 0.923777 | 0.9369 R.TAWVFDDK[325.13]YK.R                           |
| 0.923775 | 0.6967 R.K[325.13]VIDDTNITR.L                           |
| 0.923747 | 0.4729 R.SSIAGLLLK[325.13]ATNEK.L                       |
| 0.923657 | 0.9642 R.LGC[160.03]FNLT VK[325.13]GHAK.C               |
| 0.923625 | 0.9891 R.TAHEISLK[325.13]R.S                            |
| 0.923427 | 0.9055 K.K[325.13]DVLEFTVK.S                            |
| 0.92341  | 0.9345 R.YVASYLLAALGGNSSPSAK[325.13]DIKK.I              |
| 0.923409 | 0.9884 R.AYNYVAQEVDYHAFQTLTHIYNK[325.13]VR.T            |
| 0.923401 | 0.8641 R.GREFSFEAWNAK[325.13]ITDLK.Q                    |
| 0.923295 | 0.9721 K.FFSAYK[325.13]SHFR.N                           |
| 0.923269 | 0.8113 K.GRPC[160.03]K[325.13]IVEM[147.04]STSK.T        |

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| 0.923254 | 0.7241 K.MK[325.13]GYSFGHPSSVAGEVVFNTGLGGYPEAITDPAYI     |
| 0.923179 | 0.9594 R.EIPSHVLSK[325.13]VC[160.03]MYFTYK.V             |
| 0.923049 | 0.9107 K.GVTIPYRPK[325.13]PSSSPVIFAGGQDR.Y               |
| 0.923019 | 0.8181 R.HK[325.13]NM[147.04]SVHLSPC[160.03]FR.D         |
| 0.922995 | 0.8666 K.VVDPFSK[325.13]KDWYDVK.A                        |
| 0.922917 | 0.4959 R.VAPEEHPVLLTEAPLNPK[325.13]ANREK.M               |
| 0.922882 | 0.9889 R.K[325.13]LVIPSELGYGER.G                         |
| 0.922824 | 0.5445 K.FEDENFILK[325.13]HTGPGILSMANAGPNTNGSQFFIC[16    |
| 0.922751 | 0.8805 R.AAVATFLQSVQVPEFTPK[325.13]SGVK.I                |
| 0.922705 | 0.979 K.IQKEPTAVLK[325.13]DEAMVLHLTLGK.Y                 |
| 0.922704 | 0.6615 R.TVPQYK[325.13]YAAGVR.N                          |
| 0.922696 | 0.8606 R.VIIEK[325.13]YYTR.L                             |
| 0.922509 | 0.9204 K.IMSSPLSK[325.13]ELR.Q                           |
| 0.922432 | 0.9757 K.HGYIPGK[325.13]NR.D                             |
| 0.92238  | 0.6446 R.GFEVVYM[147.04]TEPIDEYC[160.03]VQQLK[325.13]EF  |
| 0.922292 | 0.7348 R.LKPYVAAQLDVLPEFTLGDK[325.13]KNYR.G              |
| 0.92229  | 0.8439 K.K[325.13]LTQTSGETTHTDKVPGGEDK.S                 |
| 0.922276 | 0.6957 R.EKIK[325.13]SDHPGISITDLSK.K                     |
| 0.922259 | 0.9034 K.ISK[325.13]PAPYWEGTAVIDGEFK.E                   |
| 0.922212 | 0.6544 R.DC[160.03]QLNAHK[325.13]DHQYQFLEDAVR.N          |
| 0.922177 | 0.8455 K.LNSGDYK[325.13]TIHLSSIRPPR.L                    |
| 0.922169 | 0.8836 R.HLTASEAK[325.13]K.L                             |
| 0.922127 | 0.987 K.K[325.13]IC[160.03]C[160.03]IGAGYVGGPTC[160.03]S |
| 0.922001 | 0.469 K.LVINGNPITIFQERDPSK[325.13]IK.W                   |
| 0.921995 | 0.7869 R.TDDVHAK[325.13]DNTRPGANSPEMWSEAIK.I             |
| 0.921987 | 0.9435 R.LLLETHLPSK[325.13]K.K                           |
| 0.921968 | 0.8751 K.VPSPPPGHK[325.13]WK.E                           |
| 0.921939 | 0.8666 K.APLKPYPVSPSDK[325.13]VLIQEK.T                   |
| 0.921922 | 0.7611 R.K[325.13]LADQC[160.03]TGLQGFLVFHSFGGGTGSGFTS    |
| 0.921865 | 0.2367 K.VDWLTEK[325.13]MHAR.D                           |
| 0.921815 | 0.7265 R.K[325.13]PVTVHSR.A                              |
| 0.921792 | 0.9619 K.LLASADDFGK[325.13]VHLFSYPC[160.03]C[160.03]QPR. |
| 0.921775 | 0.823 K.SFPKDDPSK[325.13]PVHLTAFLGYK.A                   |
| 0.921771 | 0.9676 R.YTIHSQLEHLQSK[325.13]YIGTGHADTTK.W              |
| 0.921771 | 0.722 K.VKAEPK[325.13]IEAFR.A                            |
| 0.921737 | 0.3608 K.LSPDAIPGK[325.13]WTSQDSLLGMEFSGR.D              |
| 0.921607 | 0.5448 K.KAPK[325.13]SPAK.A                              |
| 0.92145  | 0.2263 R.K[325.13]GHAVGDIPGVR.F                          |
| 0.921403 | 0.9415 R.HSDENDGGQPHK[325.13]R.R                         |
| 0.921371 | 0.7323 K.QLEAIDQLHLEYAK[325.13]R.A                       |
| 0.921334 | 0.9043 R.DMHSAKY[325.13]HADGK.K                          |
| 0.921333 | 0.6152 K.IGYNPDTVAFVPISGWNGDNM[147.04]LEPSANMPWFK[       |
| 0.921239 | 0.7398 R.RPGEK[325.13]TYTQR.C                            |
| 0.921164 | 0.9875 R.NHSTSFSLSNLTLPK[325.13]GAR.E                    |
| 0.921009 | 0.5763 R.DLQQYQSQAK[325.13]QLFR.K                        |
| 0.920992 | 0.8466 R.LQLELSK[325.13]VR.E                             |
| 0.92089  | 0.731 K.AKKPAAATVTK[325.13]K.V                           |

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| 0.920864 | 0.9655 K.AQITQK[325.13]IGVHAFQQR.L                        |
| 0.920784 | 0.767 K.VEVNDRQGFVPAAYVK[325.13]K.L                       |
| 0.920769 | 0.9206 K.TENQQK[325.13]STNVVYQAHVSR.N                     |
| 0.920756 | 0.9848 R.FPSHFSSDLK[325.13]DLLR.N                         |
| 0.92068  | 0.6591 K.DISLSDYK[325.13]GK.Y                             |
| 0.920621 | 0.7852 R.LLEDGEDFNLGDALDSSNSM[147.04]QTIQK[325.13]TTTI    |
| 0.920568 | 0.4628 R.HNGTGGK[325.13]SIYGEKFEDENFILK.H                 |
| 0.92051  | 0.8642 K.LFVTGLFSLNQDIPAFK[325.13]EHLR.D                  |
| 0.920485 | 0.8513 K.TEILPPFFK[325.13]HFWQHR.M                        |
| 0.920452 | 0.9865 K.KPLK[325.13]VIFVGEDAVDAGGVR.K                    |
| 0.920373 | 0.6957 R.QLMWSATWPK[325.13]EVR.Q                          |
| 0.920307 | 0.8492 R.VMEHFIK[325.13]LYK.K                             |
| 0.920259 | 0.9794 R.YFK[325.13]VWLYHDGR.L                            |
| 0.92022  | 0.8679 R.FPPVVFYTPK[325.13]ELGGLGMLSMGHVLIPQSDLR.W        |
| 0.920202 | 0.9191 R.MELLAHLLGEK[325.13]WMGPIPPAVNAR.L                |
| 0.920183 | 0.9372 R.NDEELNK[325.13]LLGR.V                            |
| 0.920128 | 0.958 R.FKEK[325.13]LPAPIPLEFFAVVMGTGISAGFNLK.E           |
| 0.920115 | 0.9667 R.YFILPDSLPLDTLLVDVEPK[325.13]VK.S                 |
| 0.920107 | 0.2097 K.WK[325.13]PPM[147.04]IDNPSYQGIWKPR.K             |
| 0.920031 | 0.4606 K.K[325.13]LLEAQSHFR.K                             |
| 0.91993  | 0.9201 R.VTSLGK[325.13]DWHRPC[160.03]LK.C                 |
| 0.919908 | 0.6401 R.AK[325.13]LTPGC[160.03]EAEAETEAIK[160.03]FFVQQF  |
| 0.919865 | 0.7831 R.NNFEGEVTK[325.13]ENLLDFIK.H                      |
| 0.919823 | 0.9162 R.K[325.13]IHESAGLPFFEIVDAPLNIC[160.03]ESR.D       |
| 0.91967  | 0.9888 K.RPHLSVILVGENPASHSYVLNK[325.13]TR.A               |
| 0.919583 | 0.8176 R.ETAQAIK[325.13]GM[147.04]HIR.K                   |
| 0.919573 | 0.0553 K.ADKDYHFK[325.13]VDNDENEHQLSLR.T                  |
| 0.919541 | 0.7371 R.GLPYK[325.13]ATENDIYNFFSPLNPVR.V                 |
| 0.919539 | 0.5357 R.K[325.13]TVTAMDVVYALK.R                          |
| 0.919525 | 0.9799 R.EVPEYLHHVVK[325.13]R.L                           |
| 0.919525 | 0.933 K.RFTAQGLPDLNHSQVYAVK[325.13]TVLQRPLSLIQGPPGT       |
| 0.919498 | 0.6112 R.AGQK[325.13]GYHHR.T                              |
| 0.919485 | 0.7272 K.LLK[325.13]ELHK.E                                |
| 0.919485 | 0.7708 K.FEDENFILK[325.13]HTGPGILSM[147.04]ANAGPNTNGS     |
| 0.919468 | 0.9465 K.TEKHESQK[325.13]DYVK.G                           |
| 0.919366 | 0.9827 R.DMFYK[325.13]ILHGFK.D                            |
| 0.919337 | 0.9869 K.SC[160.03]K[325.13]MITEHTSNDPYC[160.03]FVEFYEHF  |
| 0.919224 | 0.9012 R.YHPDK[325.13]NKEPGAEEK.F                         |
| 0.919154 | 0.8298 K.K[325.13]FISDKDASIVGFFDDSFSEAHSEFLK.A            |
| 0.919106 | 0.4031 K.FINYVK[325.13]NC[160.03]FR.M                     |
| 0.919078 | 0.9055 R.FGGGNPELLTQMVS[325.13]GFLGR.K                    |
| 0.919071 | 0.9821 R.VIGTLLGTVDK[325.13]HSVEVTNC[160.03]FSVPHNESED    |
| 0.919056 | 0.1817 R.LKDLEALLNSK[325.13]EAALSTALSEK.R                 |
| 0.919002 | 0.8799 R.RPFVK[325.13]SR.L                                |
| 0.9189   | 0.9556 K.DK[325.13]HILAK.I                                |
| 0.918862 | 0.7186 R.EGNDLYHEMIESGVINLK[325.13]DATSK.V                |
| 0.918853 | 0.9808 R.AC[160.03]GVSRPVIAC[160.03]SVTIK[325.13]EGSQLK.C |

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| 0.918848 | 0.7767 K.SLC[160.03]IPFKPLC[160.03]ELQPGAK[325.13]C[160.03] |
| 0.91881  | 0.0987 K.K[325.13]IGYNPDTVAFVPISGWNGDNM[147.04]LEPSAI       |
| 0.918808 | 0.6209 R.FK[325.13]KPGSK.N                                  |
| 0.918804 | 0.9758 K.K[325.13]FGPVVAPKPK.V                              |
| 0.918753 | 0.7272 K.TLNNKFASFIDK[325.13]VR.F                           |
| 0.918712 | 0.931 R.ELTDYLMK[325.13]ILTER.G                             |
| 0.918638 | 0.6318 R.KQLATK[325.13]AAR.K                                |
| 0.918593 | 0.9868 R.LVK[325.13]LFNHANQEVQR.H                           |
| 0.918581 | 0.8036 R.GYISPYFINTSK[325.13]GQK.C                          |
| 0.918554 | 0.6108 K.NQQFHK[325.13]ER.E                                 |
| 0.918549 | 0.8211 R.SK[325.13]GHGFITPADGGPDIFLHISDVEGEYVPVEGDEV        |
| 0.918544 | 0.7033 R.VNVPVIGGHAGK[325.13]TIIP LISQC[160.03]TPK.V        |
| 0.918525 | 0.9598 R.K[325.13]LHELTVMQDR.R                              |
| 0.918406 | 0.6591 R.GAPLAK[325.13]VVFR.D                               |
| 0.918346 | 0.8823 K.SANK[325.13]SGSSFVHQASF.K                          |
| 0.918228 | 0.9556 R.DFGSAAVSLQVAAPYSK[325.13]PSMTLEPNK.D               |
| 0.918147 | 0.8609 R.SYSK[325.13]LLC[160.03]GLLAER.L                    |
| 0.918136 | 0.9569 R.FKEK[325.13]LPAPIPLEFFAVVMGTGISAGFNLK.E            |
| 0.91813  | 0.9407 K.FNK[325.13]IVHSSMTR.A                              |
| 0.918113 | 0.9882 R.SQFSPAVFVYK[325.13]GGR.E                           |
| 0.917936 | 0.6283 K.EAHLPPGAM[147.04]AAVGLSWEEC[160.03]K[325.13]C      |
| 0.917605 | 0.9539 K.DLFHIPPSYK[325.13]STVTL SWKP VQK.V                 |
| 0.917528 | 0.8906 K.DWSK[325.13]VVLAYEPVWAI GTGK.T                     |
| 0.917514 | 0.81 K.YGK[325.13]AGEVFIHK.D                                |
| 0.917471 | 0.9801 K.KTESHK[325.13]PGK.N                                |
| 0.917471 | 0.9356 K.KGGPSPGDVEAIK[325.13]NAIANASTLAEVER.L              |
| 0.917325 | 0.9701 K.VVTTNYK[325.13]PVANHQYNIEYER.K                     |
| 0.917286 | 0.8969 K.K[325.13]LSTIALALGVER.T                            |
| 0.91718  | 0.7431 R.DQK[325.13]WHDK.Q                                  |
| 0.917179 | 0.8607 R.GVYTVEAK[325.13]NASGSAK.A                          |
| 0.917081 | 0.9671 R.RGPLVK[325.13]YSSDYFQAPSDYR.Y                      |
| 0.917028 | 0.773 R.VFITDDFHDMM[147.04]PK[325.13]YLN FVK.G              |
| 0.917016 | 0.9888 R.VHAALVYHK[325.13]HLK.R                             |
| 0.917016 | 0.9888 R.K[325.13]EVGEVSVLVN NAGVVSGHH LLEC[160.03]PDEL     |
| 0.917012 | 0.6529 K.RLK[325.13]TDNAGDQHGGGGGGGGGAGAAGGGGGGE            |
| 0.916989 | 0.935 K.AVVK[325.13]TDIQIALPSGC[160.03]YGR.V                |
| 0.916987 | 0.2403 K.TVDLKP DWGK[325.13]GYSR.K                          |
| 0.916966 | 0.724 R.DLEK[325.13]PFLLPVEAVYSVPGR.G                       |
| 0.916896 | 0.972 R.IC[160.03]LPHGAGGDAK[325.13]K.L                     |
| 0.916886 | 0.9368 R.FVELVHQQK[325.13]TPNFSTLLC[160.03]YDR.V            |
| 0.916749 | 0.7454 K.YGK[325.13]IVGC[160.03]SVHK.G                      |
| 0.916645 | 0.7297 K.DAK[325.13]TAASGIPYHSEVPVSLK.E                     |
| 0.916601 | 0.9789 R.LVPGWTK[325.13]PITIGR.H                            |
| 0.916555 | 0.8208 K.YK[325.13]QALLQYK.K                                |
| 0.916537 | 0.978 K.KKPTVTK[325.13]GR.S                                 |
| 0.916437 | 0.4718 R.QAERLKPYVAAQLDVL PETFTLGDK[325.13]K.N              |
| 0.916401 | 0.9843 R.LHLPIGDSASNLLFK[325.13]WR.N                        |

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| 0.91635  | 0.9837 R.LHSPQTHWK[325.13]TVR.E                      |
| 0.916344 | 0.9635 K.K[325.13]VPTVSRPYSFIEFDTFIQK.T              |
| 0.916343 | 0.8686 R.AITGASLADIMAK[325.13]R.N                    |
| 0.91631  | 0.7169 R.KVLGEK[325.13]GK.N                          |
| 0.916179 | 0.985 K.FLALDK[325.13]C[160.03]LPHR.D                |
| 0.916099 | 0.6652 R.LFC[160.03]VGFTK[325.13]K.R                 |
| 0.916069 | 0.4867 K.HAVSEGK[325.13]AVTKYTSSK.-                  |
| 0.916037 | 0.95 K.K[325.13]ILIEDWK.K                            |
| 0.915912 | 0.6168 K.NQQFHK[325.13]ER.E                          |
| 0.915751 | 0.7436 K.IVGC[160.03]SVHK[325.13]GFAFVQYVNER.N       |
| 0.915717 | 0.8459 R.FHM[147.04]YEGYPLWK[325.13]VTFPVR.V         |
| 0.915714 | 0.7406 R.DLYDAGVK[325.13]R.K                         |
| 0.915708 | 0.7334 K.NKPYPK[325.13]SR.F                          |
| 0.915664 | 0.5283 R.MGVVEC[160.03]AK[325.13]HELLQPFNVLYEK.E     |
| 0.915658 | 0.7245 K.NVVS GK[325.13]TSAC[160.03]FEPSLDYMVTK.I    |
| 0.915641 | 0.1842 R.GTK[325.13]VILHLK.E                         |
| 0.915565 | 0.8025 K.ALEAVFGK[325.13]YGR.I                       |
| 0.91556  | 0.5975 K.EGKPLLK[325.13]AVM[147.04]R.R               |
| 0.915542 | 0.8312 K.MFIGGLSWDTTK[325.13]K.D                     |
| 0.915477 | 0.9483 K.TIYTAPLDMQLQVTQAKK[325.13]SQAIASDVDYK.H     |
| 0.915447 | 0.8138 R.FLM[147.04]K[325.13]SYDQVHSGK.L             |
| 0.915405 | 0.3759 R.WLPAGDALLQM[147.04]ITIHLSPVTAQK[325.13]YR.C |
| 0.915251 | 0.9882 R.AAAAK[325.13]STAMEETAIWEQHTVTLHR.A          |
| 0.915241 | 0.9716 R.YSGAYGASVSDEELK[325.13]R.R                  |
| 0.915188 | 0.8393 R.VEWK[325.13]FDQGDTR.L                       |
| 0.914959 | 0.9885 R.NLVEQHK[325.13]SSSWINK.D                    |
| 0.914942 | 0.8811 R.C[160.03]AQAK[325.13]QWGWQTQGR.W            |
| 0.914857 | 0.6168 R.NLK[325.13]ASLENSLR.E                       |
| 0.914833 | 0.9785 K.K[325.13]LAPPLVTLLSGEPEVQYVALR.N            |
| 0.914751 | 0.981 R.HMVMQK[325.13]LLR.K                          |
| 0.914749 | 0.9099 K.GAVDGGLSIPHSTK[325.13]R.F                   |
| 0.914746 | 0.6131 K.VTQQGLK[325.13]M[147.04]VVPGLDGAQIPR.D      |
| 0.91464  | 0.7144 R.LK[325.13]AEATEAAR.Q                        |
| 0.914621 | 0.9887 K.FQSEK[325.13]AAGSVSK.S                      |
| 0.914553 | 0.9242 K.YGLIYHASLVGQTSPK[325.13]HK.G                |
| 0.914509 | 0.9224 R.VGVM[147.04]KPPEMPQK[325.13]R.R             |
| 0.914508 | 0.7998 R.FVTGNK[325.13]ILR.I                         |
| 0.914434 | 0.7258 R.LAK[325.13]YNQLLR.I                         |
| 0.914389 | 0.9341 R.VLTVINQTQK[325.13]ENLR.K                    |
| 0.914366 | 0.7007 K.LPVPSK[325.13]QHGGQIR.G                     |
| 0.914361 | 0.9856 K.ILIQHQK[325.13]AK.H                         |
| 0.914276 | 0.9856 R.AHFK[325.13]ELVNAVATVR.V                    |
| 0.914254 | 0.9222 K.TEISFRPNDPK[325.13]SYEAYVLNIVR.F            |
| 0.914147 | 0.8354 K.IVHK[325.13]GDEC[160.03]ILK.D               |
| 0.914145 | 0.6364 K.IAILTC[160.03]PFEPKPK[325.13]TK.H           |
| 0.914078 | 0.8591 K.LYGD LK[325.13]HLK.T                        |
| 0.914029 | 0.7745 K.K[325.13]DSEDNPQTLLFSATC[160.03]PHWVFNVAK.K |

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| 0.913991 | 0.7033 R.VRGPK[325.13]GPEEK.K                             |
| 0.913963 | 0.8608 R.NFLGEK[325.13]YIR.R                              |
| 0.913865 | 0.0977 K.SALSGHLETVILGLLK[325.13]TPAQYDASELK.A            |
| 0.913841 | 0.6662 R.VSQEHPVVLTK[325.13]FVEGAR.E                      |
| 0.913833 | 0.9419 K.LIIWDSYTTNK[325.13]VHAIPLR.S                     |
| 0.913792 | 0.838 K.KPEAK[325.13]FFTTPSK.S                            |
| 0.913691 | 0.7912 K.KLDTNSDGQLDFSEFLNLIGGLAMAC[160.03]HDSFLK[325.13] |
| 0.913649 | 0.9425 K.KEPAGHSQK[325.13]K.G                             |
| 0.913646 | 0.6455 R.HLTGEFEK[325.13]K.Y                              |
| 0.913643 | 0.9875 R.K[325.13]SALGPGVPHIINTK.L                        |
| 0.913632 | 0.8789 R.GQHTK[325.13]TTGR.R                              |
| 0.913584 | 0.9543 R.RPLYK[325.13]NIVLSGGSTMFR.D                      |
| 0.913543 | 0.8988 K.VSVYLQNWSHVLSYVSK[325.13]AESTPEIAEQR.G           |
| 0.913514 | 0.9268 R.SEFYK[325.13]HIVLSGGSTMYPGLPSR.L                 |
| 0.913488 | 0.8619 R.K[325.13]HGVVPLATYMR.I                           |
| 0.913361 | 0.8489 R.EHGSNK[325.13]K.L                                |
| 0.913345 | 0.8738 R.ELLTLDEK[325.13]DPRR.L                           |
| 0.913337 | 0.921 K.KIEISQHAK[325.13]YTC[160.03]SFC[160.03]GK.T       |
| 0.913307 | 0.8429 K.LFPDTPLALDANKK[325.13]K.R                        |
| 0.913283 | 0.9875 R.SLDSFLLSPEAAVGLLK[325.13]GTALVLAR.L              |
| 0.913219 | 0.7107 K.VTAPDVDLHLK[325.13]APK.I                         |
| 0.913058 | 0.3853 R.FTLTGLK[325.13]PDTTYDIK.V                        |
| 0.912937 | 0.8775 K.DVTLQK[325.13]QC[160.03]VPFR.R                   |
| 0.912882 | 0.9449 K.HLSASQK[325.13]ALK.E                             |
| 0.912867 | 0.985 R.TVEALYK[325.13]FVVPKPR.S                          |
| 0.912839 | 0.4124 R.GELAIKDANAK[325.13]LSELEAALQR.A                  |
| 0.912802 | 0.7636 K.AQPLEDLAGLK[325.13]ELFQTPIC[160.03]TDKPTTHEK.T   |
| 0.912752 | 0.9076 K.SSK[325.13]GELTTLIHQLEK.D                        |
| 0.912702 | 0.5575 K.IPVQLVFK[325.13]NK.I                             |
| 0.912668 | 0.6397 R.LK[325.13]GYLISGSSYAR.S                          |
| 0.912603 | 0.7652 K.YQLDK[325.13]DGVVLFK.K                           |
| 0.912522 | 0.4014 K.GATYGK[325.13]PVHHGVNQLK.F                       |
| 0.912378 | 0.7857 K.LHQAM[147.04]K[325.13]GVGTR.H                    |
| 0.912361 | 0.8638 R.GRPAATEVK[325.13]IPKPR.G                         |
| 0.912361 | 0.9507 R.IIK[325.13]PC[160.03]NHVLSLSFPIR.R               |
| 0.91225  | 0.6895 R.AK[325.13]GKPDAK.K                               |
| 0.912233 | 0.4548 K.FDLMYAK[325.13]R.A                               |
| 0.912197 | 0.9659 K.TVTQNGTHVASVPTAVHGQVNNAAASPLHMLATHASASA          |
| 0.91219  | 0.481 K.GKWKPPMIDNPSYQGIWK[325.13]PRK.I                   |
| 0.912161 | 0.9835 K.FQRPDPQSAQDK[325.13]AR.M                         |
| 0.912118 | 0.5997 K.EVQALIAEGIALVWESYK[325.13]LDPYVQR.L              |
| 0.912016 | 0.8379 R.AKGSETPGATPGSK[325.13]IWDPTPSHTPAGAATPGR.G       |
| 0.911978 | 0.9734 R.YGGETK[325.13]VYVGNLGTGAGK.G                     |
| 0.911961 | 0.8368 R.HIAMEK[325.13]VASR.T                             |
| 0.91193  | 0.8954 R.TRNEMTAEK[325.13]R.R                             |
| 0.911918 | 0.8492 K.IPQALEK[325.13]ILQLK.E                           |
| 0.911899 | 0.9137 K.FYAPWC[160.03]GHC[160.03]K[325.13]TLAPTWEELSK.   |



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| 0.911878 | 0.9608 R.IVDPEIALK[325.13]ILHR.Q                           |
| 0.911834 | 0.1168 R.QTVAVGVK[325.13]AVDKK.A                           |
| 0.911679 | 0.9879 R.FLK[325.13]LC[160.03]EEWPVDETKR.G                 |
| 0.911653 | 0.1519 R.HNGTGGK[325.13]SIYGEK.F                           |
| 0.911618 | 0.9798 R.VK[325.13]HFEAR.S                                 |
| 0.911608 | 0.3992 R.DTSFEQHVLWHTGGK[325.13]GVDLVLSLAEEK.L             |
| 0.911594 | 0.3681 R.IGSSMK[325.13]SVGEVMAIGR.T                        |
| 0.911509 | 0.7867 K.K[325.13]ALWFQGR.C                                |
| 0.911484 | 0.45 R.LPSGNHMK[325.13]ESR.E                               |
| 0.911462 | 0.6982 K.LMSAISK[325.13]TFC[160.03]PAHK.S                  |
| 0.911432 | 0.9869 K.LEPEAWK[325.13]HVEAVYIDIADR.S                     |
| 0.911219 | 0.9851 R.DAK[325.13]HTNFVEFR.N                             |
| 0.911128 | 0.9496 R.ELVHK[325.13]ANPIR.K                              |
| 0.911117 | 0.8441 R.KVMSQNFTNC[160.03]HTK[325.13]IR.H                 |
| 0.911114 | 0.8676 R.HLTASEAK[325.13]K.L                               |
| 0.911048 | 0.7705 R.EK[325.13]LC[160.03]FLDKVEPHATIAEIK.N             |
| 0.910961 | 0.7783 R.K[325.13]PSAPHGYTC[160.03]EC[160.03]PPNYLGPYC[1   |
| 0.910933 | 0.909 R.ASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGG           |
| 0.910914 | 0.9821 K.C[160.03]LNNLAASQLK[325.13]LDHYR.A                |
| 0.910803 | 0.8172 R.DQLEAAQEAVPPADIVFSVK[325.13]SPPSAGYLVMSR.G        |
| 0.910619 | 0.9787 R.AC[160.03]GVS RPVIAC[160.03]SVTIK[325.13]EGSQLK.( |
| 0.910514 | 0.9141 R.FLQPVHK[325.13]IDMNLTDLLGELQR.D                   |
| 0.910437 | 0.6568 K.SPNK[325.13]HNR.L                                 |
| 0.910379 | 0.9431 K.K[325.13]IGSGGFGLIYLAFTNKPEK.D                    |
| 0.910209 | 0.9351 R.SLNYK[325.13]STSSGHR.E                            |
| 0.910202 | 0.9838 K.DKVNC[160.03]SFYFK[325.13]IGAC[160.03]R.H         |
| 0.910141 | 0.7094 K.QHGIPIVTPK[325.13]NPWSMDENLMHISYEAGILENPK.        |
| 0.910131 | 0.6051 R.YQK[325.13]STELLIR.K                              |
| 0.909966 | 0.8138 K.IQGEYK[325.13]YTQVGPDHNR.S                        |
| 0.909927 | 0.6748 R.DYQGPK[325.13]EHEVTIFVR.R                         |
| 0.909926 | 0.5385 K.K[325.13]HGVYNPNK.I                               |
| 0.909875 | 0.8672 R.TANPPKK[325.13]R.-                                |
| 0.909859 | 0.9479 R.FAYKDPEK[325.13]NWNR.N                            |
| 0.909801 | 0.8543 K.NIILGGVK[325.13]AVTLHDQGTAWADLSSQFYLR.E           |
| 0.90979  | 0.8628 R.C[160.03]LPTPK[325.13]C[160.03]HTPPLYR.M          |
| 0.909788 | 0.6944 K.TDLLLEPYNK[325.13]YR.F                            |
| 0.909726 | 0.9572 R.ATNWAK[325.13]FTATASLGVIHK.G                      |
| 0.909712 | 0.1122 K.SVHELEKSK[325.13]R.A                              |
| 0.9097   | 0.9201 R.WPDVARPPFNPHGGAEPGADSAEGDVGDDGDFGAGVN             |
| 0.909646 | 0.7648 R.VFIGNLNTLVVK[325.13]K.S                           |
| 0.909622 | 0.9438 R.SPEEQC[160.03]LDVVTHWIIQEGEEGRPK[325.13]DDR.H     |
| 0.909611 | 0.6108 K.SDFGK[325.13]FVLSSGK.F                            |
| 0.909606 | 0.9845 R.KK[325.13]PEQVVALDAQNIVAVSC[160.03]GEAHTLALN      |
| 0.909589 | 0.865 R.SK[325.13]GTAEKLPEDITQIQPQQLVLR.L                  |
| 0.909533 | 0.956 K.LWNEVLASLK[325.13]DRPASGSPFQLFLSK.V                |
| 0.909491 | 0.6699 K.QFAEMYVAK[325.13]FAAK.G                           |
| 0.909474 | 0.9781 K.K[325.13]SSHAVELAC[160.03]R.D                     |

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| 0.909472 | 0.9377 K.WHYK[325.13]LTK.A                            |
| 0.909384 | 0.6585 R.K[325.13]VGLIAR.R                            |
| 0.909379 | 0.4203 K.GLILSLK[325.13]QQEMMAALTDAIQDK.K             |
| 0.909326 | 0.7007 K.VFDAIMNFKK[325.13]EETAK.L                    |
| 0.909325 | 0.9837 R.EHQMAK[325.13]TGGTQTDLFTC[160.03]GK.C        |
| 0.909229 | 0.979 R.SHPFIK[325.13]EYQAK.E                         |
| 0.909203 | 0.5485 R.K[325.13]IEEIKDFLLTAR.R                      |
| 0.909102 | 0.626 K.TYSAK[325.13]LDNAR.Q                          |
| 0.909056 | 0.8367 R.LILEQMOK[325.13]DPQALSEHLK.N                 |
| 0.908858 | 0.6126 K.TVWDWELMNDIK[325.13]PIWQRPSK.E               |
| 0.908844 | 0.9566 K.GFVEFAAK[325.13]PPAR.K                       |
| 0.908769 | 0.9804 K.TGVIEHEHPVKN[325.13]ISFIAR.D                 |
| 0.908717 | 0.7058 K.K[325.13]PAAAAGAK.K                          |
| 0.908707 | 0.9867 K.K[325.13]LASESVYVSLQSMNSQGR.S                |
| 0.90863  | 0.7844 R.TQLVNVAIFGPPWM[147.04]AFK[325.13]ER.K        |
| 0.90862  | 0.8582 K.TVAPMPPAQDHK[325.13]R.L                      |
| 0.908518 | 0.9867 R.VVNSETPVVDFHAQWC[160.03]GPC[160.03]K[325.13] |
| 0.908356 | 0.9379 K.ETAIELGYLTAEQFDEWVKPK[325.13]DMLGPK.-        |
| 0.908349 | 0.7019 K.NKPYPK[325.13]SR.F                           |
| 0.90834  | 0.6982 R.DLLDPAWEK[325.13]QQR.K                       |
| 0.908209 | 0.7755 K.GRPC[160.03]K[325.13]IVEMSTSK.T              |
| 0.908174 | 0.9699 R.VGQAVDVVGQAGKPK[325.13]TITGFQTHHTTPVLLAHGER  |
| 0.908158 | 0.9875 R.C[160.03]LLAYFLDK[325.13]GADELPYLR.C         |
| 0.908143 | 0.6977 R.AGTFQAFEQFGQQLAHGHYASPEIK[325.13]QK.L        |
| 0.908136 | 0.9702 K.VTK[325.13]NVSKPR.H                          |
| 0.908027 | 0.9765 K.EIPAK[325.13]IIFEDDR.C                       |
| 0.907929 | 0.983 K.SQVTLTK[325.13]EFPVSSGSQHR.K                  |
| 0.907912 | 0.1448 R.LLQDSVDFSLADAINTEFK[325.13]NTR.T             |
| 0.907868 | 0.7699 R.LSK[325.13]EETVLATVQALQTASHLSQQADLR.S        |
| 0.90782  | 0.8641 R.NVIFQPVAELK[325.13]K.Q                       |
| 0.907806 | 0.4672 K.GKWKPPMIDNPSYQGIWK[325.13]PRK.I              |
| 0.907787 | 0.8367 R.RGDDSFQDK[325.13]YR.D                        |
| 0.907774 | 0.8354 R.DFQQALYELSYHVIK[325.13]GNLK.H                |
| 0.907739 | 0.9815 R.HYQTGQPLPK[325.13]NMVSR.L                    |
| 0.90773  | 0.1074 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K       |
| 0.907512 | 0.5917 -.MQIFVK[325.13]TLTGK.T                        |
| 0.907453 | 0.5288 R.RAPFDLFENK[325.13]K.K                        |
| 0.907318 | 0.9035 R.VAHFLEK[325.13]QGFK.Q                        |
| 0.90728  | 0.8787 R.VGLK[325.13]APGIIPR.I                        |
| 0.907101 | 0.2103 R.TLSDYNIQK[325.13]ESTLHLVLR.L                 |
| 0.907084 | 0.6699 R.SGKPAELLK[325.13]MFGIDR.D                    |
| 0.906978 | 0.7681 R.AITGASLADIMAKRNQK[325.13]PEVR.K              |
| 0.906969 | 0.9853 K.EEPAIAPIEHVLSGWK[325.13]AR.T                 |
| 0.906957 | 0.4224 R.AVNYFSK[325.13]VK.Q                          |
| 0.906912 | 0.8973 R.LKPTNPAAQK[325.13]ALTPPTHYK.L                |
| 0.906888 | 0.8585 K.LPDGYEFK[325.13]FPNR.L                       |
| 0.906833 | 0.6944 K.GPK[325.13]VDINAPDVGVGPDWHLK.M               |

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| 0.906778 | 0.9819 R.FHEIC[160.03]SNLVK[325.13]TR.R                |
| 0.906719 | 0.9791 R.FQILGK[325.13]VYSVLSDR.E                      |
| 0.906718 | 0.8115 R.GTLSGWILSK[325.13]AK.K                        |
| 0.906692 | 0.7934 K.YMHSGPVVAMVWEGLNVVK[325.13]TGR.V              |
| 0.906632 | 0.0968 R.GILTLK[325.13]YPIEHGIITNWDDMEK.I              |
| 0.906603 | 0.7946 K.MGVPYC[160.03]IIK[325.13]GK.A                 |
| 0.906599 | 0.4713 R.AK[325.13]VTLNGVPAQPLGPR.A                    |
| 0.906583 | 0.9326 K.DGPLNM[147.04]ILDDGGDLTNLIHTK[325.13]YPQLLPGI |
| 0.906487 | 0.9583 R.K[325.13]SDLHPTLPAGR.Y                        |
| 0.906314 | 0.831 K.TIVFVETK[325.13]R.R                            |
| 0.906229 | 0.8591 K.MGAK[325.13]AMNWMMSGK.I                       |
| 0.906196 | 0.7521 R.K[325.13]ASVHSSGR.G                           |
| 0.906135 | 0.9872 R.LRPQDK[325.13]FLVLATDGLWETMHR.Q               |
| 0.906124 | 0.4322 K.VDIDAPDVDVHGPDWHLK[325.13]MPK.M               |
| 0.906087 | 0.9303 R.HLGK[325.13]PEEYK.M                           |
| 0.90601  | 0.939 R.HAGGHGIEFAPMYK[325.13]INYSR.D                  |
| 0.905997 | 0.8648 K.MK[325.13]LDYILGLK.I                          |
| 0.905846 | 0.6871 K.VVLK[325.13]HLK.K                             |
| 0.905843 | 0.6773 R.YK[325.13]EVYAAAAEVLGLILR.Y                   |
| 0.905835 | 0.6919 K.MSAAQALKK[325.13]GWLYYEAGQR.F                 |
| 0.905831 | 0.6773 K.EGLELLK[325.13]TAIGK.A                        |
| 0.905809 | 0.8591 R.EHC[160.03]PAGQPVK[325.13]VR.V                |
| 0.905806 | 0.9784 K.LKDIAGEFK[325.13]EQLQALIPYVLNPSK.L            |
| 0.905765 | 0.9059 R.RLSYNTASNK[325.13]TR.L                        |
| 0.905733 | 0.6591 K.KAAK[325.13]SAAK.A                            |
| 0.905678 | 0.9827 K.YRPQTLNDLISHQDILSTIQK[325.13]FINEDR.L         |
| 0.905666 | 0.8395 R.K[325.13]NPLPPSVGVVDKK.E                      |
| 0.905617 | 0.8513 K.KGK[325.13]PHC[160.03]SR.N                    |
| 0.905528 | 0.8354 R.VC[160.03]ENIPIVLC[160.03]GNK[325.13]VDIK.D   |
| 0.905524 | 0.9829 K.AGGSASAMLQPLLDNQVGFK[325.13]NMQNVFHVPLSLC     |
| 0.905473 | 0.9856 K.SESK[325.13]TSLLKAAAAAASGGS.R                 |
| 0.90541  | 0.5839 R.NVNVFK[325.13]FIIPQIVK.Y                      |
| 0.905306 | 0.6931 R.K[325.13]IVDQIRPDR.Q                          |
| 0.905289 | 0.9658 K.ELQAHGADELLK[325.13]R.V                       |
| 0.905266 | 0.7522 K.SLKDEDVLQK[325.13]LPVGTATLYFR.D               |
| 0.905238 | 0.9 K.RSSQTQNK[325.13]ASR.K                            |
| 0.905223 | 0.7391 R.WQPPLSHNGVLTGYVLSYHPLDEGGK[325.13]GQLSFNLR    |
| 0.905118 | 0.9835 R.LVNAC[160.03]LAEELPHIHAFEQK[325.13]TLTPDQWAR  |
| 0.905105 | 0.365 K.SK[325.13]DDQVTVIGAGVTLHEALAAELLK.K            |
| 0.905018 | 0.97 K.HFELGGDK[325.13]K.R                             |
| 0.904979 | 0.9594 K.SDLFFHDYSIAPLFVQENYIHVK[325.13]PVAAGGDM[147.  |
| 0.904938 | 0.3429 K.FAAK[325.13]GEGQLGPAER.A                      |
| 0.904906 | 0.0761 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K        |
| 0.904873 | 0.6895 R.WK[325.13]QSVELC[160.03]K.K                   |
| 0.904837 | 0.9642 K.APPARPVK[325.13]GAYR.E                        |
| 0.904793 | 0.8984 R.RTTTGDVQVLGLVHTQK[325.13]LGVIGDK.V            |
| 0.904781 | 0.6871 R.GK[325.13]LGLVGVNLTLDGVK.S                    |

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| 0.904777 | 0.6883 R.LRLPLDK[325.13]EPAR.E                            |
| 0.904704 | 0.7334 R.VFITDDFHDM[147.04]MPK[325.13]YLNFBK.G            |
| 0.904358 | 0.9648 R.KTPC[160.03]GEGSK[325.13]TWDR.F                  |
| 0.90432  | 0.7033 K.IISK[325.13]IENHEGVR.R                           |
| 0.904243 | 0.9599 R.AVGNIIVTGTDEQTQVVLNC[160.03]DVLSHFNPILLSHPK[3    |
| 0.90418  | 0.6062 K.K[325.13]AQLNIGNVLPVGTMPGIVC[160.03]C[160.0:     |
| 0.904119 | 0.9869 R.AMGK[325.13]AYHPGC[160.03]FTC[160.03]VVC[160.0   |
| 0.904055 | 0.9712 K.LNSLMSLVNK[325.13]TTHLIAK.E                      |
| 0.90397  | 0.5872 R.LDHLAEK[325.13]FR.Q                              |
| 0.903898 | 0.978 K.IK[325.13]LQVWDTAGQER.F                           |
| 0.903858 | 0.6727 R.AVTGYTDPYTGQQISLFQAMQK[325.13]GLIVR.E            |
| 0.903797 | 0.9489 R.FKEK[325.13]LPAPIPLEFFAVVMGTGISAGFNLK.E          |
| 0.903696 | 0.5785 R.ASNGDAWVEAHGK[325.13]LYSPSQIGAFVLMK.M            |
| 0.903695 | 0.9849 R.K[325.13]TLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR.R       |
| 0.90369  | 0.9837 K.EIDKNDHLYILLSTLEPTDAGILGTTK[325.13]DSPK.L        |
| 0.903679 | 0.0778 R.GENSWFSTQVDTVATK[325.13]VK.D                     |
| 0.903667 | 0.9305 R.IAGQVAAANK[325.13]K.H                            |
| 0.903634 | 0.8834 R.VITYLDHSTQKPLIAC[160.03]VEK[325.13]QLLGEHLTAILC  |
| 0.90353  | 0.9764 R.LNVDFALHK[325.13]ER.K                            |
| 0.903483 | 0.8172 R.VLEC[160.03]LASGIVMPDGSIGYDPC[160.03]EK[325.13   |
| 0.903429 | 0.9504 K.EPPLLLGVLHPNTK[325.13]LR.Q                       |
| 0.90326  | 0.3782 K.DDQHFTVTGLHK[325.13]GTTYIFR.L                    |
| 0.903178 | 0.8883 R.YNFFTGC[160.03]PK[325.13]AK.T                    |
| 0.903015 | 0.6849 K.HVFHPK[325.13]R.A                                |
| 0.90299  | 0.9407 K.YKETDLLILFK[325.13]DDYFAK.K                      |
| 0.902945 | 0.9588 K.EK[325.13]EQC[160.03]C[160.03]VSLAAGLPHFSSGIFR.( |
| 0.902877 | 0.5666 R.SLVEIIEHGLVDEQQK[325.13]VR.T                     |
| 0.902873 | 0.6615 K.EKPGPEDK[325.13]LHEQC[160.03]RPWR.K              |
| 0.902858 | 0.9732 K.SLEK[325.13]MGYNAC[160.03]TLHGK.G                |
| 0.902702 | 0.9455 R.GVEVDPSLIK[325.13]DTWHQVYR.R                     |
| 0.902697 | 0.789 R.ETLK[325.13]AIHYALNC[160.03]C[160.03]GLAGGVEQFI   |
| 0.902675 | 0.9677 K.QK[325.13]GHFFVEDQIYC[160.03]EK.H                |
| 0.902501 | 0.9856 R.HGLINFGIYK[325.13]R.I                            |
| 0.902449 | 0.651 K.YHTINGHNC[160.03]EVK[325.13]K.A                   |
| 0.90238  | 0.9857 R.ILPHPK[325.13]FDPR.T                             |
| 0.90232  | 0.9676 R.TLK[325.13]TLLHTLC[160.03]K.L                    |
| 0.902289 | 0.6844 R.KSAPATGGVK[325.13]KPHR.Y                         |
| 0.902244 | 0.2607 K.VVLAYEPVWAIGTGK[325.13]TATPQQAQEVHEK.L           |
| 0.902195 | 0.9857 R.SC[160.03]HYGVIDK[325.13]FR.L                    |
| 0.902176 | 0.9448 R.VLMEK[325.13]EFPGFLENQKDPLAVDK.I                 |
| 0.902111 | 0.9866 K.ANTLIAFTK[325.13]LLGAPTHILR.D                    |
| 0.902093 | 0.8163 R.VEWK[325.13]FDQGDTR.L                            |
| 0.902088 | 0.9856 R.VANPK[325.13]DIIHFFR.H                           |
| 0.902085 | 0.1012 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K           |
| 0.902079 | 0.9785 R.FAGVFHVEK[325.13]NGR.Y                           |
| 0.902034 | 0.9016 R.DGMLDDEEFALASHLIEAK[325.13]LEGHGLPANLPR.R        |
| 0.901963 | 0.8151 R.VSLDVNHFADELTVK[325.13]TK.D                      |

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| 0.901917 | 0.6723 | K.QAADAEMEK[325.13]HKK.F                        |
| 0.901904 | 0.9786 | K.VK[325.13]LEGHELPADLPPHLVPPSK.R               |
| 0.901828 | 0.9594 | K.RNEIDAEPKAK[325.13]R.H                        |
| 0.901819 | 0.8221 | K.VEVTAPDVEVSLPSVEVDVKAPGAK[325.13]LDGAR.L      |
| 0.90169  | 0.9551 | K.RKPK[325.13]SQETPATK.K                        |
| 0.901656 | 0.8441 | R.K[325.13]HGVVPLATYMR.I                        |
| 0.901597 | 0.985  | R.VGNPWDPNVLYGPLHTK[325.13]QAVSMFLGAVEEAK.K     |
| 0.901503 | 0.9493 | K.TPGQNAQK[325.13]WIPAR.S                       |
| 0.90148  | 0.4041 | K.FHGTVK[325.13]AENGK.L                         |
| 0.901288 | 0.6603 | K.YGK[325.13]IVGC[160.03]SVHK.G                 |
| 0.90126  | 0.9854 | R.THAGKK[325.13]AHGR.G                          |
| 0.901244 | 0.8328 | K.RLK[325.13]AADIDQEVK.E                        |
| 0.901221 | 0.6805 | K.MDIDAPDVDVHGPDWHLK[325.13]MPK.M               |
| 0.901195 | 0.5633 | R.AAAEK[325.13]LFGNM[147.04]EGDC[160.03]PSDWK.T |
| 0.901111 | 0.9167 | R.K[325.13]DLQHPNEFIR.G                         |
| 0.901055 | 0.9754 | K.MGYNAC[160.03]TLHGGK[325.13]GQEQR.E           |
| 0.900971 | 0.665  | K.GTGASGSFK[325.13]LNKK.A                       |
| 0.900947 | 0.7409 | K.GSREEKQK[325.13]PQAER.K                       |
| 0.900928 | 0.5886 | K.SIYGKEKFEDENFILK[325.13]HTGPGILSMANAGPNTNGSQ  |
| 0.900856 | 0.965  | K.K[325.13]IFQIPWMHAAR.H                        |
| 0.900835 | 0.9546 | K.HLPNDPMFK[325.13]LVAQLYK.I                    |
| 0.900814 | 0.3567 | R.QLFHPEQLITGK[325.13]EDAANNYAR.G               |
| 0.900698 | 0.6848 | K.FNALFAQGNYSEAAKVAANAPK[325.13]GILR.T          |
| 0.900643 | 0.8489 | R.K[325.13]AIIIFVPVPQLK.S                       |
| 0.900616 | 0.4016 | K.LDSEDKDK[325.13]EGKPLLK.A                     |
| 0.900572 | 0.122  | R.LLLPGELAKHAVSEGK[325.13]AVTK.Y                |
| 0.900511 | 0.8088 | R.DMHSAYK[325.13]HADGK.K                        |
| 0.900507 | 0.8906 | R.IGTLEK[325.13]EHNVFQNK.I                      |
| 0.900458 | 0.8417 | R.LQLLEPFDKWDGK[325.13]DLEDLQILIK.V             |
| 0.900455 | 0.9819 | R.HVYTGGK[325.13]GC[160.03]VK.V                 |
| 0.900424 | 0.8566 | K.GYAFVHFETQEAADK[325.13]AIEK.M                 |
| 0.900364 | 0.5506 | K.EVQALIAEGIALVWESYK[325.13]LDPYVQR.L           |
| 0.900239 | 0.6035 | R.ELAQQIQK[325.13]VVMALGDYMGASC[160.03]HAC[16   |
| 0.900198 | 0.6823 | R.HPFIVNHPK[325.13]VGR.V                        |
| 0.899948 | 0.6213 | K.IVLQK[325.13]YHTINGHNAEVR.K                   |
| 0.899907 | 0.6773 | K.VLNNMEIGTSLFDEEGAK[325.13]IVK.D               |
| 0.899896 | 0.9611 | K.DYGALK[325.13]DIVINANPASPLSLVLHR.L            |
| 0.899814 | 0.5699 | R.FDASFFGVHPK[325.13]QAHTM[147.04]DPQLR.L       |
| 0.899774 | 0.86   | R.GQHTK[325.13]TTGR.R                           |
| 0.899745 | 0.7805 | R.YTLHYK[325.13]TDAPLNIR.S                      |
| 0.899706 | 0.4254 | K.KPAAATVTK[325.13]K.V                          |
| 0.899671 | 0.7385 | R.IVSLEPAYPPVFYLNK[325.13]DTGEIYTTSVTLDR.E      |
| 0.899505 | 0.2015 | K.IAPSFIVESIEDALK[325.13]AADTIGYPVM[147.04]IR.S |
| 0.899484 | 0.6192 | K.SAPATGGVKK[325.13]PHR.Y                       |
| 0.899429 | 0.6073 | K.HGIK[325.13]TVSQIISLQTLK.K                    |
| 0.899377 | 0.6519 | K.AK[325.13]LGDSHDLQR.F                         |
| 0.899349 | 0.9704 | K.DIQTNVYIK[325.13]HPVSLEQYLMESYNK.V            |

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| 0.899343 | 0.9342 R.VVSSIEQK[325.13]TEGAEEK.Q                  |
| 0.899332 | 0.6253 K.GKWKPPM[147.04]IDNPSYQGIWK[325.13]PRK.I    |
| 0.899329 | 0.7884 R.LIK[325.13]VHLDK.A                         |
| 0.899328 | 0.9557 R.GK[325.13]NVVHQLSVTLEDLYNGATR.K            |
| 0.899054 | 0.9569 K.K[325.13]SMIASTAITVHYLDLSLNPSGEVTR.Q       |
| 0.89903  | 0.9774 K.SNTHEFVNLVK[325.13]ELALPGELTQSR.S          |
| 0.899029 | 0.9141 K.KGDSSAEELK[325.13]LATQLTGPVMPVR.N          |
| 0.899008 | 0.7718 K.HELQANC[160.03]YEEVK[325.13]DR.C           |
| 0.898981 | 0.876 R.ASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGG    |
| 0.898979 | 0.755 R.NYYEQWGK[325.13]LTDC[160.03]VVM[147.04]R.D  |
| 0.898888 | 0.9446 R.VMDGLLVIAMNK[325.13]HR.E                   |
| 0.898848 | 0.3971 K.FK[325.13]MPEMHFK.T                        |
| 0.89878  | 0.829 K.IIPLVVK[325.13]FC[160.03]NVDDDEL.R.E        |
| 0.89875  | 0.3398 R.TLLAK[325.13]NLPYK.V                       |
| 0.89873  | 0.4811 R.K[325.13]LAVNM[147.04]VPFPR.L              |
| 0.898574 | 0.9194 K.IFVGGLSPDTPEEK[325.13]IR.E                 |
| 0.898442 | 0.8787 K.DK[325.13]MMNGGHHYTYSEN.R.V                |
| 0.898404 | 0.8517 R.HSQYHVDGSLEK[325.13]DR.T                   |
| 0.898376 | 0.6736 R.QK[325.13]AEADKNDK.S                       |
| 0.898364 | 0.9509 R.AQK[325.13]LHFLQR.G                        |
| 0.898298 | 0.9665 R.TPALVFEHVNNTDFK[325.13]QLYQTLTDYDIR.F      |
| 0.89829  | 0.829 R.TRLAADVGK[325.13]AGAER.E                    |
| 0.898286 | 0.9497 K.GPLK[325.13]TPIAAGHPSMNLLLR.K              |
| 0.898153 | 0.7937 R.DQLEAAQEAVPPADIVFSVK[325.13]SPPSAGYLVMSR.G |
| 0.898141 | 0.8954 -.MK[325.13]FNPVFTSDR.S                      |
| 0.898138 | 0.5925 K.C[160.03]SRAEAEAWYQTK[325.13]FETLQAQAGK.H  |
| 0.898119 | 0.986 K.YNC[160.03]TGLNFGK[325.13]VDVGR.Y           |
| 0.898088 | 0.4054 R.WQLK[325.13]ANEALR.L                       |
| 0.898071 | 0.9669 K.LGEWVGLC[160.03]K[325.13]IDR.E             |
| 0.898069 | 0.1579 R.LQLETEIEALK[325.13]EELLFM[147.04]K.K       |
| 0.898062 | 0.9737 K.WAAGQNK[325.13]QHSITK.N                    |
| 0.898038 | 0.8895 R.IEHIK[325.13]HSK.S                         |
| 0.897998 | 0.7429 K.GVFTK[325.13]ELPSGK.K                      |
| 0.897918 | 0.9814 K.IHQETFGK[325.13]SGC[160.03]R.R             |
| 0.897902 | 0.6544 K.MPEMHFK[325.13]APK.I                       |
| 0.897886 | 0.9403 R.LMELFPANK[325.13]QSVEHFTK.Y                |
| 0.897839 | 0.8303 R.GKQGK[325.13]AR.A                          |
| 0.897835 | 0.6723 K.SVHELEK[325.13]SK.R                        |
| 0.897776 | 0.8505 R.EYK[325.13]VVGR.C                          |
| 0.897735 | 0.9722 K.LQHINPLLPAC[160.03]LNK[325.13]EESK.T       |
| 0.89766  | 0.6568 R.NVDSNNK[325.13]ELSIAIR.G                   |
| 0.897577 | 0.6748 K.LKGPK[325.13]FK.M                          |
| 0.897564 | 0.4449 R.MFAPTK[325.13]TWR.R                        |
| 0.897521 | 0.8194 K.VGVLAASMEAK[325.13]ASSQQEKEDKPAETK.K       |
| 0.897371 | 0.9561 R.HLPGVC[160.03]K[325.13]VSTDLLR.E           |
| 0.897208 | 0.9732 R.IHGVGFK[325.13]K.R                         |
| 0.897074 | 0.6739 K.K[325.13]AGGTKPK.K                         |

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| 0.896989 | 0.7935 R.GSTPEAAAQVVQWVSFADSDIVPPASTWVFPTLGIMHHNI      |
| 0.896957 | 0.976 K.ELWFSDDPNVTK[325.13]TLR.F                      |
| 0.896925 | 0.1046 K.YPIEHGIITNWDDM[147.04]EK[325.13]IWHHTFYNELR.V |
| 0.896924 | 0.8319 R.LPSAHTC[160.03]FNQLDLPAYESFEK[325.13]LR.H     |
| 0.896904 | 0.7346 R.RPIK[325.13]GAAGRPLELSDFR.M                   |
| 0.896721 | 0.9449 R.FKEK[325.13]LPAPILEFFAVVMGTGISAGFNLK.E        |
| 0.896691 | 0.982 K.LLGMGDIEGLIDK[325.13]VNELK.L                   |
| 0.896634 | 0.9503 R.YVQK[325.13]GEYR.T                            |
| 0.89661  | 0.9848 K.APTIVGK[325.13]SSLNPILFR.G                    |
| 0.896516 | 0.8606 R.DM[147.04]FC[160.03]K[325.13]ILHGFK.N         |
| 0.896408 | 0.9527 K.HGEK[325.13]VSLSSK.C                          |
| 0.896358 | 0.3502 R.GELAIK[325.13]DANAK.L                         |
| 0.896261 | 0.7857 K.HK[325.13]FM[147.04]VQTIFAPPNTSDMEAVWK.E      |
| 0.896052 | 0.5797 R.AAPGAEFAPNK[325.13]R.R                        |
| 0.895924 | 0.9252 R.VQIEHISSLIK[325.13]LSK.A                      |
| 0.89587  | 0.9293 R.LALK[325.13]FHPDKNHAPGATEAFK.A                |
| 0.895774 | 0.9198 K.LWC[160.03]HVHLK[325.13]K.S                   |
| 0.895647 | 0.6627 R.FMNAVFFLLPK[325.13]FHGVK.T                    |
| 0.895606 | 0.2206 K.VLK[325.13]QVHPDTGISSKAMGIMNSFVNDIFER.I       |
| 0.895566 | 0.5119 R.KQLATK[325.13]AAR.K                           |
| 0.89555  | 0.8617 K.K[325.13]LETAVNLAWTAGNSNTR.F                  |
| 0.895424 | 0.4184 R.VNFAMNVGK[325.13]AR.G                         |
| 0.895329 | 0.9417 R.IHFFLSK[325.13]K.K                            |
| 0.895194 | 0.9796 K.EK[325.13]IYVLLR.R                            |
| 0.895168 | 0.5594 R.K[325.13]VIDDTNITR.L                          |
| 0.89514  | 0.0944 K.EITALAPSTM[147.04]KIK[325.13]IIAPPER.K        |
| 0.895112 | 0.9453 R.SVLISLK[325.13]QAPLVH.-                       |
| 0.895056 | 0.9268 K.QLDDLK[325.13]VELSQLR.V                       |
| 0.894914 | 0.7854 R.IVATK[325.13]PLYVALAQR.K                      |
| 0.89491  | 0.9805 R.GDIPDLSQAPSSLLDALEQHLASLEGK[325.13]K.I        |
| 0.894813 | 0.9426 K.VTPQSDGSSSK[325.13]VK.V                       |
| 0.894785 | 0.6674 R.KK[325.13]TATAVAHC[160.03]K.R                 |
| 0.894666 | 0.829 K.LYGDLK[325.13]HLK.T                            |
| 0.894427 | 0.9808 K.SSVHQPGSHYC[160.03]QGC[160.03]AYK[325.13]K.G  |
| 0.894423 | 0.954 R.ARVQAQSTNDGLDFQESQLVK[325.13]K.L               |
| 0.894357 | 0.5648 K.VLK[325.13]QVHPDTGISSKAMGIM[147.04]NSFVNDIFEI |
| 0.894346 | 0.5853 R.GAPLAK[325.13]VVFR.D                          |
| 0.894342 | 0.9575 K.SSIIVADESTISWGPSPTFGELGYGDHK[325.13]PK.S      |
| 0.894254 | 0.907 K.ISAWHNNVEK[325.13]TLPSTK.A                     |
| 0.894198 | 0.9738 R.TEVVK[325.13]NNLNPVWRPFK.I                    |
| 0.894176 | 0.5349 R.ALTVPELTQQVFDK[325.13]NMMAAC[160.03]DPR.H     |
| 0.894131 | 0.6557 R.FLSQPFQVAEVFTGHMGK[325.13]LVPLK.E             |
| 0.894112 | 0.3423 R.SKGQESFK[325.13]K.Q                           |
| 0.894073 | 0.9812 K.YNIEK[325.13]DIAAHK.K                         |
| 0.894063 | 0.8063 R.AK[325.13]VEFNIR.K                            |
| 0.893996 | 0.9567 K.HLEEVLEMK[325.13]QEALLAAISEK.D                |
| 0.893912 | 0.8036 K.KPEAK[325.13]FFTPSK.S                         |

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| 0.89388  | 0.8698 | R.ASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGG     |
| 0.893864 | 0.9413 | R.MLQPSSSPLWGK[325.13]LR.V                     |
| 0.893802 | 0.9291 | K.NSTIVFPLPIDMLQGIIGAK[325.13]HSHLG.-          |
| 0.893787 | 0.9818 | R.EK[325.13]ELSIHFVPGSC[160.03]R.L             |
| 0.893728 | 0.4242 | K.HAVSEGTK[325.13]AVTKYTSAK.-                  |
| 0.893728 | 0.6476 | R.QLLHNFPPDQLTSSGAPFWSGPK[325.13]R.C           |
| 0.893696 | 0.9759 | R.SWHDIDK[325.13]DNAK.Y                        |
| 0.893672 | 0.9247 | R.EPSLSPK[325.13]LTC[160.03]LQNLK.W            |
| 0.893612 | 0.79   | R.NSQGK[325.13]GAHRPEHASGR.R                   |
| 0.893602 | 0.9112 | R.ELGSLPQEAFEK[325.13]YQTLCLK.Q                |
| 0.893499 | 0.981  | R.SK[325.13]EGSIWNHQPC[160.03]FLK.D            |
| 0.893475 | 0.9649 | R.YNDYK[325.13]LDFR.R                          |
| 0.893411 | 0.9245 | K.K[325.13]AAVHYDR.S                           |
| 0.89329  | 0.3964 | K.AAKPKVVK[325.13]PK.K                         |
| 0.893248 | 0.9652 | K.LGEWVGLC[160.03]K[325.13]IDR.E               |
| 0.893099 | 0.955  | R.VIPVK[325.13]LGIIIGVVNR.S                    |
| 0.892984 | 0.9762 | R.EVEHFLK[325.13]AEPEK.N                       |
| 0.892918 | 0.8354 | R.WLK[325.13]GGVVLK.E                          |
| 0.892826 | 0.314  | K.VEAK[325.13]FINYVK.N                         |
| 0.892712 | 0.931  | R.DAVHNK[325.13]LWLQR.R                        |
| 0.892694 | 0.9653 | R.NHYLK[325.13]DIER.M                          |
| 0.892599 | 0.3654 | R.AFITNIPFDVK[325.13]WQSLK.D                   |
| 0.89245  | 0.9789 | R.FHINQPALK[325.13]QR.E                        |
| 0.892444 | 0.8113 | R.GK[325.13]IGLDFC[160.03]K.Y                  |
| 0.89236  | 0.7954 | R.TDRGGDSIGETPTPGASK[325.13]R.K                |
| 0.892326 | 0.9811 | R.NC[160.03]SSFLIK[325.13]R.N                  |
| 0.892325 | 0.801  | R.GQVAK[325.13]LEAALGEAK.K                     |
| 0.892324 | 0.9045 | R.K[325.13]HFPSVNWLSYSK.Y                      |
| 0.892049 | 0.6086 | K.VK[325.13]AFGPGLQGGGAGSPAR.F                 |
| 0.891922 | 0.6583 | K.AIDDNMSLDEIEK[325.13]LTYIDKWFLYK.M           |
| 0.891869 | 0.39   | R.MVTSESKNVK[325.13]LTVSNVLK.E                 |
| 0.891806 | 0.7588 | R.AK[325.13]FYPEDVSEELIQDITQR.L                |
| 0.8918   | 0.7228 | R.KTVTAM[147.04]DVVYALK[325.13]R.Q             |
| 0.891725 | 0.916  | K.TEFLSFMNTELAFTK[325.13]NQK.D                 |
| 0.891704 | 0.9783 | K.VNIISVTNK[325.13]GLLHSFDLLK.A                |
| 0.891666 | 0.9814 | R.IK[325.13]DEFQLLQAQYHSLK.L                   |
| 0.891634 | 0.8895 | R.VLLGETGKEK[325.13]LPR.Y                      |
| 0.89163  | 0.8095 | R.ASSHSSQTQGGGSVTK[325.13]K.R                  |
| 0.891605 | 0.6296 | R.VHFK[325.13]NTR.E                            |
| 0.891598 | 0.1226 | R.HNGTGGK[325.13]SIYGEK.F                      |
| 0.891591 | 0.7915 | K.K[325.13]QHLEIELK.Q                          |
| 0.89153  | 0.3905 | R.LDHLEAK[325.13]FR.Q                          |
| 0.89151  | 0.8726 | R.IHIMPSMNPDGFEAVKK[325.13]PDC[160.03]YYSIGR.E |
| 0.891499 | 0.9319 | R.SPEEQC[160.03]LDVVTHWIEGEEGRPK[325.13]DDR.H  |
| 0.891496 | 0.9754 | R.VVLSGHHPFK[325.13]IFTK.M                     |
| 0.891462 | 0.959  | R.LKDK[325.13]WDELK.E                          |
| 0.891433 | 0.9732 | R.IEQLSPFPFDLLK[325.13]EVQK.Y                  |



|          |                                                      |
|----------|------------------------------------------------------|
| 0.891415 | 0.9588 R.YAHEK[325.13]LNASR.G                        |
| 0.891348 | 0.3458 R.TAPDLLPHK[325.13]PLPASAYIEDGRFDLSMPHVQDPSLV |
| 0.891315 | 0.5629 K.SMK[325.13]FVDGLMIHSGDPVNYYVDTAVR.H         |
| 0.891249 | 0.343 K.GATYGK[325.13]PVHHGVNQLK.F                   |
| 0.891177 | 0.9158 R.YHQIGSGK[325.13]C[160.03]EIK.V              |
| 0.891045 | 0.8095 R.K[325.13]AAALEFLNR.F                        |

| protein                        | calc_neutral_pep_mass |
|--------------------------------|-----------------------|
| sp P11387 TOP1_HUMAN           | 1708.7289             |
| sp Q09161 NCBP1_HUMAN          | 1672.6826             |
| sp Q14978 NOLC1_HUMAN          | 2017.0956             |
| sp Q14978 NOLC1_HUMAN          | 2017.0956             |
| sp P16403 H12_HUMAN            | 1219.6925             |
| sp P51397 DAP1_HUMAN           | 1942.9385             |
| sp Q14978 NOLC1_HUMAN          | 2017.0956             |
| sp Q14978 NOLC1_HUMAN          | 2017.0956             |
| sp Q14978 NOLC1_HUMAN          | 2017.0956             |
| sp Q09161 NCBP1_HUMAN          | 1672.6826             |
| sp P16403 H12_HUMAN            | 1219.6925             |
| sp P16401 H15_HUMAN            | 1346.7558             |
| sp P16401 H15_HUMAN            | 1346.7558             |
| sp P62987 RL40_HUMAN           | 1520.7154             |
| sp P46778 RL21_HUMAN           | 1187.5935             |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1501.7637             |
| sp P14866 HNRPL_HUMAN          | 3574.5078             |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1501.7637             |
| sp P08047 SP1_HUMAN            | 1661.7402             |
| sp P08047 SP1_HUMAN            | 1661.7402             |
| sp P14866 HNRPL_HUMAN          | 3574.5078             |
| sp P14866 HNRPL_HUMAN          | 3574.5078             |
| sp P08047 SP1_HUMAN            | 1661.7402             |
| sp P23246 SFPQ_HUMAN           | 1755.8176             |
| sp P51991 ROA3_HUMAN           | 1795.7948             |
| sp P23246 SFPQ_HUMAN           | 1755.8176             |
| sp P62424 RL7A_HUMAN           | 1438.7205             |
| sp P23246 SFPQ_HUMAN           | 1755.8176             |
| sp P51991 ROA3_HUMAN           | 1795.7948             |
| sp Q16891 MIC60_HUMAN          | 1931.0112             |
| sp Q16891 MIC60_HUMAN          | 1931.0112             |
| sp Q16891 MIC60_HUMAN          | 1931.0112             |
| sp P35579 MYH9_HUMAN           | 1408.6947             |
| sp Q8IWS0 PHF6_HUMAN           | 1802.7682             |
| sp O14715 RGPD8_HUMAN,sp P497  | 1731.7635             |
| sp Q8IWS0 PHF6_HUMAN           | 1802.7682             |
| sp Q8IWS0 PHF6_HUMAN           | 1802.7682             |
| sp O14715 RGPD8_HUMAN,sp P497  | 1731.7635             |
| sp Q8IWS0 PHF6_HUMAN           | 1802.7682             |
| sp Q71RC2 LARP4_HUMAN          | 1999.9963             |
| sp Q9P0L0 VAPA_HUMAN           | 1971.9286             |
| sp P41250 GARS_HUMAN           | 1833.8242             |
| sp O14715 RGPD8_HUMAN,sp P497  | 1731.7635             |
| sp O14715 RGPD8_HUMAN,sp P497  | 1731.7635             |
| sp Q71RC2 LARP4_HUMAN          | 1999.9963             |
| sp Q71RC2 LARP4_HUMAN          | 1999.9963             |

[illegible]

|                                |           |
|--------------------------------|-----------|
| sp O43707 ACTN4_HUMAN,sp P356  | 1949.8504 |
| sp P35241 RADI_HUMAN           | 2149.044  |
| sp P26038 MOES_HUMAN           | 2148.0236 |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp Q14152 EIF3A_HUMAN          | 1760.8734 |
| sp Q14152 EIF3A_HUMAN          | 1760.8734 |
| sp Q92804 RBP56_HUMAN          | 2331.178  |
| sp Q92804 RBP56_HUMAN          | 2331.178  |
| sp Q9Y3F4 STRAP_HUMAN          | 2750.3763 |
| sp Q13283 G3BP1_HUMAN          | 3095.4333 |
| sp Q06830 PRDX1_HUMAN          | 2817.3392 |
| sp Q06830 PRDX1_HUMAN          | 2817.3392 |
| sp Q06830 PRDX1_HUMAN          | 2817.3392 |
| sp Q969P0 IGSF8_HUMAN          | 1865.902  |
| sp Q13283 G3BP1_HUMAN          | 3095.4333 |
| sp Q13162 PRDX4_HUMAN          | 1687.8529 |
| sp Q06830 PRDX1_HUMAN          | 2817.3392 |
| sp Q06830 PRDX1_HUMAN          | 2817.3392 |
| sp P21333 FLNA_HUMAN           | 2564.2619 |
| sp Q13162 PRDX4_HUMAN          | 1687.8529 |
| sp Q13283 G3BP1_HUMAN          | 3095.4333 |
| sp Q13283 G3BP1_HUMAN          | 3095.4333 |
| sp P21333 FLNA_HUMAN           | 2564.2619 |
| sp P21333 FLNA_HUMAN           | 2564.2619 |
| sp P21333 FLNA_HUMAN           | 2564.2619 |
| sp P21333 FLNA_HUMAN           | 2564.2619 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P61513 RL37A_HUMAN          | 2253.0194 |
| sp P61513 RL37A_HUMAN          | 2253.0194 |
| sp P15880 RS2_HUMAN            | 2037.9731 |
| sp P61513 RL37A_HUMAN          | 2253.0194 |
| sp Q969P0 IGSF8_HUMAN          | 1865.902  |
| sp Q9NR30 DDX21_HUMAN          | 1818.9476 |
| sp Q969P0 IGSF8_HUMAN          | 1865.902  |
| sp P27816 MAP4_HUMAN           | 3280.6398 |
| sp Q969P0 IGSF8_HUMAN          | 1865.902  |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp Q9P2B2 FPRP_HUMAN           | 2816.3478 |
| sp P27816 MAP4_HUMAN           | 3280.6398 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp Q9P2B2 FPRP_HUMAN           | 2816.3478 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp Q9P2B2 FPRP_HUMAN           | 2816.3478 |
| sp O75694 NU155_HUMAN          | 2220.1175 |
| sp Q01105 SET_HUMAN            | 2424.2649 |

|                                |           |
|--------------------------------|-----------|
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp O75694 NU155_HUMAN          | 2220.1175 |
| sp P22626 ROA2_HUMAN           | 2188.1025 |
| sp Q01105 SET_HUMAN            | 2424.2649 |
| sp P22626 ROA2_HUMAN           | 2188.1025 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P62888 RL30_HUMAN           | 2693.1929 |
| sp P62888 RL30_HUMAN           | 2693.1929 |
| sp P62888 RL30_HUMAN           | 2693.1929 |
| sp Q01105 SET_HUMAN            | 2424.2649 |
| sp P09429 HMGB1_HUMAN,sp B2RF  | 1844.9632 |
| sp P22626 ROA2_HUMAN           | 2188.1025 |
| sp O43707 ACTN4_HUMAN          | 2314.1917 |
| sp P62888 RL30_HUMAN           | 2693.1929 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P09429 HMGB1_HUMAN,sp B2RF  | 1844.9632 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P61313 RL15_HUMAN           | 1915.9541 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp O43707 ACTN4_HUMAN          | 2314.1917 |
| sp O43707 ACTN4_HUMAN          | 2314.1917 |
| sp P61313 RL15_HUMAN           | 1915.9541 |
| sp P16435 NCPR_HUMAN           | 2054.9156 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P62979 RS27A_HUMAN          | 2576.0229 |
| sp P09429 HMGB1_HUMAN          | 1916.8905 |
| sp Q14839 CHD4_HUMAN           | 2451.2282 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P09429 HMGB1_HUMAN          | 1916.8905 |
| sp P49411 EFTU_HUMAN           | 1814.9713 |
| sp P35579 MYH9_HUMAN           | 2022.9681 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp P09429 HMGB1_HUMAN          | 1916.8905 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |

|                                |           |
|--------------------------------|-----------|
| sp P62854 RS26_HUMAN,sp Q5JNZ5 | 2024.9561 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp P09429 HMGB1_HUMAN          | 1916.8905 |
| sp P09429 HMGB1_HUMAN          | 1916.8905 |
| sp Q8IWS0 PHF6_HUMAN           | 2829.1584 |
| sp Q8IVF2 AHNK2_HUMAN          | 2032.0378 |
| sp P22087 FBRL_HUMAN           | 1957.0421 |
| sp P46940 IQGA1_HUMAN          | 1805.9272 |
| sp P22087 FBRL_HUMAN           | 1957.0421 |
| sp Q12788 TBL3_HUMAN           | 2119.9382 |
| sp Q9NX63 MIC19_HUMAN          | 3038.3433 |
| sp Q00839 HNRPU_HUMAN          | 1834.885  |
| sp Q00839 HNRPU_HUMAN          | 1834.885  |
| sp Q9NX63 MIC19_HUMAN          | 3038.3433 |
| sp Q9NX63 MIC19_HUMAN          | 3038.3433 |
| sp P28288 ABCD3_HUMAN          | 2359.0717 |
| sp Q00839 HNRPU_HUMAN          | 1834.885  |
| sp Q00839 HNRPU_HUMAN          | 1834.885  |
| sp P28288 ABCD3_HUMAN          | 2359.0717 |
| sp Q14126 DSG2_HUMAN           | 1916.9592 |
| sp Q92901 RL3L_HUMAN,sp P39023 | 1561.746  |
| sp P62424 RL7A_HUMAN           | 1673.8274 |
| sp P28288 ABCD3_HUMAN          | 2359.0717 |
| sp P28288 ABCD3_HUMAN          | 2359.0717 |
| sp O95573 ACSL3_HUMAN          | 2384.0822 |
| sp P62266 RS23_HUMAN           | 2044.0126 |
| sp P62424 RL7A_HUMAN           | 1673.8274 |
| sp O75083 WDR1_HUMAN           | 4211.7754 |
| sp O75083 WDR1_HUMAN           | 4211.7754 |
| sp O75475 PSIP1_HUMAN,sp Q7Z4V | 1438.6452 |
| sp P23396 RS3_HUMAN            | 2050.1099 |
| sp Q9NQC3 RTN4_HUMAN           | 2145.0603 |
| sp Q9NQC3 RTN4_HUMAN           | 2145.0603 |
| sp O95573 ACSL3_HUMAN          | 2384.0822 |
| sp P23396 RS3_HUMAN            | 2050.1099 |
| sp P62266 RS23_HUMAN           | 2044.0126 |
| sp Q9NQC3 RTN4_HUMAN           | 2145.0603 |
| sp Q9NQC3 RTN4_HUMAN           | 2145.0603 |
| sp O43707 ACTN4_HUMAN          | 2399.0455 |
| sp P38606 VATA_HUMAN           | 2450.303  |
| sp P48643 TCPE_HUMAN           | 2070.0269 |
| sp P48643 TCPE_HUMAN           | 2070.0269 |
| sp P62424 RL7A_HUMAN           | 1673.8274 |
| sp P31948 STIP1_HUMAN          | 1896.8755 |
| sp P62424 RL7A_HUMAN           | 1673.8274 |
| sp P20700 LMNB1_HUMAN          | 2431.1656 |
| sp P62424 RL7A_HUMAN           | 1673.8274 |

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|---------------------------------|-----------|
| sp P62424 RL7A_HUMAN            | 1673.8274 |
| sp P20700 LMNB1_HUMAN           | 2431.1656 |
| sp O43707 ACTN4_HUMAN           | 2399.0455 |
| sp O43707 ACTN4_HUMAN           | 2399.0455 |
| sp P27635 RL10_HUMAN            | 1874.985  |
| sp P26640 SYVC_HUMAN            | 1614.7249 |
| sp Q9Y2X3 NOP58_HUMAN           | 2195.1011 |
| sp Q9Y2X3 NOP58_HUMAN           | 2195.1011 |
| sp O43707 ACTN4_HUMAN           | 2399.0455 |
| sp P26640 SYVC_HUMAN            | 1614.7249 |
| sp O43707 ACTN4_HUMAN           | 2399.0455 |
| sp Q9Y2X3 NOP58_HUMAN           | 2195.1011 |
| sp Q9Y2X3 NOP58_HUMAN           | 2195.1011 |
| sp P26640 SYVC_HUMAN            | 1614.7249 |
| sp P10586 PTPRF_HUMAN           | 3008.39   |
| sp Q96SI9 STRBP_HUMAN,sp Q1290  | 2085.9967 |
| sp P10586 PTPRF_HUMAN           | 3008.39   |
| sp P10586 PTPRF_HUMAN           | 3008.39   |
| sp Q96SI9 STRBP_HUMAN,sp Q1290  | 2085.9967 |
| sp P10586 PTPRF_HUMAN           | 3008.39   |
| sp P47756 CAPZB_HUMAN           | 2251.0943 |
| sp P15880 RS2_HUMAN             | 2154.997  |
| sp P15880 RS2_HUMAN             | 2154.997  |
| sp Q9UQ80 PA2G4_HUMAN           | 2033.0364 |
| sp P78371 TCPB_HUMAN            | 1680.8406 |
| sp P15880 RS2_HUMAN             | 2154.997  |
| sp Q9UQ80 PA2G4_HUMAN           | 2033.0364 |
| sp P47756 CAPZB_HUMAN           | 2251.0943 |
| sp P15880 RS2_HUMAN             | 2154.997  |
| sp Q9UQ80 PA2G4_HUMAN           | 2033.0364 |
| sp P78371 TCPB_HUMAN            | 1680.8406 |
| sp P15880 RS2_HUMAN             | 2154.997  |
| sp P07814 SYEP_HUMAN            | 2172.1004 |
| sp P43121 MUC18_HUMAN           | 1471.7783 |
| sp P15880 RS2_HUMAN             | 2154.997  |
| sp P07814 SYEP_HUMAN            | 2172.1004 |
| sp P43121 MUC18_HUMAN           | 1471.7783 |
| sp P49915 GUAA_HUMAN            | 2206.1746 |
| sp P07900 HS90A_HUMAN,sp P08238 | 2497.2336 |
| sp P08238 HS90B_HUMAN           | 2107.0698 |
| sp Q9UQ80 PA2G4_HUMAN           | 2033.0364 |
| sp P07814 SYEP_HUMAN            | 2172.1004 |
| sp P13639 EF2_HUMAN             | 2657.3523 |
| sp P07900 HS90A_HUMAN,sp P08238 | 2497.2336 |
| sp P07900 HS90A_HUMAN,sp P08238 | 2497.2336 |
| sp P08238 HS90B_HUMAN           | 2107.0698 |
| sp P08238 HS90B_HUMAN           | 2107.0698 |

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|---------------------------------------------|-----------|
| sp P07900 HS90A_HUMAN,sp P08238 HS90B_HUMAN | 2497.2336 |
| sp P13639 EF2_HUMAN                         | 2657.3523 |
| sp P07900 HS90A_HUMAN,sp P08238 HS90B_HUMAN | 2497.2336 |
| sp P52272 HNRPM_HUMAN                       | 2377.1083 |
| sp P08238 HS90B_HUMAN                       | 2107.0698 |
| sp P08238 HS90B_HUMAN                       | 2107.0698 |
| sp P13639 EF2_HUMAN                         | 2657.3523 |
| sp P52272 HNRPM_HUMAN                       | 2377.1083 |
| sp P34897 GLYM_HUMAN                        | 2188.1164 |
| sp O43395 PRPF3_HUMAN                       | 2023.0011 |
| sp P08238 HS90B_HUMAN                       | 2107.0698 |
| sp P52272 HNRPM_HUMAN                       | 2377.1083 |
| sp Q9NR30 DDX21_HUMAN                       | 2260.1059 |
| sp Q9NR30 DDX21_HUMAN                       | 2260.1059 |
| sp P52272 HNRPM_HUMAN                       | 2377.1083 |
| sp P34897 GLYM_HUMAN                        | 2188.1164 |
| sp P34897 GLYM_HUMAN                        | 2188.1164 |
| sp Q71U36 TBA1A_HUMAN,sp P683 P683          | 1767.7531 |
| sp P11142 HSP7C_HUMAN                       | 1603.7453 |
| sp P39023 RL3_HUMAN                         | 2163.9895 |
| sp Q9NR30 DDX21_HUMAN                       | 2260.1059 |
| sp P11142 HSP7C_HUMAN                       | 1603.7453 |
| sp P27824 CALX_HUMAN                        | 3584.622  |
| sp P07900 HS90A_HUMAN                       | 2286.1604 |
| sp P78347 GTF2I_HUMAN                       | 2548.3286 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P181 P181          | 3040.3661 |
| sp Q15149 PLEC_HUMAN                        | 2252.1437 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P181 P181          | 3040.3661 |
| sp P08195 4F2_HUMAN                         | 1356.7765 |
| sp Q9Y3F4 STRAP_HUMAN                       | 2953.2613 |
| sp Q9Y3F4 STRAP_HUMAN                       | 2953.2613 |
| sp Q9Y3F4 STRAP_HUMAN                       | 2953.2613 |
| sp Q5JTH9 RRP12_HUMAN                       | 2515.2166 |
| sp Q5JTH9 RRP12_HUMAN                       | 2515.2166 |
| sp P51511 MMP15_HUMAN                       | 4502.9297 |
| sp P48643 TCPE_HUMAN                        | 2248.1562 |
| sp P26640 SYVC_HUMAN                        | 3093.4648 |
| sp P61353 RL27_HUMAN                        | 2978.4734 |
| sp O14980 XPO1_HUMAN                        | 2358.1063 |
| sp P61353 RL27_HUMAN                        | 2978.4734 |
| sp P51511 MMP15_HUMAN                       | 4502.9297 |
| sp P11142 HSP7C_HUMAN                       | 1587.7504 |
| sp P51511 MMP15_HUMAN                       | 4502.9297 |
| sp P11142 HSP7C_HUMAN                       | 1587.7504 |
| sp Q06830 PRDX1_HUMAN                       | 3779.8254 |
| sp P11142 HSP7C_HUMAN                       | 1587.7504 |
| sp Q06830 PRDX1_HUMAN                       | 3779.8254 |



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|-------------------------------|-----------|
| sp Q06830 PRDX1_HUMAN         | 3779.8254 |
| sp P49368 TCPG_HUMAN          | 2820.4505 |
| sp Q13813 SPTN1_HUMAN         | 2542.3027 |
| sp P11142 HSP7C_HUMAN         | 1587.7504 |
| sp Q06830 PRDX1_HUMAN         | 3779.8254 |
| sp P49368 TCPG_HUMAN          | 2820.4505 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp Q06830 PRDX1_HUMAN         | 3779.8254 |
| sp Q13813 SPTN1_HUMAN         | 2542.3027 |
| sp P07900 HS90A_HUMAN         | 2111.0647 |
| sp Q15067 ACOX1_HUMAN         | 2200.0259 |
| sp P07900 HS90A_HUMAN         | 2111.0647 |
| sp P09651 ROA1_HUMAN,sp Q32P5 | 2873.2861 |
| sp P83731 RL24_HUMAN          | 2425.1195 |
| sp P42704 LPPRC_HUMAN         | 2153.9865 |
| sp P42167 LAP2B_HUMAN         | 3771.7725 |
| sp Q9NZ01 TECR_HUMAN          | 1954.9326 |
| sp P53396 ACLY_HUMAN          | 2638.3789 |
| sp P08195 4F2_HUMAN           | 2276.1298 |
| sp Q9NZ01 TECR_HUMAN          | 1954.9326 |
| sp Q15149 PLEC_HUMAN          | 2841.3504 |
| sp P53396 ACLY_HUMAN          | 2638.3789 |
| sp P08195 4F2_HUMAN           | 2276.1298 |
| sp Q9NZ01 TECR_HUMAN          | 1954.9326 |
| sp P42167 LAP2B_HUMAN         | 3771.7725 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P42167 LAP2B_HUMAN         | 3771.7725 |
| sp P15121 ALDR_HUMAN          | 2918.3617 |
| sp P42167 LAP2B_HUMAN         | 3771.7725 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P42167 LAP2B_HUMAN         | 3771.7725 |
| sp P15121 ALDR_HUMAN          | 2918.3617 |
| sp O75821 EIF3G_HUMAN         | 2123.0072 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp O75821 EIF3G_HUMAN         | 2123.0072 |
| sp P10586 PTPRF_HUMAN         | 2432.1397 |
| sp Q13263 TIF1B_HUMAN         | 3334.4515 |
| sp Q13263 TIF1B_HUMAN         | 3334.4515 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp Q13263 TIF1B_HUMAN         | 3334.4515 |
| sp P08195 4F2_HUMAN           | 1613.8777 |

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| sp Q13263 TIF1B_HUMAN | 3334.4515 |
| sp P08195 4F2_HUMAN   | 1613.8777 |
| sp Q13263 TIF1B_HUMAN | 3334.4515 |
| sp Q15149 PLEC_HUMAN  | 2912.492  |
| sp P08195 4F2_HUMAN   | 1613.8777 |
| sp Q13263 TIF1B_HUMAN | 3334.4515 |
| sp Q13263 TIF1B_HUMAN | 3334.4515 |
| sp P08195 4F2_HUMAN   | 1613.8777 |
| sp Q14118 DAG1_HUMAN  | 2061.0895 |
| sp P61978 HNRPK_HUMAN | 1971.1153 |
| sp O95340 PAPS2_HUMAN | 2157.0491 |
| sp P61978 HNRPK_HUMAN | 1971.1153 |
| sp O95340 PAPS2_HUMAN | 2157.0491 |
| sp O95340 PAPS2_HUMAN | 2157.0491 |
| sp P49327 FAS_HUMAN   | 2697.2969 |
| sp O95340 PAPS2_HUMAN | 2157.0491 |
| sp P49327 FAS_HUMAN   | 2697.2969 |
| sp O95340 PAPS2_HUMAN | 2157.0491 |
| sp O60264 SMCA5_HUMAN | 2965.3577 |
| sp O60264 SMCA5_HUMAN | 2965.3577 |
| sp P23246 SFPQ_HUMAN  | 2938.3039 |
| sp P62917 RL8_HUMAN   | 2721.3221 |
| sp P49792 RBP2_HUMAN  | 3149.4843 |
| sp P23246 SFPQ_HUMAN  | 2938.3039 |
| sp P49327 FAS_HUMAN   | 2697.2969 |
| sp P49327 FAS_HUMAN   | 2697.2969 |
| sp P49327 FAS_HUMAN   | 2697.2969 |
| sp P49327 FAS_HUMAN   | 2697.2969 |
| sp O75367 H2AY_HUMAN  | 3055.4419 |
| sp P49327 FAS_HUMAN   | 2697.2969 |
| sp P14384 CBPM_HUMAN  | 3221.462  |
| sp O75367 H2AY_HUMAN  | 3055.4419 |
| sp P36578 RL4_HUMAN   | 1640.8998 |
| sp P36578 RL4_HUMAN   | 1640.8998 |
| sp P43243 MATR3_HUMAN | 2991.4978 |
| sp P22695 QCR2_HUMAN  | 2659.2667 |
| sp P62888 RL30_HUMAN  | 3637.6817 |
| sp P62888 RL30_HUMAN  | 3637.6817 |
| sp P62888 RL30_HUMAN  | 3637.6817 |
| sp P36578 RL4_HUMAN   | 1640.8998 |
| sp P22695 QCR2_HUMAN  | 2659.2667 |
| sp P36578 RL4_HUMAN   | 1640.8998 |
| sp P43243 MATR3_HUMAN | 2991.4978 |
| sp P08195 4F2_HUMAN   | 2051.9854 |
| sp P43243 MATR3_HUMAN | 2991.4978 |
| sp P08195 4F2_HUMAN   | 2051.9854 |
| sp Q15149 PLEC_HUMAN  | 2521.2999 |

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| sp Q06830 PRDX1_HUMAN | 3077.4488 |
| sp P43243 MATR3_HUMAN | 2991.4978 |
| sp P43243 MATR3_HUMAN | 2991.4978 |
| sp P49327 FAS_HUMAN   | 2863.3665 |
| sp P43243 MATR3_HUMAN | 2991.4978 |
| sp P49327 FAS_HUMAN   | 2863.3665 |
| sp Q99798 ACON_HUMAN  | 3189.5942 |
| sp P12236 ADT3_HUMAN  | 2027.9854 |
| sp P49327 FAS_HUMAN   | 2863.3665 |
| sp P48643 TCPE_HUMAN  | 2477.2876 |
| sp P08195 4F2_HUMAN   | 2051.9854 |
| sp P32004 L1CAM_HUMAN | 3087.5335 |
| sp P31930 QCR1_HUMAN  | 2813.3039 |
| sp P48643 TCPE_HUMAN  | 2477.2876 |
| sp P55265 DSRAD_HUMAN | 3058.4818 |
| sp P32004 L1CAM_HUMAN | 3087.5335 |
| sp P08195 4F2_HUMAN   | 2051.9854 |
| sp P55265 DSRAD_HUMAN | 3058.4818 |
| sp Q06830 PRDX1_HUMAN | 3077.4488 |
| sp P04406 G3P_HUMAN   | 3285.5798 |
| sp P31930 QCR1_HUMAN  | 2813.3039 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q24JP5 T132A_HUMAN | 2518.2063 |
| sp P04406 G3P_HUMAN   | 3285.5798 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp P55060 XPO2_HUMAN  | 2369.2227 |
| sp Q24JP5 T132A_HUMAN | 2518.2063 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q63HN8 RN213_HUMAN | 2593.2595 |
| sp P78527 PRKDC_HUMAN | 2987.5175 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp P32004 L1CAM_HUMAN | 1627.8246 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q6UVK1 CSPG4_HUMAN | 2933.6087 |
| sp Q9Y262 EIF3L_HUMAN | 3319.6302 |
| sp P53618 COPB_HUMAN  | 3338.6531 |
| sp P32004 L1CAM_HUMAN | 1627.8246 |
| sp Q9Y262 EIF3L_HUMAN | 3319.6302 |
| sp P32004 L1CAM_HUMAN | 1627.8246 |
| sp Q14166 TTL12_HUMAN | 2278.0014 |

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| sp Q14166 TTL12_HUMAN          | 2278.0014 |
| sp P49327 FAS_HUMAN            | 3542.6195 |
| sp Q14166 TTL12_HUMAN          | 2278.0014 |
| sp P51991 ROA3_HUMAN           | 3254.422  |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P78527 PRKDC_HUMAN          | 2833.4723 |
| sp P78527 PRKDC_HUMAN          | 2833.4723 |
| sp P78347 GTF2I_HUMAN          | 2092.0452 |
| sp P78347 GTF2I_HUMAN          | 2092.0452 |
| sp P78527 PRKDC_HUMAN          | 2833.4723 |
| sp P78527 PRKDC_HUMAN          | 2833.4723 |
| sp P78347 GTF2I_HUMAN          | 2092.0452 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P0DMV8 HS71A_HUMAN,sp PODI  | 3080.4338 |
| sp P00558 PGK1_HUMAN           | 3475.7367 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P11021 BIP_HUMAN            | 3302.6572 |
| sp P78371 TCPB_HUMAN           | 2404.2057 |
| sp P11021 BIP_HUMAN            | 3302.6572 |
| sp P07900 HS90A_HUMAN,sp P0825 | 3053.4155 |
| sp P11021 BIP_HUMAN            | 3302.6572 |
| sp P11021 BIP_HUMAN            | 3302.6572 |
| sp P04843 RPN1_HUMAN           | 2521.2601 |
| sp P00558 PGK1_HUMAN           | 3475.7367 |
| sp P11021 BIP_HUMAN            | 3302.6572 |
| sp P04843 RPN1_HUMAN           | 2521.2601 |
| sp P31327 CPSM_HUMAN           | 2147.1851 |
| sp P00558 PGK1_HUMAN           | 3475.7367 |
| sp P06576 ATPB_HUMAN           | 3016.4084 |
| sp P06576 ATPB_HUMAN           | 3016.4084 |
| sp P31327 CPSM_HUMAN           | 2147.1851 |
| sp P06576 ATPB_HUMAN           | 3016.4084 |
| sp P00558 PGK1_HUMAN           | 3475.7367 |
| sp P04843 RPN1_HUMAN           | 2521.2601 |
| sp P12268 IMDH2_HUMAN          | 2835.4014 |
| sp P12268 IMDH2_HUMAN          | 2835.4014 |
| sp P51991 ROA3_HUMAN           | 2765.3184 |
| sp P04843 RPN1_HUMAN           | 2521.2601 |
| sp P04843 RPN1_HUMAN           | 2521.2601 |
| sp P12268 IMDH2_HUMAN          | 2835.4014 |
| sp P12268 IMDH2_HUMAN          | 2835.4014 |
| sp P51991 ROA3_HUMAN           | 2765.3184 |
| sp P04843 RPN1_HUMAN           | 2521.2601 |
| sp P12268 IMDH2_HUMAN          | 2835.4014 |
| sp P04843 RPN1_HUMAN           | 2521.2601 |

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| sp P00558 PGK1_HUMAN  | 3136.478  |
| sp P51991 ROA3_HUMAN  | 2765.3184 |
| sp P04843 RPN1_HUMAN  | 2521.2601 |
| sp Q15365 PCBP1_HUMAN | 4823.2886 |
| sp Q15149 PLEC_HUMAN  | 2054.0585 |
| sp Q15365 PCBP1_HUMAN | 4823.2886 |
| sp Q15365 PCBP1_HUMAN | 4823.2886 |
| sp P11142 HSP7C_HUMAN | 3085.4062 |
| sp P11142 HSP7C_HUMAN | 3085.4062 |
| sp Q15149 PLEC_HUMAN  | 2054.0585 |
| sp P00533 EGFR_HUMAN  | 3103.5033 |
| sp Q15149 PLEC_HUMAN  | 2054.0585 |
| sp Q15149 PLEC_HUMAN  | 2054.0585 |
| sp P00533 EGFR_HUMAN  | 3103.5033 |
| sp Q15149 PLEC_HUMAN  | 3689.8366 |
| sp P00533 EGFR_HUMAN  | 3103.5033 |
| sp P00533 EGFR_HUMAN  | 3103.5033 |
| sp P00558 PGK1_HUMAN  | 3459.7418 |
| sp P00558 PGK1_HUMAN  | 3459.7418 |
| sp P00558 PGK1_HUMAN  | 3459.7418 |
| sp P68104 EF1A1_HUMAN | 5309.4969 |
| sp P78527 PRKDC_HUMAN | 3586.6488 |
| sp P68104 EF1A1_HUMAN | 5309.4969 |
| sp Q92973 TNPO1_HUMAN | 1591.7163 |
| sp Q13148 TADBP_HUMAN | 3333.6782 |
| sp Q9Y3T9 NOC2L_HUMAN | 1880.9785 |
| sp Q92973 TNPO1_HUMAN | 1591.7163 |
| sp P09651 ROA1_HUMAN  | 3133.4563 |
| sp Q9Y3T9 NOC2L_HUMAN | 1880.9785 |
| sp Q9Y3T9 NOC2L_HUMAN | 1880.9785 |
| sp P09651 ROA1_HUMAN  | 3133.4563 |
| sp P00491 PNPH_HUMAN  | 2382.1143 |
| sp P09651 ROA1_HUMAN  | 3133.4563 |
| sp P09651 ROA1_HUMAN  | 3133.4563 |
| sp P09651 ROA1_HUMAN  | 3133.4563 |
| sp P46940 IQGA1_HUMAN | 2132.1954 |
| sp P46940 IQGA1_HUMAN | 2132.1954 |
| sp Q13151 ROA0_HUMAN  | 3216.5979 |
| sp P46940 IQGA1_HUMAN | 2132.1954 |
| sp P00491 PNPH_HUMAN  | 2382.1143 |
| sp P04406 G3P_HUMAN   | 5043.3435 |
| sp P78371 TCPB_HUMAN  | 2109.0161 |
| sp P78371 TCPB_HUMAN  | 2109.0161 |
| sp P04406 G3P_HUMAN   | 5043.3435 |
| sp P04406 G3P_HUMAN   | 5043.3435 |
| sp P07437 TBB5_HUMAN  | 5102.3377 |
| sp P07437 TBB5_HUMAN  | 5102.3377 |

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| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp Q92598 HS105_HUMAN          | 1796.921  |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp P10586 PTPRF_HUMAN          | 3655.7439 |
| sp P04350 TBB4A_HUMAN,sp P6837 | 5116.3533 |
| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp P04350 TBB4A_HUMAN,sp P6837 | 5116.3533 |
| sp Q92598 HS105_HUMAN          | 1796.921  |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp P78371 TCPB_HUMAN           | 2109.0161 |
| sp Q92598 HS105_HUMAN          | 1796.921  |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp P04350 TBB4A_HUMAN,sp P6837 | 5116.3533 |
| sp P04350 TBB4A_HUMAN,sp P6837 | 5116.3533 |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp P04350 TBB4A_HUMAN,sp P6837 | 5116.3533 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2583.287  |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp P53396 ACLY_HUMAN           | 1973.0087 |
| sp P18084 ITB5_HUMAN           | 2614.3279 |
| sp Q16531 DDB1_HUMAN           | 2375.2195 |
| sp Q16531 DDB1_HUMAN           | 2375.2195 |
| sp P53396 ACLY_HUMAN           | 1973.0087 |
| sp P18084 ITB5_HUMAN           | 2614.3279 |
| sp Q16531 DDB1_HUMAN           | 2375.2195 |
| sp Q16531 DDB1_HUMAN           | 2375.2195 |
| sp P53396 ACLY_HUMAN           | 1973.0087 |
| sp P00491 PNPH_HUMAN           | 2366.1194 |
| sp P18084 ITB5_HUMAN           | 2614.3279 |
| sp P18084 ITB5_HUMAN           | 2614.3279 |
| sp P18084 ITB5_HUMAN           | 2614.3279 |
| sp P18084 ITB5_HUMAN           | 2614.3279 |
| sp P18084 ITB5_HUMAN           | 2614.3279 |
| sp P00491 PNPH_HUMAN           | 2366.1194 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P00491 PNPH_HUMAN           | 2366.1194 |
| sp P00491 PNPH_HUMAN           | 2366.1194 |
| sp Q13435 SF3B2_HUMAN          | 2805.4458 |
| sp P00491 PNPH_HUMAN           | 2366.1194 |
| sp P07900 HS90A_HUMAN          | 3491.6629 |
| sp P49327 FAS_HUMAN            | 3305.5841 |
| sp O00299 CLIC1_HUMAN          | 3333.7101 |
| sp P00966 ASSY_HUMAN           | 3056.4298 |
| sp P49327 FAS_HUMAN            | 3305.5841 |
| sp O00299 CLIC1_HUMAN          | 3333.7101 |

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| sp P61247 RS3A_HUMAN           | 3209.6067 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P49327 FAS_HUMAN            | 3305.5841 |
| sp O00299 CLIC1_HUMAN          | 3333.7101 |
| sp P49327 FAS_HUMAN            | 3305.5841 |
| sp P61247 RS3A_HUMAN           | 3209.6067 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q5JTH9 RRP12_HUMAN          | 2736.4408 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q5JTH9 RRP12_HUMAN          | 2736.4408 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q9UIG0 BAZ1B_HUMAN          | 2606.2655 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp O00410 IPO5_HUMAN           | 2524.2016 |
| sp P00966 ASSY_HUMAN           | 4051.9448 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P00966 ASSY_HUMAN           | 4051.9448 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q9UIG0 BAZ1B_HUMAN          | 2606.2655 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P00966 ASSY_HUMAN           | 4051.9448 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp O75475 PSIP1_HUMAN          | 3664.8454 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp O75475 PSIP1_HUMAN          | 3664.8454 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp O75475 PSIP1_HUMAN          | 3664.8454 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P17812 PYRG1_HUMAN          | 2597.2762 |
| sp O75475 PSIP1_HUMAN          | 3664.8454 |
| sp P17812 PYRG1_HUMAN          | 2597.2762 |
| sp Q15181 IPYR_HUMAN           | 3368.6176 |
| sp P17812 PYRG1_HUMAN          | 2597.2762 |
| sp O00571 DDX3X_HUMAN          | 3105.5043 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp P31930 QCR1_HUMAN           | 4623.289  |

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| sp P17812 PYRG1_HUMAN | 2597.2762 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P17812 PYRG1_HUMAN | 3079.5437 |
| sp P53621 COPA_HUMAN  | 2732.3406 |
| sp P17812 PYRG1_HUMAN | 2597.2762 |
| sp P31930 QCR1_HUMAN  | 4623.289  |
| sp O95373 IPO7_HUMAN  | 2118.0932 |
| sp O95373 IPO7_HUMAN  | 2118.0932 |
| sp P28288 ABCD3_HUMAN | 2848.4971 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P53621 COPA_HUMAN  | 2732.3406 |
| sp P17812 PYRG1_HUMAN | 2597.2762 |
| sp O95373 IPO7_HUMAN  | 2118.0932 |
| sp O95373 IPO7_HUMAN  | 2118.0932 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P10809 CH60_HUMAN  | 1909.0343 |
| sp P35606 COPB2_HUMAN | 4624.1533 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P16066 ANPRA_HUMAN | 2852.5549 |
| sp P16066 ANPRA_HUMAN | 2852.5549 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P29401 TKT_HUMAN   | 2973.5659 |
| sp P53621 COPA_HUMAN  | 2732.3406 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P53621 COPA_HUMAN  | 2732.3406 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P53621 COPA_HUMAN  | 2732.3406 |
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| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P53621 COPA_HUMAN  | 2732.3406 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp Q92900 RENT1_HUMAN | 4027.1167 |
| sp P31327 CPSM_HUMAN  | 4635.2856 |
| sp P05783 K1C18_HUMAN | 1917.8897 |
| sp P31327 CPSM_HUMAN  | 4635.2856 |
| sp P40227 TCPZ_HUMAN  | 2571.2059 |
| sp O75153 CLU_HUMAN   | 2397.258  |
| sp P40227 TCPZ_HUMAN  | 2571.2059 |
| sp P10586 PTPRF_HUMAN | 4745.4019 |
| sp Q13162 PRDX4_HUMAN | 3266.6095 |
| sp P29401 TKT_HUMAN   | 3284.7868 |
| sp P10586 PTPRF_HUMAN | 4745.4019 |
| sp P04843 RPN1_HUMAN  | 2901.4832 |
| sp P04843 RPN1_HUMAN  | 2901.4832 |
| sp P04406 G3P_HUMAN   | 3532.7508 |



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| sp P04843 RPN1_HUMAN           | 2901.4832 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp Q92841 DDX17_HUMAN          | 3701.8876 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp O75533 SF3B1_HUMAN          | 2397.2652 |
| sp Q15149 PLEC_HUMAN           | 3237.7285 |
| sp O75533 SF3B1_HUMAN          | 2397.2652 |
| sp Q15149 PLEC_HUMAN           | 3237.7285 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp Q15149 PLEC_HUMAN           | 3237.7285 |
| sp Q15149 PLEC_HUMAN           | 3237.7285 |
| sp O75475 PSIP1_HUMAN          | 3211.5543 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2282.1729 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2282.1729 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2282.1729 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 3714.7447 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp P15924 DESP_HUMAN           | 2159.0933 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp Q13283 G3BP1_HUMAN          | 3347.6649 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P13639 EF2_HUMAN            | 4552.2043 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P13639 EF2_HUMAN            | 4552.2043 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp Q14839 CHD4_HUMAN           | 2689.2548 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |

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| sp P62491 RB11A_HUMAN,sp Q159I | 2627.3231 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp P29401 TKT_HUMAN            | 3378.6554 |
| sp P29401 TKT_HUMAN            | 3378.6554 |
| sp P58107 EPIPL_HUMAN          | 5251.6911 |
| sp Q8TDD1 DDX54_HUMAN          | 2690.4432 |
| sp Q8TDD1 DDX54_HUMAN          | 2690.4432 |
| sp O00410 IPO5_HUMAN           | 2660.3165 |
| sp Q08211 DHX9_HUMAN           | 3151.6554 |
| sp Q5JTH9 RRP12_HUMAN          | 2013.0142 |
| sp Q01105 SET_HUMAN            | 4563.2598 |
| sp Q14152 EIF3A_HUMAN          | 3028.6267 |
| sp Q14152 EIF3A_HUMAN          | 3028.6267 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp Q92616 GCN1_HUMAN           | 3849.1325 |
| sp Q92616 GCN1_HUMAN           | 3849.1325 |
| sp Q92616 GCN1_HUMAN           | 3849.1325 |
| sp Q92616 GCN1_HUMAN           | 3849.1325 |
| sp Q92616 GCN1_HUMAN           | 3849.1325 |
| sp P40939 ECHA_HUMAN           | 3881.9575 |
| sp P40939 ECHA_HUMAN           | 3881.9575 |
| sp P40939 ECHA_HUMAN           | 3881.9575 |
| sp P40939 ECHA_HUMAN           | 3881.9575 |
| sp P50395 GDIB_HUMAN           | 3655.96   |
| sp P55060 XPO2_HUMAN           | 3614.8369 |
| sp P07195 LDHB_HUMAN           | 3979.9799 |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1261.6051 |
| sp P10412 H14_HUMAN            | 1390.7932 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1629.8587 |
| sp P50914 RL14_HUMAN           | 1565.7375 |
| sp Q8NC51 PAIRB_HUMAN          | 1973.8868 |
| sp Q8IWS0 PHF6_HUMAN           | 2108.9487 |
| sp P61313 RL15_HUMAN           | 2209.1141 |
| sp P61313 RL15_HUMAN           | 2209.1141 |
| sp Q8WXX5 DNJC9_HUMAN          | 1887.934  |
| sp Q8WXX5 DNJC9_HUMAN          | 1887.934  |
| sp P46781 RS9_HUMAN            | 1398.7368 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1620.7831 |

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| sp P14618 KPYM_HUMAN           | 2449.1411 |
| sp P14618 KPYM_HUMAN           | 2449.1411 |
| sp P14618 KPYM_HUMAN           | 2449.1411 |
| sp P14618 KPYM_HUMAN           | 2449.1411 |
| sp P15328 FOLR1_HUMAN          | 2358.0811 |
| sp P50238 CRIP1_HUMAN          | 1724.7399 |
| sp Q14137 BOP1_HUMAN           | 1971.9374 |
| sp P55265 DSRAD_HUMAN          | 1596.8161 |
| sp P14618 KPYM_HUMAN           | 2449.1411 |
| sp P14618 KPYM_HUMAN           | 2449.1411 |
| sp P14618 KPYM_HUMAN           | 2449.1411 |
| sp P50238 CRIP1_HUMAN          | 1724.7399 |
| sp Q14137 BOP1_HUMAN           | 1971.9374 |
| sp Q14137 BOP1_HUMAN           | 1971.9374 |
| sp Q9Y266 NUDC_HUMAN           | 2219.1083 |
| sp Q9Y266 NUDC_HUMAN           | 2219.1083 |
| sp Q14847 LASP1_HUMAN          | 2006.7862 |
| sp P62753 RS6_HUMAN            | 1782.8835 |
| sp P62280 RS11_HUMAN           | 1824.8036 |
| sp P09622 DLDH_HUMAN           | 2528.1291 |
| sp P62280 RS11_HUMAN           | 1824.8036 |
| sp P09622 DLDH_HUMAN           | 2528.1291 |
| sp P62280 RS11_HUMAN           | 1824.8036 |
| sp P62266 RS23_HUMAN           | 2172.1076 |
| sp P62266 RS23_HUMAN           | 2172.1076 |
| sp P62266 RS23_HUMAN           | 2172.1076 |
| sp P62266 RS23_HUMAN           | 2172.1076 |
| sp Q13151 ROA0_HUMAN           | 1655.8532 |
| sp Q15181 IPYR_HUMAN           | 1618.774  |
| sp O14617 AP3D1_HUMAN          | 1714.8825 |
| sp Q15181 IPYR_HUMAN           | 1618.774  |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp Q15181 IPYR_HUMAN           | 1618.774  |
| sp P22626 ROA2_HUMAN,sp P0965: | 2204.0862 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2204.0862 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P31948 STIP1_HUMAN          | 2188.0338 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2204.0862 |
| sp P31948 STIP1_HUMAN          | 2188.0338 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2204.0862 |
| sp P50238 CRIP1_HUMAN          | 1892.9203 |
| sp P31948 STIP1_HUMAN          | 2188.0338 |
| sp P31948 STIP1_HUMAN          | 2188.0338 |
| sp P84098 RL19_HUMAN           | 1630.7813 |
| sp P31327 CPSM_HUMAN           | 1575.7682 |

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| sp P62854 RS26_HUMAN,sp Q5JNZ5 | 2024.9561 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2204.0862 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp P31327 CPSM_HUMAN           | 1575.7682 |
| sp P62854 RS26_HUMAN,sp Q5JNZ5 | 2024.9561 |
| sp Q00839 HNRPU_HUMAN          | 1834.885  |
| sp P22626 ROA2_HUMAN,sp P0965: | 2204.0862 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2204.0862 |
| sp P62081 RS7_HUMAN            | 1712.8998 |
| sp P62081 RS7_HUMAN            | 1712.8998 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp P62701 RS4X_HUMAN,sp P22090 | 2736.2641 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp Q00839 HNRPU_HUMAN          | 1834.885  |
| sp P84098 RL19_HUMAN           | 1614.7864 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp P51531 SMCA2_HUMAN,sp P515  | 2384.1444 |
| sp Q00839 HNRPU_HUMAN          | 1834.885  |
| sp Q9NR30 DDX21_HUMAN          | 2038.9861 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp P51531 SMCA2_HUMAN,sp P515  | 2384.1444 |
| sp P84098 RL19_HUMAN           | 1614.7864 |
| sp P51531 SMCA2_HUMAN,sp P515  | 2384.1444 |
| sp P62266 RS23_HUMAN           | 2044.0126 |
| sp P26373 RL13_HUMAN           | 2088.9952 |
| sp P26373 RL13_HUMAN           | 2088.9952 |
| sp P12814 ACTN1_HUMAN          | 1692.8584 |
| sp Q9UHB6 LIMA1_HUMAN          | 2005.972  |
| sp P35659 DEK_HUMAN            | 2136.1328 |
| sp P55060 XPO2_HUMAN           | 2085.0426 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp P55060 XPO2_HUMAN           | 2085.0426 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2075.9912 |
| sp P30084 ECHM_HUMAN           | 1747.8682 |
| sp P50238 CRIP1_HUMAN          | 3730.614  |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp P50238 CRIP1_HUMAN          | 3730.614  |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2075.9912 |
| sp P35659 DEK_HUMAN            | 2136.1328 |
| sp O75643 U520_HUMAN           | 1578.8195 |
| sp P30084 ECHM_HUMAN           | 1747.8682 |
| sp Q15149 PLEC_HUMAN           | 2067.0385 |
| sp O75643 U520_HUMAN           | 1578.8195 |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp P62701 RS4X_HUMAN           | 2185.1644 |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |

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| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp P04439 HLAA_HUMAN,sp P01885 | 2245.095  |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp P27797 CALR_HUMAN           | 1732.842  |
| sp P07919 QCR6_HUMAN,sp A0A09  | 1791.8363 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2075.9912 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2075.9912 |
| sp P07919 QCR6_HUMAN,sp A0A09  | 1791.8363 |
| sp P61353 RL27_HUMAN           | 3106.5683 |
| sp P61353 RL27_HUMAN           | 3106.5683 |
| sp P99999 CYC_HUMAN            | 1629.8012 |
| sp P04439 HLAA_HUMAN,sp P01885 | 2245.095  |
| sp P61353 RL27_HUMAN           | 3106.5683 |
| sp P61353 RL27_HUMAN           | 3106.5683 |
| sp P04439 HLAA_HUMAN,sp P01885 | 2245.095  |
| sp P99999 CYC_HUMAN            | 1629.8012 |
| sp P07814 SYEP_HUMAN           | 2172.1004 |
| sp P31040 SDHA_HUMAN           | 2991.4297 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1709.8195 |
| sp P31040 SDHA_HUMAN           | 2991.4297 |
| sp P07814 SYEP_HUMAN           | 2172.1004 |
| sp P31040 SDHA_HUMAN           | 2991.4297 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1709.8195 |
| sp P07814 SYEP_HUMAN           | 2172.1004 |
| sp Q08945 SSRP1_HUMAN          | 1758.9206 |
| sp Q16891 MIC60_HUMAN          | 1747.8278 |
| sp Q08945 SSRP1_HUMAN          | 1758.9206 |
| sp P78310 CXAR_HUMAN           | 1712.9937 |
| sp P55072 TERA_HUMAN           | 1726.9519 |
| sp P62873 GBB1_HUMAN,sp P62875 | 2038.9319 |
| sp Q16891 MIC60_HUMAN          | 1747.8278 |
| sp P08238 HS90B_HUMAN          | 2107.0698 |
| sp P62873 GBB1_HUMAN,sp P62875 | 2038.9319 |
| sp P78310 CXAR_HUMAN           | 1712.9937 |
| sp O75643 U520_HUMAN           | 2161.0739 |
| sp P78310 CXAR_HUMAN           | 1712.9937 |
| sp P30153 2AAA_HUMAN           | 2565.2612 |
| sp P30153 2AAA_HUMAN           | 2565.2612 |
| sp O75643 U520_HUMAN           | 2161.0739 |
| sp P78310 CXAR_HUMAN           | 1712.9937 |
| sp P54886 P5CS_HUMAN           | 3298.6007 |
| sp P54886 P5CS_HUMAN           | 3298.6007 |
| sp P54886 P5CS_HUMAN           | 3298.6007 |
| sp P30101 PDIA3_HUMAN          | 1970.001  |
| sp P62701 RS4X_HUMAN           | 2057.0694 |

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| sp Q13283 G3BP1_HUMAN          | 2736.3144 |
| sp Q13283 G3BP1_HUMAN          | 2736.3144 |
| sp P08581 MET_HUMAN            | 3447.41   |
| sp O14980 XPO1_HUMAN           | 2358.1063 |
| sp P08581 MET_HUMAN            | 3447.41   |
| sp P08581 MET_HUMAN            | 3447.41   |
| sp P49327 FAS_HUMAN            | 1991.9887 |
| sp Q00341 VIGLN_HUMAN          | 2012.9051 |
| sp P52948 NUP98_HUMAN          | 2918.3228 |
| sp P32004 L1CAM_HUMAN          | 1870.9802 |
| sp P32004 L1CAM_HUMAN          | 1870.9802 |
| sp P10586 PTPRF_HUMAN          | 3846.8238 |
| sp P10586 PTPRF_HUMAN          | 3846.8238 |
| sp P32004 L1CAM_HUMAN          | 1870.9802 |
| sp P32004 L1CAM_HUMAN          | 1870.9802 |
| sp P32004 L1CAM_HUMAN          | 1870.9802 |
| sp P10586 PTPRF_HUMAN          | 3846.8238 |
| sp P10586 PTPRF_HUMAN          | 3846.8238 |
| sp Q14118 DAG1_HUMAN           | 3063.3934 |
| sp Q14118 DAG1_HUMAN           | 3063.3934 |
| sp P32004 L1CAM_HUMAN          | 1870.9802 |
| sp P32004 L1CAM_HUMAN          | 1870.9802 |
| sp Q14118 DAG1_HUMAN           | 3063.3934 |
| sp P07237 PDIA1_HUMAN          | 3188.5852 |
| sp O75369 FLNB_HUMAN           | 2759.3416 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp O75369 FLNB_HUMAN           | 2759.3416 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp P78527 PRKDC_HUMAN          | 2126.9812 |
| sp O15031 PLXB2_HUMAN          | 4398.9851 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp O15031 PLXB2_HUMAN          | 4398.9851 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp Q14315 FLNC_HUMAN,sp P2133: | 2755.3467 |
| sp P27824 CALX_HUMAN           | 2594.274  |
| sp P49327 FAS_HUMAN            | 2625.2071 |
| sp P62826 RAN_HUMAN            | 2376.2226 |
| sp P49327 FAS_HUMAN            | 2625.2071 |
| sp P27824 CALX_HUMAN           | 2594.274  |
| sp P49327 FAS_HUMAN            | 2625.2071 |
| sp P34897 GLYM_HUMAN           | 2608.205  |
| sp P34897 GLYM_HUMAN           | 2608.205  |

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| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp O00567 NOP56_HUMAN         | 2149.0626 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp P24941 CDK2_HUMAN          | 2739.4497 |
| sp P24941 CDK2_HUMAN          | 2739.4497 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp P24941 CDK2_HUMAN          | 2739.4497 |
| sp O00567 NOP56_HUMAN         | 2149.0626 |
| sp O00567 NOP56_HUMAN         | 2149.0626 |
| sp P62826 RAN_HUMAN           | 2376.2226 |
| sp Q13057 COASY_HUMAN         | 2031.0174 |
| sp P09429 HMGB1_HUMAN         | 3095.4964 |
| sp Q9Y490 TLN1_HUMAN          | 2131.1134 |
| sp Q13057 COASY_HUMAN         | 2031.0174 |
| sp P09429 HMGB1_HUMAN         | 3095.4964 |
| sp P13667 PDIA4_HUMAN         | 1901.9312 |
| sp P11142 HSP7C_HUMAN         | 3257.5022 |
| sp Q13057 COASY_HUMAN         | 2031.0174 |
| sp P09429 HMGB1_HUMAN         | 3095.4964 |
| sp Q06830 PRDX1_HUMAN         | 3077.4488 |
| sp P52948 NUP98_HUMAN         | 2119.9898 |
| sp Q9Y490 TLN1_HUMAN          | 2131.1134 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3208.5288 |
| sp Q06830 PRDX1_HUMAN         | 3077.4488 |
| sp P11142 HSP7C_HUMAN         | 3257.5022 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3208.5288 |
| sp Q06830 PRDX1_HUMAN         | 3077.4488 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3208.5288 |
| sp Q06830 PRDX1_HUMAN         | 3077.4488 |
| sp P52948 NUP98_HUMAN         | 2119.9898 |
| sp P11142 HSP7C_HUMAN         | 3257.5022 |
| sp O95340 PAPS2_HUMAN         | 2112.1156 |
| sp P17812 PYRG1_HUMAN         | 2764.318  |
| sp Q9GZT3 SLIRP_HUMAN         | 2762.3677 |
| sp P05388 RLAO_HUMAN          | 2147.1124 |
| sp Q9GZT3 SLIRP_HUMAN         | 2762.3677 |
| sp Q9GZT3 SLIRP_HUMAN         | 2762.3677 |
| sp P05388 RLAO_HUMAN          | 2147.1124 |
| sp P15531 NDKA_HUMAN          | 2230.1059 |
| sp P15531 NDKA_HUMAN          | 2230.1059 |
| sp P05388 RLAO_HUMAN          | 2147.1124 |

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| sp Q6UVK1 CSPG4_HUMAN                     | 2933.6087 |
| sp P39023 RL3_HUMAN                       | 2849.417  |
| sp P39023 RL3_HUMAN                       | 2849.417  |
| sp P32004 L1CAM_HUMAN                     | 1627.8246 |
| sp Q9UIG0 BAZ1B_HUMAN                     | 2174.116  |
| sp Q16719 KYNU_HUMAN                      | 2453.224  |
| sp Q9BQG0 MBB1A_HUMAN                     | 2380.1998 |
| sp P26599 PTBP1_HUMAN                     | 3963.0054 |
| sp P26599 PTBP1_HUMAN                     | 3963.0054 |
| sp P32004 L1CAM_HUMAN                     | 1627.8246 |
| sp P26599 PTBP1_HUMAN                     | 3963.0054 |
| sp P09429 HMGB1_HUMAN                     | 2439.2045 |
| sp P11142 HSP7C_HUMAN                     | 3241.5073 |
| sp P14618 KPYM_HUMAN                      | 2808.4449 |
| sp P11142 HSP7C_HUMAN                     | 3241.5073 |
| sp P78527 PRKDC_HUMAN                     | 1970.0374 |
| sp P16435 NCPR_HUMAN                      | 2520.1856 |
| sp P11142 HSP7C_HUMAN                     | 3241.5073 |
| sp P78527 PRKDC_HUMAN                     | 1970.0374 |
| sp P11142 HSP7C_HUMAN                     | 3241.5073 |
| sp P11142 HSP7C_HUMAN                     | 3241.5073 |
| sp P11142 HSP7C_HUMAN                     | 3241.5073 |
| sp P11142 HSP7C_HUMAN                     | 3241.5073 |
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| sp P11142 HSP7C_HUMAN                     | 3241.5073 |
| sp P78527 PRKDC_HUMAN                     | 2833.4723 |
| sp Q9GZT3 SLIRP_HUMAN                     | 2606.2666 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN | 3669.6623 |
| sp Q9GZT3 SLIRP_HUMAN                     | 2606.2666 |
| sp Q9GZT3 SLIRP_HUMAN                     | 2606.2666 |
| sp P78527 PRKDC_HUMAN                     | 1819.9443 |
| sp Q9GZT3 SLIRP_HUMAN                     | 2606.2666 |
| sp Q9GZT3 SLIRP_HUMAN                     | 2606.2666 |
| sp P08069 IGF1R_HUMAN                     | 1918.0061 |
| sp P08069 IGF1R_HUMAN                     | 1918.0061 |
| sp P68104 EF1A1_HUMAN                     | 5465.598  |
| sp P26641 EF1G_HUMAN                      | 2343.1535 |
| sp P12268 IMDH2_HUMAN                     | 2835.4014 |
| sp P26641 EF1G_HUMAN                      | 2343.1535 |
| sp Q16576 RBBP7_HUMAN                     | 4359.988  |
| sp Q9NR30 DDX21_HUMAN                     | 2473.243  |
| sp Q9NR30 DDX21_HUMAN                     | 2473.243  |
| sp Q9NR30 DDX21_HUMAN                     | 2473.243  |
| sp P53396 ACLY_HUMAN                      | 2949.6076 |
| sp P08195 4F2_HUMAN                       | 2988.4519 |
| sp P18621 RL17_HUMAN                      | 2469.221  |
| sp P68032 ACTC_HUMAN,sp P63267 ACTC_HUMAN | 2938.4535 |



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| sp P53396 ACLY_HUMAN           | 2949.6076 |
| sp P53396 ACLY_HUMAN           | 2949.6076 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2938.4535 |
| sp P53396 ACLY_HUMAN           | 2949.6076 |
| sp P18621 RL17_HUMAN           | 2469.221  |
| sp P68032 ACTC_HUMAN,sp P63267 | 2938.4535 |
| sp P53396 ACLY_HUMAN           | 2949.6076 |
| sp P53396 ACLY_HUMAN           | 2949.6076 |
| sp P00387 NB5R3_HUMAN          | 4256.0882 |
| sp P53396 ACLY_HUMAN           | 2949.6076 |
| sp P00387 NB5R3_HUMAN          | 4256.0882 |
| sp P10586 PTPRF_HUMAN          | 4179.0735 |
| sp P10586 PTPRF_HUMAN          | 4179.0735 |
| sp P10586 PTPRF_HUMAN          | 4179.0735 |
| sp Q14204 DYHC1_HUMAN          | 2763.4456 |
| sp Q00341 VIGLN_HUMAN          | 2528.3751 |
| sp Q14204 DYHC1_HUMAN          | 2763.4456 |
| sp Q16891 MIC60_HUMAN          | 3165.6128 |
| sp P25705 ATPA_HUMAN           | 2905.5086 |
| sp P25705 ATPA_HUMAN           | 2905.5086 |
| sp P04075 ALDOA_HUMAN          | 3607.8133 |
| sp P04075 ALDOA_HUMAN          | 3607.8133 |
| sp P25705 ATPA_HUMAN           | 2905.5086 |
| sp P04075 ALDOA_HUMAN          | 3607.8133 |
| sp P04075 ALDOA_HUMAN          | 3607.8133 |
| sp P04075 ALDOA_HUMAN          | 3607.8133 |
| sp P04075 ALDOA_HUMAN          | 3607.8133 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P02786 TFR1_HUMAN           | 2571.3234 |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp O75533 SF3B1_HUMAN          | 2179.0639 |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp P04350 TBB4A_HUMAN,sp P6837 | 5116.3533 |
| sp P02786 TFR1_HUMAN           | 2571.3234 |
| sp P02786 TFR1_HUMAN           | 2571.3234 |
| sp P02786 TFR1_HUMAN           | 2571.3234 |
| sp P04350 TBB4A_HUMAN,sp P6837 | 5116.3533 |
| sp P02786 TFR1_HUMAN           | 2571.3234 |
| sp P02786 TFR1_HUMAN           | 2571.3234 |
| sp P02786 TFR1_HUMAN           | 2571.3234 |
| sp P54886 P5CS_HUMAN           | 2978.6189 |
| sp P54886 P5CS_HUMAN           | 2978.6189 |
| sp P00491 PNPH_HUMAN           | 2366.1194 |
| sp Q13283 G3BP1_HUMAN          | 4291.0611 |
| sp Q13283 G3BP1_HUMAN          | 4291.0611 |
| sp Q13283 G3BP1_HUMAN          | 4291.0611 |
| sp Q13283 G3BP1_HUMAN          | 4291.0611 |
| sp Q13283 G3BP1_HUMAN          | 4291.0611 |

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| sp Q9NYF8 BCLF1_HUMAN                      | 2868.477  |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp Q9NYF8 BCLF1_HUMAN                      | 2868.477  |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P52272 HNRPM_HUMAN                      | 6173.9761 |
| sp P52272 HNRPM_HUMAN                      | 6173.9761 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P36578 RL4_HUMAN                        | 3027.6294 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN  | 3653.6674 |
| sp P50454 SERPH_HUMAN                      | 2146.0888 |
| sp P36578 RL4_HUMAN                        | 3027.6294 |
| sp P50454 SERPH_HUMAN                      | 2146.0888 |
| sp P36578 RL4_HUMAN                        | 3027.6294 |
| sp P36578 RL4_HUMAN                        | 3027.6294 |
| sp P50454 SERPH_HUMAN                      | 2146.0888 |
| sp P36578 RL4_HUMAN                        | 3027.6294 |
| sp P36578 RL4_HUMAN                        | 3027.6294 |
| sp P36578 RL4_HUMAN                        | 3027.6294 |
| sp Q05639 EF1A2_HUMAN,sp P68133 ACTC_HUMAN | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P68133 ACTC_HUMAN | 2362.2896 |
| sp P26368 U2AF2_HUMAN                      | 5542.7144 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF              | 4700.2567 |
| sp P78527 PRKDC_HUMAN                      | 4134.1022 |
| sp P78527 PRKDC_HUMAN                      | 4134.1022 |
| sp P78527 PRKDC_HUMAN                      | 4134.1022 |
| sp P78527 PRKDC_HUMAN                      | 4134.1022 |
| sp P31930 QCR1_HUMAN                       | 4623.289  |
| sp P78527 PRKDC_HUMAN                      | 4134.1022 |
| sp P78527 PRKDC_HUMAN                      | 4134.1022 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF              | 4684.2618 |
| sp P32322 P5CR1_HUMAN                      | 2707.4116 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF              | 4684.2618 |
| sp P32322 P5CR1_HUMAN                      | 2707.4116 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF              | 4684.2618 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF              | 4684.2618 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF              | 4684.2618 |
| sp P32322 P5CR1_HUMAN                      | 2707.4116 |

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| sp P31327 CPSM_HUMAN           | 4635.2856 |
| sp P32322 P5CR1_HUMAN          | 2707.4116 |
| sp P32322 P5CR1_HUMAN          | 2707.4116 |
| sp P31327 CPSM_HUMAN           | 4635.2856 |
| sp P32322 P5CR1_HUMAN          | 2707.4116 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 2536.2494 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 2536.2494 |
| sp Q9Y2Q3 GSTK1_HUMAN          | 2739.3877 |
| sp Q9Y2Q3 GSTK1_HUMAN          | 2739.3877 |
| sp P68104 EF1A1_HUMAN,sp Q5VT! | 4302.2206 |
| sp Q9BQE3 TBA1C_HUMAN          | 4698.2775 |
| sp P34897 GLYM_HUMAN           | 3829.9185 |
| sp P34897 GLYM_HUMAN           | 3829.9185 |
| sp O95373 IPO7_HUMAN           | 2133.1504 |
| sp O95373 IPO7_HUMAN           | 2133.1504 |
| sp Q16891 MIC60_HUMAN          | 4427.1591 |
| sp O95373 IPO7_HUMAN           | 2133.1504 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2674.3867 |
| sp Q92979 NEP1_HUMAN           | 1997.0227 |
| sp Q92979 NEP1_HUMAN           | 1997.0227 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2674.3867 |
| sp Q92973 TNPO1_HUMAN          | 2090.9554 |
| sp Q92979 NEP1_HUMAN           | 1997.0227 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2674.3867 |
| sp Q92979 NEP1_HUMAN           | 1997.0227 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2674.3867 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2674.3867 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2674.3867 |
| sp Q9Y262 EIF3L_HUMAN          | 2595.3445 |
| sp Q9Y262 EIF3L_HUMAN          | 2595.3445 |
| sp Q9Y262 EIF3L_HUMAN          | 2595.3445 |
| sp Q9Y262 EIF3L_HUMAN          | 2595.3445 |
| sp P68104 EF1A1_HUMAN,sp Q5VT! | 5180.718  |
| sp Q9NZN4 EHD2_HUMAN           | 4240.0383 |
| sp Q9NZN4 EHD2_HUMAN           | 4240.0383 |
| sp P29401 TKT_HUMAN            | 4178.063  |
| sp P06733 ENOA_HUMAN           | 5112.559  |
| sp P31040 SDHA_HUMAN           | 5070.2541 |
| sp P06733 ENOA_HUMAN           | 5112.559  |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |
| sp Q8WUM4 PDC6I_HUMAN          | 2671.3395 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |
| sp Q8WUM4 PDC6I_HUMAN          | 2671.3395 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |

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| sp Q9BVA1 TBB2B_HUMAN,sp Q138 | 4934.3325 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138 | 4934.3325 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138 | 4934.3325 |
| sp P22695 QCR2_HUMAN          | 2847.4775 |
| sp P22695 QCR2_HUMAN          | 2847.4775 |
| sp P22695 QCR2_HUMAN          | 2847.4775 |
| sp P06733 ENOA_HUMAN          | 5096.5641 |
| sp P58107 EPIPL_HUMAN         | 4270.1732 |
| sp Q9Y490 TLN1_HUMAN          | 3233.6541 |
| sp Q9Y490 TLN1_HUMAN          | 3233.6541 |
| sp P58107 EPIPL_HUMAN         | 4270.1732 |
| sp Q9Y490 TLN1_HUMAN          | 3233.6541 |
| sp Q13421 MSLN_HUMAN          | 4011.9717 |
| sp Q13421 MSLN_HUMAN          | 4011.9717 |
| sp Q13421 MSLN_HUMAN          | 4011.9717 |
| sp Q16836 HCDH_HUMAN          | 2481.313  |
| sp Q16836 HCDH_HUMAN          | 2481.313  |
| sp P05787 K2C8_HUMAN          | 1733.8584 |
| sp P05787 K2C8_HUMAN          | 1733.8584 |
| sp P17301 ITA2_HUMAN          | 1326.584  |
| sp P49207 RL34_HUMAN          | 1455.6235 |
| sp P49207 RL34_HUMAN          | 1455.6235 |
| sp P49207 RL34_HUMAN          | 1455.6235 |
| sp P17301 ITA2_HUMAN          | 1326.584  |
| sp P26373 RL13_HUMAN          | 1670.786  |
| sp P26373 RL13_HUMAN          | 1670.786  |
| sp P04792 HSPB1_HUMAN         | 1839.8487 |
| sp P23284 PPIB_HUMAN          | 1492.643  |
| sp P00338 LDHA_HUMAN          | 1691.8002 |
| sp P00338 LDHA_HUMAN          | 1691.8002 |
| sp P23284 PPIB_HUMAN          | 1492.643  |
| sp P00338 LDHA_HUMAN          | 1691.8002 |
| sp P00338 LDHA_HUMAN          | 1691.8002 |
| sp P00338 LDHA_HUMAN          | 1691.8002 |
| sp P00338 LDHA_HUMAN          | 1691.8002 |
| sp Q99623 PHB2_HUMAN          | 1798.881  |
| sp P07195 LDHB_HUMAN          | 1706.7999 |
| sp P07195 LDHB_HUMAN          | 1706.7999 |
| sp P07195 LDHB_HUMAN          | 1706.7999 |
| sp P06748 NPM_HUMAN           | 1453.6937 |
| sp P16402 H13_HUMAN,sp Q02539 | 1774.8122 |
| sp P13639 EF2_HUMAN           | 1626.7638 |
| sp P13639 EF2_HUMAN           | 1626.7638 |
| sp P04843 RPN1_HUMAN          | 1674.7849 |
| sp P62937 PPIA_HUMAN          | 1453.6725 |
| sp P62937 PPIA_HUMAN          | 1453.6725 |
| sp O75054 IGSF3_HUMAN         | 2837.1399 |

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| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp O75054 IGSF3_HUMAN          | 2837.1399 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P08729 K2C7_HUMAN           | 1637.8009 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P26639 SYTC_HUMAN           | 1944.9793 |
| sp P52272 HNRPM_HUMAN          | 2092.0185 |
| sp Q92945 FUBP2_HUMAN          | 2467.1285 |
| sp Q92945 FUBP2_HUMAN          | 2467.1285 |
| sp P21333 FLNA_HUMAN           | 1852.9068 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P21333 FLNA_HUMAN           | 1852.9068 |
| sp P07737 PROF1_HUMAN          | 1804.8843 |
| sp P26639 SYTC_HUMAN           | 1944.9793 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 1877.8207 |
| sp P21333 FLNA_HUMAN           | 1766.7748 |
| sp P21333 FLNA_HUMAN           | 1766.7748 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 1877.8207 |
| sp Q15233 NONO_HUMAN           | 1427.7045 |
| sp P21333 FLNA_HUMAN           | 1766.7748 |
| sp Q9Y624 JAM1_HUMAN           | 2041.9051 |
| sp Q15233 NONO_HUMAN           | 1427.7045 |
| sp P08670 VIME_HUMAN           | 1504.6794 |
| sp P21333 FLNA_HUMAN           | 1416.7249 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P10586 PTPRF_HUMAN          | 1954.9385 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P08708 RS17_HUMAN           | 1380.6925 |
| sp P10586 PTPRF_HUMAN          | 1954.9385 |
| sp P35613 BASI_HUMAN           | 1606.8203 |
| sp P35613 BASI_HUMAN           | 1606.8203 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P10586 PTPRF_HUMAN          | 1954.9385 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P35613 BASI_HUMAN           | 1606.8203 |
| sp P35613 BASI_HUMAN           | 1606.8203 |
| sp P10586 PTPRF_HUMAN          | 1954.9385 |
| sp P10586 PTPRF_HUMAN          | 1954.9385 |
| sp P52272 HNRPM_HUMAN          | 1859.836  |
| sp P23246 SFPQ_HUMAN           | 1441.7201 |
| sp P68371 TBB4B_HUMAN          | 2039.9589 |
| sp P13987 CD59_HUMAN           | 1562.7188 |

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| sp P23246 SFPQ_HUMAN           | 1441.7201 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P68371 TBB4B_HUMAN          | 2039.9589 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P68371 TBB4B_HUMAN          | 2039.9589 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp Q9Y624 JAM1_HUMAN           | 1677.7271 |
| sp Q15149 PLEC_HUMAN           | 2991.3734 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P21796 VDAC1_HUMAN          | 1724.7893 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P05556 ITB1_HUMAN           | 2854.0541 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp Q15149 PLEC_HUMAN           | 2991.3734 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P21796 VDAC1_HUMAN          | 1724.7893 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1531.7155 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1531.7155 |
| sp P10586 PTPRF_HUMAN          | 2717.2459 |
| sp Q15365 PCBP1_HUMAN          | 2040.9972 |
| sp P08174 DAF_HUMAN            | 1554.76   |
| sp O00299 CLIC1_HUMAN          | 2234.0491 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |
| sp P08174 DAF_HUMAN            | 1554.76   |
| sp O00299 CLIC1_HUMAN          | 2234.0491 |
| sp Q15365 PCBP1_HUMAN          | 2040.9972 |
| sp P08174 DAF_HUMAN            | 1554.76   |
| sp O00299 CLIC1_HUMAN          | 2234.0491 |
| sp P08174 DAF_HUMAN            | 1554.76   |
| sp O00299 CLIC1_HUMAN          | 2234.0491 |
| sp P08174 DAF_HUMAN            | 1554.76   |
| sp P32004 L1CAM_HUMAN          | 2041.0116 |
| sp Q9UHB6 LIMA1_HUMAN          | 2397.0478 |
| sp P13639 EF2_HUMAN            | 1470.7355 |
| sp P30101 PDIA3_HUMAN          | 2272.0464 |
| sp P19338 NUCL_HUMAN           | 1356.7289 |
| sp P43121 MUC18_HUMAN          | 2046.8265 |
| sp P21333 FLNA_HUMAN           | 2582.1483 |

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| sp P19338 NUCL_HUMAN           | 1356.7289 |
| sp P13639 EF2_HUMAN            | 1470.7355 |
| sp P19338 NUCL_HUMAN           | 1356.7289 |
| sp P10809 CH60_HUMAN           | 1868.952  |
| sp P45880 VDAC2_HUMAN          | 1752.8206 |
| sp P19338 NUCL_HUMAN           | 1356.7289 |
| sp Q99729 ROAA_HUMAN           | 2134.93   |
| sp P19338 NUCL_HUMAN           | 1356.7289 |
| sp P21333 FLNA_HUMAN           | 2582.1483 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P45880 VDAC2_HUMAN          | 1752.8206 |
| sp P32004 L1CAM_HUMAN          | 2041.0116 |
| sp P84098 RL19_HUMAN           | 2267.0455 |
| sp P04075 ALDOA_HUMAN          | 1496.7623 |
| sp P32004 L1CAM_HUMAN          | 2041.0116 |
| sp P60174 TPIS_HUMAN           | 1914.9072 |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp P60174 TPIS_HUMAN           | 1914.9072 |
| sp Q9UHD1 CHRD1_HUMAN          | 2042.8891 |
| sp P04075 ALDOA_HUMAN          | 1496.7623 |
| sp P53396 ACLY_HUMAN           | 1715.873  |
| sp P02786 TFR1_HUMAN           | 2571.9941 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2023.964  |
| sp P22626 ROA2_HUMAN           | 6040.4038 |
| sp P04406 G3P_HUMAN            | 1526.6745 |
| sp Q9Y624 JAM1_HUMAN           | 2419.1114 |
| sp Q00610 CLH1_HUMAN           | 1954.9061 |
| sp Q9Y624 JAM1_HUMAN           | 2419.1114 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2023.964  |
| sp Q00839 HNRPU_HUMAN          | 1893.8057 |
| sp Q9Y624 JAM1_HUMAN           | 2419.1114 |
| sp Q00839 HNRPU_HUMAN          | 1893.8057 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2023.964  |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2023.964  |
| sp P08670 VIME_HUMAN           | 1930.8401 |
| sp Q00610 CLH1_HUMAN           | 1954.9061 |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp Q9Y624 JAM1_HUMAN           | 2419.1114 |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp P12235 ADT1_HUMAN,sp P12236 | 1968.8346 |
| sp P55769 NH2L1_HUMAN          | 1804.8665 |
| sp P19338 NUCL_HUMAN           | 1351.666  |
| sp P55769 NH2L1_HUMAN          | 1804.8665 |
| sp P10809 CH60_HUMAN           | 1349.7919 |

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| sp P39023 RL3_HUMAN            | 1491.7973 |
| sp P02786 TFR1_HUMAN           | 1410.7718 |
| sp P11940 PABP1_HUMAN          | 1608.7672 |
| sp P05556 ITB1_HUMAN           | 1773.8971 |
| sp P08195 4F2_HUMAN            | 1361.7078 |
| sp P32004 L1CAM_HUMAN          | 2060.9538 |
| sp P08195 4F2_HUMAN            | 1361.7078 |
| sp P19338 NUCL_HUMAN           | 2346.9764 |
| sp P08865 RSSA_HUMAN           | 1810.9577 |
| sp Q00839 HNRPU_HUMAN          | 2694.3613 |
| sp P19338 NUCL_HUMAN           | 2346.9764 |
| sp P08865 RSSA_HUMAN           | 1810.9577 |
| sp P08865 RSSA_HUMAN           | 1810.9577 |
| sp P50990 TCPQ_HUMAN           | 1730.8475 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P10809 CH60_HUMAN           | 1349.7919 |
| sp P10809 CH60_HUMAN           | 1349.7919 |
| sp P08865 RSSA_HUMAN           | 1810.9577 |
| sp Q00839 HNRPU_HUMAN          | 2694.3613 |
| sp P08865 RSSA_HUMAN           | 1810.9577 |
| sp P35637 FUS_HUMAN            | 2566.01   |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P06703 S10A6_HUMAN          | 1839.9214 |
| sp P50990 TCPQ_HUMAN           | 1730.8475 |
| sp P31327 CPSM_HUMAN           | 1817.8652 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P06703 S10A6_HUMAN          | 1839.9214 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P35637 FUS_HUMAN            | 2566.01   |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P31327 CPSM_HUMAN           | 1817.8652 |
| sp P32004 L1CAM_HUMAN          | 2060.9538 |
| sp P32004 L1CAM_HUMAN          | 2060.9538 |
| sp P08238 HS90B_HUMAN          | 2587.2078 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P32004 L1CAM_HUMAN          | 2060.9538 |
| sp P05787 K2C8_HUMAN           | 1844.8978 |
| sp P32004 L1CAM_HUMAN          | 2060.9538 |
| sp P62829 RL23_HUMAN           | 2123.9946 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P05787 K2C8_HUMAN           | 1844.8978 |
| sp Q14964 RB39A_HUMAN,sp Q9HC  | 1753.8635 |
| sp P05141 ADT2_HUMAN           | 2012.8608 |
| sp Q14964 RB39A_HUMAN,sp Q9HC  | 1753.8635 |



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| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1965.8996 |
| sp P05141 ADT2_HUMAN           | 2012.8608 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1965.8996 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P02786 TFR1_HUMAN           | 2321.9569 |
| sp P62826 RAN_HUMAN            | 1885.8846 |
| sp P26583 HMGB2_HUMAN,sp P094  | 1877.8077 |
| sp P62826 RAN_HUMAN            | 1885.8846 |
| sp P62987 RL40_HUMAN,sp P62979 | 2484.2483 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1965.8996 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P02786 TFR1_HUMAN           | 2321.9569 |
| sp Q14964 RB39A_HUMAN,sp Q9HC  | 1753.8635 |
| sp Q14964 RB39A_HUMAN,sp Q9HC  | 1753.8635 |
| sp P05141 ADT2_HUMAN           | 2012.8608 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1965.8996 |
| sp P06733 ENOA_HUMAN           | 2385.1812 |
| sp P62826 RAN_HUMAN            | 1885.8846 |
| sp P62826 RAN_HUMAN            | 1885.8846 |
| sp P19338 NUCL_HUMAN           | 1972.8578 |
| sp P62851 RS25_HUMAN           | 2011.0262 |
| sp P33316 DUT_HUMAN            | 2144.0572 |
| sp P62851 RS25_HUMAN           | 2011.0262 |
| sp P19338 NUCL_HUMAN           | 1972.8578 |
| sp P06756 ITAV_HUMAN           | 2105.9874 |
| sp P46940 IQGA1_HUMAN          | 1924.9465 |
| sp P62987 RL40_HUMAN,sp P62979 | 1461.7538 |
| sp P62851 RS25_HUMAN           | 2011.0262 |
| sp P19338 NUCL_HUMAN           | 1972.8578 |
| sp P33316 DUT_HUMAN            | 2144.0572 |
| sp P11142 HSP7C_HUMAN,sp P5465 | 1984.0153 |
| sp P19338 NUCL_HUMAN           | 1972.8578 |
| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp P11142 HSP7C_HUMAN,sp P5465 | 1984.0153 |
| sp P06756 ITAV_HUMAN           | 2105.9874 |
| sp P62987 RL40_HUMAN,sp P62979 | 2484.2483 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp P62987 RL40_HUMAN,sp P62979 | 1461.7538 |
| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp P11142 HSP7C_HUMAN,sp P5465 | 1984.0153 |
| sp P11142 HSP7C_HUMAN,sp P5465 | 1984.0153 |
| sp P38646 GRP75_HUMAN          | 2301.1012 |
| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |

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| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp Q9H0U4 RAB1B_HUMAN,sp Q925  | 1854.9112 |
| sp P30101 PDIA3_HUMAN          | 1665.8039 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp P45880 VDAC2_HUMAN          | 1920.824  |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp Q13310 PABP4_HUMAN,sp Q9H3  | 2073.899  |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp P49327 FAS_HUMAN            | 2101.0691 |
| sp P04075 ALDOA_HUMAN          | 3537.6107 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp P04075 ALDOA_HUMAN          | 3537.6107 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp Q13310 PABP4_HUMAN,sp Q9H3  | 2073.899  |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp O15031 PLXB2_HUMAN          | 3126.559  |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp Q9H0U4 RAB1B_HUMAN,sp Q925  | 1854.9112 |
| sp P45880 VDAC2_HUMAN          | 1920.824  |
| sp P49327 FAS_HUMAN            | 2101.0691 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp P04075 ALDOA_HUMAN          | 3537.6107 |
| sp O15031 PLXB2_HUMAN          | 3126.559  |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp P11021 BIP_HUMAN            | 2012.0215 |
| sp P04075 ALDOA_HUMAN          | 3537.6107 |
| sp P11142 HSP7C_HUMAN          | 2974.4158 |
| sp O15031 PLXB2_HUMAN          | 3126.559  |
| sp P11142 HSP7C_HUMAN          | 2974.4158 |
| sp O95678 K2C75_HUMAN,sp P4866 | 1593.7675 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp P04075 ALDOA_HUMAN          | 3537.6107 |
| sp P62829 RL23_HUMAN           | 1783.8848 |
| sp P11142 HSP7C_HUMAN          | 2974.4158 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P83731 RL24_HUMAN           | 1613.8083 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp Q15149 PLEC_HUMAN           | 2432.3023 |
| sp O95678 K2C75_HUMAN,sp P4866 | 1593.7675 |
| sp P14649 MYL6B_HUMAN,sp P6061 | 2159.1222 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp Q00839 HNRPU_HUMAN          | 1784.8727 |
| sp P83731 RL24_HUMAN           | 1613.8083 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P08195 4F2_HUMAN            | 2193.0226 |

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| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P10586 PTPRF_HUMAN          | 1908.9357 |
| sp P10586 PTPRF_HUMAN          | 1908.9357 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P08195 4F2_HUMAN            | 2542.1823 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P07737 PROF1_HUMAN          | 2282.1001 |
| sp P08195 4F2_HUMAN            | 2542.1823 |
| sp P10586 PTPRF_HUMAN          | 1908.9357 |
| sp P07737 PROF1_HUMAN          | 2282.1001 |
| sp P10586 PTPRF_HUMAN          | 1908.9357 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P07737 PROF1_HUMAN          | 2282.1001 |
| sp P08195 4F2_HUMAN            | 2542.1823 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp Q15149 PLEC_HUMAN           | 1637.8625 |
| sp P53999 TCP4_HUMAN           | 1823.9054 |
| sp P53999 TCP4_HUMAN           | 1823.9054 |
| sp Q6UVK1 CSPG4_HUMAN          | 2353.0744 |
| sp P53999 TCP4_HUMAN           | 1823.9054 |
| sp P00338 LDHA_HUMAN           | 1874.9237 |
| sp P53999 TCP4_HUMAN           | 1823.9054 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P31948 STIP1_HUMAN          | 2455.0672 |
| sp Q00839 HNRPU_HUMAN          | 2367.1707 |
| sp P00338 LDHA_HUMAN           | 1874.9237 |
| sp P02786 TFR1_HUMAN           | 2596.3061 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1673.8189 |
| sp P08729 K2C7_HUMAN           | 1825.9462 |
| sp P00338 LDHA_HUMAN           | 1874.9237 |
| sp Q00839 HNRPU_HUMAN          | 2367.1707 |
| sp P08729 K2C7_HUMAN           | 1825.9462 |
| sp P02786 TFR1_HUMAN           | 2596.3061 |
| sp P49327 FAS_HUMAN            | 1439.7872 |
| sp O00148 DX39A_HUMAN,sp Q138  | 2108.9902 |
| sp Q00839 HNRPU_HUMAN          | 2367.1707 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1673.8189 |
| sp Q00839 HNRPU_HUMAN          | 2367.1707 |
| sp O00148 DX39A_HUMAN,sp Q138  | 2108.9902 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q9BQG0 MBB1A_HUMAN          | 1668.8359 |
| sp P60900 PSA6_HUMAN           | 1974.8743 |
| sp P42704 LPPRC_HUMAN          | 1989.0055 |
| sp P10586 PTPRF_HUMAN          | 1762.8349 |

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| sp P62266 RS23_HUMAN          | 1571.8559 |
| sp P07910 HNRPC_HUMAN,sp P0DN | 1640.9138 |
| sp Q9BQG0 MBB1A_HUMAN         | 1668.8359 |
| sp P55884 EIF3B_HUMAN         | 1989.9796 |
| sp P02786 TFR1_HUMAN          | 2596.3061 |
| sp P02786 TFR1_HUMAN          | 2596.3061 |
| sp P10586 PTPRF_HUMAN         | 1762.8349 |
| sp P62937 PPIA_HUMAN          | 2027.9364 |
| sp Q15149 PLEC_HUMAN          | 1961.8942 |
| sp P62937 PPIA_HUMAN          | 2027.9364 |
| sp P02786 TFR1_HUMAN          | 2596.3061 |
| sp P08729 K2C7_HUMAN          | 2466.1339 |
| sp P02786 TFR1_HUMAN          | 2596.3061 |
| sp P02786 TFR1_HUMAN          | 2596.3061 |
| sp P10586 PTPRF_HUMAN         | 1762.8349 |
| sp P08729 K2C7_HUMAN          | 2466.1339 |
| sp P02786 TFR1_HUMAN          | 2282.0347 |
| sp P62937 PPIA_HUMAN          | 2027.9364 |
| sp P10586 PTPRF_HUMAN         | 1762.8349 |
| sp Q14103 HNRPD_HUMAN         | 2116.0147 |
| sp P60900 PSA6_HUMAN          | 1974.8743 |
| sp P62937 PPIA_HUMAN          | 2027.9364 |
| sp P62277 RS13_HUMAN          | 1784.8832 |
| sp P02786 TFR1_HUMAN          | 2596.3061 |
| sp P60900 PSA6_HUMAN          | 1974.8743 |
| sp P07737 PROF1_HUMAN         | 1414.7378 |
| sp P62937 PPIA_HUMAN          | 2027.9364 |
| sp P43121 MUC18_HUMAN         | 3439.6566 |
| sp P60900 PSA6_HUMAN          | 1974.8743 |
| sp Q14103 HNRPD_HUMAN         | 2116.0147 |
| sp Q15149 PLEC_HUMAN          | 1961.8942 |
| sp P43121 MUC18_HUMAN         | 3439.6566 |
| sp P62805 H4_HUMAN            | 1678.8236 |
| sp P07737 PROF1_HUMAN         | 1414.7378 |
| sp P07737 PROF1_HUMAN         | 1414.7378 |
| sp P07910 HNRPC_HUMAN         | 2248.1522 |
| sp P43121 MUC18_HUMAN         | 3439.6566 |
| sp P60900 PSA6_HUMAN          | 1974.8743 |
| sp Q14103 HNRPD_HUMAN         | 2116.0147 |
| sp P60900 PSA6_HUMAN          | 1974.8743 |
| sp Q96E39 RMXL1_HUMAN,sp P381 | 2095.9487 |
| sp P62805 H4_HUMAN            | 1678.8236 |
| sp P22626 ROA2_HUMAN          | 2257.9772 |
| sp P62937 PPIA_HUMAN          | 1575.7821 |
| sp P34897 GLYM_HUMAN          | 2197.1379 |
| sp P62277 RS13_HUMAN          | 1784.8832 |
| sp Q96E39 RMXL1_HUMAN,sp P381 | 2095.9487 |

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| sp Q96E39 RMXL1_HUMAN,sp P381  | 2095.9487 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P62753 RS6_HUMAN            | 2501.1744 |
| sp P22626 ROA2_HUMAN           | 2257.9772 |
| sp P34897 GLYM_HUMAN           | 2197.1379 |
| sp Q9ULF5 S39AA_HUMAN          | 1456.6874 |
| sp P43121 MUC18_HUMAN          | 3439.6566 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P22626 ROA2_HUMAN           | 2257.9772 |
| sp P00338 LDHA_HUMAN           | 2270.1067 |
| sp P11142 HSP7C_HUMAN          | 3725.7697 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1687.8345 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp P43121 MUC18_HUMAN          | 3439.6566 |
| sp P43121 MUC18_HUMAN          | 3439.6566 |
| sp P05362 ICAM1_HUMAN          | 2953.4413 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P07910 HNRPC_HUMAN          | 2248.1522 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P43121 MUC18_HUMAN          | 3439.6566 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp P07910 HNRPC_HUMAN          | 2248.1522 |
| sp P05783 K1C18_HUMAN          | 3395.5311 |
| sp P15121 ALDR_HUMAN           | 2421.225  |
| sp P43121 MUC18_HUMAN          | 3439.6566 |
| sp P05783 K1C18_HUMAN          | 3395.5311 |
| sp P05362 ICAM1_HUMAN          | 2953.4413 |
| sp P62937 PPIA_HUMAN           | 1575.7821 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2386.1839 |
| sp P05783 K1C18_HUMAN          | 3395.5311 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2386.1839 |
| sp P05783 K1C18_HUMAN          | 3395.5311 |
| sp P62805 H4_HUMAN             | 1634.8226 |
| sp P09382 LEG1_HUMAN           | 1840.9207 |
| sp P62937 PPIA_HUMAN           | 1575.7821 |
| sp P09382 LEG1_HUMAN           | 1840.9207 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2386.1839 |
| sp P62937 PPIA_HUMAN           | 1575.7821 |
| sp P08670 VIME_HUMAN           | 1729.8774 |
| sp P41091 IF2G_HUMAN,sp Q2VIR3 | 2295.178  |
| sp P62805 H4_HUMAN             | 1634.8226 |
| sp P62937 PPIA_HUMAN           | 1575.7821 |
| sp P62805 H4_HUMAN             | 1634.8226 |
| sp P23284 PPIB_HUMAN           | 2113.0004 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P08670 VIME_HUMAN           | 1729.8774 |

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| sp P43121 MUC18_HUMAN          | 3439.6566 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P35637 FUS_HUMAN            | 2090.9585 |
| sp P05783 K1C18_HUMAN          | 3547.5977 |
| sp Q07020 RL18_HUMAN           | 1969.9997 |
| sp Q07020 RL18_HUMAN           | 1969.9997 |
| sp P35637 FUS_HUMAN            | 2090.9585 |
| sp Q07020 RL18_HUMAN           | 1969.9997 |
| sp Q6UVK1 CSPG4_HUMAN          | 3720.972  |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1947.856  |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P46781 RS9_HUMAN            | 1842.9363 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P02786 TFR1_HUMAN           | 2407.0928 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1947.856  |
| sp P04083 ANXA1_HUMAN          | 1874.9374 |
| sp P62753 RS6_HUMAN            | 2391.1053 |
| sp P40926 MDHM_HUMAN           | 1797.8897 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P02786 TFR1_HUMAN           | 2407.0928 |
| sp Q13332 PTPRS_HUMAN          | 2789.2708 |
| sp P04083 ANXA1_HUMAN          | 1874.9374 |
| sp P10586 PTPRF_HUMAN          | 4348.1135 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P40926 MDHM_HUMAN           | 1797.8897 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp P02786 TFR1_HUMAN           | 2407.0928 |
| sp P04083 ANXA1_HUMAN          | 1874.9374 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P05783 K1C18_HUMAN          | 3531.6028 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3379.6143 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp P10586 PTPRF_HUMAN          | 4348.1135 |
| sp P21796 VDAC1_HUMAN          | 1640.8086 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3379.6143 |

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| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P05783 K1C18_HUMAN          | 3531.6028 |
| sp P10586 PTPRF_HUMAN          | 4348.1135 |
| sp P10586 PTPRF_HUMAN          | 4348.1135 |
| sp P35579 MYH9_HUMAN           | 1872.904  |
| sp Q9Y624 JAM1_HUMAN           | 2569.4116 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P05783 K1C18_HUMAN          | 3531.6028 |
| sp P10586 PTPRF_HUMAN          | 4348.1135 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P05783 K1C18_HUMAN          | 3531.6028 |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P10586 PTPRF_HUMAN          | 4348.1135 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp P50991 TCPD_HUMAN           | 1498.8395 |
| sp O15031 PLXB2_HUMAN          | 2446.1435 |
| sp Q96AG4 LRC59_HUMAN          | 2053.0402 |
| sp Q15149 PLEC_HUMAN           | 1640.8621 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P60842 IF4A1_HUMAN          | 1697.7937 |
| sp P21333 FLNA_HUMAN           | 3425.5293 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P60842 IF4A1_HUMAN          | 1697.7937 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |
| sp P21333 FLNA_HUMAN           | 3425.5293 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P21333 FLNA_HUMAN           | 3425.5293 |
| sp P14174 MIF_HUMAN            | 1705.8345 |

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| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P13639 EF2_HUMAN            | 2059.0256 |
| sp P78347 GTF2I_HUMAN          | 2411.1865 |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |
| sp P42285 MTREX_HUMAN          | 2131.1201 |
| sp P13639 EF2_HUMAN            | 2059.0256 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp O15031 PLXB2_HUMAN          | 2446.1435 |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |
| sp P15121 ALDR_HUMAN           | 2405.2301 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp P42285 MTREX_HUMAN          | 2131.1201 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P19338 NUCL_HUMAN           | 2005.8945 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P15121 ALDR_HUMAN           | 2405.2301 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 3320.5296 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P21333 FLNA_HUMAN           | 4230.9957 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp P19338 NUCL_HUMAN           | 2005.8945 |
| sp Q14204 DYHC1_HUMAN          | 1962.8782 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp P0DMV8 HS71A_HUMAN,sp P345  | 3723.7904 |
| sp P46940 IQGA1_HUMAN          | 2360.1285 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp Q14204 DYHC1_HUMAN          | 1962.8782 |
| sp P04843 RPN1_HUMAN           | 1940.0037 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp P23396 RS3_HUMAN            | 2196.0375 |
| sp P23396 RS3_HUMAN            | 2196.0375 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P23396 RS3_HUMAN            | 2196.0375 |



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| sp P05787 K2C8_HUMAN          | 2484.1366 |
| sp P23396 RS3_HUMAN           | 2196.0375 |
| sp P09651 ROA1_HUMAN,sp Q32P5 | 2109.0266 |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P23396 RS3_HUMAN           | 2196.0375 |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P09651 ROA1_HUMAN,sp Q32P5 | 2109.0266 |
| sp P05787 K2C8_HUMAN          | 2484.1366 |
| sp P23396 RS3_HUMAN           | 2196.0375 |
| sp P62805 H4_HUMAN            | 1662.8287 |
| sp P62805 H4_HUMAN            | 1662.8287 |
| sp P02545 LMNA_HUMAN          | 2138.1219 |
| sp P51991 ROA3_HUMAN          | 2095.011  |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P23396 RS3_HUMAN           | 2196.0375 |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P09651 ROA1_HUMAN,sp Q32P5 | 2109.0266 |
| sp Q9Y262 EIF3L_HUMAN         | 2483.1492 |
| sp P20700 LMNB1_HUMAN         | 2089.0215 |
| sp P62805 H4_HUMAN            | 1662.8287 |
| sp P62805 H4_HUMAN            | 1662.8287 |
| sp P62805 H4_HUMAN            | 1662.8287 |
| sp P02545 LMNA_HUMAN          | 2138.1219 |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P20700 LMNB1_HUMAN         | 2089.0215 |
| sp P22626 ROA2_HUMAN          | 2123.0423 |
| sp P62241 RS8_HUMAN           | 2097.9895 |
| sp P22626 ROA2_HUMAN          | 2123.0423 |
| sp P02786 TFR1_HUMAN          | 2193.0412 |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P20700 LMNB1_HUMAN         | 2089.0215 |
| sp P19338 NUCL_HUMAN          | 1827.9618 |
| sp P22626 ROA2_HUMAN          | 2123.0423 |
| sp P22626 ROA2_HUMAN          | 2123.0423 |
| sp P02786 TFR1_HUMAN          | 2193.0412 |
| sp P02786 TFR1_HUMAN          | 2579.2391 |
| sp P07814 SYEP_HUMAN          | 2075.0245 |
| sp Q01813 PFKAP_HUMAN         | 1626.789  |
| sp P16402 H13_HUMAN,sp P10412 | 1921.9997 |
| sp P11021 BIP_HUMAN           | 2259.0848 |
| sp P05387 RLA2_HUMAN          | 2421.2064 |
| sp P05387 RLA2_HUMAN          | 2421.2064 |
| sp P22626 ROA2_HUMAN          | 2123.0423 |
| sp P21333 FLNA_HUMAN          | 2328.1314 |
| sp P22626 ROA2_HUMAN          | 2123.0423 |

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| sp P07814 SYEP_HUMAN           | 2075.0245 |
| sp Q16881 TRXR1_HUMAN          | 2884.3767 |
| sp P07814 SYEP_HUMAN           | 2075.0245 |
| sp P07737 PROF1_HUMAN          | 2111.0899 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3191.425  |
| sp P07737 PROF1_HUMAN          | 2111.0899 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3191.425  |
| sp P07737 PROF1_HUMAN          | 2111.0899 |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P21333 FLNA_HUMAN           | 2328.1314 |
| sp P07737 PROF1_HUMAN          | 2111.0899 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3191.425  |
| sp P05556 ITB1_HUMAN           | 2157.0954 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3191.425  |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P07355 ANXA2_HUMAN          | 1968.0164 |
| sp P61978 HNRPK_HUMAN          | 3348.6838 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2711.4092 |
| sp P15880 RS2_HUMAN            | 2169.0048 |
| sp P61978 HNRPK_HUMAN          | 3348.6838 |
| sp P61978 HNRPK_HUMAN          | 3348.6838 |
| sp P06733 ENOA_HUMAN           | 2076.0164 |
| sp P06733 ENOA_HUMAN           | 2076.0164 |
| sp P61978 HNRPK_HUMAN          | 3348.6838 |
| sp P15880 RS2_HUMAN            | 2169.0048 |
| sp P07355 ANXA2_HUMAN          | 1968.0164 |
| sp P43243 MATR3_HUMAN          | 2921.431  |
| sp P06733 ENOA_HUMAN           | 2076.0164 |
| sp P05362 ICAM1_HUMAN          | 4697.0309 |
| sp P49327 FAS_HUMAN            | 2788.3014 |
| sp P43243 MATR3_HUMAN          | 2921.431  |
| sp Q13283 G3BP1_HUMAN          | 2690.2864 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P05388 RLA0_HUMAN           | 2319.1886 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 2902.3596 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P15880 RS2_HUMAN            | 2288.0889 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 2902.3596 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P00558 PGK1_HUMAN           | 2978.4114 |
| sp P15880 RS2_HUMAN            | 2288.0889 |

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| sp P00558 PGK1_HUMAN           | 2978.4114 |
| sp P00558 PGK1_HUMAN           | 2978.4114 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P00558 PGK1_HUMAN           | 2978.4114 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P00558 PGK1_HUMAN           | 2978.4114 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P62701 RS4X_HUMAN           | 2786.2745 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P49327 FAS_HUMAN            | 2437.2523 |
| sp P53621 COPA_HUMAN           | 2898.3317 |
| sp P49327 FAS_HUMAN            | 2437.2523 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 2255.2889 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 2255.2889 |
| sp P49327 FAS_HUMAN            | 2437.2523 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 2255.2889 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 2255.2889 |
| sp P08238 HS90B_HUMAN          | 3220.4257 |
| sp P08238 HS90B_HUMAN          | 3220.4257 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 2255.2889 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 2255.2889 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 2255.2889 |
| sp P62701 RS4X_HUMAN           | 2786.2745 |
| sp P62701 RS4X_HUMAN           | 2786.2745 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp Q16881 TRXR1_HUMAN          | 3190.4151 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P22234 PUR6_HUMAN           | 2891.2751 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P46940 IQGA1_HUMAN          | 1976.0942 |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P46940 IQGA1_HUMAN          | 1976.0942 |

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| sp P14618 KPYM_HUMAN           | 3690.6665 |
| sp P14618 KPYM_HUMAN           | 3690.6665 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P14618 KPYM_HUMAN           | 3690.6665 |
| sp P14618 KPYM_HUMAN           | 3690.6665 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P14618 KPYM_HUMAN           | 3690.6665 |
| sp P31327 CPSM_HUMAN           | 2777.3793 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp Q12905 ILF2_HUMAN           | 3289.5878 |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp Q12905 ILF2_HUMAN           | 3289.5878 |
| sp P05787 K2C8_HUMAN           | 2230.0828 |
| sp P40926 MDHM_HUMAN           | 3108.5802 |
| sp P40926 MDHM_HUMAN           | 3108.5802 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P08195 4F2_HUMAN            | 3405.5736 |
| sp P08195 4F2_HUMAN            | 3405.5736 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P68363 TBA1B_HUMAN,sp P6836 | 3586.7443 |
| sp P31327 CPSM_HUMAN           | 2396.2012 |
| sp Q8NHW5 RLA0L_HUMAN,sp P05:  | 3670.8189 |
| sp P55060 XPO2_HUMAN           | 2354.2118 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P31327 CPSM_HUMAN           | 2518.2955 |
| sp Q8NHW5 RLA0L_HUMAN,sp P05:  | 3670.8189 |
| sp P38159 RBMX_HUMAN           | 2447.222  |
| sp P08195 4F2_HUMAN            | 3405.5736 |
| sp P08195 4F2_HUMAN            | 3405.5736 |
| sp P31327 CPSM_HUMAN           | 2518.2955 |
| sp P68363 TBA1B_HUMAN,sp P6836 | 3586.7443 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp P07437 TBB5_HUMAN           | 2902.3299 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q8NHW5 RLA0L_HUMAN,sp P05:  | 3670.8189 |
| sp P31327 CPSM_HUMAN           | 2518.2955 |
| sp Q8NHW5 RLA0L_HUMAN,sp P05:  | 3670.8189 |
| sp P13804 ETFA_HUMAN           | 2380.2526 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp P31327 CPSM_HUMAN           | 2518.2955 |
| sp P19338 NUCL_HUMAN           | 3133.5244 |
| sp P07437 TBB5_HUMAN           | 2902.3299 |
| sp P08670 VIME_HUMAN           | 2253.1893 |

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| sp P19338 NUCL_HUMAN          | 3133.5244 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P19338 NUCL_HUMAN          | 3133.5244 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp P19338 NUCL_HUMAN          | 3133.5244 |
| sp P58107 EPIPL_HUMAN         | 2614.265  |
| sp P14618 KPYM_HUMAN          | 2753.3007 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P58107 EPIPL_HUMAN         | 2614.265  |
| sp P19338 NUCL_HUMAN          | 3133.5244 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P14618 KPYM_HUMAN          | 2753.3007 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp P16402 H13_HUMAN,sp P10412 | 2258.1794 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp P06733 ENOA_HUMAN          | 3181.4193 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P16402 H13_HUMAN,sp P10412 | 2258.1794 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp P99999 CYC_HUMAN           | 2332.0933 |
| sp P06733 ENOA_HUMAN          | 3181.4193 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp P06733 ENOA_HUMAN          | 3181.4193 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P08758 ANXA5_HUMAN         | 2247.094  |
| sp Q6YHK3 CD109_HUMAN         | 2760.3858 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp Q6UVK1 CSPG4_HUMAN         | 3667.808  |
| sp P62829 RL23_HUMAN          | 3096.6165 |
| sp Q6YHK3 CD109_HUMAN         | 2760.3858 |
| sp P49411 EFTU_HUMAN          | 2325.1893 |
| sp P62829 RL23_HUMAN          | 3096.6165 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P49411 EFTU_HUMAN          | 2325.1893 |
| sp P62829 RL23_HUMAN          | 3096.6165 |

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| sp P46940 IQGA1_HUMAN          | 3660.685  |
| sp P46940 IQGA1_HUMAN          | 3660.685  |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P49411 EFTU_HUMAN           | 2325.1893 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P46940 IQGA1_HUMAN          | 3660.685  |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P58107 EPIPL_HUMAN          | 3239.5809 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q99714 HCD2_HUMAN           | 2323.2383 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 3003.3365 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q99714 HCD2_HUMAN           | 2323.2383 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 3003.3365 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp Q24JP5 T132A_HUMAN          | 2951.4975 |
| sp P58107 EPIPL_HUMAN          | 3239.5809 |
| sp Q9HCU4 CELR2_HUMAN          | 2747.4018 |
| sp Q9HCU4 CELR2_HUMAN          | 2747.4018 |
| sp Q24JP5 T132A_HUMAN          | 2951.4975 |
| sp Q99714 HCD2_HUMAN           | 2323.2383 |
| sp P62854 RS26_HUMAN           | 2353.1729 |
| sp P58107 EPIPL_HUMAN          | 3239.5809 |
| sp P62854 RS26_HUMAN           | 2353.1729 |
| sp P62854 RS26_HUMAN           | 2353.1729 |
| sp P58107 EPIPL_HUMAN          | 3239.5809 |
| sp P46782 RS5_HUMAN            | 2735.296  |
| sp Q24JP5 T132A_HUMAN          | 2951.4975 |
| sp Q24JP5 T132A_HUMAN          | 2951.4975 |
| sp P62854 RS26_HUMAN           | 2353.1729 |
| sp Q14126 DSG2_HUMAN           | 3597.7767 |
| sp Q14126 DSG2_HUMAN           | 3597.7767 |
| sp P46782 RS5_HUMAN            | 2735.296  |
| sp P58107 EPIPL_HUMAN          | 3239.5809 |
| sp P46782 RS5_HUMAN            | 2735.296  |
| sp P58107 EPIPL_HUMAN          | 3239.5809 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P46782 RS5_HUMAN            | 2735.296  |
| sp P26599 PTBP1_HUMAN          | 2308.2202 |
| sp P26599 PTBP1_HUMAN          | 2308.2202 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P26599 PTBP1_HUMAN          | 2308.2202 |
| sp P08195 4F2_HUMAN            | 2518.1864 |
| sp P26599 PTBP1_HUMAN          | 2308.2202 |

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| sp P58107 EPIPL_HUMAN          | 2081.0641 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4518.0731 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P31327 CPSM_HUMAN           | 2267.1362 |
| sp P08758 ANXA5_HUMAN          | 2231.0991 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P62258 1433E_HUMAN          | 2596.2068 |
| sp P23528 COF1_HUMAN           | 3258.6184 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P31327 CPSM_HUMAN           | 2267.1362 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4518.0731 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4518.0731 |
| sp P27797 CALR_HUMAN           | 3863.7326 |
| sp P07737 PROF1_HUMAN          | 3034.5652 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp O15031 PLXB2_HUMAN          | 2524.2156 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4775.2106 |
| sp O76021 RL1D1_HUMAN          | 2422.1441 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp O76021 RL1D1_HUMAN          | 2422.1441 |
| sp P07814 SYEP_HUMAN           | 2298.1743 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P07814 SYEP_HUMAN           | 2298.1743 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp Q9UHD8 SEPT9_HUMAN          | 2577.2057 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P07814 SYEP_HUMAN           | 2298.1743 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P17987 TCPA_HUMAN           | 2818.5076 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P17987 TCPA_HUMAN           | 2818.5076 |
| sp P35052 GPC1_HUMAN           | 3238.4435 |
| sp Q15149 PLEC_HUMAN           | 2507.2366 |
| sp P35052 GPC1_HUMAN           | 3238.4435 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |

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| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P52597 HNRPF_HUMAN          | 2433.2064 |
| sp P60174 TPIS_HUMAN           | 3225.6081 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P60174 TPIS_HUMAN           | 3225.6081 |
| sp P07814 SYEP_HUMAN           | 2298.1743 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp Q92973 TNPO1_HUMAN          | 2553.1372 |
| sp Q15149 PLEC_HUMAN           | 2507.2366 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P56192 SYMC_HUMAN           | 2887.3197 |
| sp P52597 HNRPF_HUMAN          | 2433.2064 |
| sp P15880 RS2_HUMAN            | 1989.071  |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P60174 TPIS_HUMAN           | 3225.6081 |
| sp P52597 HNRPF_HUMAN          | 2433.2064 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4518.0731 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P60174 TPIS_HUMAN           | 3225.6081 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp Q15149 PLEC_HUMAN           | 2507.2366 |
| sp P15880 RS2_HUMAN            | 1989.071  |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4775.2106 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P62249 RS16_HUMAN           | 1924.0921 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P62136 PP1A_HUMAN,sp P6214C | 2737.2768 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4777.1899 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P62136 PP1A_HUMAN,sp P6214C | 2737.2768 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4775.2106 |
| sp Q01082 SPTB2_HUMAN          | 2345.0482 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |



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| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4775.2106 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp O75475 PSIP1_HUMAN          | 2844.3964 |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4775.2106 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4761.195  |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp P49411 EFTU_HUMAN           | 3134.5118 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4761.195  |
| sp P49411 EFTU_HUMAN           | 3134.5118 |
| sp P13639 EF2_HUMAN            | 1938.9939 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4761.195  |
| sp P68032 ACTC_HUMAN,sp P63267 | 4761.195  |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P13639 EF2_HUMAN            | 1938.9939 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4761.195  |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp O15371 EIF3D_HUMAN          | 2678.3044 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4761.195  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P00558 PGK1_HUMAN           | 1942.0299 |
| sp P46940 IQGA1_HUMAN          | 3213.7133 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp Q96QK1 VPS35_HUMAN          | 2258.1583 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp Q9UHB9 SRP68_HUMAN          | 2283.1594 |
| sp Q9UHB9 SRP68_HUMAN          | 2283.1594 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P43121 MUC18_HUMAN          | 2985.5086 |
| sp O94979 SC31A_HUMAN          | 2920.4164 |

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| sp P43121 MUC18_HUMAN | 2985.5086 |
| sp Q7KZF4 SND1_HUMAN  | 3240.619  |
| sp P43121 MUC18_HUMAN | 2985.5086 |
| sp P15311 EZRI_HUMAN  | 2743.3552 |
| sp P15311 EZRI_HUMAN  | 2743.3552 |
| sp Q7KZF4 SND1_HUMAN  | 3240.619  |
| sp P15311 EZRI_HUMAN  | 2743.3552 |
| sp Q7KZF4 SND1_HUMAN  | 3240.619  |
| sp Q92945 FUBP2_HUMAN | 2575.2121 |
| sp P15311 EZRI_HUMAN  | 2743.3552 |
| sp P05787 K2C8_HUMAN  | 2593.1854 |
| sp P46776 RL27A_HUMAN | 2832.3389 |
| sp P05787 K2C8_HUMAN  | 2593.1854 |
| sp P46776 RL27A_HUMAN | 2832.3389 |
| sp P05787 K2C8_HUMAN  | 2593.1854 |
| sp P05787 K2C8_HUMAN  | 2593.1854 |
| sp P46776 RL27A_HUMAN | 2832.3389 |
| sp P05787 K2C8_HUMAN  | 2593.1854 |
| sp P05787 K2C8_HUMAN  | 2593.1854 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
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| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P07195 LDHB_HUMAN  | 2067.0623 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P17844 DDX5_HUMAN  | 2881.4498 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp Q1KMD3 HNRL2_HUMAN | 2453.2584 |
| sp O43390 HNRPR_HUMAN | 2714.3116 |
| sp O43390 HNRPR_HUMAN | 2714.3116 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp Q1KMD3 HNRL2_HUMAN | 2453.2584 |
| sp Q1KMD3 HNRL2_HUMAN | 2453.2584 |
| sp O43390 HNRPR_HUMAN | 2714.3116 |
| sp O43390 HNRPR_HUMAN | 2714.3116 |
| sp P05787 K2C8_HUMAN  | 2577.1905 |
| sp P06733 ENOA_HUMAN  | 2097.0306 |
| sp Q8WUM4 PDC6I_HUMAN | 2338.1117 |

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| sp Q8WUM4 PDC6I_HUMAN | 2338.1117 |
| sp P50454 SERPH_HUMAN | 3505.8516 |
| sp P50395 GDIB_HUMAN  | 2332.1257 |
| sp P50454 SERPH_HUMAN | 3505.8516 |
| sp Q15149 PLEC_HUMAN  | 3601.7022 |
| sp P02786 TFR1_HUMAN  | 2331.2032 |
| sp Q15149 PLEC_HUMAN  | 3601.7022 |
| sp P02786 TFR1_HUMAN  | 2331.2032 |
| sp P05783 K1C18_HUMAN | 2389.1974 |
| sp Q15149 PLEC_HUMAN  | 3601.7022 |
| sp P02786 TFR1_HUMAN  | 2331.2032 |
| sp P02786 TFR1_HUMAN  | 2331.2032 |
| sp P47897 SYQ_HUMAN   | 3073.5568 |
| sp P47897 SYQ_HUMAN   | 3073.5568 |
| sp Q01518 CAP1_HUMAN  | 3352.614  |
| sp Q01518 CAP1_HUMAN  | 3352.614  |
| sp P00338 LDHA_HUMAN  | 2095.0572 |
| sp Q01518 CAP1_HUMAN  | 3352.614  |
| sp P00338 LDHA_HUMAN  | 2095.0572 |
| sp P46940 IQGA1_HUMAN | 4059.0187 |
| sp P08729 K2C7_HUMAN  | 2419.1465 |
| sp Q96DG6 CMBL_HUMAN  | 3010.5903 |
| sp P08729 K2C7_HUMAN  | 2419.1465 |
| sp P08729 K2C7_HUMAN  | 2419.1465 |
| sp P37802 TAGL2_HUMAN | 2960.4226 |
| sp P08729 K2C7_HUMAN  | 2419.1465 |
| sp P37802 TAGL2_HUMAN | 2960.4226 |
| sp P37802 TAGL2_HUMAN | 2960.4226 |
| sp P37802 TAGL2_HUMAN | 2960.4226 |
| sp P62826 RAN_HUMAN   | 5583.6477 |
| sp P05783 K1C18_HUMAN | 2373.2025 |
| sp P05783 K1C18_HUMAN | 2373.2025 |
| sp P05783 K1C18_HUMAN | 2373.2025 |
| sp P05783 K1C18_HUMAN | 2373.2025 |
| sp P05783 K1C18_HUMAN | 2373.2025 |
| sp P05783 K1C18_HUMAN | 2373.2025 |
| sp P31949 S10AB_HUMAN | 3087.4059 |
| sp P05783 K1C18_HUMAN | 2373.2025 |
| sp P36871 PGM1_HUMAN  | 3222.5833 |
| sp P36871 PGM1_HUMAN  | 3222.5833 |
| sp P30044 PRDX5_HUMAN | 3173.5768 |
| sp Q7KZF4 SND1_HUMAN  | 2824.5004 |
| sp Q7KZF4 SND1_HUMAN  | 2824.5004 |
| sp Q7KZF4 SND1_HUMAN  | 2824.5004 |
| sp Q7KZF4 SND1_HUMAN  | 2824.5004 |
| sp P23588 IF4B_HUMAN  | 3383.6045 |
| sp Q7KZF4 SND1_HUMAN  | 2824.5004 |

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| sp Q7KZF4 SND1_HUMAN           | 2824.5004 |
| sp P23588 IF4B_HUMAN           | 3383.6045 |
| sp P23588 IF4B_HUMAN           | 3383.6045 |
| sp P06733 ENOA_HUMAN           | 4588.1275 |
| sp P06733 ENOA_HUMAN           | 4588.1275 |
| sp Q15365 PCBP1_HUMAN          | 3809.9002 |
| sp Q15365 PCBP1_HUMAN          | 3809.9002 |
| sp Q15365 PCBP1_HUMAN          | 3809.9002 |
| sp Q13011 ECH1_HUMAN           | 2514.2564 |
| sp Q13011 ECH1_HUMAN           | 2514.2564 |
| sp Q13011 ECH1_HUMAN           | 2514.2564 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp Q13011 ECH1_HUMAN           | 2514.2564 |
| sp Q13011 ECH1_HUMAN           | 2514.2564 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4518.0731 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P06748 NPM_HUMAN            | 1798.8082 |
| sp P06748 NPM_HUMAN            | 1798.8082 |
| sp P06748 NPM_HUMAN            | 1798.8082 |
| sp Q00839 HNRPU_HUMAN          | 1862.8507 |
| sp P00533 EGFR_HUMAN           | 2415.9049 |
| sp P61247 RS3A_HUMAN           | 1541.7223 |
| sp P00533 EGFR_HUMAN           | 2415.9049 |
| sp P00533 EGFR_HUMAN           | 2415.9049 |
| sp P00533 EGFR_HUMAN           | 2415.9049 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1423.6943 |
| sp P14866 HNRPL_HUMAN          | 3418.4067 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1423.6943 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1423.6943 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1423.6943 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1423.6943 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1423.6943 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1423.6943 |
| sp P99999 CYC_HUMAN            | 1994.9334 |
| sp P11142 HSP7C_HUMAN          | 1893.8302 |
| sp P99999 CYC_HUMAN            | 1994.9334 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P61927 RL37_HUMAN           | 1488.6667 |
| sp P61927 RL37_HUMAN           | 1488.6667 |
| sp P61927 RL37_HUMAN           | 1488.6667 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P61927 RL37_HUMAN           | 1488.6667 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P11142 HSP7C_HUMAN          | 1893.8302 |

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| sp Q15233 NONO_HUMAN           | 1736.7788 |
| sp P54709 AT1B3_HUMAN          | 1857.8341 |
| sp P11142 HSP7C_HUMAN          | 1893.8302 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P62633 CNBP_HUMAN           | 2045.8142 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp P05783 K1C18_HUMAN          | 1856.9116 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp Q99497 PARK7_HUMAN          | 1998.7836 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2148.9634 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2148.9634 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp Q99497 PARK7_HUMAN          | 1998.7836 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2148.9634 |
| sp Q00839 HNRPU_HUMAN          | 1735.8166 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1704.8683 |
| sp Q00839 HNRPU_HUMAN          | 1735.8166 |
| sp P23528 COF1_HUMAN           | 1986.8378 |
| sp Q00839 HNRPU_HUMAN          | 1735.8166 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1704.8683 |
| sp P23528 COF1_HUMAN           | 1986.8378 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1704.8683 |
| sp Q00839 HNRPU_HUMAN          | 1735.8166 |
| sp Q00839 HNRPU_HUMAN          | 1735.8166 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1704.8683 |
| sp P09874 PARP1_HUMAN          | 1758.7849 |
| sp Q01082 SPTB2_HUMAN          | 1958.9334 |
| sp P62917 RL8_HUMAN            | 2012.9439 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp Q9UHD8 SEPT9_HUMAN          | 1697.8373 |
| sp P27797 CALR_HUMAN           | 2282.9927 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp Q08211 DHX9_HUMAN           | 2100.9501 |
| sp Q9UHB6 LIMA1_HUMAN          | 2097.0127 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |

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| sp P42704 LPPRC_HUMAN          | 1584.7784 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp Q16576 RBBP7_HUMAN          | 2035.9269 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp Q16576 RBBP7_HUMAN          | 2035.9269 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp O00571 DDX3X_HUMAN          | 2175.9233 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P26368 U2AF2_HUMAN          | 1934.8469 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P26368 U2AF2_HUMAN          | 1934.8469 |
| sp Q15149 PLEC_HUMAN           | 2284.0244 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp P26368 U2AF2_HUMAN          | 1934.8469 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp Q13813 SPTN1_HUMAN          | 2138.9981 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp P09429 HMGB1_HUMAN          | 2450.0696 |
| sp P09429 HMGB1_HUMAN          | 2450.0696 |
| sp Q15149 PLEC_HUMAN           | 1893.9221 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P62826 RAN_HUMAN            | 1666.8203 |
| sp P09429 HMGB1_HUMAN          | 2450.0696 |
| sp Q15149 PLEC_HUMAN           | 2284.0244 |
| sp P09429 HMGB1_HUMAN          | 2450.0696 |
| sp P46777 RL5_HUMAN            | 1690.8275 |
| sp P48509 CD151_HUMAN          | 1987.8946 |
| sp P62826 RAN_HUMAN            | 1666.8203 |

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| sp P48509 CD151_HUMAN          | 1987.8946 |
| sp P62826 RAN_HUMAN            | 1666.8203 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P09429 HMGB1_HUMAN          | 2450.0696 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P58107 EPIPL_HUMAN          | 2163.0556 |
| sp Q15149 PLEC_HUMAN           | 2284.0244 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P48509 CD151_HUMAN          | 1987.8946 |
| sp P48509 CD151_HUMAN          | 1987.8946 |
| sp P48509 CD151_HUMAN          | 1987.8946 |
| sp P60842 IF4A1_HUMAN          | 1785.8567 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp O75054 IGSF3_HUMAN          | 2837.1399 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P48643 TCPE_HUMAN           | 1629.7522 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp O43707 ACTN4_HUMAN          | 1574.8053 |
| sp P48643 TCPE_HUMAN           | 1629.7522 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp Q13332 PTPRS_HUMAN          | 1852.8744 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp O43707 ACTN4_HUMAN          | 1574.8053 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P09382 LEG1_HUMAN           | 2901.2372 |
| sp P60842 IF4A1_HUMAN          | 2062.8361 |

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| sp P60842 IF4A1_HUMAN           | 1785.8567 |
| sp P11021 BIP_HUMAN             | 1928.9844 |
| sp P29692 EF1D_HUMAN            | 2993.3962 |
| sp P12268 IMDH2_HUMAN           | 2042.8786 |
| sp P60842 IF4A1_HUMAN           | 1785.8567 |
| sp P02786 TFR1_HUMAN            | 1437.7252 |
| sp P29692 EF1D_HUMAN            | 2993.3962 |
| sp P29692 EF1D_HUMAN            | 2993.3962 |
| sp P13639 EF2_HUMAN             | 1598.8304 |
| sp P61978 HNRPK_HUMAN           | 2265.0033 |
| sp O00571 DDX3X_HUMAN           | 2543.0547 |
| sp P60842 IF4A1_HUMAN           | 2062.8361 |
| sp P60842 IF4A1_HUMAN           | 2062.8361 |
| sp P09429 HMGB1_HUMAN           | 2434.0747 |
| sp O00571 DDX3X_HUMAN           | 2543.0547 |
| sp P09429 HMGB1_HUMAN           | 2434.0747 |
| sp P61978 HNRPK_HUMAN           | 2265.0033 |
| sp P60842 IF4A1_HUMAN           | 2062.8361 |
| sp O00571 DDX3X_HUMAN           | 2543.0547 |
| sp P09429 HMGB1_HUMAN           | 1788.7955 |
| sp P09429 HMGB1_HUMAN           | 2434.0747 |
| sp P09429 HMGB1_HUMAN           | 2434.0747 |
| sp Q9HCU4 CELR2_HUMAN           | 3050.2633 |
| sp P09429 HMGB1_HUMAN           | 2434.0747 |
| sp Q9HCU4 CELR2_HUMAN           | 3050.2633 |
| sp P05787 K2C8_HUMAN            | 2026.9232 |
| sp P00533 EGFR_HUMAN            | 3240.3118 |
| sp P08238 HS90B_HUMAN           | 2101.9878 |
| sp P08238 HS90B_HUMAN           | 2101.9878 |
| sp P09429 HMGB1_HUMAN           | 2434.0747 |
| sp P09429 HMGB1_HUMAN           | 1788.7955 |
| sp P08238 HS90B_HUMAN           | 2101.9878 |
| sp P15121 ALDR_HUMAN            | 2414.1213 |
| sp P09429 HMGB1_HUMAN           | 1788.7955 |
| sp Q08211 DHX9_HUMAN            | 2359.0573 |
| sp P08238 HS90B_HUMAN           | 2101.9878 |
| sp Q9HCU4 CELR2_HUMAN           | 3050.2633 |
| sp Q9HCU4 CELR2_HUMAN           | 3050.2633 |
| sp P17844 DDX5_HUMAN            | 2107.9018 |
| sp P17844 DDX5_HUMAN            | 2107.9018 |
| sp Q01082 SPTB2_HUMAN           | 2904.3348 |
| sp P00533 EGFR_HUMAN            | 3240.3118 |
| sp P00533 EGFR_HUMAN            | 3240.3118 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 2357.0304 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 2357.0304 |
| sp P00533 EGFR_HUMAN            | 3240.3118 |
| sp P17844 DDX5_HUMAN            | 2107.9018 |



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| sp P00533 EGFR_HUMAN            | 3240.3118 |
| sp P31948 STIP1_HUMAN           | 1817.8584 |
| sp P31948 STIP1_HUMAN           | 1817.8584 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 2357.0304 |
| sp P00533 EGFR_HUMAN            | 3240.3118 |
| sp P31948 STIP1_HUMAN           | 1817.8584 |
| sp P00533 EGFR_HUMAN            | 3240.3118 |
| sp P31948 STIP1_HUMAN           | 1817.8584 |
| sp P31948 STIP1_HUMAN           | 1817.8584 |
| sp O75533 SF3B1_HUMAN           | 3097.4377 |
| sp P31948 STIP1_HUMAN           | 1817.8584 |
| sp P02786 TFR1_HUMAN            | 1810.9214 |
| sp Q07065 CKAP4_HUMAN           | 1620.7744 |
| sp P07814 SYEP_HUMAN            | 2793.3709 |
| sp P05141 ADT2_HUMAN            | 1989.0531 |
| sp P10586 PTPRF_HUMAN           | 1954.9385 |
| sp P10586 PTPRF_HUMAN           | 1954.9385 |
| sp P10586 PTPRF_HUMAN           | 1954.9385 |
| sp P10586 PTPRF_HUMAN           | 1954.9385 |
| sp Q8NC51 PAIRB_HUMAN           | 2282.0087 |
| sp P10586 PTPRF_HUMAN           | 1954.9385 |
| sp P14625 ENPL_HUMAN            | 1839.8315 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI  | 1651.9145 |
| sp Q92841 DDX17_HUMAN           | 2179.9051 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI  | 1651.9145 |
| sp P84098 RL19_HUMAN            | 2395.1404 |
| sp P06733 ENOA_HUMAN            | 1887.0102 |
| sp P84098 RL19_HUMAN            | 2395.1404 |
| sp P06733 ENOA_HUMAN            | 1887.0102 |
| sp P06733 ENOA_HUMAN            | 1887.0102 |
| sp P06733 ENOA_HUMAN            | 1887.0102 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI  | 1651.9145 |
| sp P61978 HNRPK_HUMAN           | 2661.1435 |
| sp P04406 G3P_HUMAN             | 1411.6732 |
| sp Q14240 IF4A2_HUMAN           | 2044.8796 |
| sp P04406 G3P_HUMAN             | 1411.6732 |
| sp P62266 RS23_HUMAN            | 1891.9428 |
| sp P08670 VIME_HUMAN            | 1321.6303 |
| sp P04406 G3P_HUMAN             | 1411.6732 |
| sp Q6UVK1 CSPG4_HUMAN           | 1479.7106 |
| sp P61978 HNRPK_HUMAN           | 2661.1435 |
| sp P46778 RL21_HUMAN            | 2192.159  |
| sp P46778 RL21_HUMAN            | 2192.159  |
| sp P50993 AT1A2_HUMAN,sp P1363  | 1961.0292 |
| sp P08670 VIME_HUMAN            | 1321.6303 |
| sp P61978 HNRPK_HUMAN           | 2661.1435 |
| sp Q6UVK1 CSPG4_HUMAN           | 1479.7106 |

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| sp P50993 AT1A2_HUMAN,sp P1363 | 1961.0292 |
| sp P50993 AT1A2_HUMAN,sp P1363 | 1961.0292 |
| sp P50990 TCPQ_HUMAN           | 1935.9183 |
| sp P61978 HNRPK_HUMAN          | 2661.1435 |
| sp P50990 TCPQ_HUMAN           | 1935.9183 |
| sp P61978 HNRPK_HUMAN          | 2661.1435 |
| sp Q8IWS0 PHF6_HUMAN           | 2561.0841 |
| sp P61978 HNRPK_HUMAN          | 2661.1435 |
| sp Q9UHB6 LIMA1_HUMAN          | 2397.0478 |
| sp P50990 TCPQ_HUMAN           | 1935.9183 |
| sp P51610 HCFC1_HUMAN          | 2390.139  |
| sp P51610 HCFC1_HUMAN          | 2390.139  |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P52272 HNRPM_HUMAN          | 2004.8887 |
| sp P52272 HNRPM_HUMAN          | 2004.8887 |
| sp P26599 PTBP1_HUMAN          | 1997.9847 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P26599 PTBP1_HUMAN          | 1997.9847 |
| sp P18669 PGAM1_HUMAN          | 2332.0033 |
| sp P52272 HNRPM_HUMAN          | 2004.8887 |
| sp P18669 PGAM1_HUMAN          | 2332.0033 |
| sp Q96AE4 FUBP1_HUMAN          | 2522.2257 |
| sp P78371 TCPB_HUMAN           | 2156.0022 |
| sp P22234 PUR6_HUMAN           | 2169.0446 |
| sp P18669 PGAM1_HUMAN          | 2332.0033 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 2220.0771 |
| sp P18669 PGAM1_HUMAN          | 2332.0033 |
| sp Q14974 IMB1_HUMAN           | 2194.1481 |
| sp P07900 HS90A_HUMAN,sp Q145i | 2230.0906 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P50990 TCPQ_HUMAN           | 2096.0174 |
| sp P02786 TFR1_HUMAN           | 2891.3184 |
| sp P07900 HS90A_HUMAN,sp Q145i | 2230.0906 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P50990 TCPQ_HUMAN           | 2096.0174 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 2220.0771 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P0DPI2 GAL3A_HUMAN,sp A0A0E | 2938.3621 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P07900 HS90A_HUMAN,sp Q145i | 2230.0906 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P11021 BIP_HUMAN            | 2212.0913 |
| sp P0DPI2 GAL3A_HUMAN,sp A0A0E | 2938.3621 |
| sp P08670 VIME_HUMAN           | 2020.9702 |

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| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P15880 RS2_HUMAN            | 1855.8774 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P78347 GTF2I_HUMAN          | 2430.1339 |
| sp P15880 RS2_HUMAN            | 1855.8774 |
| sp P02786 TFR1_HUMAN           | 2875.3235 |
| sp P15880 RS2_HUMAN            | 1855.8774 |
| sp P02786 TFR1_HUMAN           | 2875.3235 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P02786 TFR1_HUMAN           | 2875.3235 |
| sp P15880 RS2_HUMAN            | 1855.8774 |
| sp P15880 RS2_HUMAN            | 1855.8774 |
| sp P11940 PABP1_HUMAN          | 2925.2512 |
| sp O43707 ACTN4_HUMAN          | 2658.1942 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P30086 PEBP1_HUMAN          | 2767.3049 |
| sp P07900 HS90A_HUMAN          | 2637.2347 |
| sp Q9UQE7 SMC3_HUMAN           | 1878.9727 |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |
| sp P36578 RL4_HUMAN            | 2230.0147 |
| sp Q15149 PLEC_HUMAN           | 1566.7103 |
| sp O43707 ACTN4_HUMAN          | 3008.5091 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P30086 PEBP1_HUMAN          | 2767.3049 |
| sp P04083 ANXA1_HUMAN          | 2854.341  |
| sp P02786 TFR1_HUMAN           | 2875.3235 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P02786 TFR1_HUMAN           | 2875.3235 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp Q9P2B2 FPRP_HUMAN           | 2659.1609 |
| sp Q12905 ILF2_HUMAN           | 2084.0426 |
| sp Q9P2B2 FPRP_HUMAN           | 2659.1609 |
| sp P02786 TFR1_HUMAN           | 2875.3235 |
| sp P02786 TFR1_HUMAN           | 2875.3235 |
| sp P04083 ANXA1_HUMAN          | 2854.341  |
| sp Q08J23 NSUN2_HUMAN          | 1541.766  |
| sp O43707 ACTN4_HUMAN          | 3008.5091 |
| sp P63173 RL38_HUMAN           | 2010.0197 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P14618 KP YM_HUMAN          | 1991.9874 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P63173 RL38_HUMAN           | 2010.0197 |
| sp P63173 RL38_HUMAN           | 2010.0197 |
| sp P62263 RS14_HUMAN           | 2688.245  |
| sp Q13263 TIF1B_HUMAN          | 1989.954  |

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| sp P18084 ITB5_HUMAN           | 2638.2446 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |
| sp P63173 RL38_HUMAN           | 2010.0197 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp Q00839 HNRPU_HUMAN          | 1893.8057 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P180  | 2884.265  |
| sp Q00839 HNRPU_HUMAN          | 1893.8057 |
| sp P14618 KP YM_HUMAN          | 1991.9874 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |
| sp P30048 PRDX3_HUMAN          | 3581.6409 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P62263 RS14_HUMAN           | 2688.245  |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 3108.3949 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 3108.3949 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 3108.3949 |
| sp Q15149 PLEC_HUMAN           | 2948.3101 |
| sp Q15067 ACOX1_HUMAN          | 2936.3828 |
| sp P26447 S10A4_HUMAN          | 1878.8822 |
| sp P21333 FLNA_HUMAN           | 2962.3291 |
| sp P21333 FLNA_HUMAN           | 2962.3291 |
| sp P21333 FLNA_HUMAN           | 2962.3291 |
| sp Q01974 ROR2_HUMAN           | 2416.0325 |
| sp Q00839 HNRPU_HUMAN          | 1893.8057 |
| sp P26447 S10A4_HUMAN          | 1878.8822 |
| sp Q01974 ROR2_HUMAN           | 2416.0325 |
| sp P26447 S10A4_HUMAN          | 1878.8822 |
| sp P21333 FLNA_HUMAN           | 2962.3291 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp Q00839 HNRPU_HUMAN          | 1893.8057 |
| sp P11142 HSP7C_HUMAN          | 2034.0382 |
| sp Q01974 ROR2_HUMAN           | 2416.0325 |
| sp P27824 CALX_HUMAN           | 2094.0269 |
| sp P06744 G6PI_HUMAN           | 2083.0222 |
| sp Q92945 FUBP2_HUMAN          | 2593.317  |
| sp Q92945 FUBP2_HUMAN          | 2593.317  |
| sp Q15149 PLEC_HUMAN           | 2948.3101 |
| sp P27824 CALX_HUMAN           | 2094.0269 |
| sp P06744 G6PI_HUMAN           | 2083.0222 |
| sp P35606 COPB2_HUMAN          | 2697.1732 |
| sp Q92945 FUBP2_HUMAN          | 2593.317  |

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| sp Q92945 FUBP2_HUMAN          | 2593.317  |
| sp P06744 G6PI_HUMAN           | 2083.0222 |
| sp P35606 COPB2_HUMAN          | 2697.1732 |
| sp P04792 HSPB1_HUMAN          | 2209.0903 |
| sp P58107 EPIPL_HUMAN          | 2812.3702 |
| sp P35606 COPB2_HUMAN          | 2697.1732 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1801.9138 |
| sp P60842 IF4A1_HUMAN          | 2370.2002 |
| sp P60842 IF4A1_HUMAN          | 2370.2002 |
| sp P26373 RL13_HUMAN           | 2078.032  |
| sp P60842 IF4A1_HUMAN          | 2370.2002 |
| sp P60842 IF4A1_HUMAN          | 2370.2002 |
| sp P26373 RL13_HUMAN           | 2078.032  |
| sp P62701 RS4X_HUMAN           | 1363.6884 |
| sp P09382 LEG1_HUMAN           | 1678.7627 |
| sp P61247 RS3A_HUMAN           | 2758.2691 |
| sp Q9NX63 MIC19_HUMAN          | 2547.1522 |
| sp P09382 LEG1_HUMAN           | 1678.7627 |
| sp P09382 LEG1_HUMAN           | 1678.7627 |
| sp Q9NX63 MIC19_HUMAN          | 2547.1522 |
| sp P61247 RS3A_HUMAN           | 2758.2691 |
| sp P61247 RS3A_HUMAN           | 2758.2691 |
| sp Q9NX63 MIC19_HUMAN          | 2547.1522 |
| sp Q92499 DDX1_HUMAN           | 2750.2494 |
| sp Q92499 DDX1_HUMAN           | 2750.2494 |
| sp Q13435 SF3B2_HUMAN          | 2194.1052 |
| sp P10586 PTPRF_HUMAN          | 2457.2176 |
| sp P15121 ALDR_HUMAN           | 2536.0675 |
| sp P26640 SYVC_HUMAN           | 2148.0521 |
| sp P10586 PTPRF_HUMAN          | 2457.2176 |
| sp P62917 RL8_HUMAN            | 1253.6768 |
| sp Q13813 SPTN1_HUMAN          | 2622.2813 |
| sp P10586 PTPRF_HUMAN          | 2457.2176 |
| sp P62906 RL10A_HUMAN          | 1775.8764 |
| sp O00571 DDX3X_HUMAN          | 2587.2402 |
| sp O00571 DDX3X_HUMAN          | 2587.2402 |
| sp P62917 RL8_HUMAN            | 1253.6768 |
| sp Q9HCU4 CELR2_HUMAN          | 2100.0099 |
| sp Q00839 HNRPU_HUMAN          | 3854.6312 |
| sp Q00839 HNRPU_HUMAN          | 3854.6312 |
| sp P26583 HMGB2_HUMAN,sp P094  | 1877.8077 |
| sp P26583 HMGB2_HUMAN,sp P094  | 1877.8077 |
| sp O75643 U520_HUMAN           | 2536.2082 |
| sp O75643 U520_HUMAN           | 2536.2082 |
| sp Q00839 HNRPU_HUMAN          | 3854.6312 |
| sp Q00839 HNRPU_HUMAN          | 3854.6312 |
| sp Q14126 DSG2_HUMAN           | 2755.2838 |

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| sp Q14126 DSG2_HUMAN           | 2755.2838 |
| sp P40429 RL13A_HUMAN          | 2369.1539 |
| sp O75643 U520_HUMAN           | 2536.2082 |
| sp P35052 GPC1_HUMAN           | 2798.3511 |
| sp O75643 U520_HUMAN           | 2536.2082 |
| sp P13639 EF2_HUMAN            | 1558.8355 |
| sp P06744 G6PI_HUMAN           | 1832.8482 |
| sp P40429 RL13A_HUMAN          | 2369.1539 |
| sp P06576 ATPB_HUMAN           | 2428.2962 |
| sp P07205 PGK2_HUMAN,sp P00558 | 2317.0975 |
| sp P06744 G6PI_HUMAN           | 1832.8482 |
| sp P07205 PGK2_HUMAN,sp P00558 | 2317.0975 |
| sp P62280 RS11_HUMAN           | 2538.2748 |
| sp Q14126 DSG2_HUMAN           | 2755.2838 |
| sp P62280 RS11_HUMAN           | 2538.2748 |
| sp P07205 PGK2_HUMAN,sp P00558 | 2317.0975 |
| sp Q14126 DSG2_HUMAN           | 2755.2838 |
| sp Q14126 DSG2_HUMAN           | 2755.2838 |
| sp P35052 GPC1_HUMAN           | 2798.3511 |
| sp Q16832 DDR2_HUMAN           | 2241.0702 |
| sp P31943 HNRH1_HUMAN          | 3196.4156 |
| sp Q15149 PLEC_HUMAN           | 1714.8526 |
| sp O60506 HNRPO_HUMAN          | 3256.6041 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp P60709 ACTB_HUMAN,sp P63261 | 3297.5282 |
| sp Q16630 CPSF6_HUMAN          | 2689.2654 |
| sp P08174 DAF_HUMAN            | 4586.9148 |
| sp Q16630 CPSF6_HUMAN          | 2689.2654 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp Q16630 CPSF6_HUMAN          | 2689.2654 |
| sp P08174 DAF_HUMAN            | 4586.9148 |
| sp P08174 DAF_HUMAN            | 4586.9148 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P08174 DAF_HUMAN            | 4586.9148 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P21796 VDAC1_HUMAN          | 1920.933  |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P21796 VDAC1_HUMAN          | 1920.933  |
| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp P21796 VDAC1_HUMAN          | 1920.933  |
| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp Q00839 HNRPU_HUMAN          | 1453.6482 |

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| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P05783 K1C18_HUMAN          | 3551.6322 |
| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp P38646 GRP75_HUMAN          | 3205.4952 |
| sp P05783 K1C18_HUMAN          | 3551.6322 |
| sp P43121 MUC18_HUMAN          | 3829.8833 |
| sp P38646 GRP75_HUMAN          | 3205.4952 |
| sp P05783 K1C18_HUMAN          | 3551.6322 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P35579 MYH9_HUMAN           | 1996.9643 |
| sp P31327 CPSM_HUMAN           | 1908.904  |
| sp P38646 GRP75_HUMAN          | 3205.4952 |
| sp P35579 MYH9_HUMAN           | 1996.9643 |
| sp P38646 GRP75_HUMAN          | 3205.4952 |
| sp P78527 PRKDC_HUMAN          | 1930.9247 |
| sp Q04637 IF4G1_HUMAN          | 2933.4519 |
| sp Q04637 IF4G1_HUMAN          | 2933.4519 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp Q9UMS4 PRP19_HUMAN          | 2797.3923 |
| sp Q9UMS4 PRP19_HUMAN          | 2797.3923 |
| sp Q04637 IF4G1_HUMAN          | 2933.4519 |
| sp P78527 PRKDC_HUMAN          | 1930.9247 |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp P61247 RS3A_HUMAN           | 2386.1263 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp P61247 RS3A_HUMAN           | 2386.1263 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp Q9UMS4 PRP19_HUMAN          | 2797.3923 |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp P17844 DDX5_HUMAN           | 1774.856  |
| sp P62826 RAN_HUMAN            | 2020.9279 |
| sp P62826 RAN_HUMAN            | 2020.9279 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2248.1528 |
| sp P62826 RAN_HUMAN            | 2020.9279 |
| sp P62826 RAN_HUMAN            | 2020.9279 |
| sp Q92841 DDX17_HUMAN          | 2514.2537 |
| sp P32004 L1CAM_HUMAN          | 2931.4324 |
| sp P32004 L1CAM_HUMAN          | 2931.4324 |
| sp Q92841 DDX17_HUMAN          | 2514.2537 |

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| sp Q92841 DDX17_HUMAN          | 2514.2537 |
| sp P22234 PUR6_HUMAN           | 2343.221  |
| sp P32004 L1CAM_HUMAN          | 2931.4324 |
| sp P16402 H13_HUMAN,sp P10412  | 2050.0946 |
| sp P16402 H13_HUMAN,sp P10412  | 2050.0946 |
| sp P05386 RLA1_HUMAN           | 4560.2919 |
| sp P32004 L1CAM_HUMAN          | 2931.4324 |
| sp P32004 L1CAM_HUMAN          | 2931.4324 |
| sp P16402 H13_HUMAN,sp P10412  | 2050.0946 |
| sp P05386 RLA1_HUMAN           | 4560.2919 |
| sp P05386 RLA1_HUMAN           | 4560.2919 |
| sp O95757 HS74L_HUMAN,sp P3493 | 1986.9656 |
| sp Q14118 DAG1_HUMAN           | 3688.7104 |
| sp P16401 H15_HUMAN            | 2064.1103 |
| sp P16401 H15_HUMAN            | 2064.1103 |
| sp P04406 G3P_HUMAN            | 3129.4787 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3635.6542 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3635.6542 |
| sp Q9ULV4 COR1C_HUMAN          | 3146.4145 |
| sp P10809 CH60_HUMAN           | 3003.4561 |
| sp P04406 G3P_HUMAN            | 3129.4787 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3635.6542 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3635.6542 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P05787 K2C8_HUMAN           | 5394.4205 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3635.6542 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp P45880 VDAC2_HUMAN          | 3573.8315 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P08670 VIME_HUMAN           | 1735.9356 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp P17813 EGLN_HUMAN           | 1894.9425 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P45880 VDAC2_HUMAN          | 3573.8315 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P61981 1433G_HUMAN,sp P631C | 1699.8893 |
| sp P45880 VDAC2_HUMAN          | 3573.8315 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |



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| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P61981 1433G_HUMAN,sp P631C | 1699.8893 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P17813 EGLN_HUMAN           | 1894.9425 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp Q9Y624 JAM1_HUMAN           | 2796.5749 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp Q15149 PLEC_HUMAN           | 3189.5982 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P61981 1433G_HUMAN,sp P631C | 1699.8893 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P05141 ADT2_HUMAN,sp P1223C | 1655.8308 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P61981 1433G_HUMAN,sp P631C | 1699.8893 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp Q13813 SPTN1_HUMAN          | 2902.4349 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3595.6673 |
| sp P40429 RL13A_HUMAN          | 1547.9035 |
| sp Q13813 SPTN1_HUMAN          | 2902.4349 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P38646 GRP75_HUMAN          | 1842.8934 |
| sp Q13813 SPTN1_HUMAN          | 2902.4349 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P83731 RL24_HUMAN           | 2084.9877 |
| sp P38646 GRP75_HUMAN          | 1842.8934 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P38646 GRP75_HUMAN          | 1842.8934 |
| sp P49327 FAS_HUMAN            | 1777.921  |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P38646 GRP75_HUMAN          | 1842.8934 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp O75369 FLNB_HUMAN           | 3606.7301 |
| sp Q9BY67 CADM1_HUMAN          | 3001.5008 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |

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| sp Q9BY67 CADM1_HUMAN          | 3001.5008 |
| sp P50990 TCPQ_HUMAN           | 2782.3596 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q13435 SF3B2_HUMAN          | 3489.741  |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P62258 1433E_HUMAN          | 3191.5445 |
| sp Q9BY67 CADM1_HUMAN          | 3001.5008 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |
| sp P62258 1433E_HUMAN          | 3191.5445 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P62258 1433E_HUMAN          | 3191.5445 |
| sp Q13740 CD166_HUMAN          | 3540.5991 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P31327 CPSM_HUMAN           | 3842.7774 |
| sp P01130 LDLR_HUMAN           | 4341.9738 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P62258 1433E_HUMAN          | 3191.5445 |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q16576 RBBP7_HUMAN          | 4304.9808 |
| sp P01130 LDLR_HUMAN           | 4341.9738 |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P78347 GTF2I_HUMAN          | 3239.5564 |
| sp P31327 CPSM_HUMAN           | 3066.5047 |
| sp P01130 LDLR_HUMAN           | 4341.9738 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P01130 LDLR_HUMAN           | 4341.9738 |
| sp P15121 ALDR_HUMAN           | 2405.2301 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |

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| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P23396 RS3_HUMAN            | 2196.0375 |
| sp Q12906 ILF3_HUMAN           | 3884.7543 |
| sp P06576 ATPB_HUMAN           | 2759.2596 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P06576 ATPB_HUMAN           | 2759.2596 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp P31327 CPSM_HUMAN           | 2485.2125 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp P31327 CPSM_HUMAN           | 2485.2125 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp P31327 CPSM_HUMAN           | 2485.2125 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp P27635 RL10_HUMAN           | 3477.5341 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P27635 RL10_HUMAN           | 3477.5341 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P11142 HSP7C_HUMAN          | 3411.6657 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P08195 4F2_HUMAN            | 3724.7704 |
| sp P08195 4F2_HUMAN            | 3724.7704 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P11142 HSP7C_HUMAN          | 3411.6657 |

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| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P11142 HSP7C_HUMAN          | 3411.6657 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P08195 4F2_HUMAN            | 3724.7704 |
| sp P00533 EGFR_HUMAN           | 2975.4083 |
| sp P08195 4F2_HUMAN            | 3724.7704 |
| sp P19338 NUCL_HUMAN           | 2892.4294 |
| sp P00533 EGFR_HUMAN           | 2975.4083 |
| sp P11021 BIP_HUMAN            | 3318.6694 |
| sp P55795 HNRH2_HUMAN,sp P319  | 2478.2278 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp P08195 4F2_HUMAN            | 3724.7704 |
| sp P00533 EGFR_HUMAN           | 2975.4083 |
| sp P19338 NUCL_HUMAN           | 2892.4294 |
| sp P14625 ENPL_HUMAN           | 3428.6122 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P08195 4F2_HUMAN            | 3724.7704 |
| sp P19338 NUCL_HUMAN           | 2892.4294 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P02545 LMNA_HUMAN           | 4073.9442 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp P06748 NPM_HUMAN            | 3125.4863 |
| sp P08195 4F2_HUMAN            | 3724.7704 |
| sp P19338 NUCL_HUMAN           | 2892.4294 |
| sp P00558 PGK1_HUMAN           | 2617.2912 |
| sp P62917 RL8_HUMAN            | 3591.7371 |
| sp P62917 RL8_HUMAN            | 3591.7371 |
| sp P08195 4F2_HUMAN            | 3775.7701 |
| sp P08195 4F2_HUMAN            | 3775.7701 |
| sp P62917 RL8_HUMAN            | 3591.7371 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P62424 RL7A_HUMAN           | 2007.0425 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P06748 NPM_HUMAN            | 3125.4863 |
| sp O60664 PLIN3_HUMAN          | 3276.6626 |
| sp P08195 4F2_HUMAN            | 3775.7701 |
| sp P08195 4F2_HUMAN            | 3775.7701 |
| sp O60664 PLIN3_HUMAN          | 3276.6626 |

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| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp O60664 PLIN3_HUMAN          | 3276.6626 |
| sp P62277 RS13_HUMAN           | 2105.0681 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P06748 NPM_HUMAN            | 3125.4863 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P06748 NPM_HUMAN            | 3125.4863 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3776.7444 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3776.7444 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P07900 HS90A_HUMAN          | 2901.3929 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P06748 NPM_HUMAN            | 3125.4863 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P06748 NPM_HUMAN            | 3125.4863 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P40925 MDHC_HUMAN           | 2004.9581 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P05026 AT1B1_HUMAN          | 2807.3766 |
| sp P38646 GRP75_HUMAN          | 3072.4651 |
| sp P08195 4F2_HUMAN            | 3775.7701 |
| sp P45880 VDAC2_HUMAN          | 1637.809  |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P45880 VDAC2_HUMAN          | 1637.809  |
| sp P08195 4F2_HUMAN            | 3775.7701 |
| sp P05026 AT1B1_HUMAN          | 2807.3766 |
| sp P05026 AT1B1_HUMAN          | 2807.3766 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp Q15149 PLEC_HUMAN           | 3544.6634 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P35579 MYH9_HUMAN           | 1811.0193 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P04843 RPN1_HUMAN           | 1798.9505 |
| sp Q15185 TEBP_HUMAN           | 1930.9214 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P23528 COF1_HUMAN           | 3377.5796 |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp P04406 G3P_HUMAN            | 3363.5354 |

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| sp P26599 PTBP1_HUMAN | 3142.5724 |
| sp P49458 SRP09_HUMAN | 2531.1672 |
| sp P04843 RPN1_HUMAN  | 1798.9505 |
| sp P49458 SRP09_HUMAN | 2531.1672 |
| sp P04406 G3P_HUMAN   | 3363.5354 |
| sp P23528 COF1_HUMAN  | 3377.5796 |
| sp P26599 PTBP1_HUMAN | 3142.5724 |
| sp P26599 PTBP1_HUMAN | 3142.5724 |
| sp P49458 SRP09_HUMAN | 2531.1672 |
| sp P23528 COF1_HUMAN  | 3377.5796 |
| sp P06576 ATPB_HUMAN  | 4039.0062 |
| sp P09661 RU2A_HUMAN  | 2890.4308 |
| sp P49458 SRP09_HUMAN | 2531.1672 |
| sp P49458 SRP09_HUMAN | 2531.1672 |
| sp P04406 G3P_HUMAN   | 3363.5354 |
| sp Q07020 RL18_HUMAN  | 2754.3898 |
| sp P26599 PTBP1_HUMAN | 3142.5724 |
| sp P26599 PTBP1_HUMAN | 3142.5724 |
| sp P49458 SRP09_HUMAN | 2531.1672 |
| sp P09661 RU2A_HUMAN  | 2890.4308 |
| sp P04406 G3P_HUMAN   | 3363.5354 |
| sp P00966 ASSY_HUMAN  | 3091.4808 |
| sp Q13057 COASY_HUMAN | 3265.6044 |
| sp P04406 G3P_HUMAN   | 3363.5354 |
| sp P48643 TCPE_HUMAN  | 2968.5492 |
| sp P48643 TCPE_HUMAN  | 2968.5492 |
| sp P00966 ASSY_HUMAN  | 3091.4808 |
| sp P58107 EPIPL_HUMAN | 3328.5306 |
| sp P58107 EPIPL_HUMAN | 3328.5306 |
| sp P26599 PTBP1_HUMAN | 3142.5724 |
| sp P60174 TPIS_HUMAN  | 3911.9615 |
| sp P52272 HNRPM_HUMAN | 2103.0677 |
| sp P08708 RS17_HUMAN  | 2959.475  |
| sp P08708 RS17_HUMAN  | 2959.475  |
| sp P52272 HNRPM_HUMAN | 2103.0677 |
| sp P08708 RS17_HUMAN  | 2959.475  |
| sp Q13151 ROAO_HUMAN  | 3088.5029 |
| sp P08708 RS17_HUMAN  | 2959.475  |
| sp P48643 TCPE_HUMAN  | 2107.0474 |
| sp Q15029 U5S1_HUMAN  | 2258.1331 |
| sp P04792 HSPB1_HUMAN | 5309.6541 |
| sp Q13098 CSN1_HUMAN  | 3416.6525 |
| sp P61158 ARP3_HUMAN  | 3192.5292 |
| sp P27824 CALX_HUMAN  | 2059.9527 |
| sp Q14980 NUMA1_HUMAN | 3391.6128 |
| sp Q13098 CSN1_HUMAN  | 3416.6525 |
| sp P27824 CALX_HUMAN  | 2059.9527 |

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| sp P62826 RAN_HUMAN           | 1980.937  |
| sp P27824 CALX_HUMAN          | 2059.9527 |
| sp P21333 FLNA_HUMAN          | 5081.3335 |
| sp Q14980 NUMA1_HUMAN         | 2381.1751 |
| sp P62826 RAN_HUMAN           | 1980.937  |
| sp P62826 RAN_HUMAN           | 1980.937  |
| sp P21333 FLNA_HUMAN          | 5081.3335 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp P61978 HNRPK_HUMAN         | 5330.4911 |
| sp P61978 HNRPK_HUMAN         | 5330.4911 |
| sp Q5VYK3 ECM29_HUMAN         | 2080.1205 |
| sp P07437 TBB5_HUMAN          | 2222.1042 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp P10809 CH60_HUMAN          | 3776.8203 |
| sp P35579 MYH9_HUMAN          | 3340.563  |
| sp P07437 TBB5_HUMAN          | 2222.1042 |
| sp P35579 MYH9_HUMAN          | 3340.563  |
| sp P38646 GRP75_HUMAN         | 2534.2839 |
| sp Q5VYK3 ECM29_HUMAN         | 2080.1205 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp P38646 GRP75_HUMAN         | 2534.2839 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp Q07065 CKAP4_HUMAN         | 1564.8825 |
| sp P08670 VIME_HUMAN          | 2253.1893 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp Q07065 CKAP4_HUMAN         | 1564.8825 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043 | 3246.5901 |
| sp P62258 1433E_HUMAN         | 2891.4045 |
| sp P02786 TFR1_HUMAN          | 2177.0463 |
| sp P62258 1433E_HUMAN         | 2891.4045 |
| sp P00966 ASSY_HUMAN          | 2474.2304 |
| sp P42704 LPPRC_HUMAN         | 3181.5092 |
| sp P42704 LPPRC_HUMAN         | 3181.5092 |
| sp P12236 ADT3_HUMAN          | 2267.1798 |
| sp Q6YHK3 CD109_HUMAN         | 2762.2824 |
| sp Q07065 CKAP4_HUMAN         | 3672.8231 |
| sp Q9BUF5 TBB6_HUMAN          | 3173.5914 |

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| sp Q6YHK3 CD109_HUMAN          | 2762.2824 |
| sp Q6YHK3 CD109_HUMAN          | 2762.2824 |
| sp P31327 CPSM_HUMAN           | 2146.1463 |
| sp P15121 ALDR_HUMAN           | 2135.1449 |
| sp Q6YHK3 CD109_HUMAN          | 2762.2824 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1892.0367 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1892.0367 |
| sp P32119 PRDX2_HUMAN          | 2059.095  |
| sp P14866 HNRPL_HUMAN          | 3266.5078 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1892.0367 |
| sp Q6YHK3 CD109_HUMAN          | 2762.2824 |
| sp P15121 ALDR_HUMAN           | 2135.1449 |
| sp P15121 ALDR_HUMAN           | 2135.1449 |
| sp Q6YHK3 CD109_HUMAN          | 2762.2824 |
| sp P14866 HNRPL_HUMAN          | 3266.5078 |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |
| sp Q14204 DYHC1_HUMAN          | 3280.571  |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |
| sp P14866 HNRPL_HUMAN          | 3266.5078 |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |
| sp Q96AG4 LRC59_HUMAN          | 3113.5413 |
| sp P32119 PRDX2_HUMAN          | 2059.095  |
| sp P32119 PRDX2_HUMAN          | 2059.095  |
| sp Q53EL6 PDCD4_HUMAN          | 3377.5762 |
| sp Q53EL6 PDCD4_HUMAN          | 3377.5762 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1803.9196 |
| sp P22102 PUR2_HUMAN           | 3632.7675 |
| sp P12814 ACTN1_HUMAN          | 3889.7377 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1803.9196 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3217.5925 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp P43243 MATR3_HUMAN          | 1972.0993 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp Q15149 PLEC_HUMAN           | 3257.6238 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3217.5925 |
| sp P43243 MATR3_HUMAN          | 1972.0993 |
| sp O43707 ACTN4_HUMAN          | 3520.7726 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1803.9196 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3217.5925 |
| sp Q15149 PLEC_HUMAN           | 3257.6238 |
| sp P43243 MATR3_HUMAN          | 1972.0993 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp O43707 ACTN4_HUMAN          | 3520.7726 |



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| sp Q15149 PLEC_HUMAN           | 3257.6238 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3217.5925 |
| sp Q15149 PLEC_HUMAN           | 3257.6238 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp P04844 RPN2_HUMAN           | 3133.5891 |
| sp Q15149 PLEC_HUMAN           | 3257.6238 |
| sp P12277 KCRB_HUMAN           | 3783.8124 |
| sp P12277 KCRB_HUMAN           | 3783.8124 |
| sp P00558 PGK1_HUMAN           | 2500.2175 |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp O75643 U520_HUMAN           | 3766.873  |
| sp P00558 PGK1_HUMAN           | 2500.2175 |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp P26368 U2AF2_HUMAN          | 3353.7044 |
| sp P04844 RPN2_HUMAN           | 3133.5891 |
| sp P16104 H2AX_HUMAN,sp Q96Qv  | 2595.5    |
| sp P00558 PGK1_HUMAN           | 2500.2175 |
| sp P00558 PGK1_HUMAN           | 2500.2175 |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp P26368 U2AF2_HUMAN          | 3353.7044 |
| sp P04844 RPN2_HUMAN           | 3133.5891 |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp P04844 RPN2_HUMAN           | 3133.5891 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp P00558 PGK1_HUMAN           | 2500.2175 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp Q15149 PLEC_HUMAN           | 2507.2366 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp Q15149 PLEC_HUMAN           | 2507.2366 |
| sp P21333 FLNA_HUMAN           | 3685.8873 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P21333 FLNA_HUMAN           | 3685.8873 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp O00425 IF2B3_HUMAN          | 2279.2525 |
| sp Q6FI13 H2A2A_HUMAN,sp P2067 | 2538.4785 |
| sp Q00610 CLH1_HUMAN           | 1547.8712 |
| sp P17301 ITA2_HUMAN           | 2002.0048 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q6FI13 H2A2A_HUMAN,sp P2067 | 2538.4785 |
| sp O00425 IF2B3_HUMAN          | 2279.2525 |

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| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp Q6FI13 H2A2A_HUMAN,sp P2067 | 2538.4785 |
| sp Q6FI13 H2A2A_HUMAN,sp P2067 | 2538.4785 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp Q9Y490 TLN1_HUMAN           | 3299.6132 |
| sp Q9Y490 TLN1_HUMAN           | 3299.6132 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp Q9Y490 TLN1_HUMAN           | 3299.6132 |
| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp P29401 TKT_HUMAN            | 2845.4709 |
| sp P29401 TKT_HUMAN            | 2845.4709 |
| sp P55072 TERA_HUMAN           | 2163.1212 |
| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp P55072 TERA_HUMAN           | 2163.1212 |
| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp P45974 UBP5_HUMAN           | 3052.5546 |
| sp P29401 TKT_HUMAN            | 2845.4709 |
| sp P45974 UBP5_HUMAN           | 3052.5546 |
| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp P45974 UBP5_HUMAN           | 3052.5546 |
| sp P07814 SYEP_HUMAN           | 3496.6245 |
| sp P07814 SYEP_HUMAN           | 3496.6245 |
| sp P07814 SYEP_HUMAN           | 3496.6245 |
| sp P07954 FUMH_HUMAN           | 3364.6034 |
| sp P07954 FUMH_HUMAN           | 3364.6034 |
| sp P07954 FUMH_HUMAN           | 3364.6034 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp P23396 RS3_HUMAN            | 2166.0633 |
| sp P43243 MATR3_HUMAN          | 3276.6766 |
| sp P43243 MATR3_HUMAN          | 3276.6766 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P43243 MATR3_HUMAN          | 3276.6766 |
| sp P23396 RS3_HUMAN            | 2166.0633 |
| sp P43243 MATR3_HUMAN          | 3276.6766 |
| sp Q99832 TCPH_HUMAN           | 3087.4713 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P22102 PUR2_HUMAN           | 3333.6769 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P06744 G6PI_HUMAN           | 4031.0198 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2178.1685 |

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| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P06744 G6PI_HUMAN           | 4031.0198 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P16435 NCPR_HUMAN           | 3155.6365 |
| sp P07195 LDHB_HUMAN           | 1855.0244 |
| sp P10809 CH60_HUMAN           | 1752.9332 |
| sp P07195 LDHB_HUMAN           | 1855.0244 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P10809 CH60_HUMAN           | 1752.9332 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P07195 LDHB_HUMAN           | 1855.0244 |
| sp P10809 CH60_HUMAN           | 1752.9332 |
| sp P10809 CH60_HUMAN           | 1752.9332 |
| sp P07195 LDHB_HUMAN           | 1855.0244 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P10809 CH60_HUMAN           | 1752.9332 |
| sp P00338 LDHA_HUMAN           | 1841.0087 |
| sp P00338 LDHA_HUMAN           | 1841.0087 |
| sp Q13421 MSLN_HUMAN           | 2723.4745 |
| sp Q13421 MSLN_HUMAN           | 2723.4745 |
| sp P10809 CH60_HUMAN           | 1752.9332 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P10809 CH60_HUMAN           | 1752.9332 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp Q13421 MSLN_HUMAN           | 2723.4745 |
| sp Q13421 MSLN_HUMAN           | 2723.4745 |
| sp P07195 LDHB_HUMAN           | 1855.0244 |
| sp P07195 LDHB_HUMAN           | 1855.0244 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P00338 LDHA_HUMAN           | 1841.0087 |
| sp P00338 LDHA_HUMAN           | 1841.0087 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P29692 EF1D_HUMAN           | 1965.0167 |
| sp P29692 EF1D_HUMAN           | 1965.0167 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P29692 EF1D_HUMAN           | 1965.0167 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P29692 EF1D_HUMAN           | 1965.0167 |
| sp P29692 EF1D_HUMAN           | 1965.0167 |
| sp Q5JTH9 RRP12_HUMAN          | 3013.5338 |
| sp P29692 EF1D_HUMAN           | 1965.0167 |

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| sp O60361 NDK8_HUMAN,sp P2239  | 2603.2512 |
| sp P46940 IQGA1_HUMAN          | 2774.4127 |
| sp Q9Y224 RTRAF_HUMAN          | 3271.6725 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp Q9Y224 RTRAF_HUMAN          | 3271.6725 |
| sp Q9Y224 RTRAF_HUMAN          | 3271.6725 |
| sp Q92616 GCN1_HUMAN           | 2670.3245 |
| sp P06576 ATPB_HUMAN           | 3860.8244 |
| sp Q9BQ39 DDX50_HUMAN          | 2919.4614 |
| sp P10809 CH60_HUMAN           | 2538.2822 |
| sp P14735 IDE_HUMAN            | 2982.4896 |
| sp P14735 IDE_HUMAN            | 2982.4896 |
| sp P10809 CH60_HUMAN           | 2538.2822 |
| sp P16435 NCPR_HUMAN           | 3139.6416 |
| sp P37802 TAGL2_HUMAN          | 2852.3473 |
| sp P16435 NCPR_HUMAN           | 3139.6416 |
| sp P14735 IDE_HUMAN            | 2982.4896 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P16435 NCPR_HUMAN           | 3139.6416 |
| sp P16435 NCPR_HUMAN           | 3139.6416 |
| sp P29401 TKT_HUMAN            | 2347.1366 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp Q9NR30 DDX21_HUMAN          | 2916.4829 |
| sp P29401 TKT_HUMAN            | 2347.1366 |
| sp P29401 TKT_HUMAN            | 2347.1366 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P29401 TKT_HUMAN            | 2347.1366 |
| sp P29401 TKT_HUMAN            | 2347.1366 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P30040 ERP29_HUMAN          | 3206.5569 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P30040 ERP29_HUMAN          | 3206.5569 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P23921 RIR1_HUMAN           | 4170.1372 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp Q9HAV4 XPO5_HUMAN           | 2945.575  |
| sp P30153 2AAA_HUMAN           | 2961.4576 |
| sp Q9HAV4 XPO5_HUMAN           | 2945.575  |
| sp P60842 IF4A1_HUMAN          | 3589.6422 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P36871 PGM1_HUMAN           | 2090.032  |
| sp P60842 IF4A1_HUMAN          | 3589.6422 |
| sp O43390 HNRPR_HUMAN          | 2439.1693 |
| sp P02786 TFR1_HUMAN           | 2331.2032 |

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| sp O43390 HNRPR_HUMAN          | 2439.1693 |
| sp P60842 IF4A1_HUMAN          | 3573.6473 |
| sp P38606 VATA_HUMAN           | 4338.2206 |
| sp P06744 G6PI_HUMAN           | 2753.222  |
| sp P60842 IF4A1_HUMAN          | 3573.6473 |
| sp P06744 G6PI_HUMAN           | 2753.222  |
| sp P06744 G6PI_HUMAN           | 2753.222  |
| sp P60842 IF4A1_HUMAN          | 3573.6473 |
| sp P30153 2AAA_HUMAN,sp P30154 | 2463.2646 |
| sp P60842 IF4A1_HUMAN          | 3573.6473 |
| sp O14980 XPO1_HUMAN           | 3696.7842 |
| sp P30153 2AAA_HUMAN,sp P30154 | 2463.2646 |
| sp P14923 PLAK_HUMAN           | 2714.4796 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 3359.5425 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P49327 FAS_HUMAN            | 3725.6072 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P49327 FAS_HUMAN            | 3725.6072 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P31327 CPSM_HUMAN           | 2198.1259 |
| sp P49327 FAS_HUMAN            | 3725.6072 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P31327 CPSM_HUMAN           | 2198.1259 |
| sp P49327 FAS_HUMAN            | 3725.6072 |
| sp P31327 CPSM_HUMAN           | 2198.1259 |
| sp P31327 CPSM_HUMAN           | 2198.1259 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P16435 NCPR_HUMAN           | 3264.5285 |
| sp P49327 FAS_HUMAN            | 3725.6072 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P49327 FAS_HUMAN            | 3725.6072 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp O60506 HNRPQ_HUMAN          | 2435.1856 |
| sp Q08J23 NSUN2_HUMAN          | 3032.4735 |
| sp P12956 XRCC6_HUMAN          | 2230.1418 |
| sp P49327 FAS_HUMAN            | 3725.6072 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp O60506 HNRPQ_HUMAN          | 2435.1856 |

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| sp O60506 HNRPQ_HUMAN          | 2435.1856 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P12956 XRCC6_HUMAN          | 2230.1418 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P07355 ANXA2_HUMAN          | 3034.4495 |
| sp P07355 ANXA2_HUMAN          | 3034.4495 |
| sp P42704 LPPRC_HUMAN          | 3594.6461 |
| sp P62140 PP1B_HUMAN           | 3239.5671 |
| sp P42704 LPPRC_HUMAN          | 3594.6461 |
| sp O60506 HNRPQ_HUMAN          | 2698.3167 |
| sp O60506 HNRPQ_HUMAN          | 2698.3167 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp Q08211 DHX9_HUMAN           | 2056.1278 |
| sp Q08211 DHX9_HUMAN           | 2056.1278 |
| sp P49327 FAS_HUMAN            | 4330.3424 |
| sp P06733 ENOA_HUMAN           | 4588.1275 |
| sp P36871 PGM1_HUMAN           | 3016.5903 |
| sp P36871 PGM1_HUMAN           | 3016.5903 |
| sp P12270 TPR_HUMAN            | 2423.2795 |
| sp Q05639 EF1A2_HUMAN,sp P6810 | 2178.1685 |
| sp Q8TCS8 PNPT1_HUMAN          | 2302.2607 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P13639 EF2_HUMAN            | 3345.6227 |
| sp P49327 FAS_HUMAN            | 2231.199  |
| sp P49327 FAS_HUMAN            | 2231.199  |
| sp P49327 FAS_HUMAN            | 2231.199  |
| sp P08195 4F2_HUMAN            | 4645.3134 |
| sp P31327 CPSM_HUMAN           | 3073.5318 |
| sp P49327 FAS_HUMAN            | 2231.199  |
| sp P31327 CPSM_HUMAN           | 3073.5318 |
| sp P31327 CPSM_HUMAN           | 3073.5318 |
| sp P08195 4F2_HUMAN            | 4645.3134 |
| sp P08195 4F2_HUMAN            | 4645.3134 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P31327 CPSM_HUMAN           | 3073.5318 |
| sp P31327 CPSM_HUMAN           | 3073.5318 |
| sp P11586 C1TC_HUMAN           | 3047.5162 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp P31327 CPSM_HUMAN           | 3073.5318 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp P31327 CPSM_HUMAN           | 3073.5318 |

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| sp Q12905 ILF2_HUMAN           | 2289.258  |
| sp P46940 IQGA1_HUMAN          | 3385.7882 |
| sp Q12905 ILF2_HUMAN           | 2289.258  |
| sp Q12905 ILF2_HUMAN           | 2289.258  |
| sp Q12905 ILF2_HUMAN           | 2289.258  |
| sp Q12905 ILF2_HUMAN           | 2289.258  |
| sp Q04637 IF4G1_HUMAN          | 2944.431  |
| sp Q12905 ILF2_HUMAN           | 2289.258  |
| sp Q12905 ILF2_HUMAN           | 2289.258  |
| sp Q04637 IF4G1_HUMAN          | 2944.431  |
| sp Q04637 IF4G1_HUMAN          | 2944.431  |
| sp Q04637 IF4G1_HUMAN          | 2944.431  |
| sp Q04637 IF4G1_HUMAN          | 2944.431  |
| sp Q9ULF5 S39AA_HUMAN          | 2203.1525 |
| sp Q9ULF5 S39AA_HUMAN          | 2203.1525 |
| sp P78527 PRKDC_HUMAN          | 2075.0939 |
| sp Q9ULF5 S39AA_HUMAN          | 2203.1525 |
| sp P42704 LPPRC_HUMAN          | 2794.4218 |
| sp P78527 PRKDC_HUMAN          | 2173.1671 |
| sp P78527 PRKDC_HUMAN          | 2173.1671 |
| sp P31949 S10AB_HUMAN          | 3752.7338 |
| sp Q7KZF4 SND1_HUMAN           | 2866.4649 |
| sp Q7KZF4 SND1_HUMAN           | 2866.4649 |
| sp P09874 PARP1_HUMAN          | 3939.9782 |
| sp Q15021 CND1_HUMAN           | 3412.6973 |
| sp Q15021 CND1_HUMAN           | 3412.6973 |
| sp Q15021 CND1_HUMAN           | 3412.6973 |
| sp P16435 NCPR_HUMAN           | 4913.3189 |
| sp P36871 PGM1_HUMAN           | 3000.5954 |
| sp P36871 PGM1_HUMAN           | 3000.5954 |
| sp P36871 PGM1_HUMAN           | 3000.5954 |
| sp P36871 PGM1_HUMAN           | 3000.5954 |
| sp P36871 PGM1_HUMAN           | 3000.5954 |
| sp P36871 PGM1_HUMAN           | 3000.5954 |
| sp P36871 PGM1_HUMAN           | 3000.5954 |
| sp P36871 PGM1_HUMAN           | 3000.5954 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp Q14980 NUMA1_HUMAN          | 1995.8882 |
| sp P06748 NPM_HUMAN            | 2240.0418 |
| sp P06748 NPM_HUMAN            | 2240.0418 |

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| sp P62249 RS16_HUMAN           | 1310.6037 |
| sp Q07065 CKAP4_HUMAN          | 2356.0316 |
| sp Q07065 CKAP4_HUMAN          | 2356.0316 |
| sp Q07065 CKAP4_HUMAN          | 2356.0316 |
| sp Q07065 CKAP4_HUMAN          | 2356.0316 |
| sp P26373 RL13_HUMAN           | 1867.9163 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1989.9643 |
| sp P08758 ANXA5_HUMAN          | 1321.6262 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp O43707 ACTN4_HUMAN          | 1261.6415 |
| sp O43707 ACTN4_HUMAN          | 1261.6415 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp Q9UNX3 RL26L_HUMAN,sp P612! | 1311.6208 |
| sp O43707 ACTN4_HUMAN          | 1261.6415 |
| sp Q9UNX3 RL26L_HUMAN,sp P612! | 1311.6208 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp Q9UNX3 RL26L_HUMAN,sp P612! | 1311.6208 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp P43121 MUC18_HUMAN          | 1451.6463 |
| sp Q96A72 MGN2_HUMAN,sp P613!  | 1147.5298 |
| sp P21333 FLNA_HUMAN           | 1830.886  |
| sp P21333 FLNA_HUMAN           | 1830.886  |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp P43121 MUC18_HUMAN          | 1451.6463 |
| sp Q96A72 MGN2_HUMAN,sp P613!  | 1147.5298 |
| sp P21333 FLNA_HUMAN           | 1830.886  |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp P21333 FLNA_HUMAN           | 1531.7743 |
| sp Q14978 NOLC1_HUMAN          | 2360.2336 |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp P35637 FUS_HUMAN            | 3382.3422 |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp Q14978 NOLC1_HUMAN          | 2360.2336 |
| sp Q13310 PABP4_HUMAN          | 1601.7256 |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp Q8NC51 PAIRB_HUMAN          | 1553.711  |
| sp Q8NC51 PAIRB_HUMAN          | 1553.711  |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp Q8NC51 PAIRB_HUMAN          | 1553.711  |
| sp P62633 CNBP_HUMAN           | 2045.8142 |



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| sp Q13310 PABP4_HUMAN          | 1601.7256 |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp Q8NC51 PAIRB_HUMAN          | 1553.711  |
| sp P62633 CNBP_HUMAN           | 2045.8142 |
| sp Q8NC51 PAIRB_HUMAN          | 1553.711  |
| sp P35637 FUS_HUMAN            | 3382.3422 |
| sp P21333 FLNA_HUMAN           | 1531.7743 |
| sp P27816 MAP4_HUMAN           | 1671.8329 |
| sp P35637 FUS_HUMAN            | 2448.9989 |
| sp P21333 FLNA_HUMAN           | 1531.7743 |
| sp P00558 PGK1_HUMAN           | 1355.5994 |
| sp P11142 HSP7C_HUMAN          | 2441.0983 |
| sp P11142 HSP7C_HUMAN          | 2441.0983 |
| sp P49327 FAS_HUMAN            | 1328.6183 |
| sp Q13442 HAP28_HUMAN          | 1409.6609 |
| sp Q13428 TCOF_HUMAN           | 1713.905  |
| sp P49327 FAS_HUMAN            | 1328.6183 |
| sp P00558 PGK1_HUMAN           | 1355.5994 |
| sp P62633 CNBP_HUMAN           | 2045.8142 |
| sp P11142 HSP7C_HUMAN          | 2441.0983 |
| sp P11142 HSP7C_HUMAN          | 2441.0983 |
| sp Q13442 HAP28_HUMAN          | 1409.6609 |
| sp P62633 CNBP_HUMAN           | 2045.8142 |
| sp P35637 FUS_HUMAN            | 2448.9989 |
| sp P52948 NUP98_HUMAN          | 1479.7318 |
| sp P35637 FUS_HUMAN            | 2448.9989 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1704.7811 |
| sp P35637 FUS_HUMAN            | 2448.9989 |
| sp P05783 K1C18_HUMAN          | 1856.9116 |
| sp O14979 HNRDL_HUMAN          | 1615.7301 |
| sp O14979 HNRDL_HUMAN          | 1615.7301 |
| sp O95831 AIFM1_HUMAN          | 2162.0491 |
| sp P50991 TCPD_HUMAN           | 1576.7594 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1704.7811 |
| sp O95831 AIFM1_HUMAN          | 2162.0491 |
| sp P50991 TCPD_HUMAN           | 1576.7594 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1704.7811 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1704.7811 |
| sp Q96AG4 LRC59_HUMAN          | 1848.8788 |
| sp O00148 DX39A_HUMAN          | 1616.7729 |
| sp P02545 LMNA_HUMAN           | 2198.0128 |
| sp Q8WW12 PCNP_HUMAN           | 1786.7871 |
| sp Q96AG4 LRC59_HUMAN          | 1848.8788 |
| sp O00148 DX39A_HUMAN          | 1616.7729 |
| sp P26639 SYTC_HUMAN           | 1645.7372 |
| sp P26639 SYTC_HUMAN           | 1645.7372 |

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| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P26639 SYTC_HUMAN           | 1645.7372 |
| sp Q969P0 IGSF8_HUMAN          | 1337.6398 |
| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp P26639 SYTC_HUMAN           | 1645.7372 |
| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp P40227 TCPZ_HUMAN           | 1432.731  |
| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp Q14974 IMB1_HUMAN           | 1390.6266 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp P18077 RL35A_HUMAN          | 1359.6895 |
| sp P46782 RS5_HUMAN            | 1458.6892 |
| sp P18077 RL35A_HUMAN          | 1359.6895 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp P46782 RS5_HUMAN            | 1458.6892 |
| sp Q13283 G3BP1_HUMAN          | 1931.8618 |
| sp P18077 RL35A_HUMAN          | 1359.6895 |
| sp P15170 ERF3A_HUMAN,sp Q8IYD | 1451.7079 |
| sp P52272 HNRPM_HUMAN          | 1802.8336 |
| sp Q13283 G3BP1_HUMAN          | 1931.8618 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P39023 RL3_HUMAN            | 1787.7785 |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp Q13838 DX39B_HUMAN          | 1630.7886 |
| sp P38919 IF4A3_HUMAN          | 1793.8697 |
| sp P38919 IF4A3_HUMAN          | 1793.8697 |
| sp P61978 HNRPK_HUMAN          | 1931.832  |
| sp P25205 MCM3_HUMAN           | 1332.715  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp Q96HS1 PGAM5_HUMAN          | 1515.714  |
| sp Q8NC51 PAIRB_HUMAN          | 1111.5662 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp P25205 MCM3_HUMAN           | 1332.715  |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp Q13838 DX39B_HUMAN          | 1630.7886 |
| sp P78527 PRKDC_HUMAN          | 1581.7246 |
| sp P38919 IF4A3_HUMAN          | 1793.8697 |
| sp Q8NC51 PAIRB_HUMAN          | 1111.5662 |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp Q15233 NONO_HUMAN           | 1680.7856 |

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| sp P78527 PRKDC_HUMAN          | 1581.7246 |
| sp P21333 FLNA_HUMAN           | 2222.0968 |
| sp P21333 FLNA_HUMAN           | 2222.0968 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp P39023 RL3_HUMAN            | 1787.7785 |
| sp Q15233 NONO_HUMAN           | 1680.7856 |
| sp P21333 FLNA_HUMAN           | 2222.0968 |
| sp Q14103 HNRPD_HUMAN          | 1643.7614 |
| sp P21333 FLNA_HUMAN           | 2222.0968 |
| sp Q15149 PLEC_HUMAN           | 1908.929  |
| sp Q8NC51 PAIRB_HUMAN          | 1948.9603 |
| sp P39023 RL3_HUMAN            | 1787.7785 |
| sp P08729 K2C7_HUMAN           | 1981.913  |
| sp Q8NC51 PAIRB_HUMAN          | 1948.9603 |
| sp P78527 PRKDC_HUMAN          | 1391.6834 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp Q04637 IF4G1_HUMAN          | 3270.5501 |
| sp P13987 CD59_HUMAN           | 1972.8659 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P13987 CD59_HUMAN           | 1972.8659 |
| sp Q04637 IF4G1_HUMAN          | 3270.5501 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P13987 CD59_HUMAN           | 1972.8659 |
| sp Q9ULF5 S39AA_HUMAN          | 3319.4402 |
| sp P13987 CD59_HUMAN           | 1972.8659 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P08729 K2C7_HUMAN           | 1981.913  |
| sp Q14152 EIF3A_HUMAN          | 1632.7784 |
| sp Q9ULF5 S39AA_HUMAN          | 3319.4402 |
| sp Q9Y3F4 STRAP_HUMAN          | 2622.2813 |
| sp Q8TEQ6 GEMI5_HUMAN          | 1969.913  |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp Q8TEQ6 GEMI5_HUMAN          | 1969.913  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp Q14152 EIF3A_HUMAN          | 1632.7784 |
| sp Q01082 SPTB2_HUMAN          | 1872.7915 |
| sp Q9ULF5 S39AA_HUMAN          | 3319.4402 |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P52272 HNRPM_HUMAN          | 2248.1196 |
| sp P52272 HNRPM_HUMAN          | 2248.1196 |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp P62826 RAN_HUMAN            | 1609.7637 |

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| sp Q8TEQ6 GEMI5_HUMAN          | 1969.913  |
| sp Q02878 RL6_HUMAN            | 1556.7835 |
| sp Q92804 RBP56_HUMAN          | 2203.0831 |
| sp Q9ULF5 S39AA_HUMAN          | 3319.4402 |
| sp P52272 HNRPM_HUMAN          | 2248.1196 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P15:  | 1826.8799 |
| sp P78527 PRKDC_HUMAN          | 1648.8355 |
| sp Q9P2B2 FPRP_HUMAN           | 2660.2467 |
| sp P52272 HNRPM_HUMAN          | 2248.1196 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp P06744 G6PI_HUMAN           | 1641.8362 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P15:  | 1826.8799 |
| sp Q9P2B2 FPRP_HUMAN           | 2660.2467 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp Q9ULF5 S39AA_HUMAN          | 3319.4402 |
| sp P29692 EF1D_HUMAN           | 1532.7583 |
| sp Q9P2B2 FPRP_HUMAN           | 2660.2467 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P15:  | 1826.8799 |
| sp O76021 RL1D1_HUMAN          | 1566.746  |
| sp Q6YHK3 CD109_HUMAN          | 1457.6939 |
| sp P78527 PRKDC_HUMAN          | 1648.8355 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P15:  | 1826.8799 |
| sp P29692 EF1D_HUMAN           | 1532.7583 |
| sp Q9ULF5 S39AA_HUMAN          | 3319.4402 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P15:  | 1826.8799 |
| sp Q14152 EIF3A_HUMAN          | 1887.9189 |
| sp P18621 RL17_HUMAN           | 1550.7511 |
| sp Q01813 PFKAP_HUMAN          | 1382.683  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp Q6YHK3 CD109_HUMAN          | 1810.7659 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp Q6YHK3 CD109_HUMAN          | 1457.6939 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp Q9P2B2 FPRP_HUMAN           | 2660.2467 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp Q01082 SPTB2_HUMAN          | 1872.7915 |
| sp O43707 ACTN4_HUMAN          | 1574.8053 |
| sp Q14152 EIF3A_HUMAN          | 1887.9189 |
| sp Q9P2B2 FPRP_HUMAN           | 2660.2467 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp Q01813 PFKAP_HUMAN          | 1382.683  |
| sp Q9P2B2 FPRP_HUMAN           | 2660.2467 |
| sp Q13332 PTPRS_HUMAN          | 1852.8744 |

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| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp Q15233 NONO_HUMAN           | 1444.6987 |
| sp P12956 XRCC6_HUMAN          | 2344.1434 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1419.6895 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1419.6895 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp Q86UP2 KTN1_HUMAN           | 1852.8955 |
| sp Q9Y3U8 RL36_HUMAN           | 1510.7238 |
| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1419.6895 |
| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp O60506 HNRPQ_HUMAN          | 1807.8635 |
| sp O43707 ACTN4_HUMAN          | 1574.8053 |
| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp Q9UHB6 LIMA1_HUMAN          | 2092.945  |
| sp P31948 STIP1_HUMAN          | 1494.6779 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 1806.8346 |
| sp Q15067 ACOX1_HUMAN          | 1735.7876 |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 1370.7082 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 1370.7082 |
| sp P09429 HMGB1_HUMAN,sp B2Rf  | 1716.8683 |
| sp P32004 L1CAM_HUMAN          | 2033.8935 |
| sp P09429 HMGB1_HUMAN,sp B2Rf  | 1716.8683 |
| sp P09429 HMGB1_HUMAN,sp B2Rf  | 1716.8683 |
| sp P19338 NUCL_HUMAN           | 1597.8352 |
| sp Q00341 VIGLN_HUMAN          | 1404.7249 |
| sp P09429 HMGB1_HUMAN,sp B2Rf  | 1716.8683 |
| sp P40939 ECHA_HUMAN           | 1823.9166 |
| sp P35579 MYH9_HUMAN           | 1781.789  |
| sp P07237 PDIA1_HUMAN          | 1482.7103 |
| sp Q04637 IF4G1_HUMAN,sp O4343 | 2111.9252 |
| sp P21333 FLNA_HUMAN           | 2783.2787 |
| sp Q01105 SET_HUMAN            | 2296.1699 |
| sp P09429 HMGB1_HUMAN,sp B2Rf  | 1716.8683 |
| sp P09429 HMGB1_HUMAN,sp B2Rf  | 1716.8683 |
| sp P31948 STIP1_HUMAN          | 3095.4254 |
| sp P09429 HMGB1_HUMAN,sp B2Rf  | 1716.8683 |
| sp P31948 STIP1_HUMAN          | 3095.4254 |
| sp P17844 DDX5_HUMAN           | 2107.9018 |

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| sp P21333 FLNA_HUMAN          | 2783.2787 |
| sp O75533 SF3B1_HUMAN         | 2206.0291 |
| sp P21333 FLNA_HUMAN          | 2783.2787 |
| sp Q13838 DX39B_HUMAN         | 1834.8486 |
| sp P21333 FLNA_HUMAN          | 2783.2787 |
| sp P31040 SDHA_HUMAN          | 1943.8982 |
| sp P21333 FLNA_HUMAN          | 2783.2787 |
| sp O75533 SF3B1_HUMAN         | 2206.0291 |
| sp P09429 HMGB1_HUMAN         | 1788.7955 |
| sp P21333 FLNA_HUMAN          | 2783.2787 |
| sp P08195 4F2_HUMAN           | 1499.8096 |
| sp Q92499 DDX1_HUMAN          | 2965.3148 |
| sp P08195 4F2_HUMAN           | 1499.8096 |
| sp P26006 ITA3_HUMAN          | 1718.8628 |
| sp P27635 RL10_HUMAN          | 1645.8424 |
| sp P08195 4F2_HUMAN           | 1499.8096 |
| sp P13639 EF2_HUMAN           | 1598.8304 |
| sp P46777 RL5_HUMAN           | 2207.9396 |
| sp P08195 4F2_HUMAN           | 1499.8096 |
| sp P26006 ITA3_HUMAN          | 1718.8628 |
| sp P46777 RL5_HUMAN           | 2207.9396 |
| sp P26006 ITA3_HUMAN          | 1718.8628 |
| sp Q16695 H31T_HUMAN,sp Q6NXT | 1602.8366 |
| sp P46777 RL5_HUMAN           | 2207.9396 |
| sp P08195 4F2_HUMAN           | 1499.8096 |
| sp P26006 ITA3_HUMAN          | 1718.8628 |
| sp P13639 EF2_HUMAN           | 1598.8304 |
| sp P13639 EF2_HUMAN           | 1598.8304 |
| sp P36871 PGM1_HUMAN          | 1709.8447 |
| sp Q9ULF5 S39AA_HUMAN         | 1757.906  |
| sp P46777 RL5_HUMAN           | 2207.9396 |
| sp P36871 PGM1_HUMAN          | 1709.8447 |
| sp P46777 RL5_HUMAN           | 2207.9396 |
| sp P31948 STIP1_HUMAN         | 1817.8584 |
| sp P27635 RL10_HUMAN          | 1645.8424 |
| sp Q99832 TCPH_HUMAN          | 1775.8798 |
| sp Q02878 RL6_HUMAN           | 1528.7562 |
| sp Q00839 HNRPU_HUMAN         | 1476.7283 |
| sp P62753 RS6_HUMAN           | 1751.8413 |
| sp P53621 COPA_HUMAN          | 1791.8574 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |
| sp Q9ULF5 S39AA_HUMAN         | 1757.906  |
| sp Q9ULF5 S39AA_HUMAN         | 1757.906  |
| sp Q99832 TCPH_HUMAN          | 1775.8798 |
| sp Q00839 HNRPU_HUMAN         | 1476.7283 |
| sp Q96CS3 FAF2_HUMAN          | 2362.0978 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |

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| sp Q9ULF5 S39AA_HUMAN         | 1757.906  |
| sp Q14126 DSG2_HUMAN          | 1788.8642 |
| sp Q02878 RL6_HUMAN           | 1528.7562 |
| sp O00148 DX39A_HUMAN         | 1848.8642 |
| sp Q9UHB6 LIMA1_HUMAN         | 2221.1015 |
| sp Q9ULF5 S39AA_HUMAN         | 1757.906  |
| sp Q71U36 TBA1A_HUMAN,sp PODF | 1592.7181 |
| sp P62266 RS23_HUMAN          | 1891.9428 |
| sp P12236 ADT3_HUMAN          | 1959.0425 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |
| sp P78527 PRKDC_HUMAN         | 1692.8107 |
| sp Q96CS3 FAF2_HUMAN          | 2362.0978 |
| sp P53621 COPA_HUMAN          | 1791.8574 |
| sp Q9UHB6 LIMA1_HUMAN         | 2221.1015 |
| sp Q9ULF5 S39AA_HUMAN         | 1757.906  |
| sp Q9ULF5 S39AA_HUMAN         | 1757.906  |
| sp Q71U36 TBA1A_HUMAN,sp PODF | 1592.7181 |
| sp Q9UHB6 LIMA1_HUMAN         | 2221.1015 |
| sp P62917 RL8_HUMAN           | 1515.7682 |
| sp P47897 SYQ_HUMAN           | 1916.9017 |
| sp Q9Y490 TLN1_HUMAN          | 2840.4053 |
| sp P47897 SYQ_HUMAN           | 1916.9017 |
| sp Q92945 FUBP2_HUMAN         | 2381.1975 |
| sp Q02790 FKBP4_HUMAN         | 1380.6561 |
| sp P62917 RL8_HUMAN           | 1515.7682 |
| sp Q9UHD1 CHRD1_HUMAN         | 2198.9902 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |
| sp Q92945 FUBP2_HUMAN         | 2381.1975 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |
| sp Q92945 FUBP2_HUMAN         | 2381.1975 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |
| sp Q06830 PRDX1_HUMAN         | 2338.1052 |
| sp P46781 RS9_HUMAN           | 1654.7951 |
| sp P62266 RS23_HUMAN          | 1891.9428 |
| sp Q07065 CKAP4_HUMAN         | 2227.0142 |
| sp P32004 L1CAM_HUMAN         | 2017.8986 |
| sp P49792 RBP2_HUMAN          | 3199.4624 |
| sp Q16881 TRXR1_HUMAN         | 2073.9908 |
| sp P32004 L1CAM_HUMAN         | 2017.8986 |
| sp P46781 RS9_HUMAN           | 1654.7951 |
| sp Q13310 PABP4_HUMAN         | 1714.889  |
| sp P26640 SYVC_HUMAN          | 2518.2088 |
| sp P32322 P5CR1_HUMAN         | 2214.1281 |
| sp Q04637 IF4G1_HUMAN         | 2510.2765 |
| sp P46781 RS9_HUMAN           | 1654.7951 |

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| sp P46781 RS9_HUMAN             | 1654.7951 |
| sp Q12931 TRAP1_HUMAN           | 1900.9319 |
| sp P18669 PGAM1_HUMAN           | 2332.0033 |
| sp P32004 L1CAM_HUMAN           | 2017.8986 |
| sp P32004 L1CAM_HUMAN           | 2017.8986 |
| sp P46781 RS9_HUMAN             | 1654.7951 |
| sp Q00610 CLH1_HUMAN            | 1903.9574 |
| sp Q00610 CLH1_HUMAN            | 1903.9574 |
| sp P26640 SYVC_HUMAN            | 2518.2088 |
| sp Q00610 CLH1_HUMAN            | 1903.9574 |
| sp P32004 L1CAM_HUMAN           | 2017.8986 |
| sp P46781 RS9_HUMAN             | 1654.7951 |
| sp P32004 L1CAM_HUMAN           | 2017.8986 |
| sp P62258 1433E_HUMAN           | 2134.0371 |
| sp P26640 SYVC_HUMAN            | 2518.2088 |
| sp P32322 P5CR1_HUMAN           | 2214.1281 |
| sp Q15149 PLEC_HUMAN            | 2520.282  |
| sp Q00610 CLH1_HUMAN            | 1903.9574 |
| sp Q15149 PLEC_HUMAN            | 2520.282  |
| sp Q00610 CLH1_HUMAN            | 1903.9574 |
| sp Q00610 CLH1_HUMAN            | 1903.9574 |
| sp P62258 1433E_HUMAN           | 2134.0371 |
| sp P00533 EGFR_HUMAN            | 1750.889  |
| sp P22314 UBA1_HUMAN            | 3250.559  |
| sp Q15149 PLEC_HUMAN            | 2520.282  |
| sp P23921 RIR1_HUMAN            | 2024.0327 |
| sp P42704 LPPRC_HUMAN           | 2259.0556 |
| sp P50502 F10A1_HUMAN,sp Q8IZP  | 1838.005  |
| sp P78371 TCPB_HUMAN            | 1688.9097 |
| sp P07900 HS90A_HUMAN,sp Q145i  | 2230.0906 |
| sp P07900 HS90A_HUMAN,sp Q145i  | 2230.0906 |
| sp P21333 FLNA_HUMAN            | 1987.0011 |
| sp P50502 F10A1_HUMAN,sp Q8IZP  | 1838.005  |
| sp P07900 HS90A_HUMAN,sp Q145i  | 2230.0906 |
| sp P21333 FLNA_HUMAN            | 1987.0011 |
| sp P07900 HS90A_HUMAN,sp Q145i  | 2230.0906 |
| sp P26038 MOES_HUMAN            | 2154.0189 |
| sp P07900 HS90A_HUMAN,sp Q145i  | 2230.0906 |
| sp Q58FF6 H90B4_HUMAN,sp P07900 | 2211.0695 |
| sp P60709 ACTB_HUMAN,sp P63261  | 2491.2707 |
| sp Q13263 TIF1B_HUMAN           | 2905.4029 |
| sp P62136 PP1A_HUMAN,sp P6214C  | 1991.9014 |
| sp P42704 LPPRC_HUMAN           | 2259.0556 |
| sp P42704 LPPRC_HUMAN           | 2259.0556 |
| sp P13987 CD59_HUMAN            | 3083.3654 |
| sp Q58FF6 H90B4_HUMAN,sp P07900 | 2211.0695 |
| sp P60709 ACTB_HUMAN,sp P63261  | 2491.2707 |



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| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1576.7232 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P62136 PP1A_HUMAN,sp P6214C | 1991.9014 |
| sp P42704 LPPRC_HUMAN          | 2259.0556 |
| sp Q13263 TIF1B_HUMAN          | 2905.4029 |
| sp Q16576 RBBP7_HUMAN          | 3438.5674 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp O43390 HNRPR_HUMAN          | 2224.9484 |
| sp Q16576 RBBP7_HUMAN          | 3438.5674 |
| sp Q06830 PRDX1_HUMAN          | 2322.1103 |
| sp O43390 HNRPR_HUMAN          | 2224.9484 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1576.7232 |
| sp P17844 DDX5_HUMAN           | 1744.9108 |
| sp Q06830 PRDX1_HUMAN          | 2322.1103 |
| sp Q16576 RBBP7_HUMAN          | 3438.5674 |
| sp Q16576 RBBP7_HUMAN          | 3438.5674 |
| sp Q06830 PRDX1_HUMAN          | 2322.1103 |
| sp Q9P2E9 RRBP1_HUMAN          | 1993.0017 |
| sp Q14204 DYHC1_HUMAN          | 1964.0003 |
| sp Q06830 PRDX1_HUMAN          | 2322.1103 |
| sp P32004 L1CAM_HUMAN          | 2017.8986 |
| sp Q9P2E9 RRBP1_HUMAN          | 1993.0017 |
| sp P32119 PRDX2_HUMAN          | 3984.8112 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2093.9946 |
| sp P17844 DDX5_HUMAN           | 1744.9108 |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2093.9946 |
| sp P32004 L1CAM_HUMAN          | 2017.8986 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2093.9946 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp Q96DU9 PABP5_HUMAN,sp P119  | 1728.9046 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2093.9946 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp Q9P2E9 RRBP1_HUMAN          | 1993.0017 |
| sp Q14697 GANAB_HUMAN          | 2473.354  |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp Q9P2E9 RRBP1_HUMAN          | 1993.0017 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp O43390 HNRPR_HUMAN          | 2224.9484 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2093.9946 |

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| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2093.9946 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2093.9946 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp O43390 HNRPR_HUMAN          | 2224.9484 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp O43390 HNRPR_HUMAN          | 2224.9484 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2093.9946 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp O43390 HNRPR_HUMAN          | 1735.7842 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp O60506 HNRPQ_HUMAN          | 2238.964  |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp O43390 HNRPR_HUMAN          | 2224.9484 |
| sp O60506 HNRPQ_HUMAN          | 2238.964  |
| sp Q12905 ILF2_HUMAN           | 1516.7773 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P78527 PRKDC_HUMAN          | 1926.8314 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp O60506 HNRPQ_HUMAN          | 2238.964  |
| sp O60506 HNRPQ_HUMAN          | 2238.964  |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp O43390 HNRPR_HUMAN          | 1735.7842 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp O60506 HNRPQ_HUMAN          | 2238.964  |
| sp Q00610 CLH1_HUMAN           | 1816.8632 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P02786 TFR1_HUMAN           | 2530.1765 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp P02786 TFR1_HUMAN           | 2530.1765 |
| sp P06733 ENOA_HUMAN           | 1793.9312 |
| sp P08174 DAF_HUMAN            | 2080.0623 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |

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| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P02786 TFR1_HUMAN           | 2530.1765 |
| sp P50991 TCPD_HUMAN           | 2135.1263 |
| sp P02786 TFR1_HUMAN           | 2530.1765 |
| sp O75369 FLNB_HUMAN           | 2326.0866 |
| sp P50895 BCAM_HUMAN           | 2579.2405 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q9BQG0 MBB1A_HUMAN          | 2022.9681 |
| sp P50895 BCAM_HUMAN           | 2579.2405 |
| sp P50991 TCPD_HUMAN           | 2135.1263 |
| sp P50991 TCPD_HUMAN           | 2135.1263 |
| sp P50990 TCPQ_HUMAN           | 2191.0514 |
| sp P23284 PPIB_HUMAN           | 1653.8151 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp O75369 FLNB_HUMAN           | 2326.0866 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P18077 RL35A_HUMAN          | 1795.9105 |
| sp P50991 TCPD_HUMAN           | 2135.1263 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P49327 FAS_HUMAN            | 3714.6492 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2611.2303 |
| sp P08708 RS17_HUMAN           | 1570.7814 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2611.2303 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp Q9BQG0 MBB1A_HUMAN          | 2022.9681 |
| sp P18077 RL35A_HUMAN          | 1795.9105 |
| sp Q00610 CLH1_HUMAN           | 1816.8632 |
| sp P08174 DAF_HUMAN            | 2080.0623 |
| sp P10809 CH60_HUMAN           | 2051.08   |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P49327 FAS_HUMAN            | 3714.6492 |
| sp P50895 BCAM_HUMAN           | 2579.2405 |
| sp P08174 DAF_HUMAN            | 2080.0623 |
| sp Q00610 CLH1_HUMAN           | 1816.8632 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp Q00610 CLH1_HUMAN           | 1816.8632 |
| sp P18077 RL35A_HUMAN          | 1795.9105 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P08174 DAF_HUMAN            | 2080.0623 |
| sp Q15067 ACOX1_HUMAN          | 2125.1055 |
| sp P50895 BCAM_HUMAN           | 2579.2405 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08174 DAF_HUMAN            | 2080.0623 |
| sp P50895 BCAM_HUMAN           | 2579.2405 |

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| sp P46783 RS10_HUMAN,sp Q9NQ3 | 1905.9441 |
| sp P13987 CD59_HUMAN          | 3083.3654 |
| sp P13987 CD59_HUMAN          | 3083.3654 |
| sp Q02543 RL18A_HUMAN         | 1950.9721 |
| sp P08195 4F2_HUMAN           | 2276.1298 |
| sp P50895 BCAM_HUMAN          | 2579.2405 |
| sp Q14118 DAG1_HUMAN          | 3790.7744 |
| sp Q15067 ACOX1_HUMAN         | 2125.1055 |
| sp Q14118 DAG1_HUMAN          | 3790.7744 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2611.2303 |
| sp P13987 CD59_HUMAN          | 3083.3654 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2611.2303 |
| sp Q08211 DHX9_HUMAN          | 2102.0684 |
| sp P11940 PABP1_HUMAN         | 2000.0037 |
| sp P60842 IF4A1_HUMAN         | 2370.2002 |
| sp P52597 HNRPF_HUMAN         | 2829.23   |
| sp P11940 PABP1_HUMAN         | 2000.0037 |
| sp P08195 4F2_HUMAN           | 2276.1298 |
| sp P51659 DHB4_HUMAN          | 1667.8308 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2611.2303 |
| sp P46783 RS10_HUMAN,sp Q9NQ3 | 1905.9441 |
| sp P13987 CD59_HUMAN          | 3083.3654 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2611.2303 |
| sp P60842 IF4A1_HUMAN         | 2370.2002 |
| sp P11940 PABP1_HUMAN         | 2000.0037 |
| sp Q08211 DHX9_HUMAN          | 2102.0684 |
| sp P52597 HNRPF_HUMAN         | 2829.23   |
| sp P52597 HNRPF_HUMAN         | 2829.23   |
| sp P08195 4F2_HUMAN           | 2276.1298 |
| sp P11940 PABP1_HUMAN         | 2000.0037 |
| sp P11940 PABP1_HUMAN         | 2000.0037 |
| sp Q00610 CLH1_HUMAN          | 2639.3344 |
| sp P32119 PRDX2_HUMAN         | 2128.0841 |
| sp Q9NZ45 CISD1_HUMAN         | 2335.0249 |
| sp P08195 4F2_HUMAN           | 2276.1298 |
| sp Q14240 IF4A2_HUMAN         | 2371.159  |
| sp P32119 PRDX2_HUMAN         | 2128.0841 |
| sp P48643 TCPE_HUMAN          | 2036.0653 |
| sp Q09666 AHNK_HUMAN          | 1745.8658 |
| sp P13987 CD59_HUMAN          | 3083.3654 |
| sp P32119 PRDX2_HUMAN         | 2128.0841 |
| sp P52597 HNRPF_HUMAN         | 2829.23   |
| sp P63244 RACK1_HUMAN         | 2175.0233 |
| sp P32119 PRDX2_HUMAN         | 2128.0841 |
| sp P48643 TCPE_HUMAN          | 2036.0653 |
| sp O75369 FLNB_HUMAN          | 2390.1754 |
| sp P60842 IF4A1_HUMAN         | 2370.2002 |

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| sp P21333 FLNA_HUMAN          | 2642.2217 |
| sp P52597 HNRPF_HUMAN         | 2829.23   |
| sp Q09666 AHNK_HUMAN          | 1745.8658 |
| sp P13987 CD59_HUMAN          | 3083.3654 |
| sp P52597 HNRPF_HUMAN         | 2829.23   |
| sp P49411 EFTU_HUMAN          | 1942.9459 |
| sp P63244 RACK1_HUMAN         | 2175.0233 |
| sp P60842 IF4A1_HUMAN         | 2370.2002 |
| sp P26373 RL13_HUMAN          | 2078.032  |
| sp P35579 MYH9_HUMAN          | 2192.0346 |
| sp Q15717 ELAV1_HUMAN         | 2450.1503 |
| sp Q15717 ELAV1_HUMAN         | 2450.1503 |
| sp P52597 HNRPF_HUMAN         | 2829.23   |
| sp P35579 MYH9_HUMAN          | 2192.0346 |
| sp P39019 RS19_HUMAN          | 2164.949  |
| sp Q9NZ45 CISD1_HUMAN         | 2335.0249 |
| sp Q9NZ45 CISD1_HUMAN         | 2335.0249 |
| sp P52597 HNRPF_HUMAN         | 2829.23   |
| sp Q15717 ELAV1_HUMAN         | 2450.1503 |
| sp Q06830 PRDX1_HUMAN         | 2103.0783 |
| sp P53621 COPA_HUMAN          | 2128.9194 |
| sp P39019 RS19_HUMAN          | 2164.949  |
| sp Q9NZ45 CISD1_HUMAN         | 2335.0249 |
| sp Q9NZ45 CISD1_HUMAN         | 2335.0249 |
| sp P38646 GRP75_HUMAN         | 3480.6256 |
| sp Q13813 SPTN1_HUMAN         | 2298.1314 |
| sp O75533 SF3B1_HUMAN         | 2585.189  |
| sp Q9NZ45 CISD1_HUMAN         | 2335.0249 |
| sp P38646 GRP75_HUMAN         | 3480.6256 |
| sp P11021 BIP_HUMAN           | 2116.0589 |
| sp P49411 EFTU_HUMAN          | 1942.9459 |
| sp O75533 SF3B1_HUMAN         | 2585.189  |
| sp P49411 EFTU_HUMAN          | 1942.9459 |
| sp P07910 HNRPC_HUMAN         | 2406.1427 |
| sp P07910 HNRPC_HUMAN         | 2406.1427 |
| sp O75533 SF3B1_HUMAN         | 2585.189  |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P49411 EFTU_HUMAN          | 1942.9459 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P0DMV8 HS71A_HUMAN,sp PODI | 2018.0433 |
| sp P49411 EFTU_HUMAN          | 1942.9459 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P07910 HNRPC_HUMAN         | 2406.1427 |
| sp P07910 HNRPC_HUMAN         | 2406.1427 |
| sp O43707 ACTN4_HUMAN         | 2371.0321 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp O75367 H2AY_HUMAN          | 2727.2309 |

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| sp P53396 ACLY_HUMAN          | 2127.0273 |
| sp O75367 H2AY_HUMAN          | 2727.2309 |
| sp O75643 U520_HUMAN          | 2536.2082 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P49411 EFTU_HUMAN          | 1942.9459 |
| sp P49411 EFTU_HUMAN          | 1942.9459 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q7KZF4 SND1_HUMAN          | 2204.0538 |
| sp P07910 HNRPC_HUMAN         | 2406.1427 |
| sp P38646 GRP75_HUMAN         | 3464.6307 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P38646 GRP75_HUMAN         | 3464.6307 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp P62847 RS24_HUMAN          | 2578.1322 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P38646 GRP75_HUMAN         | 3464.6307 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P38646 GRP75_HUMAN         | 3464.6307 |
| sp P32004 L1CAM_HUMAN         | 4479.1978 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P51991 ROA3_HUMAN          | 2203.9667 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P51991 ROA3_HUMAN          | 2203.9667 |
| sp P32004 L1CAM_HUMAN         | 4479.1978 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P51991 ROA3_HUMAN          | 2203.9667 |
| sp P47897 SYQ_HUMAN           | 2375.1182 |
| sp P51991 ROA3_HUMAN          | 2203.9667 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp P47897 SYQ_HUMAN           | 2375.1182 |
| sp O75643 U520_HUMAN          | 2536.2082 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp O15031 PLXB2_HUMAN         | 5121.4704 |
| sp P47897 SYQ_HUMAN           | 2375.1182 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp P47897 SYQ_HUMAN           | 2375.1182 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q13151 ROA0_HUMAN          | 2671.2701 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 2358.2795 |

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| sp P11142 HSP7C_HUMAN         | 3227.4466 |
| sp O00148 DX39A_HUMAN,sp Q138 | 1900.0094 |
| sp Q14126 DSG2_HUMAN          | 2755.2838 |
| sp O15031 PLXB2_HUMAN         | 5121.4704 |
| sp P50395 GDIB_HUMAN          | 2036.9844 |
| sp Q14789 GOGB1_HUMAN         | 1979.98   |
| sp P40429 RL13A_HUMAN         | 2369.1539 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp Q14126 DSG2_HUMAN          | 2755.2838 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp P68366 TBA4A_HUMAN         | 2022.0058 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P11142 HSP7C_HUMAN         | 3227.4466 |
| sp O00148 DX39A_HUMAN,sp Q138 | 1900.0094 |
| sp P50395 GDIB_HUMAN          | 2036.9844 |
| sp P40429 RL13A_HUMAN         | 2369.1539 |
| sp P62847 RS24_HUMAN          | 2578.1322 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp P40429 RL13A_HUMAN         | 2369.1539 |
| sp P00338 LDHA_HUMAN          | 1838.9601 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp Q15067 ACOX1_HUMAN         | 1890.0211 |
| sp Q15717 ELAV1_HUMAN         | 2749.3572 |
| sp Q15717 ELAV1_HUMAN         | 2749.3572 |
| sp P49327 FAS_HUMAN           | 2633.2003 |
| sp P62847 RS24_HUMAN          | 2578.1322 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp P49327 FAS_HUMAN           | 2633.2003 |
| sp O00231 PSD11_HUMAN         | 1676.8734 |
| sp Q15149 PLEC_HUMAN          | 2859.3093 |
| sp Q13151 ROA0_HUMAN          | 2671.2701 |
| sp P21333 FLNA_HUMAN          | 4248.0287 |
| sp Q15149 PLEC_HUMAN          | 2859.3093 |
| sp Q15717 ELAV1_HUMAN         | 2749.3572 |
| sp P49327 FAS_HUMAN           | 2633.2003 |
| sp P49327 FAS_HUMAN           | 2633.2003 |
| sp Q15717 ELAV1_HUMAN         | 2749.3572 |
| sp P62847 RS24_HUMAN          | 2578.1322 |
| sp Q13151 ROA0_HUMAN          | 2671.2701 |
| sp P49327 FAS_HUMAN           | 2002.0484 |
| sp P62851 RS25_HUMAN          | 2093.0317 |
| sp P49327 FAS_HUMAN           | 2633.2003 |
| sp O00231 PSD11_HUMAN         | 1676.8734 |
| sp Q13151 ROA0_HUMAN          | 2671.2701 |

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| sp P32004 L1CAM_HUMAN          | 4463.2029 |
| sp P21333 FLNA_HUMAN           | 4248.0287 |
| sp Q6YHK3 CD109_HUMAN          | 2385.1812 |
| sp P49327 FAS_HUMAN            | 2633.2003 |
| sp P32004 L1CAM_HUMAN          | 4463.2029 |
| sp P50990 TCPQ_HUMAN           | 2143.0983 |
| sp Q6YHK3 CD109_HUMAN          | 2385.1812 |
| sp P08670 VIME_HUMAN           | 1857.9724 |
| sp P50990 TCPQ_HUMAN           | 2143.0983 |
| sp P49327 FAS_HUMAN            | 2002.0484 |
| sp P33992 MCM5_HUMAN           | 2203.0797 |
| sp Q13151 ROA0_HUMAN           | 2671.2701 |
| sp P08670 VIME_HUMAN           | 1857.9724 |
| sp P22102 PUR2_HUMAN           | 2261.1077 |
| sp P61160 ARP2_HUMAN           | 2622.2424 |
| sp Q16832 DDR2_HUMAN           | 2241.0702 |
| sp P61160 ARP2_HUMAN           | 2622.2424 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp Q16832 DDR2_HUMAN           | 2241.0702 |
| sp P09382 LEG1_HUMAN           | 2096.0902 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P33992 MCM5_HUMAN           | 2203.0797 |
| sp Q9Y490 TLN1_HUMAN           | 1975.0123 |
| sp P22102 PUR2_HUMAN           | 2261.1077 |
| sp Q9Y490 TLN1_HUMAN           | 1975.0123 |
| sp P25786 PSA1_HUMAN           | 2469.221  |
| sp P22102 PUR2_HUMAN           | 2261.1077 |
| sp Q16832 DDR2_HUMAN           | 2241.0702 |
| sp P25786 PSA1_HUMAN           | 2469.221  |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp Q16832 DDR2_HUMAN           | 2241.0702 |
| sp Q9H0A0 NAT10_HUMAN          | 2210.0103 |
| sp P33992 MCM5_HUMAN           | 2203.0797 |
| sp Q9Y490 TLN1_HUMAN           | 1975.0123 |
| sp P21796 VDAC1_HUMAN          | 2004.0276 |
| sp P22102 PUR2_HUMAN           | 2261.1077 |
| sp P25786 PSA1_HUMAN           | 2469.221  |
| sp Q9Y490 TLN1_HUMAN           | 1975.0123 |
| sp Q08J23 NSUN2_HUMAN          | 2472.0805 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp P21796 VDAC1_HUMAN          | 2004.0276 |
| sp P08670 VIME_HUMAN           | 1857.9724 |
| sp P08670 VIME_HUMAN           | 1857.9724 |
| sp P05783 K1C18_HUMAN          | 3551.6322 |
| sp P08670 VIME_HUMAN           | 1857.9724 |
| sp P08670 VIME_HUMAN           | 1857.9724 |



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| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp P20908 CO5A1_HUMAN          | 2559.2064 |
| sp P09382 LEG1_HUMAN           | 2096.0902 |
| sp P08670 VIME_HUMAN           | 1857.9724 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp Q13813 SPTN1_HUMAN          | 2373.1271 |
| sp P08670 VIME_HUMAN           | 1857.9724 |
| sp P61247 RS3A_HUMAN           | 2386.1263 |
| sp P09382 LEG1_HUMAN           | 2096.0902 |
| sp P21333 FLNA_HUMAN           | 4236.958  |
| sp O15143 ARC1B_HUMAN          | 2601.2751 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P09382 LEG1_HUMAN           | 2096.0902 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp O15143 ARC1B_HUMAN          | 2601.2751 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp Q14118 DAG1_HUMAN           | 1932.9945 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp Q14118 DAG1_HUMAN           | 1932.9945 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp P35579 MYH9_HUMAN,sp P3558  | 1770.9264 |
| sp P04843 RPN1_HUMAN           | 2322.1703 |
| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp P21333 FLNA_HUMAN           | 4236.958  |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp O76021 RL1D1_HUMAN          | 1962.0786 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp P04843 RPN1_HUMAN           | 2322.1703 |
| sp P04843 RPN1_HUMAN           | 2322.1703 |
| sp P12956 XRCC6_HUMAN          | 1897.9058 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp O14579 COPE_HUMAN           | 2479.2959 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp O76021 RL1D1_HUMAN          | 1962.0786 |
| sp Q9HB71 CYBP_HUMAN           | 4017.9848 |
| sp O14579 COPE_HUMAN           | 2479.2959 |
| sp O14579 COPE_HUMAN           | 2479.2959 |
| sp P61247 RS3A_HUMAN           | 2386.1263 |
| sp Q14318 FKBP8_HUMAN          | 2323.1267 |
| sp Q9UHX1 PUF60_HUMAN          | 2913.4944 |
| sp Q9HB71 CYBP_HUMAN           | 4017.9848 |
| sp P30050 RL12_HUMAN           | 2237.1077 |

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| sp P33316 DUT_HUMAN           | 2429.1499 |
| sp P62937 PPIA_HUMAN          | 2294.1219 |
| sp P62937 PPIA_HUMAN          | 2294.1219 |
| sp P62937 PPIA_HUMAN          | 2294.1219 |
| sp Q08211 DHX9_HUMAN          | 3904.8351 |
| sp P62937 PPIA_HUMAN          | 2294.1219 |
| sp Q92616 GCN1_HUMAN          | 2243.162  |
| sp P62847 RS24_HUMAN          | 2562.1373 |
| sp P35606 COPB2_HUMAN         | 4728.1351 |
| sp O15031 PLXB2_HUMAN         | 2207.0681 |
| sp Q15149 PLEC_HUMAN          | 3280.5735 |
| sp Q08211 DHX9_HUMAN          | 3904.8351 |
| sp O15031 PLXB2_HUMAN         | 2207.0681 |
| sp Q9UHX1 PUF60_HUMAN         | 2913.4944 |
| sp O75153 CLU_HUMAN           | 2537.1975 |
| sp P62937 PPIA_HUMAN          | 2294.1219 |
| sp P62847 RS24_HUMAN          | 2562.1373 |
| sp P62937 PPIA_HUMAN          | 2294.1219 |
| sp P35606 COPB2_HUMAN         | 4728.1351 |
| sp O43390 HNRPR_HUMAN         | 3197.6033 |
| sp Q15149 PLEC_HUMAN          | 3280.5735 |
| sp O75153 CLU_HUMAN           | 2537.1975 |
| sp O43390 HNRPR_HUMAN         | 3197.6033 |
| sp P63173 RL38_HUMAN          | 1771.9356 |
| sp Q9UHX1 PUF60_HUMAN         | 2913.4944 |
| sp Q9UHX1 PUF60_HUMAN         | 2913.4944 |
| sp Q14318 FKBP8_HUMAN         | 2323.1267 |
| sp P26447 S10A4_HUMAN         | 2292.0441 |
| sp P30050 RL12_HUMAN          | 2237.1077 |
| sp P30050 RL12_HUMAN          | 2237.1077 |
| sp Q09666 AHNK_HUMAN          | 1807.8815 |
| sp Q09666 AHNK_HUMAN          | 1807.8815 |
| sp P63173 RL38_HUMAN          | 1771.9356 |
| sp P0DMV8 HS71A_HUMAN,sp PODI | 3535.7154 |
| sp Q14318 FKBP8_HUMAN         | 2323.1267 |
| sp Q15691 MARE1_HUMAN         | 2274.1321 |
| sp Q15691 MARE1_HUMAN         | 2274.1321 |
| sp P0DMV8 HS71A_HUMAN,sp PODI | 3535.7154 |
| sp P30050 RL12_HUMAN          | 2237.1077 |
| sp Q92804 RBP56_HUMAN         | 2157.0167 |
| sp P30050 RL12_HUMAN          | 2237.1077 |
| sp Q92804 RBP56_HUMAN         | 2157.0167 |
| sp P62847 RS24_HUMAN          | 2562.1373 |
| sp P63173 RL38_HUMAN          | 1771.9356 |
| sp P0DMV8 HS71A_HUMAN,sp PODI | 3535.7154 |
| sp P16402 H13_HUMAN,sp P10412 | 2050.0946 |
| sp P0DMV8 HS71A_HUMAN,sp PODI | 3535.7154 |

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| sp P62847 RS24_HUMAN           | 2562.1373 |
| sp Q15691 MARE1_HUMAN          | 2274.1321 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P62805 H4_HUMAN             | 1790.9237 |
| sp P62805 H4_HUMAN             | 1790.9237 |
| sp P30050 RL12_HUMAN           | 2237.1077 |
| sp P30050 RL12_HUMAN           | 2237.1077 |
| sp P62847 RS24_HUMAN           | 2562.1373 |
| sp P05141 ADT2_HUMAN,sp Q9H0C  | 2177.047  |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3535.7154 |
| sp Q15691 MARE1_HUMAN          | 2274.1321 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P42166 LAP2A_HUMAN,sp P4216 | 2043.0425 |
| sp P62805 H4_HUMAN             | 1790.9237 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P50454 SERPH_HUMAN          | 3093.4641 |
| sp P50454 SERPH_HUMAN          | 3093.4641 |
| sp P62805 H4_HUMAN             | 1790.9237 |
| sp P62847 RS24_HUMAN           | 2562.1373 |
| sp P62847 RS24_HUMAN           | 2562.1373 |
| sp P62805 H4_HUMAN             | 1790.9237 |
| sp P62847 RS24_HUMAN           | 2562.1373 |
| sp P42166 LAP2A_HUMAN,sp P4216 | 2043.0425 |
| sp P30086 PEBP1_HUMAN          | 2989.428  |
| sp P20908 CO5A1_HUMAN          | 2760.2708 |
| sp P41250 GARS_HUMAN           | 2862.3937 |
| sp Q86VP6 CAND1_HUMAN          | 2314.1304 |
| sp P20908 CO5A1_HUMAN          | 2760.2708 |
| sp P41250 GARS_HUMAN           | 2862.3937 |
| sp P20908 CO5A1_HUMAN          | 2760.2708 |
| sp P30086 PEBP1_HUMAN          | 2989.428  |
| sp P20908 CO5A1_HUMAN          | 2760.2708 |
| sp P20908 CO5A1_HUMAN          | 2760.2708 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp P46060 RAGP1_HUMAN          | 2609.2149 |
| sp P09382 LEG1_HUMAN           | 2541.2071 |
| sp Q9Y624 JAM1_HUMAN           | 2796.5749 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp Q9Y624 JAM1_HUMAN           | 2796.5749 |
| sp P09382 LEG1_HUMAN           | 2541.2071 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp P08237 PFKAM_HUMAN          | 2439.1707 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp P08237 PFKAM_HUMAN          | 2439.1707 |
| sp P09382 LEG1_HUMAN           | 2541.2071 |
| sp P63173 RL38_HUMAN           | 1771.9356 |

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| sp Q15149 PLEC_HUMAN          | 2421.2322 |
| sp P09382 LEG1_HUMAN          | 2541.2071 |
| sp Q15149 PLEC_HUMAN          | 2421.2322 |
| sp P63173 RL38_HUMAN          | 1771.9356 |
| sp Q6YHK3 CD109_HUMAN         | 2904.4618 |
| sp Q6YHK3 CD109_HUMAN         | 2904.4618 |
| sp Q6YHK3 CD109_HUMAN         | 2904.4618 |
| sp P62906 RL10A_HUMAN         | 2175.1212 |
| sp Q6YHK3 CD109_HUMAN         | 2904.4618 |
| sp Q6YHK3 CD109_HUMAN         | 2904.4618 |
| sp P62906 RL10A_HUMAN         | 2175.1212 |
| sp Q13283 G3BP1_HUMAN         | 3169.6448 |
| sp Q13283 G3BP1_HUMAN         | 3169.6448 |
| sp Q9Y624 JAM1_HUMAN          | 2796.5749 |
| sp P62906 RL10A_HUMAN         | 2175.1212 |
| sp P08865 RSSA_HUMAN          | 2969.4018 |
| sp Q9Y624 JAM1_HUMAN          | 2796.5749 |
| sp O43143 DHX15_HUMAN         | 2059.0197 |
| sp O43143 DHX15_HUMAN         | 2059.0197 |
| sp P62829 RL23_HUMAN          | 2494.2129 |
| sp Q6YHK3 CD109_HUMAN         | 2904.4618 |
| sp P62906 RL10A_HUMAN         | 2175.1212 |
| sp Q6YHK3 CD109_HUMAN         | 2904.4618 |
| sp Q13283 G3BP1_HUMAN         | 3169.6448 |
| sp Q9Y624 JAM1_HUMAN          | 2796.5749 |
| sp P78527 PRKDC_HUMAN         | 2859.4225 |
| sp P62906 RL10A_HUMAN         | 2175.1212 |
| sp P08865 RSSA_HUMAN          | 2969.4018 |
| sp Q9Y624 JAM1_HUMAN          | 2796.5749 |
| sp P08865 RSSA_HUMAN          | 2969.4018 |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp O43143 DHX15_HUMAN         | 2059.0197 |
| sp O43143 DHX15_HUMAN         | 2059.0197 |
| sp P78527 PRKDC_HUMAN         | 2859.4225 |
| sp P78527 PRKDC_HUMAN         | 2859.4225 |
| sp Q9Y624 JAM1_HUMAN          | 2796.5749 |
| sp Q10589 BST2_HUMAN          | 3034.4731 |
| sp Q10589 BST2_HUMAN          | 3034.4731 |
| sp P78527 PRKDC_HUMAN         | 2859.4225 |
| sp Q10589 BST2_HUMAN          | 3034.4731 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i | 2350.1957 |
| sp P21333 FLNA_HUMAN          | 2544.29   |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp P30048 PRDX3_HUMAN         | 2078.0466 |
| sp Q10589 BST2_HUMAN          | 3034.4731 |
| sp Q10589 BST2_HUMAN          | 3034.4731 |
| sp P21333 FLNA_HUMAN          | 2544.29   |

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| sp P21333 FLNA_HUMAN           | 2544.29   |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2133.0783 |
| sp Q10589 BST2_HUMAN           | 3034.4731 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2133.0783 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2133.0783 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2133.0783 |
| sp P60228 EIF3E_HUMAN          | 2909.3358 |
| sp P60228 EIF3E_HUMAN          | 2909.3358 |
| sp Q9ULF5 S39AA_HUMAN          | 2182.0616 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2133.0783 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q99798 ACON_HUMAN           | 2942.4846 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2133.0783 |
| sp P10809 CH60_HUMAN           | 2243.191  |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2133.0783 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp P05198 IF2A_HUMAN           | 2630.25   |
| sp P05198 IF2A_HUMAN           | 2630.25   |
| sp P08195 4F2_HUMAN            | 2276.278  |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P58107 EPIPL_HUMAN          | 2530.2591 |
| sp Q92621 NU205_HUMAN          | 3121.455  |
| sp Q92621 NU205_HUMAN          | 3121.455  |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2290.127  |
| sp Q9BS26 ERP44_HUMAN          | 2757.2704 |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp Q9BQG0 MBB1A_HUMAN          | 2560.3034 |
| sp Q14974 IMB1_HUMAN           | 2298.1492 |
| sp Q9Y3I0 RTCB_HUMAN           | 2166.0449 |
| sp P40939 ECHA_HUMAN           | 3774.8775 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |

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| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp Q9BQG0 MBB1A_HUMAN          | 2560.3034 |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P11717 MPRI_HUMAN           | 3176.4509 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp P35606 COPB2_HUMAN          | 4967.3131 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp O75131 CPNE3_HUMAN          | 2821.4221 |
| sp O75131 CPNE3_HUMAN          | 2821.4221 |
| sp P11717 MPRI_HUMAN           | 3176.4509 |
| sp P35606 COPB2_HUMAN          | 4967.3131 |
| sp Q05639 EF1A2_HUMAN,sp P6810 | 2178.1685 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp O75131 CPNE3_HUMAN          | 2821.4221 |
| sp O75131 CPNE3_HUMAN          | 2821.4221 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P23381 SYWC_HUMAN           | 2681.3853 |
| sp P22626 ROA2_HUMAN           | 2473.1802 |
| sp P23381 SYWC_HUMAN           | 2681.3853 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P22626 ROA2_HUMAN           | 2473.1802 |
| sp Q58FG0 HS905_HUMAN,sp P0790 | 2103.0677 |
| sp P06213 INSR_HUMAN           | 2060.0003 |
| sp P23381 SYWC_HUMAN           | 2681.3853 |

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| sp P43487 RANG_HUMAN           | 2935.3599 |
| sp Q58FG0 HS905_HUMAN,sp P079  | 2103.0677 |
| sp P51858 HDGF_HUMAN           | 2686.2704 |
| sp P06213 INSR_HUMAN           | 2060.0003 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P21964 COMT_HUMAN           | 2659.3428 |
| sp P51858 HDGF_HUMAN           | 2686.2704 |
| sp P43487 RANG_HUMAN           | 2935.3599 |
| sp Q58FG0 HS905_HUMAN,sp P079  | 2103.0677 |
| sp P06213 INSR_HUMAN           | 2060.0003 |
| sp P51858 HDGF_HUMAN           | 2686.2704 |
| sp P21964 COMT_HUMAN           | 2659.3428 |
| sp P51858 HDGF_HUMAN           | 2686.2704 |
| sp P21964 COMT_HUMAN           | 2659.3428 |
| sp Q58FG0 HS905_HUMAN,sp P079  | 2103.0677 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp P06213 INSR_HUMAN           | 2060.0003 |
| sp P51858 HDGF_HUMAN           | 2686.2704 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P21964 COMT_HUMAN           | 2659.3428 |
| sp Q9Y4D7 PLXD1_HUMAN          | 2653.321  |
| sp Q58FG0 HS905_HUMAN,sp P079  | 2103.0677 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp O00148 DX39A_HUMAN,sp Q138  | 4307.9418 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P12268 IMDH2_HUMAN          | 2631.3868 |
| sp P12268 IMDH2_HUMAN          | 2631.3868 |
| sp Q9Y2V2 CHSP1_HUMAN          | 4270.9859 |
| sp O00148 DX39A_HUMAN,sp Q138  | 4307.9418 |
| sp P13010 XRCC5_HUMAN          | 1824.9622 |
| sp Q9Y2V2 CHSP1_HUMAN          | 4270.9859 |
| sp P12268 IMDH2_HUMAN          | 2631.3868 |
| sp Q9Y2V2 CHSP1_HUMAN          | 4270.9859 |
| sp P13010 XRCC5_HUMAN          | 1824.9622 |
| sp P12268 IMDH2_HUMAN          | 2631.3868 |
| sp P23381 SYWC_HUMAN           | 2125.1532 |
| sp Q9Y2V2 CHSP1_HUMAN          | 4270.9859 |
| sp Q9Y2V2 CHSP1_HUMAN          | 4270.9859 |
| sp P23381 SYWC_HUMAN           | 2125.1532 |
| sp P62937 PPIA_HUMAN           | 3832.7461 |
| sp P78527 PRKDC_HUMAN          | 2549.1971 |
| sp P63244 RACK1_HUMAN          | 3222.5768 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P68104 EF1A1_HUMAN,sp Q5VT  | 3579.6724 |
| sp P62937 PPIA_HUMAN           | 3832.7461 |
| sp P78527 PRKDC_HUMAN          | 2549.1971 |

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| sp P78527 PRKDC_HUMAN          | 2549.1971 |
| sp Q01082 SPTB2_HUMAN          | 2563.3534 |
| sp P07900 HS90A_HUMAN          | 2901.3929 |
| sp P63244 RACK1_HUMAN          | 3222.5768 |
| sp P10586 PTPRF_HUMAN          | 3515.6377 |
| sp Q01082 SPTB2_HUMAN          | 2563.3534 |
| sp Q01082 SPTB2_HUMAN          | 2563.3534 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3313.5449 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P53396 ACLY_HUMAN           | 3048.5339 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3313.5449 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp O75533 SF3B1_HUMAN          | 2288.1648 |
| sp O75533 SF3B1_HUMAN          | 2288.1648 |
| sp P36578 RL4_HUMAN            | 2483.2301 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp O75533 SF3B1_HUMAN          | 2288.1648 |
| sp P63244 RACK1_HUMAN          | 3222.5768 |
| sp O75153 CLU_HUMAN            | 2279.1474 |
| sp Q00341 VIGLN_HUMAN          | 2865.4549 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q12788 TBL3_HUMAN           | 3524.7068 |
| sp P63244 RACK1_HUMAN          | 3222.5768 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp P32119 PRDX2_HUMAN          | 3023.4811 |
| sp P15170 ERF3A_HUMAN          | 3206.5012 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P36578 RL4_HUMAN            | 2483.2301 |
| sp P32119 PRDX2_HUMAN          | 3023.4811 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P36578 RL4_HUMAN            | 2483.2301 |
| sp O43747 AP1G1_HUMAN          | 3211.586  |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp O43747 AP1G1_HUMAN          | 3211.586  |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |



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| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P32119 PRDX2_HUMAN          | 3023.4811 |
| sp P36578 RL4_HUMAN            | 2483.2301 |
| sp P32119 PRDX2_HUMAN          | 3023.4811 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |
| sp P36578 RL4_HUMAN            | 2483.2301 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp O43747 AP1G1_HUMAN          | 3211.586  |
| sp P10809 CH60_HUMAN           | 3904.9153 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp O43747 AP1G1_HUMAN          | 3211.586  |
| sp P11586 C1TC_HUMAN           | 3174.5907 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P32119 PRDX2_HUMAN          | 3023.4811 |
| sp P23921 RIR1_HUMAN           | 2504.2911 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P11586 C1TC_HUMAN           | 3174.5907 |
| sp Q96C36 P5CR2_HUMAN          | 3148.6227 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P48643 TCPE_HUMAN           | 3286.7184 |
| sp P32119 PRDX2_HUMAN          | 3023.4811 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp O14980 XPO1_HUMAN           | 2547.2792 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp P11586 C1TC_HUMAN           | 3158.5958 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp P61604 CH10_HUMAN           | 2783.4058 |
| sp P11586 C1TC_HUMAN           | 3158.5958 |
| sp P41252 SYIC_HUMAN           | 2848.4681 |
| sp P61604 CH10_HUMAN           | 2783.4058 |
| sp P21333 FLNA_HUMAN           | 3297.6056 |
| sp Q96C36 P5CR2_HUMAN          | 3148.6227 |
| sp P41252 SYIC_HUMAN           | 2848.4681 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |
| sp P21333 FLNA_HUMAN           | 3297.6056 |
| sp Q96C36 P5CR2_HUMAN          | 3148.6227 |
| sp P41252 SYIC_HUMAN           | 2848.4681 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |
| sp P20042 IF2B_HUMAN           | 2046.9833 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |

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| sp P41091 IF2G_HUMAN,sp Q2VIR3 | 3621.8137 |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |
| sp P62277 RS13_HUMAN           | 2018.0361 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |
| sp P10586 PTPRF_HUMAN          | 3499.6428 |
| sp P10586 PTPRF_HUMAN          | 3499.6428 |
| sp P10586 PTPRF_HUMAN          | 3499.6428 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 2401.2206 |
| sp O14980 XPO1_HUMAN           | 2827.2541 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 2401.2206 |
| sp P46013 KI67_HUMAN           | 3206.5467 |
| sp P21399 ACOC_HUMAN           | 3105.5407 |
| sp Q15021 CND1_HUMAN           | 2757.445  |
| sp O14980 XPO1_HUMAN           | 2827.2541 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 2401.2206 |
| sp Q15021 CND1_HUMAN           | 2757.445  |
| sp P06756 ITAV_HUMAN           | 2298.2583 |
| sp Q15021 CND1_HUMAN           | 2757.445  |
| sp Q9NVJ2 ARL8B_HUMAN,sp Q96B  | 2748.481  |
| sp Q15021 CND1_HUMAN           | 2757.445  |
| sp P21399 ACOC_HUMAN           | 3105.5407 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2928.4691 |
| sp Q9NVJ2 ARL8B_HUMAN,sp Q96B  | 2748.481  |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2928.4691 |
| sp O75643 U520_HUMAN           | 2644.2592 |
| sp Q6UVK1 CSPG4_HUMAN          | 3823.9091 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2928.4691 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2928.4691 |
| sp P08133 ANXA6_HUMAN          | 2295.1053 |
| sp P62826 RAN_HUMAN            | 3176.5244 |
| sp P62826 RAN_HUMAN            | 3176.5244 |
| sp P42704 LPPRC_HUMAN          | 2308.1699 |
| sp P62826 RAN_HUMAN            | 3176.5244 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp P04843 RPN1_HUMAN           | 2199.1392 |
| sp P14625 ENPL_HUMAN           | 2556.1705 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp A5YKK6 CNOT1_HUMAN          | 2942.4087 |
| sp P30048 PRDX3_HUMAN          | 2669.4177 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp P14625 ENPL_HUMAN           | 2556.1705 |
| sp P14625 ENPL_HUMAN           | 2556.1705 |

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| sp P04843 RPN1_HUMAN  | 2199.1392 |
| sp P08195 4F2_HUMAN   | 3456.7525 |
| sp P17301 ITA2_HUMAN  | 3283.6877 |
| sp A5YKK6 CNOT1_HUMAN | 2942.4087 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp Q9BXP5 SRRT_HUMAN  | 2638.265  |
| sp Q9BXP5 SRRT_HUMAN  | 2638.265  |
| sp P30048 PRDX3_HUMAN | 2669.4177 |
| sp Q14980 NUMA1_HUMAN | 4609.297  |
| sp P14625 ENPL_HUMAN  | 2556.1705 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P14625 ENPL_HUMAN  | 2556.1705 |
| sp P14625 ENPL_HUMAN  | 2738.3163 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp Q15149 PLEC_HUMAN  | 3489.7124 |
| sp Q9H3P7 GCP60_HUMAN | 3697.7545 |
| sp P17301 ITA2_HUMAN  | 3283.6877 |
| sp P17301 ITA2_HUMAN  | 3283.6877 |
| sp Q9H3P7 GCP60_HUMAN | 3697.7545 |
| sp Q9H3P7 GCP60_HUMAN | 3697.7545 |
| sp P30041 PRDX6_HUMAN | 2793.3929 |
| sp P09622 DLDH_HUMAN  | 2679.3731 |
| sp P02545 LMNA_HUMAN  | 3218.64   |
| sp P22314 UBA1_HUMAN  | 3497.7579 |
| sp P30041 PRDX6_HUMAN | 2793.3929 |
| sp O14617 AP3D1_HUMAN | 2657.3119 |
| sp P49327 FAS_HUMAN   | 3832.8189 |
| sp O14617 AP3D1_HUMAN | 2657.3119 |
| sp O76094 SRP72_HUMAN | 3083.6074 |
| sp O76094 SRP72_HUMAN | 3083.6074 |
| sp P09622 DLDH_HUMAN  | 2679.3731 |
| sp P78527 PRKDC_HUMAN | 2211.1457 |
| sp P78527 PRKDC_HUMAN | 2211.1457 |
| sp Q9UHB9 SRP68_HUMAN | 2651.3847 |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp P09622 DLDH_HUMAN  | 2679.3731 |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp Q86VP6 CAND1_HUMAN | 3221.5955 |
| sp P02545 LMNA_HUMAN  | 2540.3221 |
| sp P02545 LMNA_HUMAN  | 2540.3221 |
| sp Q86VP6 CAND1_HUMAN | 3221.5955 |
| sp P42704 LPPRC_HUMAN | 2743.3857 |
| sp P42704 LPPRC_HUMAN | 2743.3857 |
| sp P02545 LMNA_HUMAN  | 2540.3221 |
| sp P62081 RS7_HUMAN   | 2719.4069 |
| sp Q9Y3E5 PTH2_HUMAN  | 3079.619  |

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| sp P02545 LMNA_HUMAN  | 2540.3221 |
| sp P02545 LMNA_HUMAN  | 2540.3221 |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp P62081 RS7_HUMAN   | 2719.4069 |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp P49327 FAS_HUMAN   | 3666.8134 |
| sp P02545 LMNA_HUMAN  | 2540.3221 |
| sp P62081 RS7_HUMAN   | 2719.4069 |
| sp P02545 LMNA_HUMAN  | 2540.3221 |
| sp O00299 CLIC1_HUMAN | 3205.6152 |
| sp P17844 DDX5_HUMAN  | 3169.475  |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp Q6YHK3 CD109_HUMAN | 2762.2824 |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp O00299 CLIC1_HUMAN | 3205.6152 |
| sp Q6YHK3 CD109_HUMAN | 2762.2824 |
| sp P17844 DDX5_HUMAN  | 3169.475  |
| sp O00299 CLIC1_HUMAN | 3205.6152 |
| sp P17844 DDX5_HUMAN  | 3169.475  |
| sp Q24JP5 T132A_HUMAN | 3029.655  |
| sp Q9Y3E5 PTH2_HUMAN  | 3079.619  |
| sp Q6YHK3 CD109_HUMAN | 2762.2824 |
| sp Q6YHK3 CD109_HUMAN | 2762.2824 |
| sp P17844 DDX5_HUMAN  | 3169.475  |
| sp P17844 DDX5_HUMAN  | 3169.475  |
| sp Q9Y3E5 PTH2_HUMAN  | 3079.619  |
| sp Q6YHK3 CD109_HUMAN | 2762.2824 |
| sp P60174 TPIS_HUMAN  | 2517.2533 |
| sp Q9Y3E5 PTH2_HUMAN  | 3079.619  |
| sp P60174 TPIS_HUMAN  | 2517.2533 |
| sp Q9Y3E5 PTH2_HUMAN  | 3079.619  |
| sp P60174 TPIS_HUMAN  | 2517.2533 |
| sp P60174 TPIS_HUMAN  | 2517.2533 |
| sp P60174 TPIS_HUMAN  | 2517.2533 |
| sp P08581 MET_HUMAN   | 3088.474  |
| sp P08581 MET_HUMAN   | 3088.474  |
| sp O15371 EIF3D_HUMAN | 2806.3994 |
| sp O15371 EIF3D_HUMAN | 2806.3994 |
| sp P08581 MET_HUMAN   | 3088.474  |
| sp O15371 EIF3D_HUMAN | 2806.3994 |
| sp O15371 EIF3D_HUMAN | 2806.3994 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P21266 GSTM3_HUMAN | 2790.4302 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |

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| sp Q9NZB2 F120A_HUMAN | 2559.3155 |
| sp O60264 SMCA5_HUMAN | 2718.3694 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp P53618 COPB_HUMAN  | 4358.1475 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P15924 DESP_HUMAN  | 2943.5012 |
| sp P53618 COPB_HUMAN  | 4358.1475 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp P53618 COPB_HUMAN  | 4358.1475 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp O75369 FLNB_HUMAN  | 3464.718  |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P38646 GRP75_HUMAN | 3887.7176 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp P07237 PDIA1_HUMAN | 2905.4862 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp O75054 IGSF3_HUMAN | 3815.8294 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp P07237 PDIA1_HUMAN | 2905.4862 |
| sp O75054 IGSF3_HUMAN | 3815.8294 |
| sp P08758 ANXA5_HUMAN | 2046.9997 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp P08758 ANXA5_HUMAN | 2046.9997 |
| sp P07237 PDIA1_HUMAN | 2905.4862 |
| sp P43121 MUC18_HUMAN | 3153.6558 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp O75054 IGSF3_HUMAN | 3815.8294 |
| sp P08758 ANXA5_HUMAN | 2046.9997 |
| sp P07237 PDIA1_HUMAN | 2905.4862 |
| sp Q13332 PTPRS_HUMAN | 4748.1864 |
| sp P08758 ANXA5_HUMAN | 2046.9997 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp Q9P2B2 FPRP_HUMAN  | 3050.4291 |
| sp Q13332 PTPRS_HUMAN | 4748.1864 |
| sp Q9P2B2 FPRP_HUMAN  | 3050.4291 |
| sp P62805 H4_HUMAN    | 1582.8719 |
| sp Q13813 SPTN1_HUMAN | 2783.3879 |
| sp P50991 TCPD_HUMAN  | 1927.9349 |
| sp Q13332 PTPRS_HUMAN | 4748.1864 |
| sp Q13813 SPTN1_HUMAN | 2783.3879 |
| sp Q9UQ80 PA2G4_HUMAN | 2861.3912 |

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| sp Q13813 SPTN1_HUMAN         | 2783.3879 |
| sp P62805 H4_HUMAN            | 1582.8719 |
| sp Q9UQ80 PA2G4_HUMAN         | 2861.3912 |
| sp P21926 CD9_HUMAN           | 3460.6101 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q13813 SPTN1_HUMAN         | 2783.3879 |
| sp O76094 SRP72_HUMAN         | 2508.2748 |
| sp Q9UQ80 PA2G4_HUMAN         | 2861.3912 |
| sp P46940 IQGA1_HUMAN         | 4231.1147 |
| sp P62805 H4_HUMAN            | 1582.8719 |
| sp Q13813 SPTN1_HUMAN         | 2783.3879 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp Q7KZF4 SND1_HUMAN          | 2412.2723 |
| sp O76094 SRP72_HUMAN         | 2508.2748 |
| sp Q13332 PTPRS_HUMAN         | 4748.1864 |
| sp O76094 SRP72_HUMAN         | 2508.2748 |
| sp Q13332 PTPRS_HUMAN         | 4732.1915 |
| sp Q08J23 NSUN2_HUMAN         | 3610.7072 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P28288 ABCD3_HUMAN         | 2720.4021 |
| sp P28288 ABCD3_HUMAN         | 2720.4021 |
| sp P62805 H4_HUMAN            | 1582.8719 |
| sp Q08J23 NSUN2_HUMAN         | 3610.7072 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P78347 GTF2I_HUMAN         | 3664.8454 |
| sp P28288 ABCD3_HUMAN         | 2720.4021 |
| sp P62805 H4_HUMAN            | 1582.8719 |
| sp P28288 ABCD3_HUMAN         | 2720.4021 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q13332 PTPRS_HUMAN         | 4732.1915 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q13332 PTPRS_HUMAN         | 4732.1915 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q9BSJ8 ESYT1_HUMAN         | 3465.7093 |
| sp Q92616 GCN1_HUMAN          | 2798.4194 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P35232 PHB_HUMAN           | 3319.67   |
| sp Q15738 NSDHL_HUMAN         | 3045.4509 |
| sp Q92973 TNPO1_HUMAN         | 2925.4623 |
| sp Q92973 TNPO1_HUMAN         | 2925.4623 |
| sp P35232 PHB_HUMAN           | 3319.67   |
| sp Q00610 CLH1_HUMAN          | 2564.2871 |
| sp Q00610 CLH1_HUMAN          | 2564.2871 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |

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| sp P35232 PHB_HUMAN           | 3319.67   |
| sp Q92973 TNPO1_HUMAN         | 2925.4623 |
| sp Q15738 NSDHL_HUMAN         | 3045.4509 |
| sp Q00610 CLH1_HUMAN          | 2564.2871 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp Q92973 TNPO1_HUMAN         | 2925.4623 |
| sp Q15738 NSDHL_HUMAN         | 3045.4509 |
| sp Q92973 TNPO1_HUMAN         | 2925.4623 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P29401 TKT_HUMAN           | 2475.2315 |
| sp Q09666 AHNK_HUMAN          | 4466.2064 |
| sp O95347 SMC2_HUMAN          | 2737.403  |
| sp O00231 PSD11_HUMAN         | 2890.4713 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P29401 TKT_HUMAN           | 2475.2315 |
| sp Q9BQG0 MBB1A_HUMAN         | 3089.6146 |
| sp Q8WUM4 PDC6I_HUMAN         | 2597.2472 |
| sp O95347 SMC2_HUMAN          | 2737.403  |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q9BQG0 MBB1A_HUMAN         | 3089.6146 |
| sp Q9BQG0 MBB1A_HUMAN         | 3089.6146 |
| sp Q8WUM4 PDC6I_HUMAN         | 2597.2472 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q9BQG0 MBB1A_HUMAN         | 3089.6146 |
| sp Q9BQG0 MBB1A_HUMAN         | 3089.6146 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q8NI27 THOC2_HUMAN         | 2462.2118 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P05783 K1C18_HUMAN         | 2501.2975 |
| sp P05783 K1C18_HUMAN         | 2501.2975 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 3050.5812 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 3050.5812 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 3050.5812 |
| sp P08195 4F2_HUMAN           | 2374.1594 |
| sp Q13421 MSLN_HUMAN          | 2723.4745 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 3050.5812 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 3050.5812 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 3050.5812 |
| sp P08195 4F2_HUMAN           | 2374.1594 |
| sp Q13421 MSLN_HUMAN          | 2723.4745 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 3050.5812 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |

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| sp P05783 K1C18_HUMAN         | 2501.2975 |
| sp P26640 SYVC_HUMAN          | 4609.1451 |
| sp P05783 K1C18_HUMAN         | 2501.2975 |
| sp P05783 K1C18_HUMAN         | 2501.2975 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P26640 SYVC_HUMAN          | 4609.1451 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp Q12906 ILF3_HUMAN          | 2740.4323 |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp Q12906 ILF3_HUMAN          | 2740.4323 |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q6UVK1 CSPG4_HUMAN         | 3838.953  |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp P21926 CD9_HUMAN           | 4149.985  |
| sp P50991 TCPD_HUMAN          | 1911.94   |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |



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| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp P21926 CD9_HUMAN           | 4149.985  |
| sp P07355 ANXA2_HUMAN         | 3518.7504 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp O75694 NU155_HUMAN         | 3589.845  |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp P08758 ANXA5_HUMAN         | 3066.4645 |
| sp O60568 PLOD3_HUMAN         | 2937.5084 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp O75694 NU155_HUMAN         | 3589.845  |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp O60568 PLOD3_HUMAN         | 2937.5084 |
| sp O60568 PLOD3_HUMAN         | 2937.5084 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp P14735 IDE_HUMAN           | 2982.4896 |
| sp O75694 NU155_HUMAN         | 3589.845  |
| sp P14735 IDE_HUMAN           | 2982.4896 |
| sp P08758 ANXA5_HUMAN         | 3066.4645 |
| sp P08758 ANXA5_HUMAN         | 3066.4645 |
| sp P14735 IDE_HUMAN           | 2982.4896 |
| sp P14735 IDE_HUMAN           | 2982.4896 |
| sp P14735 IDE_HUMAN           | 2982.4896 |
| sp P08758 ANXA5_HUMAN         | 3066.4645 |
| sp P08758 ANXA5_HUMAN         | 3066.4645 |
| sp P46940 IQGA1_HUMAN         | 4215.1198 |
| sp P14735 IDE_HUMAN           | 2982.4896 |
| sp P02786 TFR1_HUMAN          | 2997.472  |
| sp P14735 IDE_HUMAN           | 2982.4896 |
| sp P02786 TFR1_HUMAN          | 2997.472  |
| sp P14735 IDE_HUMAN           | 2982.4896 |
| sp P46940 IQGA1_HUMAN         | 4215.1198 |
| sp P02786 TFR1_HUMAN          | 2997.472  |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp P04844 RPN2_HUMAN          | 3577.794  |
| sp P68431 H31_HUMAN           | 3954.8226 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3089.4223 |
| sp Q92499 DDX1_HUMAN          | 2888.4808 |
| sp P49327 FAS_HUMAN           | 3666.8134 |
| sp P30153 2AAA_HUMAN          | 2946.4433 |
| sp P30153 2AAA_HUMAN          | 2946.4433 |
| sp P49327 FAS_HUMAN           | 3666.8134 |
| sp P30153 2AAA_HUMAN          | 2946.4433 |

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| sp Q01082 SPTB2_HUMAN          | 2351.2373 |
| sp P49327 FAS_HUMAN            | 3666.8134 |
| sp P60842 IF4A1_HUMAN          | 3573.6473 |
| sp P49327 FAS_HUMAN            | 3666.8134 |
| sp Q01082 SPTB2_HUMAN          | 2351.2373 |
| sp Q01082 SPTB2_HUMAN          | 2351.2373 |
| sp P49327 FAS_HUMAN            | 3666.8134 |
| sp P60842 IF4A1_HUMAN          | 3573.6473 |
| sp Q5VYK3 ECM29_HUMAN          | 2899.5331 |
| sp P07355 ANXA2_HUMAN          | 3390.6554 |
| sp P07355 ANXA2_HUMAN          | 3390.6554 |
| sp P07355 ANXA2_HUMAN          | 3390.6554 |
| sp P07355 ANXA2_HUMAN          | 3390.6554 |
| sp P46940 IQGA1_HUMAN          | 3903.8302 |
| sp Q00610 CLH1_HUMAN           | 5212.6292 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P14923 PLAK_HUMAN           | 3204.6303 |
| sp P14923 PLAK_HUMAN           | 3204.6303 |
| sp P78527 PRKDC_HUMAN          | 2994.5008 |
| sp P14923 PLAK_HUMAN           | 3204.6303 |
| sp P78527 PRKDC_HUMAN          | 2994.5008 |
| sp P78527 PRKDC_HUMAN          | 2994.5008 |
| sp P78527 PRKDC_HUMAN          | 2994.5008 |
| sp Q07065 CKAP4_HUMAN          | 3672.8384 |
| sp P14923 PLAK_HUMAN           | 3204.6303 |
| sp P14923 PLAK_HUMAN           | 3204.6303 |
| sp P68032 ACTC_HUMAN,sp P63267 | 3345.5269 |
| sp P20700 LMNB1_HUMAN          | 2852.4291 |
| sp P84243 H33_HUMAN            | 3789.8308 |
| sp P20700 LMNB1_HUMAN          | 2852.4291 |
| sp P20700 LMNB1_HUMAN          | 2852.4291 |
| sp P20700 LMNB1_HUMAN          | 2852.4291 |
| sp P84243 H33_HUMAN            | 3789.8308 |
| sp P20700 LMNB1_HUMAN          | 2852.4291 |
| sp P68032 ACTC_HUMAN,sp P63267 | 3345.5269 |
| sp P84243 H33_HUMAN            | 3789.8308 |
| sp P84243 H33_HUMAN            | 3789.8308 |
| sp P26599 PTBP1_HUMAN          | 3220.7669 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P26599 PTBP1_HUMAN          | 3220.7669 |
| sp P49327 FAS_HUMAN            | 3924.1248 |
| sp P49327 FAS_HUMAN            | 3924.1248 |
| sp P49327 FAS_HUMAN            | 3924.1248 |
| sp P49327 FAS_HUMAN            | 3924.1248 |
| sp P54819 KAD2_HUMAN           | 3201.5652 |
| sp P54819 KAD2_HUMAN           | 3201.5652 |
| sp P54819 KAD2_HUMAN           | 3201.5652 |
| sp P54819 KAD2_HUMAN           | 3201.5652 |

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| sp P49327 FAS_HUMAN           | 4330.3424 |
| sp P54819 KAD2_HUMAN          | 3201.5652 |
| sp Q6YHK3 CD109_HUMAN         | 3212.6717 |
| sp Q6YHK3 CD109_HUMAN         | 3212.6717 |
| sp Q6YHK3 CD109_HUMAN         | 3212.6717 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 2559.416  |
| sp A6NMY6 AXA2L_HUMAN,sp P073 | 2559.416  |
| sp Q71U36 TBA1A_HUMAN,sp P0DF | 2693.1994 |
| sp P50454 SERPH_HUMAN         | 1700.6849 |
| sp P10412 H14_HUMAN           | 1307.7197 |
| sp P10412 H14_HUMAN           | 1307.7197 |
| sp P10412 H14_HUMAN           | 1307.7197 |
| sp P36578 RL4_HUMAN           | 1418.7405 |
| sp Q00839 HNRPU_HUMAN         | 1990.9457 |
| sp Q00839 HNRPU_HUMAN         | 1990.9457 |
| sp P36578 RL4_HUMAN           | 1418.7405 |
| sp P16403 H12_HUMAN           | 1505.8202 |
| sp Q00839 HNRPU_HUMAN         | 1990.9457 |
| sp P16403 H12_HUMAN           | 1505.8202 |
| sp P16403 H12_HUMAN           | 1409.7878 |
| sp P16403 H12_HUMAN           | 1409.7878 |
| sp P62633 CNBP_HUMAN          | 1535.7038 |
| sp P16403 H12_HUMAN           | 1409.7878 |
| sp Q00839 HNRPU_HUMAN         | 2349.0945 |
| sp P62633 CNBP_HUMAN          | 1535.7038 |
| sp P26373 RL13_HUMAN          | 1867.9163 |
| sp P40926 MDHM_HUMAN          | 1252.5837 |
| sp P40926 MDHM_HUMAN          | 1252.5837 |
| sp P27816 MAP4_HUMAN          | 1804.8414 |
| sp P35637 FUS_HUMAN           | 3398.3371 |
| sp Q9P0L0 VAPA_HUMAN          | 1971.9286 |
| sp Q9P0L0 VAPA_HUMAN          | 1971.9286 |
| sp P35637 FUS_HUMAN           | 3398.3371 |
| sp Q9P0L0 VAPA_HUMAN          | 1971.9286 |
| sp Q15293 RCN1_HUMAN          | 1800.8166 |
| sp Q15293 RCN1_HUMAN          | 1800.8166 |
| sp P08621 RU17_HUMAN          | 1555.6362 |
| sp P00558 PGK1_HUMAN          | 1927.8548 |
| sp P00558 PGK1_HUMAN          | 1927.8548 |
| sp P35637 FUS_HUMAN           | 3398.3371 |
| sp Q9P0L0 VAPA_HUMAN          | 1971.9286 |
| sp Q9P0L0 VAPA_HUMAN          | 1971.9286 |
| sp Q9P0L0 VAPA_HUMAN          | 1971.9286 |
| sp Q9P0L0 VAPA_HUMAN          | 1971.9286 |
| sp P35637 FUS_HUMAN           | 3398.3371 |
| sp P00558 PGK1_HUMAN          | 1927.8548 |
| sp P08621 RU17_HUMAN          | 1555.6362 |

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| sp P08621 RU17_HUMAN  | 1555.6362 |
| sp P43121 MUC18_HUMAN | 1451.6463 |
| sp P00558 PGK1_HUMAN  | 1927.8548 |
| sp P35637 FUS_HUMAN   | 3398.3371 |
| sp Q15293 RCN1_HUMAN  | 1800.8166 |
| sp P35637 FUS_HUMAN   | 3398.3371 |
| sp P62081 RS7_HUMAN   | 1855.8813 |
| sp P00558 PGK1_HUMAN  | 1927.8548 |
| sp P35637 FUS_HUMAN   | 3382.3422 |
| sp P35637 FUS_HUMAN   | 3398.3371 |
| sp Q15293 RCN1_HUMAN  | 1800.8166 |
| sp P00558 PGK1_HUMAN  | 1927.8548 |
| sp Q16629 SRSF7_HUMAN | 2300.831  |
| sp P00558 PGK1_HUMAN  | 1927.8548 |
| sp Q16629 SRSF7_HUMAN | 2300.831  |
| sp Q12906 ILF3_HUMAN  | 4604.0402 |
| sp Q8IWS0 PHF6_HUMAN  | 2061.8673 |
| sp Q8IWS0 PHF6_HUMAN  | 2061.8673 |
| sp P11388 TOP2A_HUMAN | 2205.1026 |
| sp P35637 FUS_HUMAN   | 3382.3422 |
| sp P35637 FUS_HUMAN   | 3382.3422 |
| sp P35637 FUS_HUMAN   | 3382.3422 |
| sp Q8IWS0 PHF6_HUMAN  | 2061.8673 |
| sp Q12906 ILF3_HUMAN  | 4604.0402 |
| sp Q14847 LASP1_HUMAN | 1950.857  |
| sp P35637 FUS_HUMAN   | 3382.3422 |
| sp Q12906 ILF3_HUMAN  | 4604.0402 |
| sp P12270 TPR_HUMAN   | 2411.0989 |
| sp P12270 TPR_HUMAN   | 2411.0989 |
| sp Q16629 SRSF7_HUMAN | 2300.831  |
| sp P35637 FUS_HUMAN   | 3382.3422 |
| sp Q16629 SRSF7_HUMAN | 2300.831  |
| sp P35637 FUS_HUMAN   | 3382.3422 |
| sp Q12906 ILF3_HUMAN  | 4604.0402 |
| sp Q12906 ILF3_HUMAN  | 4604.0402 |
| sp Q16629 SRSF7_HUMAN | 2300.831  |
| sp Q12906 ILF3_HUMAN  | 4604.0402 |
| sp Q16629 SRSF7_HUMAN | 2300.831  |
| sp Q16629 SRSF7_HUMAN | 2300.831  |
| sp P61313 RL15_HUMAN  | 1901.9384 |
| sp P61313 RL15_HUMAN  | 1901.9384 |
| sp P61313 RL15_HUMAN  | 1901.9384 |
| sp P61313 RL15_HUMAN  | 1901.9384 |
| sp P61313 RL15_HUMAN  | 1901.9384 |
| sp P04406 G3P_HUMAN   | 1643.8407 |
| sp P04406 G3P_HUMAN   | 1643.8407 |
| sp Q12906 ILF3_HUMAN  | 4604.0402 |

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| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp Q6DD88 ATLA3_HUMAN          | 2083.0083 |
| sp Q12906 ILF3_HUMAN           | 4604.0402 |
| sp P18124 RL7_HUMAN            | 2440.1003 |
| sp Q14690 RRP5_HUMAN           | 1799.8802 |
| sp Q96DG6 CMBL_HUMAN           | 2245.991  |
| sp Q96DG6 CMBL_HUMAN           | 2245.991  |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp Q6DD88 ATLA3_HUMAN          | 2083.0083 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2735.1915 |
| sp P04083 ANXA1_HUMAN          | 1393.6772 |
| sp P51991 ROA3_HUMAN           | 1704.8683 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp Q96DG6 CMBL_HUMAN           | 2245.991  |
| sp P04083 ANXA1_HUMAN          | 1393.6772 |
| sp P04083 ANXA1_HUMAN          | 1393.6772 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P12268 IMDH2_HUMAN          | 2268.0407 |
| sp P12268 IMDH2_HUMAN          | 2268.0407 |
| sp P08708 RS17_HUMAN           | 1397.6324 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P08708 RS17_HUMAN           | 1397.6324 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P12268 IMDH2_HUMAN          | 2268.0407 |
| sp P04792 HSPB1_HUMAN          | 1893.9068 |
| sp P04792 HSPB1_HUMAN          | 1893.9068 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P12268 IMDH2_HUMAN          | 2268.0407 |
| sp O95831 AIFM1_HUMAN          | 2162.0491 |
| sp P12268 IMDH2_HUMAN          | 2268.0407 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P04792 HSPB1_HUMAN          | 1893.9068 |
| sp P04792 HSPB1_HUMAN          | 1893.9068 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P17812 PYRG1_HUMAN          | 1457.6721 |
| sp P12268 IMDH2_HUMAN          | 2268.0407 |
| sp P17812 PYRG1_HUMAN          | 1457.6721 |
| sp P27797 CALR_HUMAN           | 2124.96   |
| sp P27797 CALR_HUMAN           | 2124.96   |
| sp P15151 PVR_HUMAN            | 2719.1569 |

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| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp O95831 AIFM1_HUMAN          | 2162.0491 |
| sp P17812 PYRG1_HUMAN          | 1457.6721 |
| sp O95831 AIFM1_HUMAN          | 2162.0491 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P27797 CALR_HUMAN           | 2124.96   |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp Q13148 TADBP_HUMAN          | 2055.9722 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2735.1915 |
| sp P27797 CALR_HUMAN           | 2124.96   |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp Q13148 TADBP_HUMAN          | 2055.9722 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P14866 HNRPL_HUMAN          | 4234.8309 |
| sp P14866 HNRPL_HUMAN          | 4234.8309 |
| sp P14866 HNRPL_HUMAN          | 4234.8309 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp Q13162 PRDX4_HUMAN          | 1687.8529 |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P22102 PUR2_HUMAN           | 2698.3133 |
| sp P22102 PUR2_HUMAN           | 2698.3133 |
| sp Q13162 PRDX4_HUMAN          | 1687.8529 |
| sp P22102 PUR2_HUMAN           | 2698.3133 |
| sp P22102 PUR2_HUMAN           | 2698.3133 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P07900 HS90A_HUMAN          | 2179.0256 |
| sp P07900 HS90A_HUMAN          | 2179.0256 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P07900 HS90A_HUMAN          | 2179.0256 |
| sp P07900 HS90A_HUMAN          | 2179.0256 |
| sp Q02543 RL18A_HUMAN          | 1534.7892 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |

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| sp P48643 TCPE_HUMAN           | 1858.8949 |
| sp P29692 EF1D_HUMAN           | 3220.5345 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P78527 PRKDC_HUMAN          | 2460.1591 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P48643 TCPE_HUMAN           | 1858.8949 |
| sp P48643 TCPE_HUMAN           | 1858.8949 |
| sp P62979 RS27A_HUMAN          | 2576.0229 |
| sp Q00839 HNRPU_HUMAN          | 1958.9949 |
| sp Q00839 HNRPU_HUMAN          | 1958.9949 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp Q02543 RL18A_HUMAN          | 1534.7892 |
| sp Q02543 RL18A_HUMAN          | 1534.7892 |
| sp P22392 NDKB_HUMAN           | 1906.9061 |
| sp P22392 NDKB_HUMAN           | 1906.9061 |
| sp P29692 EF1D_HUMAN           | 3220.5345 |
| sp P22392 NDKB_HUMAN           | 1906.9061 |
| sp Q02543 RL18A_HUMAN          | 1534.7892 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp Q12788 TBL3_HUMAN           | 3115.3151 |
| sp P29692 EF1D_HUMAN           | 3220.5345 |
| sp P29692 EF1D_HUMAN           | 3220.5345 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp P62979 RS27A_HUMAN          | 2576.0229 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp P62979 RS27A_HUMAN          | 2576.0229 |
| sp O43175 SERA_HUMAN           | 2815.3195 |
| sp Q9ULF5 S39AA_HUMAN          | 3319.4402 |
| sp P62979 RS27A_HUMAN          | 2576.0229 |
| sp P62979 RS27A_HUMAN          | 2576.0229 |
| sp P21333 FLNA_HUMAN           | 2222.1331 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp P27797 CALR_HUMAN           | 3155.4207 |
| sp Q06830 PRDX1_HUMAN          | 2602.2122 |
| sp P27797 CALR_HUMAN           | 3155.4207 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp Q06830 PRDX1_HUMAN          | 2602.2122 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp O43175 SERA_HUMAN           | 2815.3195 |
| sp P27797 CALR_HUMAN           | 3155.4207 |
| sp O43175 SERA_HUMAN           | 2815.3195 |

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| sp Q06830 PRDX1_HUMAN           | 2602.2122 |
| sp P27797 CALR_HUMAN            | 3155.4207 |
| sp P12268 IMDH2_HUMAN           | 2271.059  |
| sp O43175 SERA_HUMAN            | 2815.3195 |
| sp Q06830 PRDX1_HUMAN           | 2602.2122 |
| sp Q06830 PRDX1_HUMAN           | 2602.2122 |
| sp P06748 NPM_HUMAN             | 2769.2267 |
| sp P05787 K2C8_HUMAN            | 2183.0243 |
| sp O43175 SERA_HUMAN            | 2815.3195 |
| sp P13010 XRCC5_HUMAN           | 2695.2362 |
| sp P12268 IMDH2_HUMAN           | 2271.059  |
| sp P12268 IMDH2_HUMAN           | 2271.059  |
| sp P13010 XRCC5_HUMAN           | 2695.2362 |
| sp O43175 SERA_HUMAN            | 2815.3195 |
| sp Q06830 PRDX1_HUMAN           | 2602.2122 |
| sp Q06830 PRDX1_HUMAN           | 2602.2122 |
| sp P12268 IMDH2_HUMAN           | 2271.059  |
| sp Q06830 PRDX1_HUMAN           | 2602.2122 |
| sp Q92901 RL3L_HUMAN,sp P39023  | 1561.7161 |
| sp P23528 COF1_HUMAN            | 2499.17   |
| sp P23528 COF1_HUMAN            | 2499.17   |
| sp P62277 RS13_HUMAN            | 1924.9101 |
| sp P23528 COF1_HUMAN            | 2499.17   |
| sp P23528 COF1_HUMAN            | 2499.17   |
| sp P62277 RS13_HUMAN            | 1924.9101 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 2513.1315 |
| sp O75369 FLNB_HUMAN            | 2891.3032 |
| sp O75369 FLNB_HUMAN            | 2891.3032 |
| sp O75369 FLNB_HUMAN            | 2891.3032 |
| sp P08670 VIME_HUMAN            | 1768.8778 |
| sp O75369 FLNB_HUMAN            | 2891.3032 |
| sp Q92901 RL3L_HUMAN,sp P39023  | 1561.746  |
| sp P62277 RS13_HUMAN            | 1908.9152 |
| sp Q92901 RL3L_HUMAN,sp P39023  | 1561.746  |
| sp Q92901 RL3L_HUMAN,sp P39023  | 1561.746  |
| sp O75369 FLNB_HUMAN            | 1767.858  |
| sp Q16719 KYNU_HUMAN            | 2285.2016 |
| sp Q14320 FA50A_HUMAN           | 2363.1969 |
| sp P26599 PTBP1_HUMAN           | 1729.9111 |
| sp Q14320 FA50A_HUMAN           | 2363.1969 |
| sp P21333 FLNA_HUMAN            | 2783.2787 |
| sp O75369 FLNB_HUMAN            | 1767.858  |
| sp Q92901 RL3L_HUMAN,sp P39023  | 1561.746  |
| sp Q92901 RL3L_HUMAN,sp P39023  | 1561.746  |
| sp Q14320 FA50A_HUMAN           | 2363.1969 |
| sp Q14320 FA50A_HUMAN           | 2363.1969 |
| sp P21333 FLNA_HUMAN            | 2783.2787 |



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| sp Q92901 RL3L_HUMAN,sp P39023 | 1561.746  |
| sp Q92901 RL3L_HUMAN,sp P39023 | 1561.746  |
| sp Q14320 FA50A_HUMAN          | 2363.1969 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp Q14320 FA50A_HUMAN          | 2363.1969 |
| sp P08670 VIME_HUMAN           | 1768.8778 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp Q02878 RL6_HUMAN            | 2705.2093 |
| sp P08670 VIME_HUMAN           | 1768.8778 |
| sp P08670 VIME_HUMAN           | 1768.8778 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1716.7678 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp P08195 4F2_HUMAN            | 1499.8096 |
| sp P20908 CO5A1_HUMAN          | 1478.6902 |
| sp P21333 FLNA_HUMAN           | 2783.2787 |
| sp P06748 NPM_HUMAN            | 2455.0676 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1716.7678 |
| sp P11940 PABP1_HUMAN          | 2417.2187 |
| sp P11940 PABP1_HUMAN          | 2417.2187 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1716.7678 |
| sp P40925 MDHC_HUMAN           | 2703.3041 |
| sp P21333 FLNA_HUMAN           | 1774.8315 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1716.7678 |
| sp Q15365 PCBP1_HUMAN,sp P577  | 1693.8709 |
| sp P63244 RACK1_HUMAN          | 3180.5146 |
| sp P11940 PABP1_HUMAN          | 2417.2187 |
| sp P11940 PABP1_HUMAN          | 2417.2187 |
| sp P63244 RACK1_HUMAN          | 3180.5146 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1716.7678 |
| sp P40925 MDHC_HUMAN           | 2703.3041 |
| sp P40925 MDHC_HUMAN           | 2703.3041 |
| sp Q02878 RL6_HUMAN            | 2705.2093 |
| sp Q9BUJ2 HNRL1_HUMAN          | 2592.282  |
| sp P21333 FLNA_HUMAN           | 1774.8315 |
| sp Q02878 RL6_HUMAN            | 2705.2093 |
| sp P17987 TCPA_HUMAN           | 1493.7297 |
| sp P63244 RACK1_HUMAN          | 3180.5146 |
| sp Q9BUJ2 HNRL1_HUMAN          | 2592.282  |
| sp P22314 UBA1_HUMAN           | 1640.7981 |
| sp Q7L1Q6 BZW1_HUMAN,sp Q9Y6I  | 1831.968  |
| sp P22314 UBA1_HUMAN           | 1640.7981 |
| sp P62081 RS7_HUMAN            | 1584.8049 |
| sp Q01813 PFKAP_HUMAN          | 2134.9854 |
| sp P62753 RS6_HUMAN            | 1751.8413 |
| sp P62081 RS7_HUMAN            | 1584.8049 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |

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| sp P62081 RS7_HUMAN            | 1584.8049 |
| sp Q01813 PFKAP_HUMAN          | 2134.9854 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp P55884 EIF3B_HUMAN          | 1281.6717 |
| sp P23284 PPIB_HUMAN           | 1911.8938 |
| sp P42166 LAP2A_HUMAN,sp P4216 | 3998.8995 |
| sp P23284 PPIB_HUMAN           | 1911.8938 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp P42166 LAP2A_HUMAN,sp P4216 | 3998.8995 |
| sp Q7L1Q6 BZW1_HUMAN,sp Q9Y6I  | 1831.968  |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp Q9GZT3 SLIRP_HUMAN          | 2495.2517 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp Q14847 LASP1_HUMAN          | 3063.3855 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1613.7838 |
| sp O75367 H2AY_HUMAN           | 2268.1862 |
| sp P07900 HS90A_HUMAN,sp P0823 | 2497.2336 |
| sp P53396 ACLY_HUMAN           | 2781.2518 |
| sp Q99798 ACON_HUMAN           | 2840.3763 |
| sp P53621 COPA_HUMAN           | 2031.0749 |
| sp P07900 HS90A_HUMAN,sp P0823 | 2497.2336 |
| sp P43121 MUC18_HUMAN          | 1471.7783 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp Q00610 CLH1_HUMAN           | 1903.9574 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P43121 MUC18_HUMAN          | 1471.7783 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp P43243 MATR3_HUMAN          | 2806.1055 |
| sp P43243 MATR3_HUMAN          | 2806.1055 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1613.7838 |
| sp Q09666 AHNK_HUMAN           | 1882.9214 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp P43243 MATR3_HUMAN          | 2806.1055 |
| sp P43243 MATR3_HUMAN          | 2806.1055 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp Q15365 PCBP1_HUMAN,sp P5773 | 1677.876  |
| sp Q15365 PCBP1_HUMAN,sp P5773 | 1677.876  |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1613.7838 |
| sp Q16891 MIC60_HUMAN          | 2764.4144 |
| sp Q15365 PCBP1_HUMAN,sp P5773 | 1677.876  |
| sp Q16576 RBBP7_HUMAN          | 3490.4644 |

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| sp Q71U36 TBA1A_HUMAN,sp P683  | 1767.7531 |
| sp Q15084 PDIA6_HUMAN          | 2777.3409 |
| sp P15924 DESP_HUMAN           | 2386.1951 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp Q15365 PCBP1_HUMAN,sp P577: | 1677.876  |
| sp P07900 HS90A_HUMAN          | 2286.1604 |
| sp Q16576 RBBP7_HUMAN          | 3490.4644 |
| sp Q16576 RBBP7_HUMAN          | 3490.4644 |
| sp P15924 DESP_HUMAN           | 2386.1951 |
| sp Q15084 PDIA6_HUMAN          | 2777.3409 |
| sp Q15365 PCBP1_HUMAN,sp P577: | 1677.876  |
| sp Q00610 CLH1_HUMAN           | 1903.9574 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp P07900 HS90A_HUMAN          | 2286.1604 |
| sp Q13263 TIF1B_HUMAN          | 2683.1721 |
| sp Q13263 TIF1B_HUMAN          | 2683.1721 |
| sp P11142 HSP7C_HUMAN          | 2348.1972 |
| sp P46778 RL21_HUMAN           | 1567.7817 |
| sp P61353 RL27_HUMAN           | 2978.4734 |
| sp P13639 EF2_HUMAN            | 2608.2261 |
| sp P13639 EF2_HUMAN            | 2608.2261 |
| sp Q00796 DH5O_HUMAN           | 2550.3152 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp Q13263 TIF1B_HUMAN          | 2683.1721 |
| sp Q13263 TIF1B_HUMAN          | 2683.1721 |
| sp Q00796 DH5O_HUMAN           | 2550.3152 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp Q13263 TIF1B_HUMAN          | 2683.1721 |
| sp P46778 RL21_HUMAN           | 1567.7817 |
| sp P15121 ALDR_HUMAN           | 3434.6275 |
| sp P30740 ILEU_HUMAN           | 2669.247  |
| sp P61353 RL27_HUMAN           | 2978.4734 |
| sp P61353 RL27_HUMAN           | 2978.4734 |
| sp P61353 RL27_HUMAN           | 2978.4734 |
| sp P30740 ILEU_HUMAN           | 2669.247  |
| sp P61353 RL27_HUMAN           | 2978.4734 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q13310 PABP4_HUMAN          | 1898.9486 |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 1576.7232 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 1576.7232 |
| sp P13010 XRCC5_HUMAN          | 2090.0433 |

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| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P13010 XRCC5_HUMAN          | 2090.0433 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1736.9243 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1736.9243 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2332.2023 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1736.9243 |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1581.7246 |
| sp P42704 LPPRC_HUMAN          | 2153.9865 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P11586 C1TC_HUMAN           | 2028.9905 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1581.7246 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P32119 PRDX2_HUMAN          | 4639.1126 |
| sp P32119 PRDX2_HUMAN          | 4639.1126 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q13813 SPTN1_HUMAN          | 1723.857  |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp O14980 XPO1_HUMAN           | 1848.9305 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P08195 4F2_HUMAN            | 2276.1298 |

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| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P29692 EF1D_HUMAN          | 1928.8581 |
| sp P29692 EF1D_HUMAN          | 1928.8581 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P46013 KI67_HUMAN          | 1811.8295 |
| sp P46013 KI67_HUMAN          | 1811.8295 |
| sp P29692 EF1D_HUMAN          | 1928.8581 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp Q15149 PLEC_HUMAN          | 2912.492  |
| sp Q92688 AN32B_HUMAN         | 1857.9949 |
| sp P30101 PDIA3_HUMAN         | 1841.906  |
| sp P49257 LMAN1_HUMAN         | 3283.5891 |
| sp Q13263 TIF1B_HUMAN         | 3334.4515 |
| sp P61978 HNRPK_HUMAN         | 1971.1153 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P46013 KI67_HUMAN          | 1811.8295 |
| sp P29692 EF1D_HUMAN          | 1928.8581 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp Q15149 PLEC_HUMAN          | 2912.492  |
| sp Q92688 AN32B_HUMAN         | 1857.9949 |
| sp P29692 EF1D_HUMAN          | 1928.8581 |
| sp P61978 HNRPK_HUMAN         | 1971.1153 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P23396 RS3_HUMAN           | 3106.6074 |
| sp Q13263 TIF1B_HUMAN         | 3334.4515 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q92688 AN32B_HUMAN         | 1857.9949 |
| sp P49257 LMAN1_HUMAN         | 3283.5891 |
| sp P35579 MYH9_HUMAN          | 1724.9825 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P49257 LMAN1_HUMAN         | 3283.5891 |
| sp P38606 VATA_HUMAN          | 2620.3133 |
| sp P52948 NUP98_HUMAN         | 3133.4557 |
| sp P35579 MYH9_HUMAN          | 1724.9825 |
| sp P49257 LMAN1_HUMAN         | 3283.5891 |
| sp P52948 NUP98_HUMAN         | 3133.4557 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P52948 NUP98_HUMAN         | 3133.4557 |
| sp P49257 LMAN1_HUMAN         | 3283.5891 |
| sp O75083 WDR1_HUMAN          | 3097.4265 |
| sp P08195 4F2_HUMAN           | 1613.8777 |

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| sp P61978 HNRPK_HUMAN         | 1971.1153 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P61978 HNRPK_HUMAN         | 1971.1153 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp O75083 WDR1_HUMAN          | 3097.4265 |
| sp P61978 HNRPK_HUMAN         | 1971.1153 |
| sp P13010 XRCC5_HUMAN         | 3686.7812 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P61978 HNRPK_HUMAN         | 1971.1153 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P13010 XRCC5_HUMAN         | 3686.7812 |
| sp P09874 PARP1_HUMAN         | 2984.426  |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q9Y639 NPTN_HUMAN          | 3464.4826 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q9Y639 NPTN_HUMAN          | 3464.4826 |
| sp Q9NZ01 TECR_HUMAN          | 2437.2199 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q09666 AHNK_HUMAN          | 2580.1955 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P07910 HNRPC_HUMAN         | 2406.1427 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q9Y6N7 ROBO1_HUMAN         | 2398.123  |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q9BQG0 MBB1A_HUMAN         | 1894.9393 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q99798 ACON_HUMAN          | 2730.2636 |
| sp Q9BQG0 MBB1A_HUMAN         | 1894.9393 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp Q9BQG0 MBB1A_HUMAN         | 1894.9393 |
| sp Q99798 ACON_HUMAN          | 2730.2636 |
| sp P08195 4F2_HUMAN           | 2051.9854 |
| sp Q9BQG0 MBB1A_HUMAN         | 1894.9393 |
| sp Q9Y6N7 ROBO1_HUMAN         | 2398.123  |
| sp Q9BQG0 MBB1A_HUMAN         | 1894.9393 |
| sp P62750 RL23A_HUMAN         | 2483.2908 |
| sp P49327 FAS_HUMAN           | 2633.2003 |
| sp P08195 4F2_HUMAN           | 2051.9854 |
| sp P62750 RL23A_HUMAN         | 2483.2908 |
| sp P08195 4F2_HUMAN           | 2051.9854 |
| sp Q16891 MIC60_HUMAN         | 1718.8992 |

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| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp Q6P2Q9 PRP8_HUMAN            | 2429.2379 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P07237 PDIA1_HUMAN           | 3200.5183 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P27797 CALR_HUMAN            | 3909.7105 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P08195 4F2_HUMAN             | 2051.9854 |
| sp P27797 CALR_HUMAN            | 3909.7105 |
| sp P63244 RACK1_HUMAN           | 4396.9965 |
| sp P08581 MET_HUMAN             | 2815.4868 |
| sp O00571 DDX3X_HUMAN,sp O155   | 2937.2512 |
| sp P02786 TFR1_HUMAN            | 2378.1219 |
| sp P08581 MET_HUMAN             | 2815.4868 |
| sp Q15067 ACOX1_HUMAN           | 1826.9138 |
| sp P02786 TFR1_HUMAN            | 2378.1219 |
| sp O00571 DDX3X_HUMAN,sp O155   | 2937.2512 |
| sp P02786 TFR1_HUMAN            | 2378.1219 |
| sp P49327 FAS_HUMAN             | 3542.6195 |
| sp O00571 DDX3X_HUMAN,sp O155   | 2937.2512 |
| sp O14967 CLGN_HUMAN,sp P2782   | 1780.7879 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 1622.8668 |
| sp O14967 CLGN_HUMAN,sp P2782   | 1780.7879 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 1622.8668 |
| sp P55884 EIF3B_HUMAN           | 3497.7638 |
| sp Q9P0L0 VAPA_HUMAN            | 2032.0629 |
| sp P17812 PYRG1_HUMAN           | 3258.4784 |
| sp Q9P0L0 VAPA_HUMAN            | 2032.0629 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 1622.8668 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 1622.8668 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 1622.8668 |
| sp P55884 EIF3B_HUMAN           | 3497.7638 |
| sp Q9P0L0 VAPA_HUMAN            | 2032.0629 |
| sp P02786 TFR1_HUMAN            | 2378.1219 |
| sp P49327 FAS_HUMAN             | 3542.6195 |
| sp P49327 FAS_HUMAN             | 3542.6195 |
| sp P27824 CALX_HUMAN            | 2409.1576 |
| sp P08195 4F2_HUMAN             | 3456.7525 |
| sp P07237 PDIA1_HUMAN           | 2015.9741 |
| sp P18621 RL17_HUMAN            | 1512.7647 |

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| sp P07237 PDIA1_HUMAN         | 2015.9741 |
| sp P46940 IQGA1_HUMAN         | 1878.9258 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3080.4338 |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp Q15067 ACOX1_HUMAN         | 3271.6587 |
| sp Q15067 ACOX1_HUMAN         | 3271.6587 |
| sp P46940 IQGA1_HUMAN         | 1878.9258 |
| sp P46940 IQGA1_HUMAN         | 1878.9258 |
| sp O00159 MYO1C_HUMAN         | 1778.9315 |
| sp O00159 MYO1C_HUMAN         | 1778.9315 |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp Q08J23 NSUN2_HUMAN         | 2104.1065 |
| sp Q08J23 NSUN2_HUMAN         | 2104.1065 |
| sp P18621 RL17_HUMAN          | 1512.7647 |
| sp Q08J23 NSUN2_HUMAN         | 2104.1065 |
| sp P23284 PPIB_HUMAN          | 1894.9611 |
| sp O00159 MYO1C_HUMAN         | 1778.9315 |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp P23284 PPIB_HUMAN          | 1894.9611 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3535.7154 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3535.7154 |
| sp Q08J23 NSUN2_HUMAN         | 2104.1065 |
| sp Q08J23 NSUN2_HUMAN         | 2104.1065 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3535.7154 |
| sp P62258 1433E_HUMAN         | 3319.6395 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3535.7154 |
| sp Q08J23 NSUN2_HUMAN         | 2104.1065 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3535.7154 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI | 3535.7154 |
| sp P46940 IQGA1_HUMAN         | 1878.9258 |
| sp O00159 MYO1C_HUMAN         | 1778.9315 |
| sp Q08J23 NSUN2_HUMAN         | 2104.1065 |
| sp P46940 IQGA1_HUMAN         | 1878.9258 |
| sp P08195 4F2_HUMAN           | 3456.7525 |
| sp P23284 PPIB_HUMAN          | 1894.9611 |
| sp Q96QK1 VPS35_HUMAN         | 1994.9554 |
| sp P26599 PTBP1_HUMAN         | 3687.8421 |
| sp P31327 CPSM_HUMAN          | 3339.6697 |
| sp P78527 PRKDC_HUMAN         | 2471.187  |
| sp Q92499 DDX1_HUMAN          | 3072.5305 |
| sp P09382 LEG1_HUMAN          | 2541.2071 |
| sp P32969 RL9_HUMAN           | 2257.0984 |
| sp P31327 CPSM_HUMAN          | 3339.6697 |
| sp P31327 CPSM_HUMAN          | 3339.6697 |



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| sp P78371 TCPB_HUMAN           | 1694.8628 |
| sp P09382 LEG1_HUMAN           | 2541.2071 |
| sp P32969 RL9_HUMAN            | 2257.0984 |
| sp P32969 RL9_HUMAN            | 2257.0984 |
| sp P32969 RL9_HUMAN            | 2257.0984 |
| sp P09382 LEG1_HUMAN           | 2541.2071 |
| sp P53621 COPA_HUMAN           | 4402.9722 |
| sp P32969 RL9_HUMAN            | 2257.0984 |
| sp P32969 RL9_HUMAN            | 2257.0984 |
| sp P32969 RL9_HUMAN            | 2257.0984 |
| sp Q10589 BST2_HUMAN           | 3034.4731 |
| sp P31327 CPSM_HUMAN           | 3323.6748 |
| sp P31327 CPSM_HUMAN           | 3323.6748 |
| sp Q92598 HS105_HUMAN          | 3019.4352 |
| sp Q92598 HS105_HUMAN          | 3019.4352 |
| sp P07237 PDIA1_HUMAN          | 2877.4549 |
| sp Q12906 ILF3_HUMAN           | 2218.1456 |
| sp Q15149 PLEC_HUMAN           | 2311.1808 |
| sp Q01082 SPTB2_HUMAN          | 2878.3733 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3904.8394 |
| sp P78527 PRKDC_HUMAN          | 3586.6488 |
| sp P78527 PRKDC_HUMAN          | 3586.6488 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp P08238 HS90B_HUMAN,sp Q58FI | 2290.127  |
| sp P78527 PRKDC_HUMAN          | 3586.6488 |
| sp P78527 PRKDC_HUMAN          | 3586.6488 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp P27797 CALR_HUMAN           | 3052.4124 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P14618 KPYM_HUMAN           | 2587.2853 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp P14618 KPYM_HUMAN           | 2587.2853 |
| sp Q01082 SPTB2_HUMAN          | 2437.1121 |
| sp Q01082 SPTB2_HUMAN          | 2437.1121 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3904.8394 |
| sp P14618 KPYM_HUMAN           | 2587.2853 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3904.8394 |
| sp P53396 ACLY_HUMAN           | 1933.9898 |
| sp P46781 RS9_HUMAN            | 2086.0695 |
| sp P09622 DLDH_HUMAN           | 2393.2227 |
| sp P53396 ACLY_HUMAN           | 1933.9898 |
| sp P09622 DLDH_HUMAN           | 2393.2227 |
| sp P29401 TKT_HUMAN            | 3255.4754 |
| sp Q92973 TNPO1_HUMAN          | 1591.7163 |

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| sp P53396 ACLY_HUMAN          | 1933.9898 |
| sp P36871 PGM1_HUMAN          | 3171.3914 |
| sp P09622 DLDH_HUMAN          | 2393.2227 |
| sp P08670 VIME_HUMAN          | 4119.0396 |
| sp P21964 COMT_HUMAN          | 2659.3428 |
| sp P21964 COMT_HUMAN          | 2659.3428 |
| sp P08670 VIME_HUMAN          | 4119.0396 |
| sp P08670 VIME_HUMAN          | 4119.0396 |
| sp P40926 MDHM_HUMAN          | 2930.5026 |
| sp P36871 PGM1_HUMAN          | 3171.3914 |
| sp P40926 MDHM_HUMAN          | 2930.5026 |
| sp P08670 VIME_HUMAN          | 4119.0396 |
| sp O43707 ACTN4_HUMAN         | 2841.3868 |
| sp O76021 RL1D1_HUMAN         | 1912.0346 |
| sp Q13435 SF3B2_HUMAN         | 5289.4666 |
| sp P12814 ACTN1_HUMAN         | 3464.7464 |
| sp Q13435 SF3B2_HUMAN         | 5289.4666 |
| sp Q02790 FKBP4_HUMAN         | 2652.2496 |
| sp P21964 COMT_HUMAN          | 2659.3428 |
| sp P21964 COMT_HUMAN          | 2659.3428 |
| sp P61769 B2MG_HUMAN          | 3483.6041 |
| sp Q7KZF4 SND1_HUMAN          | 2108.0401 |
| sp P21964 COMT_HUMAN          | 2659.3428 |
| sp Q687X5 STEA4_HUMAN         | 3854.9843 |
| sp P21964 COMT_HUMAN          | 2659.3428 |
| sp Q7KZF4 SND1_HUMAN          | 2108.0401 |
| sp P62701 RS4X_HUMAN          | 2335.2689 |
| sp P21964 COMT_HUMAN          | 2659.3428 |
| sp Q7KZF4 SND1_HUMAN          | 2108.0401 |
| sp P62701 RS4X_HUMAN          | 2335.2689 |
| sp Q9Y2V2 CHSP1_HUMAN         | 4270.9859 |
| sp P07900 HS90A_HUMAN         | 2260.1164 |
| sp P07900 HS90A_HUMAN         | 2260.1164 |
| sp P62701 RS4X_HUMAN          | 2335.2689 |
| sp O00148 DX39A_HUMAN,sp Q138 | 4307.9418 |
| sp P31948 STIP1_HUMAN         | 3708.7478 |
| sp Q15185 TEBP_HUMAN          | 3689.6403 |
| sp Q9Y2V2 CHSP1_HUMAN         | 4270.9859 |
| sp P61769 B2MG_HUMAN          | 3483.6041 |
| sp Q01082 SPTB2_HUMAN         | 2298.1202 |
| sp Q01082 SPTB2_HUMAN         | 2298.1202 |
| sp Q9Y2V2 CHSP1_HUMAN         | 4270.9859 |
| sp P78371 TCPB_HUMAN          | 2109.0161 |
| sp Q9Y2V2 CHSP1_HUMAN         | 4270.9859 |
| sp P61769 B2MG_HUMAN          | 3483.6041 |
| sp P04406 G3P_HUMAN           | 5043.3435 |
| sp P04406 G3P_HUMAN           | 5043.3435 |

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| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp Q9P0L0 VAPA_HUMAN           | 2773.288  |
| sp Q9P0L0 VAPA_HUMAN           | 2773.288  |
| sp Q14527 HLTF_HUMAN           | 2600.2448 |
| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp Q13435 SF3B2_HUMAN          | 3232.6074 |
| sp Q9P0L0 VAPA_HUMAN           | 2773.288  |
| sp P78371 TCPB_HUMAN           | 2109.0161 |
| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp P78371 TCPB_HUMAN           | 2109.0161 |
| sp P18206 VINC_HUMAN           | 2026.0695 |
| sp Q9P0L0 VAPA_HUMAN           | 2773.288  |
| sp P78371 TCPB_HUMAN           | 2109.0161 |
| sp Q14258 TRI25_HUMAN          | 2835.5422 |
| sp Q9NTJ3 SMC4_HUMAN           | 2343.207  |
| sp P78371 TCPB_HUMAN           | 2109.0161 |
| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2583.287  |
| sp Q6P2Q9 PRP8_HUMAN           | 2223.1688 |
| sp Q16891 MIC60_HUMAN          | 2862.3454 |
| sp Q6P2Q9 PRP8_HUMAN           | 2223.1688 |
| sp Q16891 MIC60_HUMAN          | 2862.3454 |
| sp Q16891 MIC60_HUMAN          | 2862.3454 |
| sp Q6P2Q9 PRP8_HUMAN           | 2223.1688 |
| sp Q6P2Q9 PRP8_HUMAN           | 2223.1688 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P31327 CPSM_HUMAN           | 2274.2412 |
| sp P78527 PRKDC_HUMAN          | 1978.9822 |
| sp P10809 CH60_HUMAN           | 3904.9153 |
| sp Q8IYD1 ERF3B_HUMAN          | 2890.513  |
| sp Q8IYD1 ERF3B_HUMAN          | 2890.513  |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp O60832 DKC1_HUMAN           | 2461.3693 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp Q8IYD1 ERF3B_HUMAN          | 2890.513  |
| sp Q8IYD1 ERF3B_HUMAN          | 2890.513  |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp O60832 DKC1_HUMAN           | 2461.3693 |
| sp O60832 DKC1_HUMAN           | 2461.3693 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp P50990 TCPQ_HUMAN           | 2494.289  |

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| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp P50990 TCPQ_HUMAN           | 2494.289  |
| sp Q15392 DHC24_HUMAN          | 2282.9943 |
| sp P55265 DSRAD_HUMAN          | 2575.1505 |
| sp P55265 DSRAD_HUMAN          | 2575.1505 |
| sp Q01650 LAT1_HUMAN           | 2457.2726 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp Q15392 DHC24_HUMAN          | 2282.9943 |
| sp P55265 DSRAD_HUMAN          | 2575.1505 |
| sp Q9NVP1 DDX18_HUMAN          | 3317.5155 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P50990 TCPQ_HUMAN           | 2494.289  |
| sp P62841 RS15_HUMAN           | 3364.669  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp O00264 PGRC1_HUMAN          | 4541.0459 |
| sp Q9NVP1 DDX18_HUMAN          | 3317.5155 |
| sp P62841 RS15_HUMAN           | 3364.669  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp O00264 PGRC1_HUMAN          | 4541.0459 |
| sp O00264 PGRC1_HUMAN          | 4541.0459 |
| sp O00264 PGRC1_HUMAN          | 4541.0459 |
| sp O00264 PGRC1_HUMAN          | 4541.0459 |
| sp O00264 PGRC1_HUMAN          | 4541.0459 |
| sp O00264 PGRC1_HUMAN          | 4541.0459 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q86UP2 KTN1_HUMAN           | 2792.3253 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q63HN8 RN213_HUMAN          | 2562.3152 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q86UP2 KTN1_HUMAN           | 2792.3253 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q9Y3I0 RTCB_HUMAN           | 2712.417  |
| sp Q63HN8 RN213_HUMAN          | 2562.3152 |
| sp P30101 PDIA3_HUMAN          | 3262.4983 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P18621 RL17_HUMAN           | 2341.126  |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp O75533 SF3B1_HUMAN          | 1809.9335 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |

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| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P06748 NPM_HUMAN            | 3851.9503 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp O00571 DDX3X_HUMAN          | 3105.5043 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P06748 NPM_HUMAN            | 3851.9503 |
| sp P06748 NPM_HUMAN            | 3851.9503 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp O00571 DDX3X_HUMAN          | 3105.5043 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp O00571 DDX3X_HUMAN          | 3105.5043 |
| sp O00571 DDX3X_HUMAN          | 3105.5043 |
| sp P29401 TKT_HUMAN            | 2973.5659 |
| sp P17812 PYRG1_HUMAN          | 2597.2762 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4674.5347 |
| sp P17812 PYRG1_HUMAN          | 2597.2762 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp P50914 RL14_HUMAN           | 2764.4184 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P50914 RL14_HUMAN           | 2764.4184 |
| sp P50914 RL14_HUMAN           | 2764.4184 |
| sp P41252 SYIC_HUMAN           | 2701.2483 |
| sp P41252 SYIC_HUMAN           | 2701.2483 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp P50914 RL14_HUMAN           | 2764.4184 |
| sp P29401 TKT_HUMAN            | 2973.5659 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P15531 NDKA_HUMAN           | 2626.2672 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P41252 SYIC_HUMAN           | 2701.2483 |
| sp P41252 SYIC_HUMAN           | 2701.2483 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |

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| sp P15531 NDKA_HUMAN           | 2626.2672 |
| sp P29401 TKT_HUMAN            | 2973.5659 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P62081 RS7_HUMAN            | 2719.4069 |
| sp P62081 RS7_HUMAN            | 2719.4069 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P62081 RS7_HUMAN            | 2719.4069 |
| sp P62081 RS7_HUMAN            | 2719.4069 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp P62081 RS7_HUMAN            | 2719.4069 |
| sp P34897 GLYM_HUMAN           | 2773.3415 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp Q99497 PARK7_HUMAN          | 2591.3418 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp Q99497 PARK7_HUMAN          | 2591.3418 |
| sp Q15149 PLEC_HUMAN           | 3067.623  |
| sp Q15149 PLEC_HUMAN           | 3067.623  |
| sp Q99497 PARK7_HUMAN          | 2591.3418 |
| sp Q99497 PARK7_HUMAN          | 2591.3418 |
| sp P62081 RS7_HUMAN            | 3994.9834 |
| sp Q15149 PLEC_HUMAN           | 3067.623  |
| sp Q15149 PLEC_HUMAN           | 3067.623  |
| sp Q99497 PARK7_HUMAN          | 2591.3418 |
| sp Q99497 PARK7_HUMAN          | 2591.3418 |
| sp P30048 PRDX3_HUMAN          | 2669.4177 |
| sp P30048 PRDX3_HUMAN          | 2669.4177 |
| sp P60660 MYL6_HUMAN           | 2326.1668 |
| sp P60660 MYL6_HUMAN           | 2326.1668 |
| sp P30048 PRDX3_HUMAN          | 2669.4177 |
| sp P30048 PRDX3_HUMAN          | 2669.4177 |
| sp P60660 MYL6_HUMAN           | 2326.1668 |
| sp P60660 MYL6_HUMAN           | 2326.1668 |
| sp P60660 MYL6_HUMAN           | 2326.1668 |
| sp P22314 UBA1_HUMAN           | 2805.3908 |
| sp P22314 UBA1_HUMAN           | 2805.3908 |

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| sp P22314 UBA1_HUMAN          | 2805.3908 |
| sp P22314 UBA1_HUMAN          | 2805.3908 |
| sp P22314 UBA1_HUMAN          | 2805.3908 |
| sp P78527 PRKDC_HUMAN         | 2240.2205 |
| sp P78527 PRKDC_HUMAN         | 2240.2205 |
| sp Q63HN8 RN213_HUMAN         | 2730.4381 |
| sp P78527 PRKDC_HUMAN         | 2240.2205 |
| sp P07237 PDIA1_HUMAN         | 2905.4862 |
| sp Q63HN8 RN213_HUMAN         | 2730.4381 |
| sp P78527 PRKDC_HUMAN         | 2240.2205 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 3730.7396 |
| sp P78527 PRKDC_HUMAN         | 2240.2205 |
| sp P07237 PDIA1_HUMAN         | 2905.4862 |
| sp P53396 ACLY_HUMAN          | 2361.3056 |
| sp P78527 PRKDC_HUMAN         | 2240.2205 |
| sp O75643 U520_HUMAN          | 3145.7063 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp P53396 ACLY_HUMAN          | 2361.3056 |
| sp P53396 ACLY_HUMAN          | 2361.3056 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp P49327 FAS_HUMAN           | 2875.3925 |
| sp P49327 FAS_HUMAN           | 2875.3925 |
| sp O75643 U520_HUMAN          | 3145.7063 |
| sp O75643 U520_HUMAN          | 3145.7063 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp P53396 ACLY_HUMAN          | 2361.3056 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp Q9NR30 DDX21_HUMAN         | 2410.2169 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 2038.0371 |
| sp P06576 ATPB_HUMAN          | 2769.42   |
| sp Q6PKG0 LARP1_HUMAN         | 2228.0936 |
| sp P04843 RPN1_HUMAN          | 1960.0266 |
| sp Q6PKG0 LARP1_HUMAN         | 2228.0936 |
| sp Q6PKG0 LARP1_HUMAN         | 2228.0936 |
| sp Q9BSJ8 ESYT1_HUMAN         | 3465.7093 |
| sp Q96AG4 LRC59_HUMAN         | 3026.6805 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 3714.7447 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 3714.7447 |
| sp Q9BQG0 MBB1A_HUMAN         | 2824.5521 |
| sp Q9BQG0 MBB1A_HUMAN         | 2824.5521 |
| sp Q71U36 TBA1A_HUMAN,sp P683 | 3714.7447 |

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| sp Q15437 SC23B_HUMAN          | 2676.3581 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 3714.7447 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp Q15437 SC23B_HUMAN          | 2676.3581 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp Q96AG4 LRC59_HUMAN          | 3026.6805 |
| sp Q15437 SC23B_HUMAN          | 2676.3581 |
| sp Q96AG4 LRC59_HUMAN          | 3026.6805 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp Q96AG4 LRC59_HUMAN          | 3026.6805 |
| sp Q96AG4 LRC59_HUMAN          | 3026.6805 |
| sp P53396 ACLY_HUMAN           | 2697.3538 |
| sp P00558 PGK1_HUMAN           | 2830.4541 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4174.1256 |
| sp P00558 PGK1_HUMAN           | 2830.4541 |
| sp P18124 RL7_HUMAN            | 2506.1872 |
| sp P18124 RL7_HUMAN            | 2506.1872 |
| sp P38919 IF4A3_HUMAN          | 2346.1856 |
| sp P00558 PGK1_HUMAN           | 2830.4541 |
| sp Q9BSJ8 ESYT1_HUMAN          | 3271.6626 |
| sp Q8TEQ6 GEMI5_HUMAN          | 2695.3857 |
| sp Q9BSJ8 ESYT1_HUMAN          | 3271.6626 |
| sp P04083 ANXA1_HUMAN          | 1930.0775 |
| sp O14617 AP3D1_HUMAN          | 2315.0926 |
| sp P04083 ANXA1_HUMAN          | 1930.0775 |
| sp Q16719 KYNU_HUMAN           | 2724.3429 |
| sp Q8TEQ6 GEMI5_HUMAN          | 2695.3857 |
| sp Q9BSJ8 ESYT1_HUMAN          | 3271.6626 |
| sp P04083 ANXA1_HUMAN          | 1930.0775 |
| sp P04083 ANXA1_HUMAN          | 1930.0775 |
| sp Q9BSJ8 ESYT1_HUMAN          | 3271.6626 |
| sp P62491 RB11A_HUMAN,sp Q159I | 2627.3231 |
| sp Q16719 KYNU_HUMAN           | 2724.3429 |
| sp O14617 AP3D1_HUMAN          | 2315.0926 |
| sp P62491 RB11A_HUMAN,sp Q159I | 2627.3231 |
| sp Q92616 GCN1_HUMAN           | 2356.3254 |
| sp P04083 ANXA1_HUMAN          | 1930.0775 |
| sp P62491 RB11A_HUMAN,sp Q159I | 2627.3231 |
| sp Q92616 GCN1_HUMAN           | 2356.3254 |
| sp Q92616 GCN1_HUMAN           | 2356.3254 |
| sp P04083 ANXA1_HUMAN          | 1930.0775 |
| sp P49321 NASP_HUMAN           | 2676.3581 |
| sp P49321 NASP_HUMAN           | 2676.3581 |
| sp P31327 CPSM_HUMAN           | 5734.7605 |
| sp P62491 RB11A_HUMAN,sp Q159I | 2627.3231 |
| sp Q92616 GCN1_HUMAN           | 2356.3254 |
| sp P62491 RB11A_HUMAN,sp Q159I | 2627.3231 |



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| sp A6NMY6 AXA2L_HUMAN,sp P073  | 3050.5812 |
| sp Q92616 GCN1_HUMAN           | 2356.3254 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 3050.5812 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P62491 RB11A_HUMAN,sp Q159i | 2627.3231 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp Q14204 DYHC1_HUMAN          | 3187.703  |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp Q14204 DYHC1_HUMAN          | 3187.703  |
| sp Q14204 DYHC1_HUMAN          | 3187.703  |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp Q14204 DYHC1_HUMAN          | 3187.703  |
| sp Q6UVK1 CSPG4_HUMAN          | 3838.953  |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P09874 PARP1_HUMAN          | 3381.7609 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp Q9NZN4 EHD2_HUMAN           | 3554.6988 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp P14174 MIF_HUMAN            | 6019.9071 |
| sp O94776 MTA2_HUMAN           | 2211.2879 |
| sp O94776 MTA2_HUMAN           | 2211.2879 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp P14174 MIF_HUMAN            | 6019.9071 |
| sp O94776 MTA2_HUMAN           | 2211.2879 |
| sp O94776 MTA2_HUMAN           | 2211.2879 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp O94776 MTA2_HUMAN           | 2211.2879 |
| sp O94776 MTA2_HUMAN           | 2211.2879 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp P14174 MIF_HUMAN            | 6019.9071 |
| sp P14174 MIF_HUMAN            | 6019.9071 |
| sp P52272 HNRPM_HUMAN          | 4881.3744 |
| sp P14174 MIF_HUMAN            | 6019.9071 |

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| sp P14174 MIF_HUMAN           | 6019.9071 |
| sp P14174 MIF_HUMAN           | 6019.9071 |
| sp Q08211 DHX9_HUMAN          | 3151.6554 |
| sp Q08211 DHX9_HUMAN          | 3151.6554 |
| sp Q08211 DHX9_HUMAN          | 3151.6554 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3429.6697 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp Q08211 DHX9_HUMAN          | 3151.6554 |
| sp P14174 MIF_HUMAN           | 6019.9071 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P14174 MIF_HUMAN           | 6019.9071 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P55060 XPO2_HUMAN          | 3157.6441 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P12814 ACTN1_HUMAN         | 3944.8237 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P55060 XPO2_HUMAN          | 3157.6441 |
| sp P14174 MIF_HUMAN           | 6019.9071 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P49327 FAS_HUMAN           | 3666.8134 |
| sp P14174 MIF_HUMAN           | 6019.9071 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P13639 EF2_HUMAN           | 3473.7177 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P14174 MIF_HUMAN           | 6019.9071 |
| sp P49327 FAS_HUMAN           | 3666.8134 |
| sp P13639 EF2_HUMAN           | 3473.7177 |
| sp P14174 MIF_HUMAN           | 6019.9071 |
| sp P13639 EF2_HUMAN           | 3473.7177 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P49327 FAS_HUMAN           | 3666.8134 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp P55060 XPO2_HUMAN          | 3210.6812 |
| sp P55060 XPO2_HUMAN          | 3210.6812 |
| sp P14174 MIF_HUMAN           | 6003.9122 |
| sp Q5VYK3 ECM29_HUMAN         | 2899.5331 |
| sp P55060 XPO2_HUMAN          | 3210.6812 |
| sp Q5VYK3 ECM29_HUMAN         | 2899.5331 |
| sp P55060 XPO2_HUMAN          | 3210.6812 |
| sp Q5VYK3 ECM29_HUMAN         | 2899.5331 |
| sp Q5VYK3 ECM29_HUMAN         | 2899.5331 |
| sp P49321 NASP_HUMAN          | 3257.7118 |
| sp P07195 LDHB_HUMAN          | 3484.7193 |

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| sp P02786 TFR1_HUMAN           | 2866.5018 |
| sp P49321 NASP_HUMAN           | 3257.7118 |
| sp P07195 LDHB_HUMAN           | 3484.7193 |
| sp P02786 TFR1_HUMAN           | 2866.5018 |
| sp P49321 NASP_HUMAN           | 3257.7118 |
| sp P07195 LDHB_HUMAN           | 3484.7193 |
| sp Q9Y5B9 SP16H_HUMAN          | 2763.3643 |
| sp P02786 TFR1_HUMAN           | 2866.5018 |
| sp P49321 NASP_HUMAN           | 3257.7118 |
| sp P07195 LDHB_HUMAN           | 3484.7193 |
| sp P49321 NASP_HUMAN           | 3257.7118 |
| sp O43707 ACTN4_HUMAN          | 4001.8452 |
| sp O43707 ACTN4_HUMAN          | 4001.8452 |
| sp P07195 LDHB_HUMAN           | 3484.7193 |
| sp P02786 TFR1_HUMAN           | 2866.5018 |
| sp P02786 TFR1_HUMAN           | 2866.5018 |
| sp P02786 TFR1_HUMAN           | 2866.5018 |
| sp P02786 TFR1_HUMAN           | 2866.5018 |
| sp P02786 TFR1_HUMAN           | 2866.5018 |
| sp P54819 KAD2_HUMAN           | 3201.5652 |
| sp P54819 KAD2_HUMAN           | 3201.5652 |
| sp O00629 IMA3_HUMAN           | 2708.4207 |
| sp P54819 KAD2_HUMAN           | 3201.5652 |
| sp Q92616 GCN1_HUMAN           | 2351.1427 |
| sp Q92616 GCN1_HUMAN           | 2351.1427 |
| sp Q92616 GCN1_HUMAN           | 2351.1427 |
| sp Q92616 GCN1_HUMAN           | 2351.1427 |
| sp Q92616 GCN1_HUMAN           | 2351.1427 |
| sp Q92616 GCN1_HUMAN           | 2351.1427 |
| sp P31949 S10AB_HUMAN          | 4363.0777 |
| sp Q6YHK3 CD109_HUMAN          | 3212.6717 |
| sp Q6YHK3 CD109_HUMAN          | 3212.6717 |
| sp Q6YHK3 CD109_HUMAN          | 3212.6717 |
| sp O43175 SERA_HUMAN           | 3733.9138 |
| sp O43175 SERA_HUMAN           | 3733.9138 |
| sp O43175 SERA_HUMAN           | 3733.9138 |
| sp Q6YHK3 CD109_HUMAN          | 3212.6717 |
| sp Q6YHK3 CD109_HUMAN          | 3212.6717 |
| sp O43175 SERA_HUMAN           | 3733.9138 |
| sp O43175 SERA_HUMAN           | 3733.9138 |
| sp Q6YHK3 CD109_HUMAN          | 3212.6717 |
| sp P40227 TCPZ_HUMAN           | 2530.353  |
| sp P04406 G3P_HUMAN            | 4606.287  |
| sp P50395 GDIB_HUMAN           | 3172.7271 |
| sp P50395 GDIB_HUMAN           | 3172.7271 |
| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |

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| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P04406 G3P_HUMAN            | 5043.3435 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp Q14181 DPOA2_HUMAN          | 1579.6434 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp P51397 DAP1_HUMAN           | 1942.9385 |
| sp Q13444 ADA15_HUMAN          | 1709.6635 |
| sp O15355 PPM1G_HUMAN          | 1705.7267 |
| sp O15355 PPM1G_HUMAN          | 1705.7267 |
| sp O15355 PPM1G_HUMAN          | 1705.7267 |
| sp Q14061 COX17_HUMAN          | 1912.8845 |
| sp Q14061 COX17_HUMAN          | 1912.8845 |
| sp Q14061 COX17_HUMAN          | 1912.8845 |
| sp Q02241 KIF23_HUMAN          | 2027.9562 |
| sp Q8NEY8 PPHLN_HUMAN          | 1687.7339 |
| sp Q8NEY8 PPHLN_HUMAN          | 1687.7339 |
| sp Q15125 EBP_HUMAN            | 1817.8908 |
| sp Q15125 EBP_HUMAN            | 1817.8908 |
| sp Q15125 EBP_HUMAN            | 1817.8908 |
| sp Q9NWH9 SLTM_HUMAN           | 2174.9406 |
| sp Q9NWH9 SLTM_HUMAN           | 2174.9406 |
| sp Q9NWH9 SLTM_HUMAN           | 2174.9406 |
| sp Q9NWH9 SLTM_HUMAN           | 2174.9406 |
| sp Q9NWH9 SLTM_HUMAN           | 2174.9406 |
| sp Q9NWH9 SLTM_HUMAN           | 2174.9406 |
| sp Q7Z2W4 ZCCHV_HUMAN          | 2087.8976 |
| sp Q15061 WDR43_HUMAN          | 1815.85   |
| sp Q15061 WDR43_HUMAN          | 1815.85   |
| sp Q15061 WDR43_HUMAN          | 1815.85   |
| sp Q15061 WDR43_HUMAN          | 1815.85   |
| sp Q15061 WDR43_HUMAN          | 1815.85   |
| sp Q15061 WDR43_HUMAN          | 1815.85   |
| sp P20839 IMDH1_HUMAN          | 2296.0542 |
| sp P20839 IMDH1_HUMAN          | 2296.0542 |
| sp Q9Y4W6 AFG32_HUMAN          | 2248.0509 |
| sp Q8NI27 THOC2_HUMAN          | 2311.0903 |
| sp Q8NI27 THOC2_HUMAN          | 2311.0903 |

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| sp P49755 TMEDA_HUMAN        | 1965.9796 |
| sp P49755 TMEDA_HUMAN        | 1965.9796 |
| sp P49755 TMEDA_HUMAN        | 1965.9796 |
| sp P49755 TMEDA_HUMAN        | 1965.9796 |
| sp P49755 TMEDA_HUMAN        | 1965.9796 |
| sp Q14677 EPN4_HUMAN         | 2567.1677 |
| sp Q9H8Y5 ANKZ1_HUMAN        | 2146.0695 |
| sp Q13547 HDAC1_HUMAN        | 2397.1826 |
| sp P11142 HSP7C_HUMAN        | 1603.7453 |
| sp P33176 KINH_HUMAN         | 2315.0675 |
| sp P11498 PYC_HUMAN          | 2218.1495 |
| sp P11498 PYC_HUMAN          | 2218.1495 |
| sp P11142 HSP7C_HUMAN        | 1603.7453 |
| sp Q14697 GANAB_HUMAN        | 2106.111  |
| sp P11142 HSP7C_HUMAN        | 1587.7504 |
| sp O43157 PLXB1_HUMAN        | 2596.1983 |
| sp O43157 PLXB1_HUMAN        | 2596.1983 |
| sp Q9ULW0 TPX2_HUMAN         | 2486.3057 |
| sp E9PAV3 NACAM_HUMAN,sp Q13 | 2089.1459 |
| sp E9PAV3 NACAM_HUMAN,sp Q13 | 2089.1459 |
| sp P08195 4F2_HUMAN          | 2051.9854 |
| sp O95292 VAPB_HUMAN         | 2544.2609 |
| sp O95292 VAPB_HUMAN         | 2544.2609 |
| sp Q96ER9 MITOK_HUMAN        | 2335.1404 |
| sp Q96ER9 MITOK_HUMAN        | 2335.1404 |
| sp Q96ER9 MITOK_HUMAN        | 2335.1404 |
| sp Q14203 DCTN1_HUMAN        | 3234.6673 |
| sp P00505 AATM_HUMAN         | 2221.0956 |
| sp P00505 AATM_HUMAN         | 2221.0956 |
| sp P12277 KCRB_HUMAN         | 3650.6988 |
| sp P49915 GUAA_HUMAN         | 3236.6176 |
| sp O60568 PLOD3_HUMAN        | 2593.1662 |
| sp Q96FW1 OTUB1_HUMAN        | 2372.1285 |
| sp O43169 CYB5B_HUMAN        | 1760.921  |
| sp O43169 CYB5B_HUMAN        | 1760.921  |
| sp O43169 CYB5B_HUMAN        | 1760.921  |
| sp O43169 CYB5B_HUMAN        | 1760.921  |
| sp P32004 L1CAM_HUMAN        | 3975.9544 |
| sp O43169 CYB5B_HUMAN        | 1760.921  |
| sp P42126 ECI1_HUMAN         | 2371.1386 |
| sp P42126 ECI1_HUMAN         | 2371.1386 |
| sp P42126 ECI1_HUMAN         | 2371.1386 |
| sp P42892 ECE1_HUMAN         | 3104.4952 |
| sp P42892 ECE1_HUMAN         | 3104.4952 |
| sp P42892 ECE1_HUMAN         | 3104.4952 |
| sp P31930 QCR1_HUMAN         | 4639.2839 |
| sp P31930 QCR1_HUMAN         | 4639.2839 |

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| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P62910 RL32_HUMAN           | 2282.1439 |
| sp Q8NE71 ABCF1_HUMAN          | 2277.2039 |
| sp Q01518 CAP1_HUMAN           | 3306.6747 |
| sp Q01518 CAP1_HUMAN           | 3306.6747 |
| sp P11498 PYC_HUMAN            | 4836.4188 |
| sp A6ZKI3 RTL8C_HUMAN          | 2069.2361 |
| sp P21926 CD9_HUMAN            | 4149.985  |
| sp Q14527 HLTF_HUMAN           | 3298.7085 |
| sp Q96F86 EDC3_HUMAN           | 4078.1164 |
| sp Q96F86 EDC3_HUMAN           | 4078.1164 |
| sp Q96KA5 CLP1L_HUMAN          | 2795.468  |
| sp Q96KA5 CLP1L_HUMAN          | 2795.468  |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp P11498 PYC_HUMAN            | 4521.0747 |
| sp Q96MU7 YTDC1_HUMAN          | 2280.14   |
| sp Q96KB5 TOPK_HUMAN           | 1842.9741 |
| sp Q96KB5 TOPK_HUMAN           | 1842.9741 |
| sp Q9NXW2 DJB12_HUMAN          | 2388.1862 |
| sp P48637 GSHB_HUMAN           | 1713.8985 |
| sp P48637 GSHB_HUMAN           | 1713.8985 |
| sp Q8NE71 ABCF1_HUMAN          | 2407.159  |
| sp Q8NE71 ABCF1_HUMAN          | 2407.159  |
| sp Q13505 MTX1_HUMAN           | 2220.1651 |
| sp Q13505 MTX1_HUMAN           | 2220.1651 |
| sp P62873 GBB1_HUMAN,sp P62873 | 2038.9319 |
| sp Q9UBQ5 EIF3K_HUMAN          | 2182.063  |
| sp P54136 SYRC_HUMAN           | 1926.984  |
| sp Q9UBQ5 EIF3K_HUMAN          | 2182.063  |
| sp Q9UBQ5 EIF3K_HUMAN          | 2182.063  |
| sp Q71UI9 H2AV_HUMAN,sp POCOS! | 2065.132  |
| sp Q9H0A0 NAT10_HUMAN          | 2200.1674 |
| sp Q71UI9 H2AV_HUMAN,sp POCOS! | 2065.132  |
| sp Q16832 DDR2_HUMAN           | 2344.0695 |
| sp P11413 G6PD_HUMAN           | 2295.0491 |
| sp P11413 G6PD_HUMAN           | 2295.0491 |
| sp Q16832 DDR2_HUMAN           | 2344.0695 |
| sp Q16832 DDR2_HUMAN           | 2344.0695 |
| sp P78344 IF4G2_HUMAN          | 1914.9873 |
| sp O75880 SCO1_HUMAN           | 2314.1706 |

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| sp O75880 SCO1_HUMAN           | 2314.1706 |
| sp Q13501 SQSTM_HUMAN          | 2592.2146 |
| sp Q13501 SQSTM_HUMAN          | 2592.2146 |
| sp O75880 SCO1_HUMAN           | 2314.1706 |
| sp Q13501 SQSTM_HUMAN          | 2592.2146 |
| sp P54136 SYRC_HUMAN           | 2445.2111 |
| sp P54136 SYRC_HUMAN           | 2445.2111 |
| sp P78417 GSTO1_HUMAN          | 2352.1903 |
| sp P78417 GSTO1_HUMAN          | 2352.1903 |
| sp Q8NCW5 NNRE_HUMAN           | 3568.8065 |
| sp O75844 FACE1_HUMAN          | 2662.3504 |
| sp Q7L2H7 EIF3M_HUMAN          | 2476.3366 |
| sp Q7L2H7 EIF3M_HUMAN          | 2476.3366 |
| sp Q7L2H7 EIF3M_HUMAN          | 2476.3366 |
| sp Q7L2H7 EIF3M_HUMAN          | 2476.3366 |
| sp Q14160 SCRIB_HUMAN          | 3694.8744 |
| sp P28482 MK01_HUMAN           | 3640.8308 |
| sp P28482 MK01_HUMAN           | 3640.8308 |
| sp P28482 MK01_HUMAN           | 3640.8308 |
| sp Q13421 MSLN_HUMAN           | 2992.6597 |
| sp Q12905 ILF2_HUMAN           | 2539.401  |
| sp Q12905 ILF2_HUMAN           | 2539.401  |
| sp P51659 DHB4_HUMAN           | 4166.9949 |
| sp P51659 DHB4_HUMAN           | 4166.9949 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp Q9C005 DPY30_HUMAN          | 2325.2005 |
| sp O96008 TOM40_HUMAN          | 2167.2154 |
| sp O96008 TOM40_HUMAN          | 2167.2154 |
| sp O96008 TOM40_HUMAN          | 2167.2154 |
| sp O96008 TOM40_HUMAN          | 2167.2154 |
| sp P99999 CYC_HUMAN            | 1752.7955 |
| sp P10599 THIO_HUMAN           | 1361.6099 |
| sp P10599 THIO_HUMAN           | 1361.6099 |
| sp P47914 RL29_HUMAN           | 1729.8747 |
| sp P47914 RL29_HUMAN           | 1729.8747 |
| sp Q15424 SAFB1_HUMAN,sp Q141! | 1309.699  |
| sp P06493 CDK1_HUMAN           | 1594.7627 |
| sp Q96AE4 FUBP1_HUMAN          | 2479.1649 |
| sp Q96AE4 FUBP1_HUMAN          | 2479.1649 |
| sp Q15366 PCBP2_HUMAN          | 2026.9816 |
| sp Q14974 IMB1_HUMAN           | 1625.8625 |
| sp P60981 DEST_HUMAN           | 1875.8163 |
| sp Q8TEM1 PO210_HUMAN          | 1851.8428 |
| sp P55769 NH2L1_HUMAN          | 1804.8665 |
| sp P06703 S10A6_HUMAN          | 1839.9214 |
| sp P33316 DUT_HUMAN            | 2144.0572 |
| sp P08865 RSSA_HUMAN           | 1487.762  |

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| sp O75054 IGSF3_HUMAN          | 2179.948  |
| sp Q16658 FSCN1_HUMAN          | 2565.217  |
| sp Q9H0U4 RAB1B_HUMAN,sp Q925  | 1854.9112 |
| sp Q16658 FSCN1_HUMAN          | 2565.217  |
| sp P62913 RL11_HUMAN           | 2013.0419 |
| sp P00387 NB5R3_HUMAN          | 2097.063  |
| sp P09496 CLCA_HUMAN           | 1600.8825 |
| sp P09496 CLCA_HUMAN           | 1600.8825 |
| sp Q5ZPR3 CD276_HUMAN          | 2904.3851 |
| sp Q5ZPR3 CD276_HUMAN          | 2904.3851 |
| sp P42285 MTREX_HUMAN          | 2131.1201 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp Q16658 FSCN1_HUMAN          | 2871.3709 |
| sp Q03405 UPAR_HUMAN           | 2888.3644 |
| sp Q9UJX3 APC7_HUMAN           | 2276.2488 |
| sp Q9UJX3 APC7_HUMAN           | 2276.2488 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P13804 ETFA_HUMAN           | 2380.2526 |
| sp O75874 IDHC_HUMAN           | 2641.2119 |
| sp Q99714 HCD2_HUMAN           | 2323.2383 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P49368 TCPG_HUMAN           | 2015.0939 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P14384 CBPM_HUMAN           | 3394.6941 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P46060 RAGP1_HUMAN          | 3868.9775 |
| sp P19075 TSN8_HUMAN           | 2967.439  |
| sp P19075 TSN8_HUMAN           | 2967.439  |
| sp P19075 TSN8_HUMAN           | 2967.439  |
| sp P49915 GUAA_HUMAN           | 3440.8119 |
| sp P49915 GUAA_HUMAN           | 3440.8119 |
| sp P49748 ACADV_HUMAN          | 3887.9105 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 3062.5156 |
| sp P05787 K2C8_HUMAN           | 2577.1905 |
| sp P63104 1433Z_HUMAN          | 2958.3328 |
| sp Q9Y3T9 NOC2L_HUMAN          | 3685.0165 |
| sp P51659 DHB4_HUMAN           | 1935.8857 |
| sp Q9NYF8 BCLF1_HUMAN          | 1880.8177 |
| sp P62913 RL11_HUMAN           | 1522.7198 |
| sp O95373 IPO7_HUMAN           | 1951.8946 |
| sp O95373 IPO7_HUMAN           | 1951.8946 |
| sp Q15046 SYK_HUMAN            | 1733.8117 |
| sp Q15046 SYK_HUMAN            | 1733.8117 |
| sp Q9BUJ2 HNRL1_HUMAN          | 1968.9463 |
| sp Q16658 FSCN1_HUMAN          | 2478.1663 |
| sp Q16658 FSCN1_HUMAN          | 2478.1663 |
| sp P21291 CSRP1_HUMAN          | 2800.3192 |



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| sp P21291 CSRP1_HUMAN          | 2800.3192 |
| sp Q16658 FSCN1_HUMAN          | 2478.1663 |
| sp P21291 CSRP1_HUMAN          | 2800.3192 |
| sp Q9H0D6 XRN2_HUMAN           | 2431.1768 |
| sp Q15041 AR6P1_HUMAN          | 1918.881  |
| sp Q15041 AR6P1_HUMAN          | 1918.881  |
| sp P54819 KAD2_HUMAN           | 1785.9373 |
| sp P04080 CYTB_HUMAN           | 2654.2976 |
| sp P15151 PVR_HUMAN            | 2900.5066 |
| sp P15151 PVR_HUMAN            | 2900.5066 |
| sp P15151 PVR_HUMAN            | 2900.5066 |
| sp P15151 PVR_HUMAN            | 2900.5066 |
| sp P15151 PVR_HUMAN            | 2900.5066 |
| sp P15151 PVR_HUMAN            | 2900.5066 |
| sp Q9Y224 RTRAF_HUMAN          | 2694.1656 |
| sp P08754 GNAI3_HUMAN,sp P0947 | 1803.9043 |
| sp Q99497 PARK7_HUMAN          | 2223.1318 |
| sp Q99497 PARK7_HUMAN          | 2223.1318 |
| sp Q8WXF1 PSPC1_HUMAN          | 1485.7252 |
| sp P00367 DHE3_HUMAN           | 2360.0954 |
| sp P00367 DHE3_HUMAN           | 2360.0954 |
| sp P00367 DHE3_HUMAN           | 2360.0954 |
| sp P00367 DHE3_HUMAN           | 2360.0954 |
| sp P60228 EIF3E_HUMAN          | 2822.3909 |
| sp P60228 EIF3E_HUMAN          | 2822.3909 |
| sp Q9NZ45 CISD1_HUMAN          | 2139.9419 |
| sp O00264 PGRC1_HUMAN          | 1840.842  |
| sp O00264 PGRC1_HUMAN          | 1840.842  |
| sp A1L0T0 ILVBL_HUMAN          | 3232.4917 |
| sp O75794 CD123_HUMAN          | 1701.7821 |
| sp E9PAV3 NACAM_HUMAN,sp Q13   | 1961.051  |
| sp Q9H0X4 F234A_HUMAN          | 3014.3613 |
| sp O75794 CD123_HUMAN          | 1701.7821 |
| sp O75794 CD123_HUMAN          | 1701.7821 |
| sp O14817 TSN4_HUMAN           | 3867.6314 |
| sp Q9H0X4 F234A_HUMAN          | 3014.3613 |
| sp O14817 TSN4_HUMAN           | 3867.6314 |
| sp O14817 TSN4_HUMAN           | 3867.6314 |
| sp P60903 S10AA_HUMAN          | 2743.3415 |
| sp P60903 S10AA_HUMAN          | 2743.3415 |
| sp P60903 S10AA_HUMAN          | 2743.3415 |
| sp P60903 S10AA_HUMAN          | 2743.3415 |
| sp O60313 OPA1_HUMAN           | 2338.123  |
| sp O60313 OPA1_HUMAN           | 2338.123  |
| sp P08865 RSSA_HUMAN           | 1396.7351 |
| sp O60313 OPA1_HUMAN           | 2338.123  |

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| sp P61978 HNRPK_HUMAN | 1749.9513 |
| sp Q10589 BST2_HUMAN  | 2906.3781 |
| sp Q10589 BST2_HUMAN  | 2906.3781 |
| sp P22626 ROA2_HUMAN  | 2123.0423 |
| sp Q10589 BST2_HUMAN  | 2906.3781 |
| sp P22626 ROA2_HUMAN  | 2123.0423 |
| sp P62424 RL7A_HUMAN  | 2007.0425 |
| sp P22626 ROA2_HUMAN  | 2123.0423 |
| sp Q14683 SMC1A_HUMAN | 2189.0827 |
| sp P35613 BASI_HUMAN  | 4216.8783 |
| sp Q9H9B4 SFXN1_HUMAN | 2866.3655 |
| sp Q9P289 STK26_HUMAN | 2309.2307 |
| sp P18206 VINC_HUMAN  | 1869.9684 |
| sp O95163 ELP1_HUMAN  | 4898.4291 |
| sp O95163 ELP1_HUMAN  | 4898.4291 |
| sp Q8NF37 PCAT1_HUMAN | 2677.4302 |
| sp Q96CN7 ISOC1_HUMAN | 2644.396  |
| sp Q96CN7 ISOC1_HUMAN | 2644.396  |
| sp Q96CN7 ISOC1_HUMAN | 2644.396  |
| sp Q8IY81 SPB1_HUMAN  | 3708.7101 |
| sp P08195 4F2_HUMAN   | 2374.1594 |
| sp O75608 LYPA1_HUMAN | 3381.6295 |
| sp O75608 LYPA1_HUMAN | 3381.6295 |
| sp O75608 LYPA1_HUMAN | 3381.6295 |
| sp P18206 VINC_HUMAN  | 4916.3008 |
| sp Q15043 S39AE_HUMAN | 2892.4618 |
| sp Q15043 S39AE_HUMAN | 2892.4618 |
| sp Q13421 MSLN_HUMAN  | 5706.6658 |
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| sp Q15043 S39AE_HUMAN | 2892.4618 |
| sp Q15043 S39AE_HUMAN | 2892.4618 |
| sp Q15043 S39AE_HUMAN | 2892.4618 |
| sp Q15043 S39AE_HUMAN | 2892.4618 |
| sp Q15043 S39AE_HUMAN | 2892.4618 |
| sp P60033 CD81_HUMAN  | 4497.1138 |
| sp Q9HAV4 XPO5_HUMAN  | 1720.9764 |
| sp Q9BQ39 DDX50_HUMAN | 2919.4614 |
| sp Q9HAV4 XPO5_HUMAN  | 1720.9764 |
| sp P08195 4F2_HUMAN   | 2374.1594 |
| sp Q9NXF1 TEX10_HUMAN | 1877.0775 |
| sp P30040 ERP29_HUMAN | 3206.5569 |
| sp P08195 4F2_HUMAN   | 2374.1594 |
| sp P02786 TFR1_HUMAN  | 2997.472  |
| sp Q12849 GRSF1_HUMAN | 2652.37   |
| sp Q12849 GRSF1_HUMAN | 2652.37   |
| sp Q8TEX9 IPO4_HUMAN  | 2570.3778 |
| sp Q8TEX9 IPO4_HUMAN  | 2570.3778 |

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| sp Q8TEX9 IPO4_HUMAN           | 2570.3778 |
| sp Q8TEX9 IPO4_HUMAN           | 2570.3778 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp P11441 UBL4A_HUMAN          | 2314.2321 |
| sp P11441 UBL4A_HUMAN          | 2314.2321 |
| sp P11441 UBL4A_HUMAN          | 2314.2321 |
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| sp P11441 UBL4A_HUMAN          | 2314.2321 |
| sp Q15393 SF3B3_HUMAN          | 2784.4851 |
| sp P42166 LAP2A_HUMAN          | 4200.0434 |
| sp Q8TCS8 PNPT1_HUMAN          | 2302.2607 |
| sp Q9Y3I0 RTCB_HUMAN           | 2343.1417 |
| sp Q9Y3I0 RTCB_HUMAN           | 2343.1417 |
| sp Q99714 HCD2_HUMAN           | 3899.9842 |
| sp Q99714 HCD2_HUMAN           | 3899.9842 |
| sp Q99714 HCD2_HUMAN           | 3899.9842 |
| sp Q99714 HCD2_HUMAN           | 3899.9842 |
| sp P04632 CPNS1_HUMAN          | 3174.5577 |
| sp P04632 CPNS1_HUMAN          | 3174.5577 |
| sp Q13442 HAP28_HUMAN          | 1409.6609 |
| sp Q13442 HAP28_HUMAN          | 1409.6609 |
| sp Q96GM5 SMRD1_HUMAN          | 2441.2524 |
| sp Q96GM5 SMRD1_HUMAN          | 2441.2524 |
| sp Q96GM5 SMRD1_HUMAN          | 2441.2524 |
| sp Q96GM5 SMRD1_HUMAN          | 2441.2524 |
| sp O15042 SR140_HUMAN          | 1881.8969 |
| sp P62633 CNBP_HUMAN           | 2780.0537 |
| sp O15042 SR140_HUMAN          | 1881.8969 |
| sp O15042 SR140_HUMAN          | 1881.8969 |
| sp P62633 CNBP_HUMAN           | 2780.0537 |
| sp Q9NV96 CC50A_HUMAN          | 1487.7369 |
| sp Q9UIW2 PLXA1_HUMAN          | 3886.7163 |
| sp Q9NV96 CC50A_HUMAN          | 1487.7369 |
| sp Q9NV96 CC50A_HUMAN          | 1487.7369 |
| sp Q9BUJ2 HNRL1_HUMAN          | 1707.8216 |
| sp Q9UIW2 PLXA1_HUMAN          | 3886.7163 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp Q9BWF3 RBM4_HUMAN           | 2034.9793 |
| sp Q15459 SF3A1_HUMAN          | 2909.3138 |
| sp P08237 PFKAM_HUMAN          | 2164.996  |
| sp P08237 PFKAM_HUMAN          | 2164.996  |
| sp P05161 ISG15_HUMAN          | 1920.9806 |
| sp Q96CS3 FAF2_HUMAN           | 2362.0978 |
| sp Q96DI7 SNR40_HUMAN          | 1915.8887 |
| sp Q96CS3 FAF2_HUMAN           | 2362.0978 |
| sp Q8IZL8 PELP1_HUMAN          | 2077.044  |
| sp O43819 SCO2_HUMAN           | 2213.1077 |

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| sp O43819 SCO2_HUMAN           | 2213.1077 |
| sp O43819 SCO2_HUMAN           | 2213.1077 |
| sp O43819 SCO2_HUMAN           | 2213.1077 |
| sp Q8IZL8 PELP1_HUMAN          | 2077.044  |
| sp Q8IZL8 PELP1_HUMAN          | 2077.044  |
| sp Q15262 PTPRK_HUMAN          | 1575.7794 |
| sp Q15691 MARE1_HUMAN          | 1990.9425 |
| sp Q15691 MARE1_HUMAN          | 1990.9425 |
| sp Q9BPX3 CND3_HUMAN           | 2197.1604 |
| sp Q01518 CAP1_HUMAN           | 2025.9796 |
| sp Q9BPX3 CND3_HUMAN           | 2197.1604 |
| sp Q01518 CAP1_HUMAN           | 2025.9796 |
| sp Q14527 HLTF_HUMAN           | 1910.9374 |
| sp Q9BPX3 CND3_HUMAN           | 2197.1604 |
| sp P46776 RL27A_HUMAN          | 1781.8049 |
| sp P46776 RL27A_HUMAN          | 1781.8049 |
| sp P46776 RL27A_HUMAN          | 1781.8049 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp O75153 CLU_HUMAN            | 2491.1557 |
| sp P08754 GNAI3_HUMAN,sp P0947 | 1803.9043 |
| sp O75153 CLU_HUMAN            | 2491.1557 |
| sp Q8WTT2 NOC3L_HUMAN          | 2475.2394 |
| sp P12277 KCRB_HUMAN           | 1442.7882 |
| sp Q8WTT2 NOC3L_HUMAN          | 2475.2394 |
| sp Q8WTT2 NOC3L_HUMAN          | 2475.2394 |
| sp P12277 KCRB_HUMAN           | 1442.7882 |
| sp Q8WTT2 NOC3L_HUMAN          | 2475.2394 |
| sp Q92769 HDAC2_HUMAN          | 1666.7627 |
| sp P08865 RSSA_HUMAN           | 1615.857  |
| sp P08865 RSSA_HUMAN           | 1615.857  |
| sp P00390 GSHR_HUMAN           | 2336.2125 |
| sp P00390 GSHR_HUMAN           | 2336.2125 |
| sp P00390 GSHR_HUMAN           | 2336.2125 |
| sp Q9UMR2 DD19B_HUMAN,sp Q9N   | 2195.0463 |
| sp Q9UMR2 DD19B_HUMAN,sp Q9N   | 2195.0463 |
| sp P15170 ERF3A_HUMAN,sp Q8IYD | 1601.9141 |
| sp P32320 CDD_HUMAN            | 2811.3354 |
| sp P32320 CDD_HUMAN            | 2811.3354 |
| sp P30048 PRDX3_HUMAN          | 3921.8884 |
| sp Q8IYB8 SUV3_HUMAN           | 2951.3971 |
| sp Q9Y285 SYFA_HUMAN           | 2454.1672 |
| sp Q9Y285 SYFA_HUMAN           | 2454.1672 |
| sp Q9Y285 SYFA_HUMAN           | 2454.1672 |
| sp P04040 CATA_HUMAN           | 2287.0433 |
| sp Q07955 SRSF1_HUMAN          | 2404.1481 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp Q99460 PSMD1_HUMAN          | 2112.064  |

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| sp Q14318 FKBP8_HUMAN          | 2323.1267 |
| sp P35221 CTNA1_HUMAN          | 2453.171  |
| sp Q14318 FKBP8_HUMAN          | 2323.1267 |
| sp P52907 CAZA1_HUMAN          | 2668.2922 |
| sp P52907 CAZA1_HUMAN          | 2668.2922 |
| sp Q86YQ8 CPNE8_HUMAN          | 2607.3445 |
| sp Q86YQ8 CPNE8_HUMAN          | 2607.3445 |
| sp Q86YQ8 CPNE8_HUMAN          | 2607.3445 |
| sp O95834 EMAL2_HUMAN          | 2777.2578 |
| sp Q15631 TSN_HUMAN            | 2516.3023 |
| sp Q8NBU5 ATAD1_HUMAN          | 2932.2855 |
| sp Q8NBU5 ATAD1_HUMAN          | 2932.2855 |
| sp Q15631 TSN_HUMAN            | 2516.3023 |
| sp Q8NBU5 ATAD1_HUMAN          | 2932.2855 |
| sp Q8NBU5 ATAD1_HUMAN          | 2932.2855 |
| sp Q3ZCQ8 TIM50_HUMAN          | 2412.1598 |
| sp Q99459 CDC5L_HUMAN          | 2460.138  |
| sp A0AVT1 UBA6_HUMAN           | 2018.0684 |
| sp P13693 TCTP_HUMAN           | 2177.9939 |
| sp P13693 TCTP_HUMAN           | 2177.9939 |
| sp P62873 GBB1_HUMAN,sp P62873 | 2336.2165 |
| sp A0AVT1 UBA6_HUMAN           | 2018.0684 |
| sp P32969 RL9_HUMAN            | 1922.9738 |
| sp P13693 TCTP_HUMAN           | 2177.9939 |
| sp P13693 TCTP_HUMAN           | 2177.9939 |
| sp Q9H0B6 KLC2_HUMAN,sp Q0786  | 2219.1335 |
| sp Q9H0B6 KLC2_HUMAN,sp Q0786  | 2219.1335 |
| sp Q9H0B6 KLC2_HUMAN,sp Q0786  | 2219.1335 |
| sp Q3ZCQ8 TIM50_HUMAN          | 2412.1598 |
| sp Q9H0B6 KLC2_HUMAN,sp Q0786  | 2219.1335 |
| sp Q96KP4 CNDP2_HUMAN          | 2640.3184 |
| sp Q3ZCQ8 TIM50_HUMAN          | 2412.1598 |
| sp Q3ZCQ8 TIM50_HUMAN          | 2412.1598 |
| sp Q9HCS7 SYF1_HUMAN           | 2024.9803 |
| sp Q99797 MIPEP_HUMAN          | 2192.0902 |
| sp Q969G5 CAVN3_HUMAN          | 2152.0396 |
| sp Q15369 ELOC_HUMAN           | 3444.5892 |
| sp Q15369 ELOC_HUMAN           | 3444.5892 |
| sp Q99797 MIPEP_HUMAN          | 2192.0902 |
| sp Q7L5N1 CSN6_HUMAN           | 2723.3806 |
| sp Q7L5N1 CSN6_HUMAN           | 2723.3806 |
| sp Q15369 ELOC_HUMAN           | 2298.0701 |
| sp Q15005 SPCS2_HUMAN          | 2809.2905 |
| sp Q15005 SPCS2_HUMAN          | 2809.2905 |
| sp Q15005 SPCS2_HUMAN          | 2809.2905 |
| sp Q9UNS2 CSN3_HUMAN           | 3087.4938 |
| sp O75396 SC22B_HUMAN          | 2598.3006 |

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| sp Q9UNS2 CSN3_HUMAN  | 3087.4938 |
| sp Q9UNS2 CSN3_HUMAN  | 3087.4938 |
| sp Q14114 LRP8_HUMAN  | 2618.2401 |
| sp Q9UNS2 CSN3_HUMAN  | 3087.4938 |
| sp Q14114 LRP8_HUMAN  | 2618.2401 |
| sp P62316 SMD2_HUMAN  | 2440.0861 |
| sp P62316 SMD2_HUMAN  | 2440.0861 |
| sp P62316 SMD2_HUMAN  | 2440.0861 |
| sp O43159 RRP8_HUMAN  | 2382.1532 |
| sp O43159 RRP8_HUMAN  | 2382.1532 |
| sp Q15019 SEPT2_HUMAN | 2750.334  |
| sp Q9Y221 NIP7_HUMAN  | 2483.2155 |
| sp O43159 RRP8_HUMAN  | 2382.1532 |
| sp Q9Y221 NIP7_HUMAN  | 2483.2155 |
| sp P61019 RAB2A_HUMAN | 3034.423  |
| sp P61019 RAB2A_HUMAN | 3034.423  |
| sp P61019 RAB2A_HUMAN | 3034.423  |
| sp P61019 RAB2A_HUMAN | 3034.423  |
| sp P68036 UB2L3_HUMAN | 2475.2726 |
| sp Q13228 SBP1_HUMAN  | 2370.2795 |
| sp Q13228 SBP1_HUMAN  | 2370.2795 |
| sp P43686 PRS6B_HUMAN | 2761.3963 |
| sp P43686 PRS6B_HUMAN | 2761.3963 |
| sp P62937 PPIA_HUMAN  | 3816.7512 |
| sp P31937 3HIDH_HUMAN | 2590.2236 |
| sp Q96C36 P5CR2_HUMAN | 3148.6227 |
| sp P21399 ACOC_HUMAN  | 3105.5407 |
| sp P49720 PSB3_HUMAN  | 2006.9983 |
| sp O15294 OGT1_HUMAN  | 3145.572  |
| sp O15294 OGT1_HUMAN  | 3145.572  |
| sp P24928 RPB1_HUMAN  | 2760.3566 |
| sp O00566 MPP10_HUMAN | 2851.4062 |
| sp P20839 IMDH1_HUMAN | 2824.3966 |
| sp P20839 IMDH1_HUMAN | 2824.3966 |
| sp Q9UIW2 PLXA1_HUMAN | 3066.5047 |
| sp Q9UKX7 NUP50_HUMAN | 2606.2839 |
| sp Q9UKX7 NUP50_HUMAN | 2606.2839 |
| sp Q14114 LRP8_HUMAN  | 2648.301  |
| sp Q9UKX7 NUP50_HUMAN | 2606.2839 |
| sp Q14114 LRP8_HUMAN  | 2648.301  |
| sp Q9BR76 COR1B_HUMAN | 3182.4873 |
| sp Q9UKX7 NUP50_HUMAN | 2606.2839 |
| sp Q9BR76 COR1B_HUMAN | 3182.4873 |
| sp Q12907 LMAN2_HUMAN | 3645.7264 |
| sp Q12907 LMAN2_HUMAN | 3645.7264 |
| sp O95336 6PGL_HUMAN  | 3827.8465 |
| sp Q9UKG1 DP13A_HUMAN | 2693.3297 |

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| sp O95336 6PGL_HUMAN          | 3827.8465 |
| sp P56945 BCAR1_HUMAN         | 2580.2973 |
| sp P56945 BCAR1_HUMAN         | 2580.2973 |
| sp P61619 S61A1_HUMAN         | 2651.4033 |
| sp Q13573 SNW1_HUMAN          | 2782.3926 |
| sp P61619 S61A1_HUMAN         | 2651.4033 |
| sp Q9UBX3 DIC_HUMAN           | 3671.8948 |
| sp Q9UBX3 DIC_HUMAN           | 3671.8948 |
| sp Q9UBX3 DIC_HUMAN           | 3671.8948 |
| sp P49915 GUAA_HUMAN          | 3207.642  |
| sp P62805 H4_HUMAN            | 1582.8719 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp P08648 ITA5_HUMAN          | 5766.8112 |
| sp Q15738 NSDHL_HUMAN         | 3045.4509 |
| sp P08648 ITA5_HUMAN          | 5766.8112 |
| sp P08648 ITA5_HUMAN          | 5766.8112 |
| sp P14735 IDE_HUMAN           | 2998.4845 |
| sp P14735 IDE_HUMAN           | 2998.4845 |
| sp Q86Y56 DAAF5_HUMAN         | 2604.3006 |
| sp Q9H0A0 NAT10_HUMAN         | 3646.758  |
| sp P14735 IDE_HUMAN           | 2998.4845 |
| sp Q14254 FLOT2_HUMAN         | 2272.1812 |
| sp Q14254 FLOT2_HUMAN         | 2272.1812 |
| sp Q14254 FLOT2_HUMAN         | 2272.1812 |
| sp O75608 LYPA1_HUMAN         | 3381.6295 |
| sp P45974 UBP5_HUMAN          | 5334.4788 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp P13804 ETFA_HUMAN          | 3684.8498 |
| sp P13804 ETFA_HUMAN          | 3684.8498 |
| sp P46060 RAGP1_HUMAN         | 3057.5092 |
| sp P14735 IDE_HUMAN           | 2998.4845 |
| sp Q15043 S39AE_HUMAN         | 2892.4618 |
| sp P23526 SAHH_HUMAN          | 3485.7501 |
| sp P23526 SAHH_HUMAN          | 3485.7501 |
| sp P27105 STOM_HUMAN          | 2854.4688 |
| sp Q99808 S29A1_HUMAN         | 1991.1278 |
| sp Q99808 S29A1_HUMAN         | 1991.1278 |
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| sp P25789 PSA4_HUMAN          | 1551.6801 |
| sp P25789 PSA4_HUMAN          | 1551.6801 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1097.5254 |
| sp P55809 SCOT1_HUMAN         | 1803.8574 |

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| sp P55809 SCOT1_HUMAN          | 1803.8574 |
| sp P55809 SCOT1_HUMAN          | 1803.8574 |
| sp Q9UKD2 MRT4_HUMAN           | 2098.9556 |
| sp Q9UKD2 MRT4_HUMAN           | 2098.9556 |
| sp Q9UKD2 MRT4_HUMAN           | 2098.9556 |
| sp Q6DD88 ATLA3_HUMAN          | 2083.0083 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2735.1915 |
| sp Q9C0J8 WDR33_HUMAN          | 1902.8319 |
| sp Q9C0J8 WDR33_HUMAN          | 1902.8319 |
| sp Q9C0J8 WDR33_HUMAN          | 1902.8319 |
| sp Q9C0J8 WDR33_HUMAN          | 1902.8319 |
| sp Q02543 RL18A_HUMAN          | 1534.7892 |
| sp O43929 ORC4_HUMAN           | 1972.9717 |
| sp O43929 ORC4_HUMAN           | 1972.9717 |
| sp Q9UBS4 DJB11_HUMAN          | 2509.2197 |
| sp O43929 ORC4_HUMAN           | 1972.9717 |
| sp O43929 ORC4_HUMAN           | 1972.9717 |
| sp Q9NTJ3 SMC4_HUMAN           | 2027.9912 |
| sp P05023 AT1A1_HUMAN          | 2119.948  |
| sp Q8N1F7 NUP93_HUMAN          | 2197.163  |
| sp Q8N1F7 NUP93_HUMAN          | 2197.163  |
| sp Q07065 CKAP4_HUMAN          | 2227.0142 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P54819 KAD2_HUMAN           | 3038.3968 |
| sp Q9UJU6 DBNL_HUMAN           | 2210.0756 |
| sp Q9UJU6 DBNL_HUMAN           | 2210.0756 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1736.9243 |
| sp P14923 PLAK_HUMAN           | 3414.7024 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P21266 GSTM3_HUMAN          | 2971.4273 |
| sp Q9Y224 RTRAF_HUMAN          | 1830.8213 |
| sp P30044 PRDX5_HUMAN          | 1934.9738 |
| sp P00367 DHE3_HUMAN           | 2266.1018 |
| sp Q9NYF8 BCLF1_HUMAN          | 1679.8519 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp Q14697 GANAB_HUMAN          | 1888.9432 |
| sp Q10713 MPPA_HUMAN           | 3018.3699 |
| sp P34932 HSP74_HUMAN          | 1846.9002 |
| sp P34932 HSP74_HUMAN          | 1846.9002 |
| sp Q03405 UPAR_HUMAN           | 3305.4531 |
| sp Q03405 UPAR_HUMAN           | 3305.4531 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp Q03405 UPAR_HUMAN           | 3305.4531 |
| sp P63218 GBG5_HUMAN           | 4150.0178 |
| sp P63218 GBG5_HUMAN           | 4150.0178 |
| sp P63218 GBG5_HUMAN           | 4150.0178 |



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| sp P24534 EF1B_HUMAN           | 2966.4947 |
| sp Q06265 EXOS9_HUMAN          | 1792.8964 |
| sp P53701 CCHL_HUMAN           | 2646.257  |
| sp P24534 EF1B_HUMAN           | 2966.4947 |
| sp P57088 TMM33_HUMAN          | 2218.1643 |
| sp P57088 TMM33_HUMAN          | 2218.1643 |
| sp P57088 TMM33_HUMAN          | 2218.1643 |
| sp P57088 TMM33_HUMAN          | 2218.1643 |
| sp P00505 AATM_HUMAN           | 2221.0956 |
| sp A1L0T0 ILVBL_HUMAN          | 2389.1849 |
| sp Q6DD87 ZN787_HUMAN          | 2168.159  |
| sp Q8TDN6 BRX1_HUMAN           | 3720.8927 |
| sp Q9NTJ3 SMC4_HUMAN           | 1838.905  |
| sp Q8TDN6 BRX1_HUMAN           | 3720.8927 |
| sp Q14203 DCTN1_HUMAN          | 2830.4461 |
| sp Q14203 DCTN1_HUMAN          | 2830.4461 |
| sp P33240 CSTF2_HUMAN          | 1712.9461 |
| sp P33240 CSTF2_HUMAN          | 1712.9461 |
| sp P51398 RT29_HUMAN           | 2537.2299 |
| sp P51398 RT29_HUMAN           | 2537.2299 |
| sp P51398 RT29_HUMAN           | 2537.2299 |
| sp Q14690 RRP5_HUMAN           | 3744.921  |
| sp Q15020 SART3_HUMAN          | 2399.1944 |
| sp Q15020 SART3_HUMAN          | 2399.1944 |
| sp Q5VT66 MARC1_HUMAN          | 2695.3898 |
| sp Q5VT66 MARC1_HUMAN          | 2695.3898 |
| sp Q8TDD1 DDX54_HUMAN          | 2166.0779 |
| sp Q9Y305 ACOT9_HUMAN          | 2433.1886 |
| sp Q15185 TEBP_HUMAN           | 3689.6403 |
| sp O43143 DHX15_HUMAN          | 2266.2281 |
| sp O43143 DHX15_HUMAN          | 3745.8628 |
| sp O43143 DHX15_HUMAN          | 3745.8628 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp Q8WWQ0 PHIP_HUMAN           | 2595.2493 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp Q8NE71 ABCF1_HUMAN          | 2277.2039 |
| sp P12277 KCRB_HUMAN           | 2380.2234 |
| sp Q8NE71 ABCF1_HUMAN          | 2277.2039 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp O14817 TSN4_HUMAN           | 3085.5257 |
| sp Q9BT22 ALG1_HUMAN           | 2960.5066 |
| sp P25398 RS12_HUMAN           | 4062.9312 |
| sp Q15008 PSMD6_HUMAN          | 2140.1892 |
| sp Q15008 PSMD6_HUMAN          | 2140.1892 |
| sp P25398 RS12_HUMAN           | 4062.9312 |
| sp Q15008 PSMD6_HUMAN          | 2140.1892 |

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| sp Q15008 PSMD6_HUMAN         | 2140.1892 |
| sp P21926 CD9_HUMAN           | 4149.985  |
| sp P21926 CD9_HUMAN           | 4149.985  |
| sp P05023 AT1A1_HUMAN         | 4025.9317 |
| sp P05023 AT1A1_HUMAN         | 4025.9317 |
| sp O76031 CLPX_HUMAN          | 2792.5324 |
| sp O76031 CLPX_HUMAN          | 2792.5324 |
| sp O76031 CLPX_HUMAN          | 2792.5324 |
| sp Q92688 AN32B_HUMAN         | 2791.4215 |
| sp Q92688 AN32B_HUMAN         | 2791.4215 |
| sp Q92688 AN32B_HUMAN         | 2791.4215 |
| sp Q7L1Q6 BZW1_HUMAN          | 2996.5859 |
| sp Q7L1Q6 BZW1_HUMAN          | 2996.5859 |
| sp Q9H0D6 XRN2_HUMAN          | 3268.6379 |
| sp Q9H0D6 XRN2_HUMAN          | 3268.6379 |
| sp Q8TEM1 PO210_HUMAN         | 6271.9282 |
| sp Q8TEM1 PO210_HUMAN         | 6255.9333 |
| sp P27105 STOM_HUMAN          | 2854.4688 |
| sp P27105 STOM_HUMAN          | 2854.4688 |
| sp P27105 STOM_HUMAN          | 2854.4688 |
| sp P27105 STOM_HUMAN          | 2854.4688 |
| sp P27105 STOM_HUMAN          | 2854.4688 |
| sp O00629 IMA3_HUMAN          | 2708.4207 |
| sp P35579 MYH9_HUMAN          | 1408.6947 |
| sp P50570 DYN2_HUMAN          | 1682.7359 |
| sp P15151 PVR_HUMAN           | 2719.1569 |
| sp Q9H2P0 ADNP_HUMAN          | 2092.0014 |
| sp Q9H2P0 ADNP_HUMAN          | 2092.0014 |
| sp P35658 NU214_HUMAN         | 2602.3252 |
| sp P15328 FOLR1_HUMAN         | 1890.8717 |
| sp P62424 RL7A_HUMAN          | 1673.8274 |
| sp Q96EE3 SEH1_HUMAN          | 2657.099  |
| sp Q14166 TTL12_HUMAN         | 1902.9799 |
| sp P11142 HSP7C_HUMAN         | 1603.7453 |
| sp Q14160 SCRIB_HUMAN         | 2903.3798 |
| sp P11142 HSP7C_HUMAN         | 1587.7504 |
| sp Q9UHN6 CEIP2_HUMAN         | 2448.1856 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp Q9NX63 MIC19_HUMAN         | 2703.2534 |
| sp O95672 ECEL1_HUMAN         | 2481.1925 |
| sp P48960 CD97_HUMAN,sp Q9UHX | 3933.7687 |
| sp P48960 CD97_HUMAN,sp Q9UHX | 3933.7687 |
| sp Q9BZK7 TBL1R_HUMAN         | 2908.3814 |
| sp Q9BZK7 TBL1R_HUMAN         | 2908.3814 |
| sp P08069 IGF1R_HUMAN         | 2958.3025 |
| sp P48960 CD97_HUMAN,sp Q9UHX | 3933.7687 |
| sp P08069 IGF1R_HUMAN         | 2958.3025 |

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| sp P48960 CD97_HUMAN,sp Q9UHX  | 3933.7687 |
| sp Q96DI7 SNR40_HUMAN          | 3153.5367 |
| sp Q96DI7 SNR40_HUMAN          | 3153.5367 |
| sp P08195 4F2_HUMAN            | 2051.9854 |
| sp P0DPI2 GAL3A_HUMAN,sp AOA0E | 2816.4717 |
| sp P49257 LMAN1_HUMAN          | 3678.7492 |
| sp P49257 LMAN1_HUMAN          | 3678.7492 |
| sp P21964 COMT_HUMAN           | 2492.1318 |
| sp P21964 COMT_HUMAN           | 2349.0987 |
| sp Q14166 TTL12_HUMAN          | 3546.6112 |
| sp Q96FW1 OTUB1_HUMAN          | 2372.1285 |
| sp O14732 IMPA2_HUMAN          | 4079.9146 |
| sp Q02880 TOP2B_HUMAN          | 2446.234  |
| sp Q8IVT2 MISP_HUMAN           | 3236.7405 |
| sp P35251 RFC1_HUMAN           | 3804.8134 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp Q6PL18 ATAD2_HUMAN          | 3808.9959 |
| sp Q29983 MICA_HUMAN           | 2307.0161 |
| sp Q9BWJ5 SF3B5_HUMAN          | 2924.3941 |
| sp O00151 PDLI1_HUMAN          | 2824.3351 |
| sp Q02750 MP2K1_HUMAN,sp P365  | 1626.9457 |
| sp Q02750 MP2K1_HUMAN,sp P365  | 1626.9457 |
| sp Q02750 MP2K1_HUMAN,sp P365  | 1626.9457 |
| sp Q02750 MP2K1_HUMAN,sp P365  | 1626.9457 |
| sp Q6PKG0 LARP1_HUMAN          | 2169.1041 |
| sp P21399 ACOC_HUMAN           | 3350.716  |
| sp Q96A72 MGN2_HUMAN,sp P613   | 2236.0225 |
| sp Q8TDN6 BRX1_HUMAN           | 2757.3187 |
| sp P61201 CSN2_HUMAN           | 2782.484  |
| sp P61201 CSN2_HUMAN           | 2782.484  |
| sp P50895 BCAM_HUMAN           | 3288.4856 |
| sp P50895 BCAM_HUMAN           | 3288.4856 |
| sp P00491 PNPH_HUMAN           | 4165.0691 |
| sp Q9H2P0 ADNP_HUMAN           | 2815.4149 |
| sp P68400 CSK21_HUMAN,sp Q8NE  | 2903.4454 |
| sp P68400 CSK21_HUMAN,sp Q8NE  | 2903.4454 |
| sp P49321 NASP_HUMAN           | 3385.8068 |
| sp P53999 TCP4_HUMAN           | 1420.643  |
| sp P53999 TCP4_HUMAN           | 1420.643  |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P62888 RL30_HUMAN           | 1748.9243 |
| sp Q93009 UBP7_HUMAN           | 1751.8301 |
| sp P15328 FOLR1_HUMAN          | 2732.1305 |
| sp P15328 FOLR1_HUMAN          | 2732.1305 |
| sp P51511 MMP15_HUMAN          | 2290.127  |
| sp P51511 MMP15_HUMAN          | 2290.127  |

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| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P62241 RS8_HUMAN            | 2088.0561 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P00491 PNPH_HUMAN           | 2449.2887 |
| sp P00491 PNPH_HUMAN           | 2449.2887 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp Q6PKG0 LARP1_HUMAN          | 2767.3817 |
| sp P24534 EF1B_HUMAN           | 2470.2744 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P36776 LONM_HUMAN           | 2005.019  |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P05387 RLA2_HUMAN           | 4208.1237 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp Q9Y678 COPG1_HUMAN          | 2373.2275 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P05386 RLA1_HUMAN           | 5688.8311 |
| sp P62910 RL32_HUMAN           | 1931.8432 |
| sp Q8NBS9 TXND5_HUMAN          | 2460.0798 |
| sp P61769 B2MG_HUMAN           | 1714.805  |
| sp P08069 IGF1R_HUMAN          | 2337.0179 |
| sp P27694 RFA1_HUMAN           | 1830.9186 |
| sp P27694 RFA1_HUMAN           | 1830.9186 |
| sp Q04837 SSBP_HUMAN           | 2489.1095 |
| sp P52565 GDIR1_HUMAN          | 1920.904  |
| sp Q9Y6N8 CAD10_HUMAN          | 2081.0065 |
| sp P05387 RLA2_HUMAN           | 2097.0226 |
| sp P05387 RLA2_HUMAN           | 2097.0226 |
| sp Q04837 SSBP_HUMAN           | 2489.1095 |
| sp Q04837 SSBP_HUMAN           | 2489.1095 |
| sp Q04837 SSBP_HUMAN           | 2489.1095 |
| sp P25788 PSA3_HUMAN           | 1831.9316 |
| sp P07900 HS90A_HUMAN,sp Q145i | 2230.0906 |
| sp O15144 ARPC2_HUMAN          | 1957.9422 |
| sp O15144 ARPC2_HUMAN          | 1957.9422 |
| sp P31930 QCR1_HUMAN           | 1960.9167 |
| sp P68400 CSK21_HUMAN,sp Q8NE\ | 2280.0157 |
| sp Q13263 TIF1B_HUMAN          | 1989.954  |
| sp P36952 SPB5_HUMAN           | 2238.1168 |
| sp Q49A26 GLYR1_HUMAN          | 1688.8562 |
| sp P57081 WDR4_HUMAN           | 2688.249  |
| sp P40925 MDHC_HUMAN           | 2374.1693 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp P16066 ANPRA_HUMAN          | 2663.3371 |

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| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P62424 RL7A_HUMAN           | 2007.0425 |
| sp Q15437 SC23B_HUMAN          | 2919.4874 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp Q6PL18 ATAD2_HUMAN          | 3652.8948 |
| sp P19387 RPB3_HUMAN           | 2354.2369 |
| sp P60033 CD81_HUMAN           | 4497.1138 |
| sp P19387 RPB3_HUMAN           | 2354.2369 |
| sp Q13057 COASY_HUMAN          | 1950.0649 |
| sp P49588 SYAC_HUMAN           | 2657.3081 |
| sp Q99714 HCD2_HUMAN           | 3883.9893 |
| sp Q99714 HCD2_HUMAN           | 3883.9893 |
| sp Q9P258 RCC2_HUMAN           | 1264.5796 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp Q13098 CSN1_HUMAN           | 1371.6895 |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp P38919 IF4A3_HUMAN          | 1793.8697 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp Q16513 PKN2_HUMAN           | 1762.885  |
| sp O15260 SURF4_HUMAN          | 1507.7783 |
| sp Q9ULV4 COR1C_HUMAN          | 2260.9807 |
| sp Q9ULV4 COR1C_HUMAN          | 2260.9807 |
| sp O43776 SYNC_HUMAN           | 1960.8738 |
| sp Q14683 SMC1A_HUMAN          | 1711.8642 |
| sp P56192 SYMC_HUMAN           | 1964.9129 |
| sp P56192 SYMC_HUMAN           | 1964.9129 |
| sp P13984 T2FB_HUMAN           | 3446.6743 |
| sp P13984 T2FB_HUMAN           | 3446.6743 |
| sp P49257 LMAN1_HUMAN          | 3799.7721 |
| sp Q9BXP5 SRRT_HUMAN           | 1561.81   |
| sp Q08380 LG3BP_HUMAN          | 2445.1237 |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp P62847 RS24_HUMAN           | 1560.797  |
| sp Q9BS26 ERP44_HUMAN          | 1889.8366 |
| sp P36776 LONM_HUMAN           | 1899.8785 |
| sp P23284 PIIB_HUMAN           | 1653.8151 |
| sp Q00610 CLH1_HUMAN           | 1816.8632 |
| sp Q08AF3 SLFN5_HUMAN          | 2783.3047 |
| sp Q9Y5J7 TIM9_HUMAN           | 2778.3725 |
| sp Q9Y5J7 TIM9_HUMAN           | 2778.3725 |
| sp P22087 FBRL_HUMAN           | 2068.1317 |
| sp Q15006 EMC2_HUMAN           | 2360.1471 |
| sp P46063 RECQ1_HUMAN          | 2459.2479 |
| sp P48739 PIPNB_HUMAN          | 2835.2785 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp Q96KP4 CNDP2_HUMAN          | 2640.3184 |

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| sp Q9Y6X3 SCC4_HUMAN           | 2592.286  |
| sp Q9HCS7 SYF1_HUMAN           | 2024.9803 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P49588 SYAC_HUMAN           | 2366.1866 |
| sp Q53EL6 PDCD4_HUMAN          | 2087.1011 |
| sp O43159 RRP8_HUMAN           | 2382.1532 |
| sp O43159 RRP8_HUMAN           | 2382.1532 |
| sp P10586 PTPRF_HUMAN          | 3499.6428 |
| sp O00116 ADAS_HUMAN           | 2901.4405 |
| sp O00116 ADAS_HUMAN           | 2901.4405 |
| sp Q9H4A3 WNK1_HUMAN           | 2463.1707 |
| sp O95336 6PGL_HUMAN           | 3827.8465 |
| sp P61619 S61A1_HUMAN          | 2651.4033 |
| sp Q9H8H0 NOL11_HUMAN          | 2867.4705 |
| sp P68400 CSK21_HUMAN,sp Q8NE\ | 3437.6416 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q9UFC0 LRWD1_HUMAN          | 2604.3105 |
| sp Q8NI36 WDR36_HUMAN          | 3418.8137 |
| sp Q9UFC0 LRWD1_HUMAN          | 2604.3105 |
| sp Q8NI36 WDR36_HUMAN          | 3418.8137 |
| sp P43487 RANG_HUMAN           | 5492.3612 |
| sp P43487 RANG_HUMAN           | 5492.3612 |
| sp Q6UVK1 CSPG4_HUMAN          | 3838.953  |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P30084 ECHM_HUMAN           | 3614.8726 |
| sp P30084 ECHM_HUMAN           | 3614.8726 |
| sp Q15029 U5S1_HUMAN           | 3869.9152 |
| sp Q15029 U5S1_HUMAN           | 3869.9152 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q9GZP8 IMUP_HUMAN           | 1729.802  |
| sp Q9GZP8 IMUP_HUMAN           | 1729.802  |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp P15328 FOLR1_HUMAN          | 2073.8244 |
| sp P15328 FOLR1_HUMAN          | 2073.8244 |
| sp O00151 PDLI1_HUMAN          | 2078.0069 |
| sp O00151 PDLI1_HUMAN          | 2078.0069 |
| sp Q9NUP9 LIN7C_HUMAN          | 2361.1098 |
| sp P13987 CD59_HUMAN           | 2209.8946 |
| sp P13987 CD59_HUMAN           | 2209.8946 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P08621 RU17_HUMAN           | 3279.4527 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P48960 CD97_HUMAN,sp Q9UHX  | 3933.7687 |
| sp Q13098 CSN1_HUMAN           | 2977.2243 |
| sp P48960 CD97_HUMAN,sp Q9UHX  | 3933.7687 |
| sp Q07666 KHDR1_HUMAN          | 2322.011  |

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| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp P61978 HNRPK_HUMAN          | 1971.1153 |
| sp P24941 CDK2_HUMAN           | 1897.8992 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp Q7L2H7 EIF3M_HUMAN          | 2279.1369 |
| sp Q14166 TTL12_HUMAN          | 3546.6112 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp O00571 DDX3X_HUMAN          | 3105.5043 |
| sp Q16666 IF16_HUMAN           | 2230.0762 |
| sp Q9UIJ7 KAD3_HUMAN           | 2710.3755 |
| sp Q14320 FA50A_HUMAN          | 2214.1467 |
| sp P35579 MYH9_HUMAN           | 1408.6947 |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp Q9Y383 LC7L2_HUMAN          | 2449.0937 |
| sp Q96KG9 SCYL1_HUMAN          | 2684.3493 |
| sp Q15287 RNPS1_HUMAN          | 2787.2123 |
| sp Q15287 RNPS1_HUMAN          | 2787.2123 |
| sp Q92922 SMRC1_HUMAN          | 2071.095  |
| sp P60900 PSA6_HUMAN           | 2124.1103 |
| sp O75165 DJC13_HUMAN          | 2290.1706 |
| sp O75165 DJC13_HUMAN          | 2290.1706 |
| sp P30419 NMT1_HUMAN           | 2553.3479 |
| sp O15027 SC16A_HUMAN          | 3626.8257 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp Q9NVJ2 ARL8B_HUMAN,sp Q96B  | 2520.2609 |
| sp Q09161 NCBP1_HUMAN          | 1960.9863 |
| sp Q9NVP1 DDX18_HUMAN          | 2723.3959 |
| sp Q9NVP1 DDX18_HUMAN          | 2723.3959 |
| sp Q13085 ACACA_HUMAN          | 3443.7541 |
| sp O94973 AP2A2_HUMAN          | 3682.9206 |
| sp Q687X5 STEA4_HUMAN          | 2445.2726 |
| sp Q687X5 STEA4_HUMAN          | 2445.2726 |
| sp Q92538 GBF1_HUMAN           | 1767.9169 |
| sp Q96EE3 SEH1_HUMAN           | 2476.1408 |
| sp Q9UG63 ABCF2_HUMAN          | 2383.0804 |
| sp Q9NXE4 NSMA3_HUMAN          | 2305.1855 |
| sp Q09161 NCBP1_HUMAN          | 2165.0218 |
| sp Q09161 NCBP1_HUMAN          | 2165.0218 |
| sp Q9Y383 LC7L2_HUMAN          | 2119.0851 |
| sp Q9Y383 LC7L2_HUMAN          | 2119.0851 |
| sp P48735 IDHP_HUMAN           | 2053.9785 |
| sp P50502 F10A1_HUMAN          | 3481.5806 |
| sp O75691 UTP20_HUMAN          | 2496.3087 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp O14880 MGST3_HUMAN          | 1962.9    |
| sp P62491 RB11A_HUMAN,sp Q159I | 1812.8642 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |

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| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P14314 GLU2B_HUMAN          | 2784.3243 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp O60684 IMA7_HUMAN           | 2630.3626 |
| sp O60684 IMA7_HUMAN           | 2630.3626 |
| sp Q9Y3E5 PTH2_HUMAN           | 1843.8523 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp Q9UKM9 RALY_HUMAN           | 2368.0542 |
| sp P52565 GDIR1_HUMAN          | 2081.9728 |
| sp P26006 ITA3_HUMAN           | 2301.9994 |
| sp P26006 ITA3_HUMAN           | 2301.9994 |
| sp P63096 GNAI1_HUMAN          | 1776.789  |
| sp Q96T37 RBM15_HUMAN          | 2230.0138 |
| sp P02786 TFR1_HUMAN           | 2891.3184 |
| sp Q9BQ67 GRWD1_HUMAN          | 2955.3491 |
| sp O95782 AP2A1_HUMAN          | 3322.6582 |
| sp P04406 G3P_HUMAN            | 3129.4787 |
| sp Q92466 DDB2_HUMAN           | 3056.4372 |
| sp P62491 RB11A_HUMAN,sp Q159I | 2293.1009 |
| sp P27695 APEX1_HUMAN          | 3780.8271 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3246.5901 |
| sp P30419 NMT1_HUMAN           | 2388.1426 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1892.0367 |
| sp O60664 PLIN3_HUMAN          | 4062.9561 |
| sp P10809 CH60_HUMAN           | 1752.9332 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P04183 KITH_HUMAN           | 2091.1616 |
| sp P04183 KITH_HUMAN           | 2091.1616 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp Q9HD20 AT131_HUMAN          | 3616.8195 |
| sp Q9Y570 PPME1_HUMAN          | 2592.3985 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp O60684 IMA7_HUMAN           | 2630.3626 |
| sp O00425 IF2B3_HUMAN          | 2013.9617 |
| sp O00425 IF2B3_HUMAN          | 2013.9617 |



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| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp O14745 NHRF1_HUMAN          | 1702.7587 |
| sp Q96KR1 ZFR_HUMAN            | 2222.882  |
| sp O14745 NHRF1_HUMAN          | 1702.7587 |
| sp Q9NVP1 DDX18_HUMAN          | 1794.8213 |
| sp O14745 NHRF1_HUMAN          | 1702.7587 |
| sp P36542 ATPG_HUMAN           | 1796.8549 |
| sp P36542 ATPG_HUMAN           | 1796.8549 |
| sp O14975 S27A2_HUMAN          | 1875.8066 |
| sp O14975 S27A2_HUMAN          | 1875.8066 |
| sp P45973 CBX5_HUMAN           | 2099.8861 |
| sp P52701 MSH6_HUMAN           | 1670.8053 |
| sp P61086 UBE2K_HUMAN          | 2300.1113 |
| sp P48729 KC1A_HUMAN           | 1714.8566 |
| sp Q15477 SKIV2_HUMAN          | 2060.9949 |
| sp P47756 CAPZB_HUMAN          | 2269.007  |
| sp Q9UBB4 ATX10_HUMAN          | 2458.1369 |
| sp P47756 CAPZB_HUMAN          | 2269.007  |
| sp Q9BWT3 PAPOG_HUMAN,sp P51   | 2089.0262 |
| sp O75131 CPNE3_HUMAN          | 2137.0956 |
| sp P25788 PSA3_HUMAN           | 1940.9381 |
| sp Q9Y383 LC7L2_HUMAN          | 1965.9288 |
| sp P36542 ATPG_HUMAN           | 1929.9221 |
| sp P36542 ATPG_HUMAN           | 1929.9221 |
| sp P36542 ATPG_HUMAN           | 1929.9221 |
| sp Q5TFE4 NT5D1_HUMAN          | 2031.9724 |
| sp Q5TFE4 NT5D1_HUMAN          | 2031.9724 |
| sp Q9Y2X3 NOP58_HUMAN          | 2008.0378 |
| sp Q9Y2X3 NOP58_HUMAN          | 2008.0378 |
| sp Q15287 RNPS1_HUMAN          | 2078.9619 |
| sp Q15287 RNPS1_HUMAN          | 2078.9619 |
| sp P30419 NMT1_HUMAN           | 2425.2529 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P29317 EPHA2_HUMAN          | 4847.3171 |
| sp Q9NVJ2 ARL8B_HUMAN          | 2517.217  |
| sp Q9NVJ2 ARL8B_HUMAN          | 2517.217  |
| sp P29317 EPHA2_HUMAN          | 4613.9517 |
| sp P60174 TPIS_HUMAN           | 2517.2533 |
| sp P47756 CAPZB_HUMAN          | 4069.0929 |
| sp P47756 CAPZB_HUMAN          | 4069.0929 |
| sp P47756 CAPZB_HUMAN          | 4069.0929 |
| sp P47756 CAPZB_HUMAN          | 4069.0929 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp O75131 CPNE3_HUMAN          | 2396.1932 |
| sp Q9BY67 CADM1_HUMAN          | 3222.5364 |

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| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp Q9H0S4 DDX47_HUMAN          | 2181.0637 |
| sp P60891 PRPS1_HUMAN          | 1650.8366 |
| sp O75436 VP26A_HUMAN          | 1689.9124 |
| sp P52565 GDIR1_HUMAN          | 2688.2344 |
| sp P06493 CDK1_HUMAN           | 1997.9483 |
| sp P06493 CDK1_HUMAN           | 1997.9483 |
| sp Q8WUM0 NU133_HUMAN          | 3341.463  |
| sp Q8WUM0 NU133_HUMAN          | 3341.463  |
| sp Q8N752 KC1AL_HUMAN,sp P487: | 1871.924  |
| sp Q8N752 KC1AL_HUMAN,sp P487: | 1871.924  |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q9NxE4 NSMA3_HUMAN          | 3442.7595 |
| sp P16401 H15_HUMAN            | 1346.7558 |
| sp Q9UGU0 TCF20_HUMAN          | 2308.0621 |
| sp P49916 DNLI3_HUMAN          | 1775.957  |
| sp Q9Y6C9 MTCH2_HUMAN          | 3779.7915 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp P08195 4F2_HUMAN            | 2051.9854 |
| sp Q8NAV1 PR38A_HUMAN          | 2387.187  |
| sp P35610 SOAT1_HUMAN          | 2219.1548 |
| sp P09960 LKHA4_HUMAN          | 1864.936  |
| sp P35610 SOAT1_HUMAN          | 2219.1548 |
| sp Q16836 HCDH_HUMAN           | 3611.6991 |
| sp P09960 LKHA4_HUMAN          | 1864.936  |
| sp Q15149 PLEC_HUMAN           | 2054.0585 |
| sp Q8IY17 PLPL6_HUMAN          | 2054.0295 |
| sp O15067 PUR4_HUMAN           | 2588.3785 |
| sp O15067 PUR4_HUMAN           | 2588.3785 |
| sp O43795 MYO1B_HUMAN          | 3178.5724 |
| sp Q7Z4V5 HDGR2_HUMAN          | 3698.8297 |
| sp Q7Z4V5 HDGR2_HUMAN          | 3698.8297 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P51153 RAB13_HUMAN          | 2142.0997 |
| sp O75937 DNJC8_HUMAN          | 3830.9003 |
| sp Q6DD88 ATLA3_HUMAN          | 2774.3511 |
| sp Q10570 CPSF1_HUMAN          | 1701.8951 |
| sp Q13347 EIF3I_HUMAN          | 2103.0174 |
| sp Q03167 TGBR3_HUMAN          | 2568.3489 |
| sp P30046 DOPD_HUMAN,sp A6NH   | 2529.1925 |
| sp P30046 DOPD_HUMAN,sp A6NH   | 2529.1925 |
| sp P68032 ACTC_HUMAN,sp P6813  | 3653.6674 |
| sp Q9P275 UBP36_HUMAN          | 4424.1682 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp Q8IVD9 NUDC3_HUMAN          | 2844.3727 |

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| sp Q8IVD9 NUDC3_HUMAN          | 2828.3778 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1614.8175 |
| sp P51114 FXR1_HUMAN           | 2144.0273 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp P04439 HLAA_HUMAN,sp P01892 | 4241.9261 |
| sp P62995 TRA2B_HUMAN          | 2597.2286 |
| sp P62995 TRA2B_HUMAN          | 2597.2286 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp P08648 ITA5_HUMAN           | 2765.3184 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q8N684 CPSF7_HUMAN          | 3003.5037 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp P16615 AT2A2_HUMAN          | 1850.8291 |
| sp P16615 AT2A2_HUMAN          | 1850.8291 |
| sp Q53H96 P5CR3_HUMAN          | 1959.965  |
| sp Q00610 CLH1_HUMAN           | 2040.9905 |
| sp Q9UKX7 NUP50_HUMAN          | 2328.0739 |
| sp Q9UKX7 NUP50_HUMAN          | 2328.0739 |
| sp Q9UKX7 NUP50_HUMAN          | 2328.0739 |
| sp Q9UKX7 NUP50_HUMAN          | 2328.0739 |
| sp P31948 STIP1_HUMAN          | 1817.8584 |
| sp Q969X5 ERGI1_HUMAN          | 2596.1506 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1651.9145 |
| sp Q10471 GALT2_HUMAN          | 1495.7453 |
| sp Q96EP5 DAZP1_HUMAN          | 2324.0855 |
| sp Q96EP5 DAZP1_HUMAN          | 2324.0855 |
| sp Q96EP5 DAZP1_HUMAN          | 2324.0855 |
| sp Q15738 NSDHL_HUMAN          | 2817.2817 |
| sp Q15738 NSDHL_HUMAN          | 2817.2817 |
| sp P54727 RD23B_HUMAN          | 1959.0102 |
| sp P54727 RD23B_HUMAN          | 1959.0102 |
| sp Q8N684 CPSF7_HUMAN          | 1979.0034 |
| sp Q09028 RBBP4_HUMAN          | 4291.924  |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P09012 SNRPA_HUMAN          | 2134.0695 |
| sp P09012 SNRPA_HUMAN          | 2134.0695 |
| sp P60891 PRPS1_HUMAN          | 3241.5053 |
| sp Q8WWI5 CTL1_HUMAN           | 2223.067  |
| sp Q6FI13 H2A2A_HUMAN,sp P2067 | 2538.4785 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P52292 IMA1_HUMAN           | 2667.5211 |
| sp P36897 TGFR1_HUMAN          | 4744.3066 |
| sp P24752 THIL_HUMAN           | 3078.6853 |
| sp Q15785 TOM34_HUMAN          | 1497.6089 |
| sp Q15785 TOM34_HUMAN          | 1497.6089 |

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| sp P24752 THIL_HUMAN          | 1642.7079 |
| sp P04183 KITH_HUMAN          | 2998.4203 |
| sp P04183 KITH_HUMAN          | 2998.4203 |
| sp Q14157 UBP2L_HUMAN         | 1738.7911 |
| sp P36897 TGFR1_HUMAN         | 3486.4333 |
| sp Q14157 UBP2L_HUMAN         | 1738.7911 |
| sp P36897 TGFR1_HUMAN         | 3486.4333 |
| sp Q9NXW2 DJB12_HUMAN         | 3220.5385 |
| sp Q9NXW2 DJB12_HUMAN         | 3220.5385 |
| sp Q8IY67 RAVR1_HUMAN         | 1547.8308 |
| sp P61106 RAB14_HUMAN         | 3474.6764 |
| sp P69849 NOMO3_HUMAN,sp Q15  | 1847.924  |
| sp P32004 L1CAM_HUMAN         | 2017.8986 |
| sp O43852 CALU_HUMAN          | 2945.2661 |
| sp O43852 CALU_HUMAN          | 2945.2661 |
| sp Q09028 RBBP4_HUMAN         | 3454.5623 |
| sp P63279 UBC9_HUMAN          | 1638.8042 |
| sp P61106 RAB14_HUMAN         | 2161.9561 |
| sp P53701 CCHL_HUMAN          | 2060.9916 |
| sp P78406 RAE1L_HUMAN         | 2382.1644 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P55209 NP1L1_HUMAN         | 1836.941  |
| sp P25787 PSA2_HUMAN          | 2428.1733 |
| sp Q9UN86 G3BP2_HUMAN         | 2105.0218 |
| sp P49773 HINT1_HUMAN         | 1995.0538 |
| sp P63162 RSMN_HUMAN,sp P1467 | 2379.9922 |
| sp P18754 RCC1_HUMAN          | 3060.526  |
| sp O15020 SPTN2_HUMAN         | 3052.5578 |
| sp O15020 SPTN2_HUMAN         | 3052.5578 |
| sp Q6YHK3 CD109_HUMAN         | 2904.4618 |
| sp Q13085 ACACA_HUMAN         | 2600.3922 |
| sp Q6PD62 CTR9_HUMAN          | 2896.5083 |
| sp Q03701 CEBPZ_HUMAN         | 1893.987  |
| sp P69849 NOMO3_HUMAN,sp Q15  | 2964.4869 |
| sp Q03701 CEBPZ_HUMAN         | 1893.987  |
| sp Q03701 CEBPZ_HUMAN         | 1893.987  |
| sp P98155 VLDLR_HUMAN         | 2642.2839 |
| sp P33993 MCM7_HUMAN          | 3005.5492 |
| sp Q9BWD1 THIC_HUMAN          | 4211.9272 |
| sp Q9BWD1 THIC_HUMAN          | 4211.9272 |
| sp Q9Y6M7 S4A7_HUMAN          | 2349.1199 |
| sp Q9BTE3 MCMBP_HUMAN         | 4324.1322 |
| sp Q13813 SPTN1_HUMAN         | 2783.3879 |
| sp P50991 TCPD_HUMAN          | 1927.9349 |
| sp Q14764 MVP_HUMAN           | 3865.0553 |
| sp Q16851 UGPA_HUMAN          | 4878.3182 |
| sp P53004 BIEA_HUMAN          | 3250.622  |

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| sp Q99575 POP1_HUMAN           | 2113.9665 |
| sp O60271 JIP4_HUMAN           | 2291.0778 |
| sp Q08379 GOGA2_HUMAN          | 3394.5848 |
| sp Q08379 GOGA2_HUMAN          | 3394.5848 |
| sp Q13155 AIMP2_HUMAN          | 2371.2383 |
| sp Q13155 AIMP2_HUMAN          | 2371.2383 |
| sp Q9Y230 RUVB2_HUMAN          | 2271.1495 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp Q9Y639 NPTN_HUMAN           | 3480.4775 |
| sp Q9Y639 NPTN_HUMAN           | 3480.4775 |
| sp P61978 HNRPK_HUMAN          | 1971.1153 |
| sp Q13505 MTX1_HUMAN           | 2284.16   |
| sp Q13505 MTX1_HUMAN           | 2284.16   |
| sp P0DN76 U2AF5_HUMAN,sp Q010  | 1859.8447 |
| sp P0DN76 U2AF5_HUMAN,sp Q010  | 1859.8447 |
| sp P0DN76 U2AF5_HUMAN,sp Q010  | 1859.8447 |
| sp Q6UB35 C1TM_HUMAN           | 2498.2839 |
| sp Q6UB35 C1TM_HUMAN           | 2498.2839 |
| sp Q6UB35 C1TM_HUMAN           | 2498.2839 |
| sp Q15149 PLEC_HUMAN           | 2054.0585 |
| sp P52209 6PGD_HUMAN           | 2006.0262 |
| sp Q9NZT2 OGFR_HUMAN           | 2316.2478 |
| sp Q9UUK9 NUDT5_HUMAN          | 1840.9148 |
| sp Q9UUK9 NUDT5_HUMAN          | 1840.9148 |
| sp Q02218 ODO1_HUMAN           | 3774.9541 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P61160 ARP2_HUMAN           | 1925.9743 |
| sp Q9P287 BCCIP_HUMAN          | 3058.5699 |
| sp Q9P287 BCCIP_HUMAN          | 3058.5699 |
| sp Q8IY67 RAVR1_HUMAN          | 5872.7043 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp Q9UHX1 PUF60_HUMAN          | 3517.6646 |
| sp Q9BU23 LMF2_HUMAN           | 3070.3759 |
| sp P24928 RPB1_HUMAN           | 2717.1477 |
| sp P24928 RPB1_HUMAN           | 2717.1477 |
| sp Q8WW11 LMO7_HUMAN           | 3081.5116 |
| sp Q8WWQ0 PHIP_HUMAN           | 2395.1153 |
| sp Q15428 SF3A2_HUMAN          | 2480.1754 |
| sp Q16762 THTR_HUMAN           | 2701.3136 |
| sp Q13347 EIF3I_HUMAN          | 3133.3802 |
| sp P32970 CD70_HUMAN           | 1792.8744 |
| sp Q9NP77 SSU72_HUMAN          | 2768.3446 |
| sp Q9NP77 SSU72_HUMAN          | 2768.3446 |
| sp P49327 FAS_HUMAN            | 2863.3665 |
| sp P08195 4F2_HUMAN            | 2051.9854 |
| sp P82930 RT34_HUMAN           | 2726.3453 |

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| sp Q9UKV8 AGO2_HUMAN           | 3604.6641 |
| sp Q6P996 PDXD1_HUMAN          | 2558.2976 |
| sp P43897 EFTS_HUMAN           | 3054.5273 |
| sp Q01433 AMPD2_HUMAN          | 2114.0619 |
| sp O95834 EMAL2_HUMAN          | 3278.5203 |
| sp Q15637 SF01_HUMAN           | 3131.5386 |
| sp Q15637 SF01_HUMAN           | 3131.5386 |
| sp Q9H6B4 CLMP_HUMAN           | 3809.8207 |
| sp Q92552 RT27_HUMAN           | 2652.1836 |
| sp Q9NRF8 PYRG2_HUMAN          | 2470.1587 |
| sp Q9NRF8 PYRG2_HUMAN          | 2470.1587 |
| sp Q6GMV3 PTRD1_HUMAN          | 4165.0289 |
| sp Q969Z0 FAKD4_HUMAN          | 3372.6984 |
| sp Q71UI9 H2AV_HUMAN,sp POCOS! | 2666.3552 |
| sp Q13228 SBP1_HUMAN           | 2743.397  |
| sp Q15003 CND2_HUMAN           | 1987.0448 |
| sp P11766 ADHX_HUMAN           | 3918.9687 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp Q7Z460 CLAP1_HUMAN          | 2825.3468 |
| sp Q99829 CPNE1_HUMAN          | 4462.2512 |
| sp Q96T60 PNKP_HUMAN           | 1675.8431 |
| sp Q9NQG5 RPR1B_HUMAN          | 1582.8005 |
| sp Q9NQG5 RPR1B_HUMAN          | 1582.8005 |
| sp Q6PGP7 TTC37_HUMAN          | 1979.949  |
| sp O43670 ZN207_HUMAN          | 2149.0449 |
| sp Q7L0Y3 TM10C_HUMAN          | 2367.1244 |
| sp Q7L0Y3 TM10C_HUMAN          | 2367.1244 |
| sp P30043 BLVRB_HUMAN          | 1748.8668 |
| sp P40261 NNMT_HUMAN           | 1699.8893 |
| sp Q9UBM7 DHCR7_HUMAN          | 1889.9537 |
| sp Q9UBM7 DHCR7_HUMAN          | 1889.9537 |
| sp Q9UBQ0 VPS29_HUMAN          | 2489.3134 |
| sp Q9NSD9 SYFB_HUMAN           | 2825.3595 |
| sp Q6GMV3 PTRD1_HUMAN          | 3479.6793 |
| sp O75608 LYPA1_HUMAN          | 2962.4726 |
| sp Q9BQ52 RNZ2_HUMAN           | 2914.5341 |
| sp Q56UQ5 TPT1L_HUMAN,sp P136  | 2439.2621 |
| sp Q9BQ52 RNZ2_HUMAN           | 2914.5341 |
| sp Q56UQ5 TPT1L_HUMAN,sp P136  | 2439.2621 |
| sp O60610 DIAP1_HUMAN          | 2412.2801 |
| sp Q96EP5 DAZP1_HUMAN          | 2039.8933 |
| sp P13639 EF2_HUMAN            | 1626.7638 |
| sp P05787 K2C8_HUMAN           | 1537.7736 |
| sp P30046 DOPD_HUMAN,sp A6NH   | 1709.8407 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P20618 PSB1_HUMAN           | 1543.7882 |
| sp P08195 4F2_HUMAN            | 2542.1823 |

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| sp P49458 SRP09_HUMAN          | 2406.1261 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P35998 PRS7_HUMAN           | 3544.7322 |
| sp P58107 EPIPL_HUMAN          | 3239.5809 |
| sp O00499 BIN1_HUMAN           | 2720.3367 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4761.195  |
| sp P54826 GAS1_HUMAN           | 2550.0057 |
| sp Q93052 LPP_HUMAN            | 2296.9734 |
| sp P98155 VLDLR_HUMAN          | 3006.0433 |
| sp P63220 RS21_HUMAN           | 2235.0841 |
| sp P63220 RS21_HUMAN           | 2235.0841 |
| sp Q9UNN8 EPCR_HUMAN           | 2735.2385 |
| sp Q9UNN8 EPCR_HUMAN           | 2735.2385 |
| sp P12004 PCNA_HUMAN           | 2180.0419 |
| sp Q12792 TWF1_HUMAN           | 3048.5152 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp Q9H3U1 UN45A_HUMAN          | 4045.8752 |
| sp P54826 GAS1_HUMAN           | 3843.7861 |
| sp P08582 TRFM_HUMAN           | 3611.7202 |
| sp P08582 TRFM_HUMAN           | 3611.7202 |
| sp Q13425 SNTB2_HUMAN          | 2153.1191 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp Q96RP9 EFGM_HUMAN           | 1935.9731 |
| sp Q9UHQ9 NB5R1_HUMAN          | 4026.9521 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P17174 AATC_HUMAN           | 2195.1144 |
| sp P06748 NPM_HUMAN            | 2240.0418 |
| sp O95817 BAG3_HUMAN           | 2173.0903 |
| sp Q9UNN8 EPCR_HUMAN           | 1711.7762 |
| sp Q9UNN8 EPCR_HUMAN           | 1711.7762 |
| sp Q9UNN8 EPCR_HUMAN           | 1711.7762 |
| sp O00422 SAP18_HUMAN          | 2135.0746 |
| sp P00558 PGK1_HUMAN           | 1355.5994 |
| sp P82933 RT09_HUMAN           | 1739.7897 |
| sp Q12860 CNTN1_HUMAN          | 1756.7441 |
| sp Q6UB35 C1TM_HUMAN           | 2011.9599 |
| sp P40763 STAT3_HUMAN          | 2927.3032 |
| sp P40763 STAT3_HUMAN          | 2927.3032 |
| sp Q9UK59 DBR1_HUMAN           | 1988.8687 |
| sp Q9UK59 DBR1_HUMAN           | 1988.8687 |
| sp Q9NZL9 MAT2B_HUMAN          | 2171.9443 |
| sp Q9NZL9 MAT2B_HUMAN          | 2171.9443 |

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| sp Q9BR76 COR1B_HUMAN          | 2301.012  |
| sp P31942 HNRH3_HUMAN          | 1660.7845 |
| sp Q9NRZ9 HELLS_HUMAN          | 1768.8996 |
| sp P19338 NUCL_HUMAN           | 1597.8352 |
| sp P10606 COX5B_HUMAN          | 1817.8519 |
| sp P56211 ARP19_HUMAN          | 3263.6058 |
| sp Q9NWT1 PK1IP_HUMAN          | 1887.9228 |
| sp Q9H910 JUPI2_HUMAN          | 2563.2303 |
| sp Q9H910 JUPI2_HUMAN          | 2563.2303 |
| sp Q96CP2 FWCH2_HUMAN          | 2118.0602 |
| sp Q06210 GFPT1_HUMAN          | 2055.0459 |
| sp Q9BVP2 GNL3_HUMAN           | 2035.0375 |
| sp Q9UH65 SWP70_HUMAN          | 1936.0088 |
| sp O60313 OPA1_HUMAN           | 2351.1757 |
| sp Q9UKY7 CDV3_HUMAN           | 4210.0793 |
| sp Q9Y221 NIP7_HUMAN           | 2062.0411 |
| sp Q5ZPR3 CD276_HUMAN          | 4726.2531 |
| sp P78527 PRKDC_HUMAN          | 2859.4225 |
| sp O60216 RAD21_HUMAN,sp Q9H4  | 1809.9665 |
| sp P08134 RHOC_HUMAN,sp P6158  | 2544.2835 |
| sp P08134 RHOC_HUMAN,sp P6158  | 2544.2835 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp Q9BRR6 ADPGK_HUMAN          | 2302.0324 |
| sp Q96GD4 AURKB_HUMAN          | 1976.083  |
| sp Q96GD4 AURKB_HUMAN          | 1976.083  |
| sp Q99627 CSN8_HUMAN           | 3836.0149 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp O75937 DNJC8_HUMAN          | 3674.7992 |
| sp Q96T60 PNKP_HUMAN           | 2791.4909 |
| sp Q14181 DPOA2_HUMAN          | 2402.1754 |
| sp Q14181 DPOA2_HUMAN          | 2402.1754 |
| sp P14550 AK1A1_HUMAN          | 3061.5397 |
| sp P43897 EFTS_HUMAN           | 2537.3411 |
| sp Q99627 CSN8_HUMAN           | 4675.2687 |
| sp Q9H3P2 NELFA_HUMAN          | 4184.1066 |
| sp Q9H3P2 NELFA_HUMAN          | 4184.1066 |
| sp P05204 HMG2_HUMAN           | 1780.9723 |
| sp Q9P021 CRIPT_HUMAN          | 2563.0679 |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp Q08117 TLE5_HUMAN           | 2584.1248 |
| sp Q08117 TLE5_HUMAN           | 2584.1248 |
| sp Q15041 AR6P1_HUMAN          | 1699.7988 |
| sp P50552 VASP_HUMAN           | 2041.9395 |
| sp P50552 VASP_HUMAN           | 2041.9395 |
| sp P46977 STT3A_HUMAN          | 2063.9701 |
| sp P46977 STT3A_HUMAN          | 2063.9701 |



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| sp P32970 CD70_HUMAN           | 1792.8744 |
| sp Q9UKY7 CDV3_HUMAN           | 3324.5899 |
| sp P61978 HNRPK_HUMAN          | 1971.1153 |
| sp P82930 RT34_HUMAN           | 2186.9269 |
| sp P68036 UB2L3_HUMAN,sp A0A1F | 3303.6234 |
| sp Q9NSD9 SYFB_HUMAN           | 3183.6088 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P50579 MAP2_HUMAN           | 2443.1954 |
| sp Q92508 PIEZ1_HUMAN          | 3140.6506 |
| sp P20674 COX5A_HUMAN          | 4115.1103 |
| sp P20674 COX5A_HUMAN          | 4115.1103 |
| sp Q08379 GOGA2_HUMAN          | 5561.7703 |
| sp Q9UH99 SUN2_HUMAN           | 4309.2918 |
| sp P16401 H15_HUMAN            | 1346.7558 |
| sp P13498 CY24A_HUMAN          | 2886.4737 |
| sp Q9BTX1 NDC1_HUMAN           | 2534.215  |
| sp Q96SB4 SRPK1_HUMAN,sp Q9UP  | 2707.2449 |
| sp Q9BSY4 CHCH5_HUMAN          | 2613.1774 |
| sp O00487 PSDE_HUMAN           | 1933.9931 |
| sp Q12888 TP53B_HUMAN          | 3347.6018 |
| sp Q12888 TP53B_HUMAN          | 3347.6018 |
| sp P53396 ACLY_HUMAN           | 2638.3789 |
| sp Q9GZR7 DDX24_HUMAN          | 2195.1487 |
| sp O60493 SNX3_HUMAN           | 2573.2986 |
| sp O60493 SNX3_HUMAN           | 2573.2986 |
| sp P08195 4F2_HUMAN            | 2051.9854 |
| sp Q15149 PLEC_HUMAN           | 2054.0585 |
| sp Q12872 SFSWA_HUMAN          | 2679.4306 |
| sp Q9UHA4 LTOR3_HUMAN          | 3831.9068 |
| sp Q9UHA4 LTOR3_HUMAN          | 3831.9068 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp P46940 IQGA1_HUMAN          | 2132.1954 |
| sp P37268 FDFT_HUMAN           | 3100.4349 |
| sp Q9NRX1 PNO1_HUMAN           | 2983.4815 |
| sp Q9NU22 MDN1_HUMAN           | 2735.3443 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 3714.7447 |
| sp P19784 CSK22_HUMAN          | 2028.0892 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1261.6051 |
| sp Q8N766 EMC1_HUMAN           | 1838.9639 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp Q01780 EXOSX_HUMAN          | 1740.0046 |
| sp Q01780 EXOSX_HUMAN          | 1740.0046 |
| sp Q9NNW7 TRXR2_HUMAN          | 2900.363  |
| sp Q9NNW7 TRXR2_HUMAN          | 2900.363  |
| sp P62424 RL7A_HUMAN           | 1673.8274 |
| sp Q14332 FZD2_HUMAN           | 2691.2322 |
| sp Q14332 FZD2_HUMAN           | 2691.2322 |

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| sp Q9Y4L1 HYOU1_HUMAN          | 2665.3037 |
| sp Q9Y4L1 HYOU1_HUMAN          | 2665.3037 |
| sp O75096 LRP4_HUMAN           | 2180.0585 |
| sp Q9UBQ7 GRHPR_HUMAN          | 2214.0851 |
| sp P30519 HMOX2_HUMAN          | 2379.1106 |
| sp Q9H2U2 IPYR2_HUMAN          | 2569.3005 |
| sp Q9H2U2 IPYR2_HUMAN          | 2569.3005 |
| sp O95202 LETM1_HUMAN          | 3034.624  |
| sp O95202 LETM1_HUMAN          | 3034.624  |
| sp Q9BV38 WDR18_HUMAN          | 3998.1339 |
| sp P28074 PSB5_HUMAN           | 1604.8046 |
| sp P09972 ALDOC_HUMAN          | 2811.341  |
| sp P10321 HLAC_HUMAN           | 2502.0823 |
| sp P09972 ALDOC_HUMAN          | 2811.341  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp O43813 LANC1_HUMAN          | 2733.1983 |
| sp P19338 NUCL_HUMAN           | 1827.9618 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp Q16643 DREB_HUMAN           | 2752.3344 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q04721 NOTC2_HUMAN          | 1622.7107 |
| sp P80723 BASP1_HUMAN          | 3522.6234 |
| sp P80723 BASP1_HUMAN          | 3522.6234 |
| sp P30530 UFO_HUMAN            | 2135.9178 |
| sp P30530 UFO_HUMAN            | 2135.9178 |
| sp P30530 UFO_HUMAN            | 2135.9178 |
| sp Q8N8Z6 DCBD1_HUMAN          | 2377.0319 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp Q9BVL2 NUP58_HUMAN          | 2486.1503 |
| sp Q8N4H5 TOM5_HUMAN           | 1921.9455 |
| sp P20020 AT2B1_HUMAN          | 1919.9087 |
| sp Q9BYJ9 YTHD1_HUMAN,sp Q7Z7: | 1917.9109 |
| sp Q9BYJ9 YTHD1_HUMAN,sp Q7Z7: | 1917.9109 |
| sp Q15149 PLEC_HUMAN           | 1714.8526 |
| sp O15173 PGRC2_HUMAN          | 1940.9057 |
| sp Q92692 NECT2_HUMAN          | 3279.5969 |
| sp Q92692 NECT2_HUMAN          | 3279.5969 |
| sp Q02487 DSC2_HUMAN           | 3868.9557 |
| sp Q02487 DSC2_HUMAN           | 3868.9557 |
| sp Q02487 DSC2_HUMAN           | 3868.9557 |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp P08238 HS90B_HUMAN          | 3552.5481 |
| sp O75489 NDUS3_HUMAN          | 2525.2438 |

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| sp Q00610 CLH1_HUMAN,sp P5367: | 1803.9196 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp Q14019 COTL1_HUMAN          | 2215.1273 |
| sp Q9Y4W2 LAS1L_HUMAN          | 2574.3152 |
| sp O15230 LAMA5_HUMAN          | 2745.4297 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P52294 IMA5_HUMAN           | 2742.3687 |
| sp P52294 IMA5_HUMAN           | 2742.3687 |
| sp P61221 ABCE1_HUMAN          | 4309.0849 |
| sp P61221 ABCE1_HUMAN          | 4309.0849 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp P28066 PSA5_HUMAN           | 3692.7987 |
| sp P28066 PSA5_HUMAN           | 3692.7987 |
| sp P06241 FYN_HUMAN            | 2641.3244 |
| sp P07947 YES_HUMAN            | 2805.3717 |
| sp Q04721 NOTC2_HUMAN          | 1622.7107 |
| sp Q9B XK1 KLF16_HUMAN         | 1487.7117 |
| sp Q9Y3D3 RT16_HUMAN           | 1361.651  |
| sp O43719 HTSF1_HUMAN          | 2348.9928 |
| sp Q9HB07 MYG1_HUMAN           | 1908.8788 |
| sp Q9Y2T4 2ABG_HUMAN,sp P6315  | 1880.8177 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp Q9UPN9 TRI33_HUMAN          | 1871.8915 |
| sp Q96BR5 COA7_HUMAN           | 3139.4629 |
| sp Q96BR5 COA7_HUMAN           | 3139.4629 |
| sp Q14192 FHL2_HUMAN           | 2203.8874 |
| sp Q14192 FHL2_HUMAN           | 2203.8874 |
| sp Q13523 PRP4B_HUMAN          | 1303.6884 |
| sp P51692 STA5B_HUMAN          | 2117.0178 |
| sp P36543 VATE1_HUMAN          | 1667.8883 |
| sp Q86XL3 ANKL2_HUMAN          | 2169.0127 |
| sp P36543 VATE1_HUMAN          | 1667.8883 |
| sp Q5VTL8 PR38B_HUMAN          | 2055.0095 |
| sp Q9Y5J1 UTP18_HUMAN          | 2343.1819 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp Q9UQB8 BAIP2_HUMAN          | 2202.0957 |
| sp Q9ULT8 HECD1_HUMAN          | 3798.7393 |
| sp Q9UQB8 BAIP2_HUMAN          | 2202.0957 |
| sp Q9ULT8 HECD1_HUMAN          | 3798.7393 |
| sp Q9BSH4 TACO1_HUMAN          | 2693.2715 |
| sp Q7Z6E9 RBBP6_HUMAN          | 3748.7097 |
| sp P15559 NQO1_HUMAN           | 3653.789  |
| sp Q96ME7 ZN512_HUMAN          | 2238.1532 |
| sp P08238 HS90B_HUMAN,sp Q58F1 | 2133.0783 |
| sp P21333 FLNA_HUMAN           | 2544.29   |
| sp Q15418 KS6A1_HUMAN          | 2226.0957 |
| sp Q5SSJ5 HP1B3_HUMAN          | 2182.1998 |

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| sp Q9Y2A7 NCKP1_HUMAN          | 2364.2074 |
| sp Q15257 PTPA_HUMAN           | 3432.6851 |
| sp Q9NYQ6 CELR1_HUMAN          | 2994.5451 |
| sp Q9NYQ6 CELR1_HUMAN          | 2994.5451 |
| sp Q9UP83 COG5_HUMAN           | 3265.6579 |
| sp Q9H6R0 DHX33_HUMAN          | 3446.7367 |
| sp P49184 DNSL1_HUMAN          | 3553.9072 |
| sp P28340 DPOD1_HUMAN          | 3751.8985 |
| sp Q15004 PAF15_HUMAN          | 2282.1114 |
| sp Q9H6F5 CCD86_HUMAN          | 2473.1874 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp Q96SB3 NEB2_HUMAN           | 2277.0814 |
| sp P51571 SSRD_HUMAN           | 2530.1513 |
| sp Q9H078 CLPB_HUMAN           | 2733.3035 |
| sp P84095 RHOG_HUMAN           | 2906.5363 |
| sp P84095 RHOG_HUMAN           | 2906.5363 |
| sp Q9Y237 PIN4_HUMAN           | 1746.8399 |
| sp Q9BRP8 PYM1_HUMAN           | 3700.8625 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp Q9HAV7 GRPE1_HUMAN          | 3193.5244 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp Q9HAV7 GRPE1_HUMAN          | 3193.5244 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp Q8WWY3 PRP31_HUMAN          | 3711.8421 |
| sp P07900 HS90A_HUMAN          | 2260.1164 |
| sp Q15257 PTPA_HUMAN           | 3432.6851 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4674.5347 |
| sp Q14534 ERG1_HUMAN           | 2196.1215 |
| sp P49327 FAS_HUMAN            | 2875.3925 |
| sp Q9BXS5 AP1M1_HUMAN          | 2215.1889 |
| sp Q9BXS5 AP1M1_HUMAN          | 2215.1889 |
| sp P11908 PRPS2_HUMAN          | 2739.4596 |
| sp P16403 H12_HUMAN            | 1219.6925 |
| sp Q00613 HSF1_HUMAN           | 1885.0058 |
| sp Q96EY7 PTCD3_HUMAN          | 1482.7004 |
| sp Q5U5X0 LYRM7_HUMAN          | 2325.2077 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q9NZM5 NOP53_HUMAN          | 4592.2208 |
| sp Q04912 RON_HUMAN            | 4590.085  |
| sp P08195 4F2_HUMAN            | 2051.9854 |
| sp P53992 SC24C_HUMAN          | 2503.126  |
| sp Q8WVB6 CTF18_HUMAN          | 3415.712  |
| sp O00291 HIP1_HUMAN           | 2808.4406 |
| sp P36915 GNL1_HUMAN           | 2763.2565 |
| sp Q92754 AP2C_HUMAN           | 2411.2809 |
| sp Q9NPR2 SEM4B_HUMAN          | 2128.0412 |
| sp Q96DH6 MSI2H_HUMAN          | 3094.4672 |

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| sp P49005 DPOD2_HUMAN          | 4948.1924 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp P49589 SYCC_HUMAN           | 2763.4443 |
| sp Q969V3 NCLN_HUMAN           | 1610.8165 |
| sp Q16795 NDUA9_HUMAN          | 2005.997  |
| sp Q9HCC0 MCCB_HUMAN           | 2491.1629 |
| sp Q96RQ1 ERGI2_HUMAN          | 2010.0435 |
| sp P46934 NEDD4_HUMAN          | 2114.0585 |
| sp P62993 GRB2_HUMAN           | 3612.551  |
| sp Q03426 KIME_HUMAN           | 2916.5531 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp Q5VT52 RPRD2_HUMAN          | 4331.1247 |
| sp P27361 MK03_HUMAN           | 3658.7872 |
| sp Q9H6X2 ANTR1_HUMAN          | 2772.4235 |
| sp Q9H6X2 ANTR1_HUMAN          | 2772.4235 |
| sp Q6NUM9 RETST_HUMAN          | 2878.6321 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 2727.4041 |
| sp P15121 ALDR_HUMAN           | 2405.2301 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp Q9UBI6 GBG12_HUMAN          | 2149.9045 |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 1651.9145 |
| sp Q8N1G4 LRC47_HUMAN          | 2316.2114 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp Q7Z2T5 TRM1L_HUMAN          | 2726.3875 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp Q96H55 MYO19_HUMAN          | 2120.0321 |
| sp O75369 FLNB_HUMAN           | 2072.999  |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 1576.7232 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp Q86YP4 P66A_HUMAN           | 2664.3507 |
| sp Q9Y2Z0 SGT1_HUMAN           | 2362.1086 |
| sp Q96GE9 DMAC1_HUMAN          | 3947.933  |
| sp P49327 FAS_HUMAN            | 2633.2003 |
| sp Q9BTT0 AN32E_HUMAN          | 2123.1474 |
| sp Q14BN4 SLMAP_HUMAN          | 2060.0538 |
| sp P52788 SPSY_HUMAN           | 2243.078  |
| sp Q14694 UBP10_HUMAN          | 2466.3482 |
| sp Q12824 SNF5_HUMAN           | 3081.5196 |
| sp Q96EK9 KTI12_HUMAN          | 2085.0531 |
| sp Q8TB96 TIP_HUMAN            | 3009.5712 |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp Q9UIQ6 LCAP_HUMAN           | 3664.7548 |
| sp O75940 SPF30_HUMAN          | 4286.039  |
| sp O43660 PLRG1_HUMAN          | 2146.0767 |

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| sp Q969G3 SMCE1_HUMAN          | 2135.0072 |
| sp P53367 ARFP1_HUMAN          | 2978.4258 |
| sp P55735 SEC13_HUMAN          | 4021.9745 |
| sp Q13418 ILK_HUMAN            | 1843.9105 |
| sp Q9Y3B2 EXOS1_HUMAN          | 1898.9964 |
| sp Q13601 KRR1_HUMAN           | 1879.9866 |
| sp Q01082 SPTB2_HUMAN          | 2437.1121 |
| sp Q6YP21 KAT3_HUMAN           | 2105.047  |
| sp Q9H0H5 RGAP1_HUMAN          | 2911.4902 |
| sp O00625 PIR_HUMAN            | 2574.3006 |
| sp Q9HCD6 TANC2_HUMAN          | 3571.8603 |
| sp Q9C0D5 TANC1_HUMAN          | 3586.8963 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp Q9BXS9 S26A6_HUMAN          | 3528.8473 |
| sp Q9C0B0 UNK_HUMAN            | 3689.8941 |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp P10586 PTPRF_HUMAN          | 1778.8298 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp Q00839 HNRPU_HUMAN          | 1453.6482 |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp P38646 GRP75_HUMAN          | 2534.2839 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2133.0783 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp Q6UVK1 CSPG4_HUMAN          | 3838.953  |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp P35579 MYH9_HUMAN           | 1408.6947 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2038.0371 |
| sp P11142 HSP7C_HUMAN          | 3241.5073 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2386.1839 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 2727.4041 |
| sp P15121 ALDR_HUMAN           | 2405.2301 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P13639 EF2_HUMAN            | 1598.8304 |
| sp P10586 PTPRF_HUMAN          | 1954.9385 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P62805 H4_HUMAN             | 1582.8719 |

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| sp Q15149 PLEC_HUMAN           | 2507.2366 |
| sp P07900 HS90A_HUMAN,sp Q145i | 1204.6816 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2693.1994 |
| sp P62937 PPIA_HUMAN           | 2294.1219 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P61978 HNRPK_HUMAN          | 1971.1153 |
| sp P08195 4F2_HUMAN            | 2051.9854 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp Q06830 PRDX1_HUMAN          | 3779.8254 |
| sp P32004 L1CAM_HUMAN          | 1627.8246 |
| sp P00558 PGK1_HUMAN           | 3459.7418 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P39023 RL3_HUMAN            | 1491.7973 |
| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp Q00610 CLH1_HUMAN,sp P53675 | 1892.0367 |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2018.0433 |
| sp P62937 PPIA_HUMAN           | 2294.1219 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3653.6674 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 4934.3325 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1598.8226 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P19338 NUCL_HUMAN           | 1351.666  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp P08670 VIME_HUMAN           | 1735.9356 |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp P36578 RL4_HUMAN            | 2483.2301 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp P53396 ACLY_HUMAN           | 2361.3056 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P08670 VIME_HUMAN           | 1369.7453 |

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| sp P13639 EF2_HUMAN            | 1938.8636 |
| sp P05787 K2C8_HUMAN           | 1844.8978 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P18669 PGAM1_HUMAN          | 2332.0033 |
| sp P09382 LEG1_HUMAN           | 2096.0902 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp P14174 MIF_HUMAN            | 6003.9122 |
| sp P27824 CALX_HUMAN           | 1639.7842 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P19338 NUCL_HUMAN           | 1827.9618 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P05787 K2C8_HUMAN           | 2436.2496 |
| sp Q92616 GCN1_HUMAN           | 2843.4957 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp P26640 SYVC_HUMAN           | 2518.2088 |
| sp P11021 BIP_HUMAN            | 2116.0589 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P78527 PRKDC_HUMAN          | 2471.187  |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1501.7637 |
| sp P21333 FLNA_HUMAN           | 2742.2926 |
| sp Q14204 DYHC1_HUMAN          | 3084.588  |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P13639 EF2_HUMAN            | 1938.8636 |
| sp P08729 K2C7_HUMAN           | 2466.1339 |
| sp P23284 PIIB_HUMAN           | 2113.0004 |
| sp P10586 PTPRF_HUMAN          | 4348.1135 |
| sp P58107 EPIPL_HUMAN          | 2750.3974 |
| sp P13639 EF2_HUMAN            | 2743.3229 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp P61978 HNRPK_HUMAN          | 2661.1435 |



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| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp P16401 H15_HUMAN,sp P10412  | 1381.7201 |
| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp P68366 TBA4A_HUMAN          | 2753.2028 |
| sp P62081 RS7_HUMAN            | 2719.4069 |
| sp P22314 UBA1_HUMAN           | 2805.3908 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp P29401 TKT_HUMAN            | 2475.2315 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P18621 RL17_HUMAN           | 1512.7647 |
| sp P51991 ROA3_HUMAN           | 1972.8875 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P62937 PPIA_HUMAN           | 1575.7821 |
| sp P14618 KPYM_HUMAN           | 2753.3007 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P15121 ALDR_HUMAN           | 2135.1449 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 4518.0731 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P07237 PDIA1_HUMAN          | 1482.7103 |
| sp Q00610 CLH1_HUMAN           | 1509.7464 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P62805 H4_HUMAN             | 1614.7638 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp Q06830 PRDX1_HUMAN          | 2322.1103 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q6UVK1 CSPG4_HUMAN          | 2933.6087 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P30101 PDIA3_HUMAN          | 1665.8039 |
| sp O15031 PLXB2_HUMAN          | 3126.559  |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp P52272 HNRPM_HUMAN          | 1802.8336 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1419.6895 |

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| sp Q9ULF5 S39AA_HUMAN          | 1757.906  |
| sp P49411 EFTU_HUMAN           | 1958.9408 |
| sp Q13283 G3BP1_HUMAN          | 3169.6448 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp Q8WUM4 PDC6I_HUMAN          | 2597.2472 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 3050.5812 |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp Q01082 SPTB2_HUMAN          | 2878.3733 |
| sp P14618 KPYM_HUMAN           | 2587.2853 |
| sp P62266 RS23_HUMAN           | 2044.0126 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3653.6674 |
| sp P36578 RL4_HUMAN            | 3027.6294 |
| sp P23528 COF1_HUMAN           | 1505.7072 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2404.2387 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1535.7216 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp P31948 STIP1_HUMAN          | 1817.8584 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp P08670 VIME_HUMAN           | 1768.8778 |
| sp P16401 H15_HUMAN            | 1346.7558 |
| sp O43707 ACTN4_HUMAN          | 1764.8795 |
| sp Q15149 PLEC_HUMAN           | 1637.8625 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1673.8189 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P06748 NPM_HUMAN            | 3149.7046 |
| sp P06748 NPM_HUMAN            | 3067.506  |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 1370.7082 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P62424 RL7A_HUMAN           | 1673.8274 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1440.746  |
| sp Q14204 DYHC1_HUMAN          | 1962.8782 |
| sp P07195 LDHB_HUMAN           | 2067.0623 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp P31327 CPSM_HUMAN           | 2092.0589 |

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| sp P26641 EF1G_HUMAN            | 1571.8559 |
| sp P35613 BASI_HUMAN            | 3646.6232 |
| sp O60361 NDK8_HUMAN,sp P2239   | 2603.2512 |
| sp Q9BQG0 MBB1A_HUMAN           | 2560.3034 |
| sp P02545 LMNA_HUMAN            | 2540.3221 |
| sp Q02543 RL18A_HUMAN           | 1534.7892 |
| sp P08195 4F2_HUMAN             | 2276.1298 |
| sp Q06830 PRDX1_HUMAN           | 2103.0783 |
| sp P27824 CALX_HUMAN            | 1158.5782 |
| sp P11142 HSP7C_HUMAN           | 1587.7504 |
| sp P08195 4F2_HUMAN             | 1613.8777 |
| sp Q05639 EF1A2_HUMAN,sp P68104 | 2886.4876 |
| sp P07237 PDIA1_HUMAN           | 3188.5852 |
| sp P62937 PIIA_HUMAN            | 1543.6903 |
| sp P13639 EF2_HUMAN             | 1626.7638 |
| sp P60709 ACTB_HUMAN,sp P63261  | 2555.185  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI  | 2727.4041 |
| sp Q15149 PLEC_HUMAN            | 3601.7022 |
| sp P02786 TFR1_HUMAN            | 1437.7252 |
| sp P31327 CPSM_HUMAN            | 1908.904  |
| sp Q6YHK3 CD109_HUMAN           | 2762.2824 |
| sp P60709 ACTB_HUMAN,sp P68032  | 1822.8659 |
| sp P31327 CPSM_HUMAN            | 3089.5267 |
| sp P04406 G3P_HUMAN             | 1261.6163 |
| sp P10809 CH60_HUMAN            | 2243.191  |
| sp P10809 CH60_HUMAN            | 2243.191  |
| sp P14625 ENPL_HUMAN            | 2556.1705 |
| sp P08758 ANXA5_HUMAN           | 2046.9997 |
| sp Q8N257 H2B3B_HUMAN,sp P628   | 3089.4223 |
| sp Q16695 H31T_HUMAN,sp Q6NXT   | 1602.8366 |
| sp P43121 MUC18_HUMAN           | 1471.7783 |
| sp Q00610 CLH1_HUMAN            | 2269.1743 |
| sp P49411 EFTU_HUMAN            | 1814.9713 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI  | 3345.6875 |
| sp P62491 RB11A_HUMAN,sp Q159I  | 2627.3231 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C  | 1261.6051 |
| sp P68104 EF1A1_HUMAN           | 5465.598  |
| sp P05787 K2C8_HUMAN            | 1733.8584 |
| sp P60709 ACTB_HUMAN,sp P63261  | 2539.1901 |
| sp P08670 VIME_HUMAN            | 2693.2821 |
| sp P06733 ENOA_HUMAN            | 2097.0306 |
| sp P06733 ENOA_HUMAN            | 2097.0306 |
| sp Q00610 CLH1_HUMAN            | 2040.9905 |
| sp Q00610 CLH1_HUMAN            | 2040.9905 |
| sp P02786 TFR1_HUMAN            | 2891.3184 |
| sp P42704 LPPRC_HUMAN           | 2794.4218 |
| sp P18621 RL17_HUMAN            | 1550.7511 |

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| sp Q09666 AHNK_HUMAN           | 2373.1747 |
| sp P53396 ACLY_HUMAN           | 2127.0273 |
| sp P21796 VDAC1_HUMAN          | 2004.0276 |
| sp P35579 MYH9_HUMAN,sp P3558  | 1770.9264 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P62424 RL7A_HUMAN           | 1673.8274 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp P49327 FAS_HUMAN            | 2625.2071 |
| sp P39023 RL3_HUMAN            | 1491.7973 |
| sp P21796 VDAC1_HUMAN          | 1640.8086 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P31327 CPSM_HUMAN           | 2133.026  |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp P08195 4F2_HUMAN            | 1499.8096 |
| sp P16402 H13_HUMAN,sp P10412  | 1191.6612 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2404.2387 |
| sp P62753 RS6_HUMAN            | 2391.1053 |
| sp Q01082 SPTB2_HUMAN          | 2345.0482 |
| sp Q00839 HNRPU_HUMAN          | 1453.6482 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp P46781 RS9_HUMAN            | 1654.7951 |
| sp O75367 H2AY_HUMAN           | 2727.2309 |
| sp P17301 ITA2_HUMAN           | 3283.6877 |
| sp Q9BSJ8 ESYT1_HUMAN          | 3271.6626 |
| sp P61313 RL15_HUMAN           | 1901.9384 |
| sp Q15149 PLEC_HUMAN           | 1965.0068 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1370.7082 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1613.7838 |
| sp Q9BSJ8 ESYT1_HUMAN          | 3271.6626 |
| sp P05787 K2C8_HUMAN           | 1537.7736 |
| sp P10586 PTPRF_HUMAN          | 1762.8349 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp P02786 TFR1_HUMAN           | 2875.3235 |
| sp Q14126 DSG2_HUMAN           | 2755.2838 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1467.7544 |
| sp P14618 KPYM_HUMAN           | 3213.6194 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P18621 RL17_HUMAN           | 1550.7511 |
| sp P18621 RL17_HUMAN           | 1550.7511 |
| sp P23284 PPIB_HUMAN           | 1653.8151 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |

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| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P07814 SYEP_HUMAN           | 2943.4192 |
| sp Q15149 PLEC_HUMAN           | 2118.993  |
| sp O75367 H2AY_HUMAN           | 3055.4419 |
| sp P36578 RL4_HUMAN            | 3027.6294 |
| sp P05787 K2C8_HUMAN           | 1277.5888 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1614.8175 |
| sp P13639 EF2_HUMAN            | 1938.8636 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P08195 4F2_HUMAN            | 2542.1823 |
| sp Q01082 SPTB2_HUMAN          | 1872.9218 |
| sp P62249 RS16_HUMAN           | 1924.0921 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp Q09666 AHNK_HUMAN           | 1365.6097 |
| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P52272 HNRPM_HUMAN          | 2248.1196 |
| sp P10586 PTPRF_HUMAN          | 2457.2176 |
| sp Q09666 AHNK_HUMAN           | 1759.8815 |
| sp P23921 RIR1_HUMAN           | 2504.2911 |
| sp P62937 PPIA_HUMAN           | 4122.9092 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P07900 HS90A_HUMAN,sp P0823 | 2497.2336 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1709.8195 |
| sp P05787 K2C8_HUMAN           | 1844.8978 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2711.4092 |
| sp Q99832 TCPH_HUMAN           | 2288.1689 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P09874 PARP1_HUMAN          | 1758.7849 |
| sp P49327 FAS_HUMAN            | 1775.9669 |
| sp O43707 ACTN4_HUMAN          | 2371.0321 |
| sp P07900 HS90A_HUMAN          | 2901.3929 |
| sp P46940 IQGA1_HUMAN          | 1878.9258 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P43243 MATR3_HUMAN          | 2991.4978 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1550.6485 |
| sp P11021 BIP_HUMAN            | 1512.7168 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1704.8683 |
| sp P16401 H15_HUMAN            | 2064.1103 |

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| sp P40429 RL13A_HUMAN          | 1547.9035 |
| sp O43707 ACTN4_HUMAN          | 3520.7726 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1704.8683 |
| sp P40429 RL13A_HUMAN          | 2369.1539 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P10412 H14_HUMAN            | 1307.7197 |
| sp Q00839 HNRPU_HUMAN          | 2349.0945 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P78527 PRKDC_HUMAN          | 2460.1591 |
| sp P08670 VIME_HUMAN           | 1768.8778 |
| sp P78527 PRKDC_HUMAN          | 2471.187  |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp P06733 ENOA_HUMAN           | 1268.5561 |
| sp P00338 LDHA_HUMAN           | 1874.9237 |
| sp P11586 C1TC_HUMAN           | 2561.3013 |
| sp P31327 CPSM_HUMAN           | 3066.5047 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P08195 4F2_HUMAN            | 1499.8096 |
| sp P08670 VIME_HUMAN           | 2623.3857 |
| sp P16403 H12_HUMAN            | 1261.7394 |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp P38646 GRP75_HUMAN          | 3464.6307 |
| sp Q14126 DSG2_HUMAN           | 1916.9592 |
| sp P13639 EF2_HUMAN            | 3131.6114 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3669.6623 |
| sp P31327 CPSM_HUMAN           | 4635.2856 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P15121 ALDR_HUMAN           | 2405.2301 |
| sp P62424 RL7A_HUMAN           | 2007.0425 |
| sp P35579 MYH9_HUMAN           | 1350.5913 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp P08195 4F2_HUMAN            | 1499.8096 |
| sp P21333 FLNA_HUMAN           | 4166.9604 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp P27797 CALR_HUMAN           | 1732.842  |
| sp P43243 MATR3_HUMAN          | 2921.431  |
| sp Q15149 PLEC_HUMAN           | 2337.2216 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P29401 TKT_HUMAN            | 2421.1383 |
| sp Q00839 HNRPU_HUMAN          | 1453.6482 |
| sp Q00610 CLH1_HUMAN           | 1509.7464 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |

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| sp P04406 G3P_HUMAN           | 1261.6163 |
| sp P43121 MUC18_HUMAN         | 1471.7783 |
| sp P18124 RL7_HUMAN           | 2506.1872 |
| sp P15151 PVR_HUMAN           | 2719.1569 |
| sp O00264 PGRC1_HUMAN         | 4541.0459 |
| sp P08670 VIME_HUMAN          | 1504.6794 |
| sp P10586 PTPRF_HUMAN         | 1762.8349 |
| sp Q00839 HNRPU_HUMAN         | 1769.8771 |
| sp Q13162 PRDX4_HUMAN,sp Q068 | 1555.8246 |
| sp Q00610 CLH1_HUMAN          | 2278.1991 |
| sp P10412 H14_HUMAN           | 1307.7197 |
| sp P23396 RS3_HUMAN           | 3106.6074 |
| sp Q92598 HS105_HUMAN         | 3019.4352 |
| sp P62937 PPIA_HUMAN          | 1511.6252 |
| sp P05787 K2C8_HUMAN          | 1844.8978 |
| sp P62937 PPIA_HUMAN          | 2027.9364 |
| sp P62937 PPIA_HUMAN          | 1511.6252 |
| sp P08195 4F2_HUMAN           | 2051.9854 |
| sp Q09666 AHNK_HUMAN          | 2580.1955 |
| sp P17844 DDX5_HUMAN,sp Q9284 | 1490.7075 |
| sp P38646 GRP75_HUMAN         | 2301.1012 |
| sp P10586 PTPRF_HUMAN         | 1778.8298 |
| sp P05787 K2C8_HUMAN          | 2593.1854 |
| sp P63244 RACK1_HUMAN         | 3222.5768 |
| sp P36578 RL4_HUMAN           | 2499.225  |
| sp P36578 RL4_HUMAN           | 2483.2301 |
| sp P08195 4F2_HUMAN           | 1613.8777 |
| sp P43243 MATR3_HUMAN         | 2991.4978 |
| sp P50454 SERPH_HUMAN         | 1379.6041 |
| sp P06733 ENOA_HUMAN          | 5112.559  |
| sp P08238 HS90B_HUMAN         | 1442.6718 |
| sp P09651 ROA1_HUMAN,sp Q32P5 | 2109.0266 |
| sp Q00839 HNRPU_HUMAN         | 2920.3807 |
| sp P02786 TFR1_HUMAN          | 2193.0412 |
| sp P58107 EPIPL_HUMAN         | 2614.265  |
| sp P43121 MUC18_HUMAN         | 3001.5035 |
| sp P06744 G6PI_HUMAN          | 1832.8482 |
| sp P09651 ROA1_HUMAN,sp Q32P5 | 2109.0266 |
| sp P09651 ROA1_HUMAN,sp Q32P5 | 2109.0266 |
| sp P21333 FLNA_HUMAN          | 1830.886  |
| sp P43121 MUC18_HUMAN         | 1451.6463 |
| sp P48643 TCPE_HUMAN          | 2036.0653 |
| sp O15031 PLXB2_HUMAN         | 2207.0681 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1959.0313 |
| sp P25705 ATPA_HUMAN          | 2905.5086 |
| sp P19338 NUCL_HUMAN          | 1972.8578 |
| sp P38646 GRP75_HUMAN         | 2602.2255 |

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| sp P13639 EF2_HUMAN            | 1558.8355 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp P29401 TKT_HUMAN            | 2845.4709 |
| sp P49327 FAS_HUMAN            | 2231.199  |
| sp P09429 HMGB1_HUMAN,sp B2RF  | 1716.8683 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp Q86VP6 CAND1_HUMAN          | 2366.1788 |
| sp P32004 L1CAM_HUMAN          | 3665.7923 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp P36578 RL4_HUMAN            | 1769.8407 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp Q6YHK3 CD109_HUMAN          | 1810.7659 |
| sp O75369 FLNB_HUMAN           | 3464.718  |
| sp P12268 IMDH2_HUMAN          | 2268.0407 |
| sp O00571 DDX3X_HUMAN          | 3105.5043 |
| sp P07237 PDIA1_HUMAN          | 2905.4862 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3669.6623 |
| sp P31327 CPSM_HUMAN           | 2267.1362 |
| sp P21333 FLNA_HUMAN           | 1820.8727 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp P17301 ITA2_HUMAN           | 3283.6877 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp P16403 H12_HUMAN            | 1409.7878 |
| sp P62081 RS7_HUMAN            | 1855.8813 |
| sp P23284 PPIB_HUMAN           | 1653.8151 |
| sp P61978 HNRPK_HUMAN          | 1971.1153 |
| sp P13639 EF2_HUMAN            | 1938.8636 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1673.8189 |
| sp P07737 PROF1_HUMAN          | 2111.0899 |
| sp P42704 LPPRC_HUMAN          | 2794.4218 |
| sp P42704 LPPRC_HUMAN          | 2794.4218 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1467.7544 |
| sp Q00610 CLH1_HUMAN           | 1509.7464 |
| sp P08670 VIME_HUMAN           | 1857.9724 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P10809 CH60_HUMAN           | 2561.3588 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2386.1839 |
| sp P25787 PSA2_HUMAN           | 2845.465  |
| sp P61978 HNRPK_HUMAN          | 2265.0033 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P02786 TFR1_HUMAN           | 2997.472  |



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| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp Q15233 NONO_HUMAN           | 1444.6987 |
| sp P53618 COPB_HUMAN           | 4358.1475 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P12268 IMDH2_HUMAN          | 2271.059  |
| sp P60660 MYL6_HUMAN           | 2326.1668 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P14625 ENPL_HUMAN           | 2333.0448 |
| sp P49327 FAS_HUMAN            | 1938.9608 |
| sp P49327 FAS_HUMAN            | 1439.7872 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P08729 K2C7_HUMAN           | 2419.1465 |
| sp P61247 RS3A_HUMAN           | 2358.0281 |
| sp Q15149 PLEC_HUMAN           | 2948.3101 |
| sp P62258 1433E_HUMAN          | 1713.905  |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P12814 ACTN1_HUMAN          | 1234.6306 |
| sp Q09666 AHNK_HUMAN           | 1793.8658 |
| sp Q09666 AHNK_HUMAN           | 1793.8658 |
| sp Q09666 AHNK_HUMAN           | 1807.8815 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1613.7838 |
| sp P29401 TKT_HUMAN            | 3411.5765 |
| sp P10586 PTPRF_HUMAN          | 4179.0735 |
| sp P19338 NUCL_HUMAN           | 1351.666  |
| sp P49327 FAS_HUMAN            | 1908.0316 |
| sp P07737 PROF1_HUMAN          | 2111.0899 |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P31327 CPSM_HUMAN           | 2777.3793 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp Q15149 PLEC_HUMAN           | 1424.7048 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp P11142 HSP7C_HUMAN          | 2441.0983 |
| sp P13639 EF2_HUMAN            | 1437.765  |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1581.7246 |
| sp Q00839 HNRPU_HUMAN          | 2349.0945 |
| sp Q8IWS0 PHF6_HUMAN           | 2061.8673 |
| sp P78527 PRKDC_HUMAN          | 2471.187  |
| sp O14980 XPO1_HUMAN           | 2358.1063 |
| sp P20700 LMNB1_HUMAN          | 2014.9807 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1370.7082 |
| sp Q06830 PRDX1_HUMAN          | 2119.0732 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp Q12906 ILF3_HUMAN           | 2218.1456 |
| sp P06748 NPM_HUMAN            | 2769.2267 |

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| sp P07900 HS90A_HUMAN          | 2111.0647 |
| sp P62491 RB11A_HUMAN,sp Q159I | 2627.3231 |
| sp P05787 K2C8_HUMAN           | 1537.7736 |
| sp P00558 PGK1_HUMAN           | 2724.1466 |
| sp Q00610 CLH1_HUMAN           | 2040.9905 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1467.7544 |
| sp O75369 FLNB_HUMAN           | 3606.7301 |
| sp P31327 CPSM_HUMAN           | 2967.5553 |
| sp Q7KZF4 SND1_HUMAN           | 2607.199  |
| sp P13639 EF2_HUMAN            | 2339.103  |
| sp O43707 ACTN4_HUMAN          | 2371.0321 |
| sp P62937 PPIA_HUMAN           | 2294.1219 |
| sp P05141 ADT2_HUMAN,sp Q9H0C  | 2177.047  |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P43121 MUC18_HUMAN          | 1451.6463 |
| sp P42704 LPPRC_HUMAN          | 2153.9865 |
| sp Q15149 PLEC_HUMAN           | 2118.993  |
| sp P05787 K2C8_HUMAN           | 1733.8584 |
| sp P10809 CH60_HUMAN           | 1349.7919 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P78527 PRKDC_HUMAN          | 2698.3272 |
| sp P42704 LPPRC_HUMAN          | 2794.4218 |
| sp P06748 NPM_HUMAN            | 2240.0418 |
| sp P36578 RL4_HUMAN            | 1581.7886 |
| sp P00558 PGK1_HUMAN           | 1355.5994 |
| sp P00558 PGK1_HUMAN           | 1355.5994 |
| sp Q9Y490 TLN1_HUMAN           | 2840.4053 |
| sp P11142 HSP7C_HUMAN          | 3227.4466 |
| sp P78527 PRKDC_HUMAN          | 2994.5008 |
| sp P15924 DESP_HUMAN           | 1900.0418 |
| sp Q02543 RL18A_HUMAN          | 1534.7892 |
| sp P10586 PTPRF_HUMAN          | 1908.9357 |
| sp P43121 MUC18_HUMAN          | 3439.6566 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P27816 MAP4_HUMAN           | 2169.0776 |
| sp O43390 HNRPR_HUMAN,sp O605  | 1628.7327 |
| sp P27816 MAP4_HUMAN           | 1671.8329 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp P46013 KI67_HUMAN           | 1575.8257 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2290.127  |
| sp P10586 PTPRF_HUMAN          | 3499.6428 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q969P0 IGSF8_HUMAN          | 1865.902  |

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| sp P68104 EF1A1_HUMAN          | 5325.4918 |
| sp P07919 QCR6_HUMAN,sp A0A09  | 1791.8363 |
| sp P05787 K2C8_HUMAN           | 1325.6463 |
| sp P21796 VDAC1_HUMAN          | 1724.7893 |
| sp P05787 K2C8_HUMAN           | 2436.2496 |
| sp Q15149 PLEC_HUMAN           | 1566.7103 |
| sp P49327 FAS_HUMAN            | 4251.0828 |
| sp Q00610 CLH1_HUMAN           | 1547.8712 |
| sp Q07065 CKAP4_HUMAN          | 2356.0316 |
| sp O75533 SF3B1_HUMAN          | 1995.9286 |
| sp P09874 PARP1_HUMAN          | 1586.7114 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1419.6895 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2611.2303 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P30084 ECHM_HUMAN           | 1747.8682 |
| sp P53621 COPA_HUMAN           | 2732.3406 |
| sp P30041 PRDX6_HUMAN          | 1358.6718 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2023.964  |
| sp P08729 K2C7_HUMAN           | 2284.1223 |
| sp P05141 ADT2_HUMAN           | 1989.0531 |
| sp P49327 FAS_HUMAN            | 1344.6132 |
| sp Q00839 HNRPU_HUMAN          | 1958.9949 |
| sp P78371 TCPB_HUMAN           | 1694.8628 |
| sp P16402 H13_HUMAN,sp P16401  | 1456.7773 |
| sp P10586 PTPRF_HUMAN          | 4348.1135 |
| sp Q00610 CLH1_HUMAN           | 1462.7205 |
| sp P38919 IF4A3_HUMAN          | 1793.8697 |
| sp O60506 HNRPO_HUMAN          | 1749.7999 |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp Q9BQG0 MBB1A_HUMAN          | 2560.3034 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P08195 4F2_HUMAN            | 1499.8096 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P26599 PTBP1_HUMAN          | 3687.8421 |
| sp Q58FG0 HS905_HUMAN,sp P079i | 2103.0677 |
| sp Q6UVK1 CSPG4_HUMAN          | 3720.972  |
| sp O00148 DX39A_HUMAN,sp Q138  | 1439.766  |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1892.0367 |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp Q96KR1 ZFR_HUMAN,sp Q96SI9  | 1239.5785 |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P10586 PTPRF_HUMAN          | 1778.8298 |

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| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P50990 TCPQ_HUMAN           | 2096.0174 |
| sp P14618 KPYM_HUMAN           | 1991.9874 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1506.8406 |
| sp P16401 H15_HUMAN,sp P10412  | 1381.7201 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp P06748 NPM_HUMAN            | 1219.5146 |
| sp P62937 PPIA_HUMAN           | 2294.1219 |
| sp Q15149 PLEC_HUMAN           | 2118.993  |
| sp Q00839 HNRPU_HUMAN          | 1834.885  |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P31327 CPSM_HUMAN           | 2198.1259 |
| sp Q12931 TRAP1_HUMAN          | 1900.9319 |
| sp P78527 PRKDC_HUMAN          | 2994.5008 |
| sp P10412 H14_HUMAN            | 1307.7197 |
| sp Q15233 NONO_HUMAN           | 1427.7045 |
| sp Q15233 NONO_HUMAN           | 1427.7045 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2404.2387 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P49327 FAS_HUMAN            | 1439.7872 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P16402 H13_HUMAN,sp P10412  | 2258.1794 |
| sp O00571 DDX3X_HUMAN          | 2175.9233 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp P52272 HNRPM_HUMAN          | 2103.0677 |
| sp P00558 PGK1_HUMAN           | 4677.1891 |
| sp P35579 MYH9_HUMAN           | 1350.5913 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1783.748  |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp P62987 RL40_HUMAN           | 1520.7154 |
| sp P43243 MATR3_HUMAN          | 1908.8788 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp Q01082 SPTB2_HUMAN          | 2878.3733 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P78527 PRKDC_HUMAN          | 2698.3272 |
| sp Q14103 HNRPD_HUMAN          | 1679.7865 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp P13639 EF2_HUMAN            | 1437.765  |
| sp P05141 ADT2_HUMAN,sp Q9H0C  | 2177.047  |
| sp Q02790 FKBP4_HUMAN          | 3455.6521 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp P11021 BIP_HUMAN            | 1512.7168 |

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| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q00610 CLH1_HUMAN           | 1816.8632 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P49327 FAS_HUMAN            | 1908.0316 |
| sp P04083 ANXA1_HUMAN          | 3094.507  |
| sp P17812 PYRG1_HUMAN          | 1457.6721 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp P61604 CH10_HUMAN           | 2783.4058 |
| sp Q6YHK3 CD109_HUMAN          | 2762.2824 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P53396 ACLY_HUMAN           | 2697.3538 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp P17301 ITA2_HUMAN           | 1326.584  |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp Q92616 GCN1_HUMAN           | 2843.4957 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2248.1528 |
| sp P02786 TFR1_HUMAN           | 1437.7252 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P27797 CALR_HUMAN           | 2124.96   |
| sp P09874 PARP1_HUMAN          | 1659.7252 |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp O95678 K2C75_HUMAN,sp P486  | 1593.7675 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P31327 CPSM_HUMAN           | 2485.2125 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P35579 MYH9_HUMAN           | 1811.0193 |
| sp P07900 HS90A_HUMAN,sp Q145  | 1204.6816 |
| sp P11387 TOP1_HUMAN           | 1894.7614 |
| sp O60506 HNRPQ_HUMAN          | 2238.964  |
| sp P11021 BIP_HUMAN            | 2116.0589 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2693.1994 |
| sp Q15691 MARE1_HUMAN          | 2274.1321 |
| sp P46940 IQGA1_HUMAN          | 2774.2745 |
| sp Q08945 SSRP1_HUMAN          | 2064.0375 |

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| sp Q8WUM4 PDC6I_HUMAN          | 2309.1652 |
| sp P11387 TOP1_HUMAN           | 1953.9618 |
| sp P49327 FAS_HUMAN            | 2437.2523 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P31327 CPSM_HUMAN           | 2886.5015 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp O75533 SF3B1_HUMAN          | 2206.0291 |
| sp P41252 SYIC_HUMAN           | 2500.3061 |
| sp P22314 UBA1_HUMAN           | 2805.3908 |
| sp P53396 ACLY_HUMAN           | 2361.3056 |
| sp Q15149 PLEC_HUMAN           | 2054.0585 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp Q00839 HNRPU_HUMAN          | 1893.8057 |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp P08195 4F2_HUMAN            | 1361.7078 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P62753 RS6_HUMAN            | 2391.1053 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P29401 TKT_HUMAN            | 2845.4709 |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp P15170 ERF3A_HUMAN,sp Q8IYD | 1451.7079 |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp P06744 G6PI_HUMAN           | 1641.8362 |
| sp P13639 EF2_HUMAN            | 1437.765  |
| sp P08195 4F2_HUMAN            | 1499.8096 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P04406 G3P_HUMAN            | 1420.7562 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P05783 K1C18_HUMAN          | 3551.6322 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp P07237 PDIA1_HUMAN          | 2015.9741 |
| sp P21333 FLNA_HUMAN           | 1416.7249 |
| sp P12236 ADT3_HUMAN           | 2267.1798 |
| sp P16402 H13_HUMAN,sp P10412  | 2258.1794 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P62424 RL7A_HUMAN           | 1568.7583 |
| sp P61978 HNRPK_HUMAN          | 2661.1435 |
| sp P05141 ADT2_HUMAN,sp Q9H0C  | 1885.8887 |
| sp P16401 H15_HUMAN,sp P10412  | 1233.7081 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp Q9UHB6 LIMA1_HUMAN          | 3045.3813 |
| sp Q13433 S39A6_HUMAN          | 1884.8575 |
| sp O60361 NDK8_HUMAN,sp P2239  | 2269.1532 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |

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| sp P16402 H13_HUMAN,sp P16401  | 1140.639  |
| sp P16402 H13_HUMAN,sp P16401  | 1140.639  |
| sp Q13162 PRDX4_HUMAN,sp Q068  | 1555.8246 |
| sp P08729 K2C7_HUMAN           | 1981.913  |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P32004 L1CAM_HUMAN          | 1627.8246 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P06733 ENOA_HUMAN           | 1223.6762 |
| sp P31327 CPSM_HUMAN           | 2485.2125 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp Q14152 EIF3A_HUMAN          | 2082.997  |
| sp P52272 HNRPM_HUMAN          | 2248.1196 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp Q15067 ACOX1_HUMAN          | 3271.6587 |
| sp Q9BQ04 RBM4B_HUMAN,sp Q9B   | 2269.124  |
| sp P23246 SFPO_HUMAN           | 2160.0375 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P62249 RS16_HUMAN           | 1924.0921 |
| sp P16401 H15_HUMAN            | 1065.5819 |
| sp P27797 CALR_HUMAN           | 1343.6874 |
| sp P62805 H4_HUMAN             | 1614.7638 |
| sp Q9NR30 DDX21_HUMAN          | 2410.2169 |
| sp Q8IWS0 PHF6_HUMAN           | 2501.1969 |
| sp O43390 HNRPR_HUMAN          | 3069.5084 |
| sp P21333 FLNA_HUMAN           | 1656.7025 |
| sp P78527 PRKDC_HUMAN          | 1798.856  |
| sp Q9Y490 TLN1_HUMAN           | 1975.0123 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1736.9243 |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 2611.2303 |
| sp P50990 TCPQ_HUMAN           | 2319.1464 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P08195 4F2_HUMAN            | 1361.7078 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P58107 EPIPL_HUMAN          | 2750.3974 |
| sp P14618 KPYM_HUMAN           | 1402.6663 |
| sp Q00610 CLH1_HUMAN           | 1462.7205 |
| sp P29401 TKT_HUMAN            | 1609.8352 |
| sp P23396 RS3_HUMAN            | 2196.0375 |
| sp P07237 PDIA1_HUMAN          | 4315.1213 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp P30041 PRDX6_HUMAN          | 2793.3929 |
| sp P08758 ANXA5_HUMAN          | 2046.9997 |
| sp Q92616 GCN1_HUMAN           | 2798.4194 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp Q92901 RL3L_HUMAN,sp P39023 | 1561.746  |

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| sp O00571 DDX3X_HUMAN          | 3105.5043 |
| sp P43243 MATR3_HUMAN          | 1908.8788 |
| sp P49327 FAS_HUMAN            | 2697.2969 |
| sp Q15149 PLEC_HUMAN           | 1961.8942 |
| sp P14618 KP YM_HUMAN          | 2753.3007 |
| sp P31327 CPSM_HUMAN           | 1908.904  |
| sp P39023 RL3_HUMAN            | 2007.8884 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P06733 ENOA_HUMAN           | 1223.6762 |
| sp O00299 CLIC1_HUMAN          | 2234.0491 |
| sp P83731 RL24_HUMAN           | 1644.7164 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P15121 ALDR_HUMAN           | 2405.2301 |
| sp P21333 FLNA_HUMAN           | 1830.886  |
| sp Q9P2B2 FPRP_HUMAN           | 2660.2467 |
| sp O43707 ACTN4_HUMAN          | 1574.8053 |
| sp O75369 FLNB_HUMAN           | 2326.0866 |
| sp P36578 RL4_HUMAN            | 2499.225  |
| sp P29401 TKT_HUMAN            | 3378.6554 |
| sp P62937 PPIA_HUMAN           | 1575.7821 |
| sp P16401 H15_HUMAN            | 1936.0153 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P46776 RL27A_HUMAN          | 2832.3389 |
| sp P36578 RL4_HUMAN            | 1333.6125 |
| sp P06744 G6PI_HUMAN           | 1641.8362 |
| sp P49327 FAS_HUMAN            | 2002.0484 |
| sp P68431 H31_HUMAN            | 3938.8277 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P35579 MYH9_HUMAN           | 1408.6947 |
| sp P00338 LDHA_HUMAN           | 1691.8002 |
| sp P32004 L1CAM_HUMAN          | 2041.0116 |
| sp P10809 CH60_HUMAN           | 1349.7919 |
| sp P08729 K2C7_HUMAN           | 2466.1339 |
| sp P05787 K2C8_HUMAN           | 2500.1315 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 2902.3596 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P00558 PGK1_HUMAN           | 2617.2912 |
| sp P07814 SYEP_HUMAN           | 2343.0808 |
| sp P27824 CALX_HUMAN           | 2059.9527 |
| sp Q00839 HNRPU_HUMAN          | 1492.7232 |
| sp Q06830 PRDX1_HUMAN          | 2338.1052 |
| sp P50990 TCPQ_HUMAN           | 2143.0983 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P16402 H13_HUMAN,sp P10412  | 1191.6612 |



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| sp P00558 PGK1_HUMAN           | 3475.7367 |
| sp P05787 K2C8_HUMAN           | 2230.0828 |
| sp P10809 CH60_HUMAN           | 2538.2822 |
| sp Q06830 PRDX1_HUMAN          | 2322.1103 |
| sp O76094 SRP72_HUMAN          | 2508.2748 |
| sp P05783 K1C18_HUMAN          | 2501.2975 |
| sp P05787 K2C8_HUMAN           | 2183.0243 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P48643 TCPE_HUMAN           | 2248.1562 |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 2404.2387 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P61978 HNRPK_HUMAN          | 2661.1435 |
| sp P31327 CPSM_HUMAN           | 2146.1463 |
| sp P0DMV8 HS71A_HUMAN,sp PODI  | 1613.7838 |
| sp P35579 MYH9_HUMAN           | 2022.9681 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P51991 ROA3_HUMAN           | 2765.3184 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp P62937 PIIA_HUMAN           | 4122.9092 |
| sp Q6UVK1 CSPG4_HUMAN          | 3838.953  |
| sp P27635 RL10_HUMAN           | 1874.985  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1550.6485 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |
| sp P15531 NDKA_HUMAN,sp P2239  | 1540.7886 |
| sp P62854 RS26_HUMAN           | 2353.1729 |
| sp P29401 TKT_HUMAN            | 2421.1383 |
| sp P04406 G3P_HUMAN            | 1526.6745 |
| sp P17844 DDX5_HUMAN           | 1774.856  |
| sp P62750 RL23A_HUMAN          | 2355.1958 |
| sp P17844 DDX5_HUMAN           | 1744.9108 |
| sp P62081 RS7_HUMAN            | 1855.8813 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp P43121 MUC18_HUMAN          | 1471.7783 |
| sp P62701 RS4X_HUMAN           | 2335.2689 |
| sp Q14152 EIF3A_HUMAN          | 1760.8734 |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp P26599 PTBP1_HUMAN          | 2308.2202 |
| sp Q00610 CLH1_HUMAN           | 2040.9905 |
| sp Q15149 PLEC_HUMAN           | 1424.7048 |
| sp P61981 1433G_HUMAN,sp P631C | 1699.8893 |
| sp P23528 COF1_HUMAN           | 3377.5796 |
| sp Q8NC51 PAIRB_HUMAN          | 1553.711  |
| sp Q15149 PLEC_HUMAN           | 1908.929  |
| sp Q8NC51 PAIRB_HUMAN          | 1948.9603 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |

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| sp P10586 PTPRF_HUMAN          | 1778.8298 |
| sp P10586 PTPRF_HUMAN          | 1778.8298 |
| sp P15880 RS2_HUMAN            | 1855.8774 |
| sp Q15233 NONO_HUMAN           | 1135.5298 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp P38646 GRP75_HUMAN          | 1096.5553 |
| sp P07900 HS90A_HUMAN          | 2195.0205 |
| sp P27824 CALX_HUMAN           | 2409.1576 |
| sp P16403 H12_HUMAN            | 1219.6925 |
| sp Q8NC51 PAIRB_HUMAN          | 1817.7857 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P78371 TCPB_HUMAN           | 2109.0161 |
| sp P49411 EFTU_HUMAN           | 1942.9459 |
| sp P61247 RS3A_HUMAN           | 2386.1263 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P78371 TCPB_HUMAN           | 1680.8406 |
| sp P13639 EF2_HUMAN            | 3131.6114 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp P07900 HS90A_HUMAN          | 1499.6933 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp P23396 RS3_HUMAN            | 1285.703  |
| sp P36578 RL4_HUMAN            | 1581.7886 |
| sp P38919 IF4A3_HUMAN          | 1793.8697 |
| sp P00558 PGK1_HUMAN           | 2228.028  |
| sp P62987 RL40_HUMAN,sp P62979 | 1461.7538 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp P09429 HMGB1_HUMAN,sp B2RF  | 1716.8683 |
| sp O75369 FLNB_HUMAN           | 2088.9939 |
| sp P62805 H4_HUMAN             | 1790.9237 |
| sp P04083 ANXA1_HUMAN          | 1393.6772 |
| sp Q09666 AHNK_HUMAN           | 1390.605  |
| sp P62987 RL40_HUMAN           | 1520.7154 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1490.7075 |
| sp P07910 HNRPC_HUMAN          | 2248.1522 |
| sp P14618 KPYM_HUMAN           | 1402.6663 |
| sp P52272 HNRPM_HUMAN          | 1466.7729 |
| sp P04843 RPN1_HUMAN           | 1798.9505 |
| sp P27797 CALR_HUMAN           | 1343.6874 |
| sp P78527 PRKDC_HUMAN          | 1692.8107 |
| sp P10586 PTPRF_HUMAN          | 2164.1052 |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp P27824 CALX_HUMAN           | 1893.9109 |
| sp P07900 HS90A_HUMAN          | 2286.1604 |
| sp Q14152 EIF3A_HUMAN          | 3028.6267 |
| sp P14625 ENPL_HUMAN           | 2333.0448 |

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| sp P14625 ENPL_HUMAN           | 2333.0448 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1360.7715 |
| sp Q06830 PRDX1_HUMAN          | 2338.1052 |
| sp P83731 RL24_HUMAN           | 2165.984  |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp O15371 EIF3D_HUMAN          | 2806.3994 |
| sp P23284 PPIB_HUMAN           | 1653.8151 |
| sp Q14118 DAG1_HUMAN           | 2208.1579 |
| sp P62424 RL7A_HUMAN           | 1673.8274 |
| sp P00338 LDHA_HUMAN           | 1691.8002 |
| sp Q00839 HNRPU_HUMAN          | 1096.5587 |
| sp P21333 FLNA_HUMAN           | 1416.7249 |
| sp P46940 IQGA1_HUMAN          | 2594.3262 |
| sp Q6YHK3 CD109_HUMAN          | 1381.7606 |
| sp Q92945 FUBP2_HUMAN          | 3049.4175 |
| sp P36578 RL4_HUMAN            | 1418.7405 |
| sp P15880 RS2_HUMAN            | 1745.8883 |
| sp Q05639 EF1A2_HUMAN,sp P6810 | 2886.4876 |
| sp P43243 MATR3_HUMAN          | 1972.0993 |
| sp Q14978 NOLC1_HUMAN          | 2360.2336 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P07237 PDIA1_HUMAN          | 2015.9741 |
| sp P61769 B2MG_HUMAN           | 3483.6041 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1614.8175 |
| sp Q09666 AHNK_HUMAN           | 1365.6097 |
| sp P05141 ADT2_HUMAN,sp P12230 | 1655.8308 |
| sp Q15149 PLEC_HUMAN           | 1305.7405 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P52272 HNRPM_HUMAN          | 1802.8336 |
| sp P11021 BIP_HUMAN            | 1512.7168 |
| sp Q00610 CLH1_HUMAN,sp P53670 | 1804.8996 |
| sp P10586 PTPRF_HUMAN          | 2657.2385 |
| sp P13639 EF2_HUMAN            | 1640.7934 |
| sp Q00839 HNRPU_HUMAN          | 1862.8507 |
| sp P60842 IF4A1_HUMAN          | 1785.8567 |
| sp P46940 IQGA1_HUMAN          | 1550.794  |
| sp P07205 PGK2_HUMAN,sp P00558 | 2710.2722 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P78527 PRKDC_HUMAN          | 1508.7875 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3776.7444 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp Q05639 EF1A2_HUMAN,sp P6810 | 1806.8346 |

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| sp P46777 RL5_HUMAN            | 1758.7818 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp P46940 IQGA1_HUMAN          | 1288.62   |
| sp Q00610 CLH1_HUMAN           | 2355.1495 |
| sp Q9Y262 EIF3L_HUMAN          | 3319.6302 |
| sp P84098 RL19_HUMAN           | 1614.7864 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp P62917 RL8_HUMAN            | 1306.7245 |
| sp O75369 FLNB_HUMAN           | 1770.8213 |
| sp P08238 HS90B_HUMAN          | 1577.7582 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp Q687X5 STEA4_HUMAN          | 3854.9843 |
| sp P10809 CH60_HUMAN           | 1349.7919 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q08211 DHX9_HUMAN           | 2056.1278 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q96KR1 ZFR_HUMAN,sp Q96SI9  | 1239.5785 |
| sp Q96KR1 ZFR_HUMAN,sp Q96SI9  | 1239.5785 |
| sp P52948 NUP98_HUMAN          | 2918.3228 |
| sp P38919 IF4A3_HUMAN          | 1613.7362 |
| sp P38919 IF4A3_HUMAN          | 1613.7362 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp Q00839 HNRPU_HUMAN          | 3854.6312 |
| sp P18621 RL17_HUMAN           | 1550.7511 |
| sp Q92973 TNPO1_HUMAN          | 1591.7163 |
| sp P23284 PPIB_HUMAN           | 1492.643  |
| sp P08729 K2C7_HUMAN           | 2466.1339 |
| sp P08729 K2C7_HUMAN           | 2466.1339 |
| sp P14618 KPYM_HUMAN           | 1236.5735 |
| sp P08670 VIME_HUMAN           | 1735.9356 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1739.8883 |
| sp P14618 KPYM_HUMAN           | 1236.5735 |
| sp P49327 FAS_HUMAN            | 2002.0484 |
| sp P23246 SFPO_HUMAN           | 1755.8176 |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp P12268 IMDH2_HUMAN          | 2835.4014 |
| sp P46782 RS5_HUMAN            | 2735.296  |
| sp P49327 FAS_HUMAN            | 3725.6072 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P04843 RPN1_HUMAN           | 2199.1392 |
| sp Q09666 AHNK_HUMAN           | 2506.1765 |
| sp P07900 HS90A_HUMAN          | 1499.6933 |
| sp Q15149 PLEC_HUMAN           | 1513.7446 |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp P21333 FLNA_HUMAN           | 2511.2275 |
| sp P21333 FLNA_HUMAN           | 1894.9425 |

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| sp P35579 MYH9_HUMAN,sp P3558  | 1733.7719 |
| sp P31327 CPSM_HUMAN           | 3153.5686 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1712.9097 |
| sp P38646 GRP75_HUMAN          | 3072.4651 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1360.7715 |
| sp P31327 CPSM_HUMAN           | 2646.3905 |
| sp Q06830 PRDX1_HUMAN          | 2602.2122 |
| sp P08670 VIME_HUMAN           | 1525.8464 |
| sp Q96SI9 STRBP_HUMAN,sp Q1290 | 2085.9967 |
| sp P05783 K1C18_HUMAN          | 1488.746  |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp P09429 HMGB1_HUMAN          | 1788.7955 |
| sp P23396 RS3_HUMAN            | 1654.8566 |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp P50395 GDIB_HUMAN           | 2036.9844 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1716.7678 |
| sp P23396 RS3_HUMAN            | 2050.1099 |
| sp P42704 LPPRC_HUMAN          | 2707.3911 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P06748 NPM_HUMAN            | 2240.0418 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2583.287  |
| sp P06733 ENOA_HUMAN           | 2076.0164 |
| sp P05141 ADT2_HUMAN           | 1989.0531 |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |
| sp P54709 AT1B3_HUMAN          | 1374.7507 |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |
| sp P83731 RL24_HUMAN           | 2084.9877 |
| sp P06744 G6PI_HUMAN           | 2753.222  |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P13987 CD59_HUMAN           | 1972.8659 |
| sp P31948 STIP1_HUMAN          | 1494.6779 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q13813 SPTN1_HUMAN          | 1627.7413 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp Q15437 SC23B_HUMAN          | 2676.3581 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1501.7637 |
| sp P17812 PYRG1_HUMAN          | 3079.5437 |
| sp P10586 PTPRF_HUMAN          | 4745.4019 |
| sp P22234 PUR6_HUMAN           | 1717.7552 |
| sp P62937 PPIA_HUMAN           | 4122.9092 |
| sp P68371 TBB4B_HUMAN          | 2039.9589 |
| sp Q6UVK1 CSPG4_HUMAN          | 1360.6987 |
| sp Q6UVK1 CSPG4_HUMAN          | 1360.6987 |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp P61978 HNRPK_HUMAN          | 1749.9513 |
| sp P09874 PARP1_HUMAN          | 2427.1302 |
| sp Q14118 DAG1_HUMAN           | 1932.9945 |

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| sp P20042 IF2B_HUMAN           | 2046.9833 |
| sp P49411 EFTU_HUMAN           | 2325.1893 |
| sp O95757 HS74L_HUMAN,sp P3493 | 1986.9656 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1900.0094 |
| sp Q8WUM4 PDC6I_HUMAN          | 2597.2472 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1752.9192 |
| sp Q14118 DAG1_HUMAN           | 2055.9722 |
| sp P23396 RS3_HUMAN            | 2352.1386 |
| sp P50990 TCPQ_HUMAN           | 2782.3596 |
| sp P50990 TCPQ_HUMAN           | 2782.3596 |
| sp Q08211 DHX9_HUMAN           | 2398.3182 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp P00966 ASSY_HUMAN           | 2347.1518 |
| sp Q01082 SPTB2_HUMAN          | 2563.3534 |
| sp Q8NBS9 TXND5_HUMAN          | 1913.9636 |
| sp P05141 ADT2_HUMAN           | 2253.1641 |
| sp P07437 TBB5_HUMAN           | 2902.3299 |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |
| sp P62937 PPIA_HUMAN           | 1109.5869 |
| sp P15121 ALDR_HUMAN           | 1729.8134 |
| sp O43707 ACTN4_HUMAN          | 2370.1757 |
| sp P39023 RL3_HUMAN            | 1491.7973 |
| sp Q8WUM4 PDC6I_HUMAN          | 2597.2472 |
| sp Q96DG6 CMBL_HUMAN           | 2245.991  |
| sp Q15149 PLEC_HUMAN           | 1416.6997 |
| sp P41250 GARS_HUMAN           | 1833.8242 |
| sp P08238 HS90B_HUMAN          | 2107.0698 |
| sp P11940 PABP1_HUMAN          | 1548.7573 |
| sp P05787 K2C8_HUMAN           | 1844.8978 |
| sp P23284 PPIB_HUMAN           | 2113.0004 |
| sp P78371 TCPB_HUMAN           | 2156.0022 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P27824 CALX_HUMAN           | 1639.7842 |
| sp Q24JP5 T132A_HUMAN          | 2518.2063 |
| sp Q86VP6 CAND1_HUMAN          | 2366.1788 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1580.8232 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P06744 G6PI_HUMAN           | 1832.8482 |
| sp P22234 PUR6_HUMAN           | 2493.2574 |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 3359.5425 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P17844 DDX5_HUMAN           | 3169.475  |
| sp Q14690 RRP5_HUMAN           | 1799.8802 |
| sp Q16891 MIC60_HUMAN          | 1903.9289 |
| sp O43390 HNRPR_HUMAN          | 3069.5084 |
| sp O43175 SERA_HUMAN           | 3148.6802 |

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| sp P15121 ALDR_HUMAN           | 2414.1213 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp P00338 LDHA_HUMAN           | 1838.9601 |
| sp P08195 4F2_HUMAN            | 2276.278  |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 2109.0266 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P68366 TBA4A_HUMAN          | 2022.0058 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1900.0094 |
| sp P18084 ITB5_HUMAN           | 2705.3523 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1783.748  |
| sp Q9NR30 DDX21_HUMAN          | 2260.1059 |
| sp P07737 PROF1_HUMAN          | 2203.2035 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q14847 LASP1_HUMAN          | 2006.7862 |
| sp P62280 RS11_HUMAN           | 1808.8087 |
| sp P02786 TFR1_HUMAN           | 2282.0347 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp O43707 ACTN4_HUMAN          | 3008.5091 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp Q00839 HNRPU_HUMAN          | 1476.7283 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1716.7678 |
| sp P27816 MAP4_HUMAN           | 1675.8166 |
| sp P25705 ATPA_HUMAN           | 2905.5086 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P49327 FAS_HUMAN            | 2303.1944 |
| sp P62753 RS6_HUMAN            | 2391.1053 |
| sp P62424 RL7A_HUMAN           | 2465.1744 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1651.9145 |
| sp P49327 FAS_HUMAN            | 1344.6132 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp Q08J23 NSUN2_HUMAN          | 2104.1065 |
| sp Q14527 HLTF_HUMAN           | 2600.2448 |
| sp P20700 LMNB1_HUMAN          | 2431.1656 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P42704 LPPRC_HUMAN          | 1989.0055 |
| sp P04406 G3P_HUMAN            | 2714.2422 |
| sp P58107 EPIPL_HUMAN          | 2081.0641 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1704.7995 |
| sp P46940 IQGA1_HUMAN          | 2079.0347 |
| sp P58107 EPIPL_HUMAN          | 1850.0302 |
| sp P32322 P5CR1_HUMAN          | 2214.1281 |
| sp Q13263 TIF1B_HUMAN          | 2905.4029 |
| sp Q13813 SPTN1_HUMAN          | 1723.857  |
| sp P22234 PUR6_HUMAN           | 4024.0153 |
| sp Q92900 RENT1_HUMAN          | 4027.1167 |
| sp Q16695 H31T_HUMAN,sp Q71DI  | 1531.7155 |
| sp P16402 H13_HUMAN,sp P10412  | 1169.6292 |

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| sp P62906 RL10A_HUMAN          | 1680.8247 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp P62917 RL8_HUMAN            | 1210.6346 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P49411 EFTU_HUMAN           | 3134.5118 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp P63244 RACK1_HUMAN          | 3222.5768 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1592.7181 |
| sp P32004 L1CAM_HUMAN          | 4479.1978 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp P08670 VIME_HUMAN           | 1768.8778 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P43243 MATR3_HUMAN          | 1908.8788 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1598.8226 |
| sp P07737 PROF1_HUMAN          | 2282.1001 |
| sp P36871 PGM1_HUMAN           | 2386.2129 |
| sp P38646 GRP75_HUMAN          | 1842.8934 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P61160 ARP2_HUMAN           | 2622.2424 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2603.265  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P61513 RL37A_HUMAN          | 2253.0194 |
| sp P15880 RS2_HUMAN            | 1745.8883 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P25705 ATPA_HUMAN           | 2172.0851 |
| sp P30086 PEBP1_HUMAN          | 2989.428  |
| sp O43707 ACTN4_HUMAN          | 2399.0455 |
| sp P07910 HNRPC_HUMAN          | 2264.1471 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp Q15149 PLEC_HUMAN           | 1724.8078 |
| sp Q13421 MSLN_HUMAN           | 1743.8792 |
| sp Q14152 EIF3A_HUMAN          | 1760.8734 |
| sp P30101 PDIA3_HUMAN          | 1364.6936 |
| sp P30101 PDIA3_HUMAN          | 1364.6936 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1370.7082 |
| sp P21333 FLNA_HUMAN           | 1820.8727 |
| sp Q00839 HNRPU_HUMAN          | 1476.7283 |
| sp P10809 CH60_HUMAN           | 2243.191  |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P18669 PGAM1_HUMAN          | 2332.0033 |
| sp Q16576 RBBP7_HUMAN          | 3438.5674 |



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| sp P02786 TFR1_HUMAN           | 2530.1765 |
| sp P46783 RS10_HUMAN,sp Q9NQ3  | 1905.9441 |
| sp O75475 PSIP1_HUMAN          | 1705.8385 |
| sp Q13162 PRDX4_HUMAN          | 1687.8529 |
| sp P62081 RS7_HUMAN            | 1584.8049 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P09651 ROA1_HUMAN           | 2263.0804 |
| sp P09651 ROA1_HUMAN           | 2263.0804 |
| sp Q92616 GCN1_HUMAN           | 1928.0805 |
| sp P21333 FLNA_HUMAN           | 1167.6499 |
| sp P52272 HNRPM_HUMAN          | 1859.836  |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp Q15149 PLEC_HUMAN           | 1893.9183 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1704.7811 |
| sp Q09666 AHNK_HUMAN           | 4076.1066 |
| sp P10586 PTPRF_HUMAN          | 2642.3843 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp O43390 HNRPR_HUMAN          | 2714.3116 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp Q06830 PRDX1_HUMAN          | 2338.1052 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp P78371 TCPB_HUMAN           | 1680.8406 |
| sp P49327 FAS_HUMAN            | 1908.0316 |
| sp Q15149 PLEC_HUMAN           | 1961.8942 |
| sp P07737 PROF1_HUMAN          | 2111.0899 |
| sp P38919 IF4A3_HUMAN          | 1793.8697 |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1736.9243 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P60174 TPIS_HUMAN           | 1914.9072 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1598.8226 |
| sp P29401 TKT_HUMAN            | 2421.1383 |
| sp P15531 NDKA_HUMAN,sp P2239  | 1540.7886 |
| sp P00966 ASSY_HUMAN           | 2474.2304 |
| sp P14866 HNRPL_HUMAN          | 3266.5078 |
| sp P13639 EF2_HUMAN            | 1598.8304 |
| sp P18124 RL7_HUMAN            | 2506.1872 |
| sp P27824 CALX_HUMAN           | 1158.5782 |
| sp P61247 RS3A_HUMAN           | 1541.7223 |
| sp Q15365 PCBP1_HUMAN,sp P577  | 1693.8709 |
| sp P46778 RL21_HUMAN           | 1567.7817 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 1761.8646 |
| sp P09429 HMGB1_HUMAN          | 1916.8905 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp Q01082 SPTB2_HUMAN          | 2345.0482 |
| sp Q01082 SPTB2_HUMAN          | 1872.7915 |
| sp Q09666 AHNK_HUMAN           | 1793.8658 |

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| sp P68366 TBA4A_HUMAN          | 2753.2028 |
| sp Q09666 AHNK_HUMAN           | 1441.637  |
| sp Q6UVK1 CSPG4_HUMAN          | 3838.953  |
| sp P07237 PDIA1_HUMAN          | 2015.9741 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4761.195  |
| sp P06748 NPM_HUMAN            | 1219.5146 |
| sp P05141 ADT2_HUMAN,sp Q9H0C  | 2177.047  |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1576.7232 |
| sp Q92616 GCN1_HUMAN           | 1703.957  |
| sp P32004 L1CAM_HUMAN          | 2041.0116 |
| sp P23396 RS3_HUMAN            | 2196.0375 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1360.7715 |
| sp Q9UHX1 PUF60_HUMAN          | 2913.4944 |
| sp P62249 RS16_HUMAN           | 1410.6925 |
| sp Q16695 H31T_HUMAN,sp Q71DI  | 1501.7637 |
| sp P49327 FAS_HUMAN            | 2697.2969 |
| sp P23528 COF1_HUMAN           | 1505.7072 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp Q01082 SPTB2_HUMAN          | 2904.3348 |
| sp P40926 MDHM_HUMAN           | 2695.4367 |
| sp P23284 PPIB_HUMAN           | 1501.8181 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp P58107 EPIPL_HUMAN          | 2812.3702 |
| sp P16435 NCPR_HUMAN           | 2804.3406 |
| sp Q07065 CKAP4_HUMAN          | 1564.8825 |
| sp P62913 RL11_HUMAN           | 2747.2827 |
| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp P26640 SYVC_HUMAN           | 2518.2088 |
| sp O75694 NU155_HUMAN          | 2534.3129 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P07910 HNRPC_HUMAN          | 2248.1522 |
| sp Q08J23 NSUN2_HUMAN          | 1541.766  |
| sp P13639 EF2_HUMAN            | 1444.7384 |
| sp P06748 NPM_HUMAN            | 2240.0418 |
| sp P78527 PRKDC_HUMAN          | 1391.6834 |
| sp Q6YHK3 CD109_HUMAN          | 2385.1812 |
| sp P12268 IMDH2_HUMAN          | 2268.0407 |
| sp P63104 1433Z_HUMAN,sp P3194 | 1432.6769 |
| sp P78371 TCPB_HUMAN           | 2289.1675 |
| sp Q13283 G3BP1_HUMAN          | 3169.6448 |
| sp P36578 RL4_HUMAN            | 1640.8998 |
| sp P18621 RL17_HUMAN           | 1512.7647 |
| sp P18124 RL7_HUMAN            | 1736.8199 |
| sp P08238 HS90B_HUMAN          | 1692.8067 |
| sp P07900 HS90A_HUMAN          | 1627.7882 |
| sp P46940 IQGA1_HUMAN          | 1288.62   |

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| sp P13010 XRCC5_HUMAN          | 2695.2362 |
| sp P31327 CPSM_HUMAN           | 2274.2412 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 1877.8207 |
| sp P62266 RS23_HUMAN           | 1891.9428 |
| sp Q00610 CLH1_HUMAN,sp P5367: | 2387.1203 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P18621 RL17_HUMAN           | 1097.5254 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P31327 CPSM_HUMAN           | 3323.6748 |
| sp P04406 G3P_HUMAN            | 2309.1652 |
| sp P30613 KPYR_HUMAN,sp P14618 | 2024.0466 |
| sp Q09666 AHNK_HUMAN           | 3183.5796 |
| sp P06576 ATPB_HUMAN           | 4039.0062 |
| sp Q14204 DYHC1_HUMAN          | 1776.8101 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp P04439 HLAA_HUMAN,sp P0188: | 2245.095  |
| sp P50454 SERPH_HUMAN          | 2739.4079 |
| sp P21333 FLNA_HUMAN           | 1766.7748 |
| sp P60709 ACTB_HUMAN,sp P6803: | 2391.2719 |
| sp Q9BQG0 MBB1A_HUMAN          | 2022.9681 |
| sp P55060 XPO2_HUMAN           | 2866.544  |
| sp Q15084 PDIA6_HUMAN          | 2777.3409 |
| sp P62081 RS7_HUMAN            | 2719.4069 |
| sp P27635 RL10_HUMAN           | 1874.985  |
| sp P62937 PPIA_HUMAN           | 1453.6725 |
| sp P26373 RL13_HUMAN           | 2078.032  |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp P55786 PSA_HUMAN            | 3262.6582 |
| sp Q01650 LAT1_HUMAN           | 2457.2726 |
| sp P32119 PRDX2_HUMAN          | 2059.095  |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp P10586 PTPRF_HUMAN          | 1954.9385 |
| sp P78527 PRKDC_HUMAN          | 1768.8592 |
| sp Q7KZF4 SND1_HUMAN           | 2943.4614 |
| sp P49327 FAS_HUMAN            | 1775.9669 |
| sp Q9H0A0 NAT10_HUMAN          | 2210.0103 |
| sp Q12788 TBL3_HUMAN           | 3524.7068 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P68104 EF1A1_HUMAN,sp Q5VT: | 3907.7862 |
| sp P62424 RL7A_HUMAN           | 1568.7583 |
| sp P45880 VDAC2_HUMAN          | 1637.809  |
| sp P02545 LMNA_HUMAN           | 3218.64   |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P22314 UBA1_HUMAN           | 2876.3882 |
| sp Q12788 TBL3_HUMAN           | 2119.9382 |

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| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1580.8232 |
| sp P31327 CPSM_HUMAN           | 2092.0589 |
| sp P13639 EF2_HUMAN            | 1558.8355 |
| sp P61247 RS3A_HUMAN           | 1541.7223 |
| sp Q14118 DAG1_HUMAN           | 2055.9722 |
| sp P16403 H12_HUMAN            | 1633.9152 |
| sp Q6UVK1 CSPG4_HUMAN          | 2933.6087 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3669.6623 |
| sp O75369 FLNB_HUMAN           | 1621.8498 |
| sp P62826 RAN_HUMAN            | 1885.8846 |
| sp Q14204 DYHC1_HUMAN          | 2775.2988 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp Q13813 SPTN1_HUMAN          | 1334.6579 |
| sp P52272 HNRPM_HUMAN          | 1916.0116 |
| sp P08865 RSSA_HUMAN           | 1810.9577 |
| sp O14980 XPO1_HUMAN           | 2827.2541 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1384.6735 |
| sp P19338 NUCL_HUMAN           | 1356.7289 |
| sp P13639 EF2_HUMAN            | 1470.7355 |
| sp P08758 ANXA5_HUMAN          | 2247.094  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P63244 RACK1_HUMAN          | 3222.5768 |
| sp O60506 HNRPQ_HUMAN          | 2698.3167 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1446.7355 |
| sp P23246 SFPQ_HUMAN           | 1755.8176 |
| sp P53396 ACLY_HUMAN           | 1715.873  |
| sp P49327 FAS_HUMAN            | 2788.3014 |
| sp P27797 CALR_HUMAN           | 2282.9927 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp P06744 G6PI_HUMAN           | 2753.222  |
| sp P10809 CH60_HUMAN           | 2051.08   |
| sp P30050 RL12_HUMAN           | 2237.1077 |
| sp P08195 4F2_HUMAN            | 2276.278  |
| sp P27797 CALR_HUMAN           | 1467.6882 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P181  | 1535.7216 |
| sp Q9UHD1 CHRD1_HUMAN          | 2044.0629 |
| sp P20908 CO5A1_HUMAN          | 2760.2708 |
| sp P07910 HNRPC_HUMAN          | 2406.1427 |
| sp P32004 L1CAM_HUMAN          | 1741.8862 |
| sp P31327 CPSM_HUMAN           | 2777.3793 |
| sp P07737 PROF1_HUMAN          | 3034.5652 |
| sp P11021 BIP_HUMAN            | 1928.9844 |
| sp P06756 ITAV_HUMAN           | 2298.2583 |
| sp P50895 BCAM_HUMAN           | 1612.7634 |
| sp P05388 RLAO_HUMAN           | 2319.1886 |

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| sp Q02790 FKBP4_HUMAN          | 1841.9233 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp Q13162 PRDX4_HUMAN          | 2599.2013 |
| sp P29401 TKT_HUMAN            | 2347.1366 |
| sp P62424 RL7A_HUMAN           | 1438.7205 |
| sp P16401 H15_HUMAN,sp P10412  | 1182.5881 |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp P12956 XRCC6_HUMAN          | 1895.9265 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1598.8226 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp P13804 ETFA_HUMAN           | 2380.2526 |
| sp P61978 HNRPK_HUMAN          | 1931.832  |
| sp P50895 BCAM_HUMAN           | 2579.2405 |
| sp Q09666 AHNK_HUMAN           | 1759.8815 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P05783 K1C18_HUMAN          | 1488.746  |
| sp P06748 NPM_HUMAN            | 1234.583  |
| sp P23284 PIIB_HUMAN           | 1501.8181 |
| sp P00966 ASSY_HUMAN           | 2474.2304 |
| sp Q16719 KYNU_HUMAN           | 2724.3429 |
| sp P46781 RS9_HUMAN            | 1398.7368 |
| sp P49327 FAS_HUMAN            | 1938.9608 |
| sp P17844 DDX5_HUMAN           | 1774.856  |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp P50454 SERPH_HUMAN          | 2146.0888 |
| sp Q9Y3U8 RL36_HUMAN           | 1510.7238 |
| sp Q15149 PLEC_HUMAN           | 2046.9687 |
| sp Q14315 FLNC_HUMAN,sp P2133: | 2755.3467 |
| sp P07737 PROF1_HUMAN          | 1414.7378 |
| sp P21333 FLNA_HUMAN           | 2642.2217 |
| sp Q09666 AHNK_HUMAN           | 1882.9214 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P19338 NUCL_HUMAN           | 1356.7289 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp P13010 XRCC5_HUMAN          | 1824.9622 |
| sp Q09666 AHNK_HUMAN           | 1338.6642 |
| sp P22234 PUR6_HUMAN           | 1605.8111 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1620.7831 |
| sp P10586 PTPRF_HUMAN          | 2717.2459 |
| sp P30740 ILEU_HUMAN           | 3916.8068 |
| sp P60660 MYL6_HUMAN           | 2326.1668 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp P06744 G6PI_HUMAN           | 1832.8482 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q99808 S29A1_HUMAN          | 1991.1278 |

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| sp P21333 FLNA_HUMAN           | 1531.7743 |
| sp P52272 HNRPM_HUMAN          | 1802.8336 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp O15031 PLXB2_HUMAN          | 2207.0681 |
| sp P29692 EF1D_HUMAN,sp P24534 | 1249.7394 |
| sp P26599 PTBP1_HUMAN          | 3687.8421 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp Q14C86 GAPD1_HUMAN          | 2468.1794 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp P13010 XRCC5_HUMAN          | 1487.762  |
| sp Q01082 SPTB2_HUMAN          | 1872.9218 |
| sp P05787 K2C8_HUMAN           | 2230.0828 |
| sp P29692 EF1D_HUMAN           | 1532.7583 |
| sp Q6YHK3 CD109_HUMAN          | 1457.6939 |
| sp P50991 TCPD_HUMAN           | 2135.1263 |
| sp Q16531 DDB1_HUMAN           | 2390.2417 |
| sp P13639 EF2_HUMAN            | 1048.4686 |
| sp P06733 ENOA_HUMAN           | 1223.6762 |
| sp Q00610 CLH1_HUMAN,sp P5367: | 1803.9196 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp P12236 ADT3_HUMAN           | 2027.9854 |
| sp Q6UVK1 CSPG4_HUMAN          | 1310.6579 |
| sp P49327 FAS_HUMAN            | 2303.1944 |
| sp Q9Y3F4 STRAP_HUMAN          | 2622.2813 |
| sp Q07955 SRSF1_HUMAN          | 2404.1481 |
| sp Q15365 PCBP1_HUMAN,sp P577: | 1693.8709 |
| sp P08708 RS17_HUMAN           | 1484.7446 |
| sp P62258 1433E_HUMAN          | 2596.2068 |
| sp P61313 RL15_HUMAN           | 1901.9384 |
| sp P10586 PTPRF_HUMAN          | 1778.8298 |
| sp P07910 HNRPC_HUMAN          | 2264.1471 |
| sp P05787 K2C8_HUMAN           | 2484.1366 |
| sp P61978 HNRPK_HUMAN          | 1249.6667 |
| sp Q9ULF5 S39AA_HUMAN          | 1757.906  |
| sp P49720 PSB3_HUMAN           | 2006.9983 |
| sp Q13162 PRDX4_HUMAN          | 1687.8529 |
| sp P21333 FLNA_HUMAN           | 1774.8315 |
| sp P35579 MYH9_HUMAN           | 2018.0473 |
| sp P42167 LAP2B_HUMAN          | 2669.1989 |
| sp P78527 PRKDC_HUMAN          | 1473.7715 |
| sp Q14204 DYHC1_HUMAN          | 1988.0466 |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp P06748 NPM_HUMAN            | 1219.5146 |
| sp Q08J23 NSUN2_HUMAN          | 1936.8843 |
| sp P00505 AATM_HUMAN           | 2221.0956 |
| sp P05783 K1C18_HUMAN          | 3531.6028 |

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| sp P43121 MUC18_HUMAN          | 2985.5086 |
| sp P51991 ROA3_HUMAN           | 1704.8683 |
| sp P17301 ITA2_HUMAN           | 1326.584  |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp Q96E39 RMXL1_HUMAN,sp P381  | 2095.9487 |
| sp Q9BQG0 MBB1A_HUMAN          | 1615.8457 |
| sp O75533 SF3B1_HUMAN          | 3097.4377 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P43243 MATR3_HUMAN          | 1908.8788 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P60660 MYL6_HUMAN           | 1995.8666 |
| sp O15031 PLXB2_HUMAN          | 2462.1384 |
| sp P49327 FAS_HUMAN            | 2437.2523 |
| sp Q99497 PARK7_HUMAN          | 1998.7836 |
| sp Q99497 PARK7_HUMAN          | 1998.7836 |
| sp Q9UHB6 LIMA1_HUMAN          | 2097.0127 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp P16402 H13_HUMAN,sp P16401  | 1456.7773 |
| sp P05783 K1C18_HUMAN          | 1488.746  |
| sp P11142 HSP7C_HUMAN          | 1893.8302 |
| sp P50395 GDIB_HUMAN           | 1598.7399 |
| sp Q14152 EIF3A_HUMAN          | 1461.7464 |
| sp P31948 STIP1_HUMAN          | 1817.8584 |
| sp P26373 RL13_HUMAN           | 2078.032  |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P05556 ITB1_HUMAN           | 1773.8971 |
| sp P31943 HNRH1_HUMAN          | 3196.4156 |
| sp P26641 EF1G_HUMAN           | 2785.2548 |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp P35579 MYH9_HUMAN           | 1724.9825 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3635.6542 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P63244 RACK1_HUMAN          | 2175.0233 |
| sp P17301 ITA2_HUMAN           | 1326.584  |
| sp P83731 RL24_HUMAN           | 2084.9877 |
| sp O95347 SMC2_HUMAN           | 2737.403  |
| sp P61978 HNRPK_HUMAN          | 1467.7318 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P05787 K2C8_HUMAN           | 1560.7202 |
| sp P21333 FLNA_HUMAN           | 1820.8727 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P62266 RS23_HUMAN           | 1200.52   |
| sp Q13435 SF3B2_HUMAN          | 4100.9711 |

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| sp Q00610 CLH1_HUMAN,sp P5367! | 1804.8996 |
| sp P06733 ENOA_HUMAN           | 2505.1296 |
| sp P08729 K2C7_HUMAN           | 2466.1339 |
| sp P05787 K2C8_HUMAN           | 1824.8854 |
| sp P49327 FAS_HUMAN            | 1777.921  |
| sp P46781 RS9_HUMAN            | 1654.7951 |
| sp P06733 ENOA_HUMAN           | 1793.9312 |
| sp Q15067 ACOX1_HUMAN          | 2125.1055 |
| sp Q86Y07 VRK2_HUMAN           | 2433.258  |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp P00558 PGK1_HUMAN           | 2228.028  |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P11586 C1TC_HUMAN           | 2529.2639 |
| sp P19338 NUCL_HUMAN           | 1594.8566 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P26641 EF1G_HUMAN           | 2785.2548 |
| sp P32004 L1CAM_HUMAN          | 1123.5298 |
| sp Q9P0L0 VAPA_HUMAN           | 3085.4775 |
| sp P11586 C1TC_HUMAN           | 2028.9905 |
| sp Q00610 CLH1_HUMAN           | 1816.8632 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp P16435 NCPR_HUMAN           | 2804.3406 |
| sp P08238 HS90B_HUMAN          | 3552.5481 |
| sp Q14126 DSG2_HUMAN           | 2755.2838 |
| sp Q9P0L0 VAPA_HUMAN           | 1971.9286 |
| sp P02786 TFR1_HUMAN           | 1460.7048 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp Q9BZZ5 API5_HUMAN           | 2224.1739 |
| sp P62249 RS16_HUMAN           | 1575.8872 |
| sp Q08211 DHX9_HUMAN           | 2100.9501 |
| sp P02786 TFR1_HUMAN           | 1437.7252 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3669.6623 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp Q04637 IF4G1_HUMAN,sp O4343 | 1414.6729 |
| sp P62140 PP1B_HUMAN           | 2026.9564 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp Q13283 G3BP1_HUMAN          | 3126.4909 |
| sp P09429 HMGB1_HUMAN,sp B2RI  | 1844.9632 |
| sp Q96SI9 STRBP_HUMAN,sp Q1290 | 1162.6346 |
| sp P08195 4F2_HUMAN            | 1574.8304 |
| sp Q9BQE3 TBA1C_HUMAN          | 4698.2775 |
| sp P13010 XRCC5_HUMAN          | 1487.762  |
| sp P08670 VIME_HUMAN           | 1735.9356 |



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| sp P07900 HS90A_HUMAN                       | 2901.3929 |
| sp P55072 TERA_HUMAN                        | 1911.0135 |
| sp P14618 KPYM_HUMAN                        | 1236.5735 |
| sp P12236 ADT3_HUMAN                        | 1959.0425 |
| sp P15924 DESP_HUMAN                        | 1828.9723 |
| sp P32004 L1CAM_HUMAN                       | 1741.8862 |
| sp P54819 KAD2_HUMAN                        | 1785.9373 |
| sp P08865 RSSA_HUMAN                        | 2969.4018 |
| sp Q7L5N1 CSN6_HUMAN                        | 2723.3806 |
| sp P50991 TCPD_HUMAN                        | 1911.94   |
| sp Q8IY81 SPB1_HUMAN                        | 1240.5837 |
| sp P42166 LAP2A_HUMAN,sp P42166 LAP2A_HUMAN | 3998.8995 |
| sp P22234 PUR6_HUMAN                        | 2891.2751 |
| sp P00558 PGK1_HUMAN                        | 1425.7715 |
| sp P00558 PGK1_HUMAN                        | 1425.7715 |
| sp P07900 HS90A_HUMAN,sp Q1451 HS90A_HUMAN  | 1204.6816 |
| sp Q09666 AHNK_HUMAN                        | 1441.637  |
| sp Q09666 AHNK_HUMAN                        | 1441.637  |
| sp P11586 C1TC_HUMAN                        | 2028.9905 |
| sp Q8N257 H2B3B_HUMAN,sp P628 H2B3B_HUMAN   | 3429.6697 |
| sp Q01082 SPTB2_HUMAN                       | 1578.7103 |
| sp Q16576 RBBP7_HUMAN                       | 4359.988  |
| sp Q15365 PCBP1_HUMAN                       | 2040.9972 |
| sp P32004 L1CAM_HUMAN                       | 2060.9538 |
| sp P32004 L1CAM_HUMAN                       | 2060.9538 |
| sp P08670 VIME_HUMAN                        | 1735.9356 |
| sp P31327 CPSM_HUMAN                        | 2146.1463 |
| sp O75694 NU155_HUMAN                       | 3226.706  |
| sp Q13151 ROA0_HUMAN                        | 1655.8532 |
| sp Q92901 RL3L_HUMAN,sp P39023 RL3L_HUMAN   | 1561.7161 |
| sp O43707 ACTN4_HUMAN,sp P356 ACTN4_HUMAN   | 1949.8504 |
| sp P43121 MUC18_HUMAN                       | 1470.7402 |
| sp P11940 PABP1_HUMAN                       | 2369.1032 |
| sp P22626 ROA2_HUMAN                        | 1662.8213 |
| sp P62266 RS23_HUMAN                        | 1571.8559 |
| sp P09874 PARP1_HUMAN                       | 1561.8716 |
| sp P35579 MYH9_HUMAN                        | 2614.2619 |
| sp Q00839 HNRPU_HUMAN                       | 2349.0945 |
| sp P35998 PRS7_HUMAN                        | 1318.6782 |
| sp P08238 HS90B_HUMAN,sp Q58F1 HS90B_HUMAN  | 1369.7201 |
| sp P06748 NPM_HUMAN                         | 3149.7046 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF TBA1A_HUMAN   | 1576.7232 |
| sp P07814 SYEP_HUMAN                        | 2113.9813 |
| sp P17844 DDX5_HUMAN                        | 2147.0859 |
| sp P63173 RL38_HUMAN                        | 2010.0197 |
| sp Q13162 PRDX4_HUMAN,sp Q068 PRDX4_HUMAN   | 1555.8246 |
| sp P60709 ACTB_HUMAN,sp P68032 ACTB_HUMAN   | 2563.0955 |

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| sp Q9Y262 EIF3L_HUMAN          | 1837.8959 |
| sp P04843 RPN1_HUMAN           | 1674.7849 |
| sp P53621 COPA_HUMAN           | 2898.3317 |
| sp P61978 HNRPK_HUMAN          | 2661.1435 |
| sp P26639 SYTC_HUMAN           | 1645.7372 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P61247 RS3A_HUMAN           | 1921.8669 |
| sp P11940 PABP1_HUMAN          | 2015.9986 |
| sp P00558 PGK1_HUMAN           | 1927.8548 |
| sp P62701 RS4X_HUMAN           | 2802.2694 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 2273.1256 |
| sp P31948 STIP1_HUMAN          | 1896.8755 |
| sp P07900 HS90A_HUMAN          | 1499.6933 |
| sp P05787 K2C8_HUMAN           | 1824.8854 |
| sp P62424 RL7A_HUMAN           | 1522.8144 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P22234 PUR6_HUMAN           | 1717.7552 |
| sp P08195 4F2_HUMAN            | 2542.1823 |
| sp Q02790 FKBP4_HUMAN          | 1841.9233 |
| sp Q9P2B2 FPRP_HUMAN           | 2471.0666 |
| sp P62277 RS13_HUMAN           | 1577.8777 |
| sp Q96A72 MGN2_HUMAN,sp P613:  | 1147.5298 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1704.7811 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1704.7811 |
| sp P78371 TCPB_HUMAN           | 2109.0161 |
| sp P0DMV8 HS71A_HUMAN,sp PODI  | 2412.0791 |
| sp P14618 KPYM_HUMAN           | 2072.9945 |
| sp P62249 RS16_HUMAN           | 1924.0921 |
| sp P62249 RS16_HUMAN           | 1924.0921 |
| sp P07205 PGK2_HUMAN,sp P00558 | 2710.2722 |
| sp P26368 U2AF2_HUMAN          | 3353.7044 |
| sp P12956 XRCC6_HUMAN          | 2003.98   |
| sp Q04637 IF4G1_HUMAN          | 1463.766  |
| sp Q14847 LASP1_HUMAN          | 1473.6347 |
| sp P08238 HS90B_HUMAN          | 1692.8067 |
| sp P07900 HS90A_HUMAN          | 1627.7882 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1283.7125 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1900.0094 |
| sp Q9BXP5 SRRT_HUMAN           | 2638.265  |
| sp P23528 COF1_HUMAN           | 2499.17   |
| sp P09622 DLDH_HUMAN           | 2528.1291 |
| sp P61978 HNRPK_HUMAN          | 1467.7318 |
| sp P45880 VDAC2_HUMAN          | 1920.824  |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P31327 CPSM_HUMAN           | 2092.0589 |
| sp P18621 RL17_HUMAN           | 1097.5254 |
| sp P13639 EF2_HUMAN            | 1910.9473 |

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| sp P43121 MUC18_HUMAN          | 1471.7783 |
| sp P35579 MYH9_HUMAN           | 1408.6947 |
| sp P49327 FAS_HUMAN            | 2804.2963 |
| sp P50990 TCPQ_HUMAN           | 2191.0514 |
| sp Q6P2Q9 PRP8_HUMAN           | 1617.8726 |
| sp P45880 VDAC2_HUMAN          | 1752.8206 |
| sp P32322 P5CR1_HUMAN          | 2723.4065 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P38159 RBMX_HUMAN           | 1406.683  |
| sp P07814 SYEP_HUMAN           | 2152.0225 |
| sp P18621 RL17_HUMAN           | 1566.746  |
| sp P55265 DSRAD_HUMAN          | 2575.1505 |
| sp P16402 H13_HUMAN,sp P10412  | 1191.6612 |
| sp P39023 RL3_HUMAN            | 2443.206  |
| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 1544.8273 |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 2693.1994 |
| sp Q9UBX3 DIC_HUMAN            | 3671.8948 |
| sp P43121 MUC18_HUMAN          | 2985.5086 |
| sp P10586 PTPRF_HUMAN          | 2164.1052 |
| sp Q14114 LRP8_HUMAN           | 2648.301  |
| sp Q09666 AHNK_HUMAN           | 1411.6264 |
| sp P04843 RPN1_HUMAN           | 1960.0266 |
| sp Q9Y3T9 NOC2L_HUMAN          | 2298.1289 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3669.6623 |
| sp Q8NBS9 TXND5_HUMAN          | 1913.9636 |
| sp P50990 TCPQ_HUMAN           | 2494.289  |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp P02786 TFR1_HUMAN           | 2331.2032 |
| sp P00966 ASSY_HUMAN           | 1324.583  |
| sp Q6YHK3 CD109_HUMAN          | 2628.198  |
| sp P50395 GDIB_HUMAN,sp P31150 | 2475.207  |
| sp P22314 UBA1_HUMAN           | 2805.3908 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp Q6UVK1 CSPG4_HUMAN          | 1310.6579 |
| sp P11940 PABP1_HUMAN          | 1548.7573 |
| sp P62424 RL7A_HUMAN           | 1547.8308 |
| sp Q969G5 CAVN3_HUMAN          | 2152.0396 |
| sp O14980 XPO1_HUMAN           | 1848.9305 |
| sp P46940 IQGA1_HUMAN          | 1878.9258 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp O60361 NDK8_HUMAN,sp P1553  | 1997.9364 |
| sp P26639 SYTC_HUMAN           | 1944.9793 |
| sp P50991 TCPD_HUMAN           | 1498.8395 |
| sp P30048 PRDX3_HUMAN          | 3581.6409 |
| sp P62906 RL10A_HUMAN          | 1680.8247 |
| sp P31327 CPSM_HUMAN           | 2579.2499 |

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| sp P30086 PEBP1_HUMAN          | 2767.3049 |
| sp Q13283 G3BP1_HUMAN          | 3347.6649 |
| sp P31327 CPSM_HUMAN           | 3181.6059 |
| sp P21333 FLNA_HUMAN           | 1875.8309 |
| sp Q00610 CLH1_HUMAN           | 1812.7447 |
| sp P36871 PGM1_HUMAN           | 2032.0153 |
| sp P31327 CPSM_HUMAN           | 3013.4557 |
| sp Q9UHB6 LIMA1_HUMAN          | 2097.0127 |
| sp Q13813 SPTN1_HUMAN          | 1652.8158 |
| sp P46940 IQGA1_HUMAN          | 1664.837  |
| sp P07900 HS90A_HUMAN          | 1785.901  |
| sp Q8NC51 PAIRB_HUMAN          | 1465.7161 |
| sp P36578 RL4_HUMAN            | 2499.225  |
| sp P02545 LMNA_HUMAN           | 1334.6103 |
| sp P13929 ENOB_HUMAN,sp P0910  | 1930.9822 |
| sp P49327 FAS_HUMAN            | 2002.0484 |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp Q6YHK3 CD109_HUMAN          | 3212.6717 |
| sp Q14103 HNRPD_HUMAN          | 1771.8563 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp P10586 PTPRF_HUMAN          | 2432.1397 |
| sp P23528 COF1_HUMAN,sp Q9Y28  | 2186.0936 |
| sp P62987 RL40_HUMAN,sp P62979 | 1477.7487 |
| sp P06756 ITAV_HUMAN           | 2624.1523 |
| sp Q14103 HNRPD_HUMAN          | 1679.7865 |
| sp Q00839 HNRPU_HUMAN          | 3854.6312 |
| sp Q09666 AHNK_HUMAN           | 1759.8815 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp Q09666 AHNK_HUMAN           | 3183.5796 |
| sp Q7Z794 K2C1B_HUMAN,sp O956  | 1278.6245 |
| sp P29401 TKT_HUMAN            | 1609.8352 |
| sp Q06830 PRDX1_HUMAN          | 2322.1103 |
| sp P26641 EF1G_HUMAN           | 1319.651  |
| sp Q9UHD1 CHRD1_HUMAN          | 2044.0629 |
| sp O76094 SRP72_HUMAN          | 2508.2748 |
| sp P13010 XRCC5_HUMAN          | 3686.7812 |
| sp P27816 MAP4_HUMAN           | 2185.1127 |
| sp Q86VP6 CAND1_HUMAN          | 2864.4055 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp Q99832 TCPH_HUMAN           | 2288.1689 |
| sp P05783 K1C18_HUMAN          | 2389.1974 |
| sp Q00839 HNRPU_HUMAN          | 1476.7283 |
| sp Q7KZF4 SND1_HUMAN           | 2607.199  |
| sp Q9P0L0 VAPA_HUMAN           | 2789.2829 |
| sp Q9P0L0 VAPA_HUMAN           | 2789.2829 |

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| sp Q14240 IF4A2_HUMAN,sp P6084 | 1581.7246 |
| sp P35580 MYH10_HUMAN          | 1724.9825 |
| sp Q9H361 PABP3_HUMAN,sp P119  | 1738.9618 |
| sp Q15149 PLEC_HUMAN           | 2507.2366 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1370.7082 |
| sp P17844 DDX5_HUMAN           | 3169.475  |
| sp P22087 FBRL_HUMAN           | 1957.0421 |
| sp Q13283 G3BP1_HUMAN          | 4291.0611 |
| sp P83731 RL24_HUMAN           | 1563.7569 |
| sp Q9UNX3 RL26L_HUMAN,sp P612! | 1311.6208 |
| sp P62249 RS16_HUMAN           | 1410.6925 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P19338 NUCL_HUMAN           | 2346.9764 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P62937 PPIA_HUMAN           | 2294.1219 |
| sp P99999 CYC_HUMAN            | 2332.0933 |
| sp Q16576 RBBP7_HUMAN          | 4304.9808 |
| sp P78371 TCPB_HUMAN           | 1688.9097 |
| sp P78371 TCPB_HUMAN           | 1688.9097 |
| sp P50990 TCPQ_HUMAN           | 1976.9765 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P07814 SYEP_HUMAN           | 2113.9813 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 1761.8646 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1892.0367 |
| sp P17812 PYRG1_HUMAN          | 1457.6721 |
| sp P54819 KAD2_HUMAN           | 3038.3968 |
| sp Q92973 TNPO1_HUMAN          | 1591.7163 |
| sp P27824 CALX_HUMAN           | 1158.5782 |
| sp P62263 RS14_HUMAN           | 1479.7318 |
| sp P17844 DDX5_HUMAN           | 2107.9018 |
| sp P52597 HNRPF_HUMAN          | 1542.8042 |
| sp P12270 TPR_HUMAN            | 1219.6561 |
| sp P55265 DSRAD_HUMAN          | 1639.7631 |
| sp Q58FF6 H90B4_HUMAN,sp P079! | 2211.0695 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P06733 ENOA_HUMAN           | 1467.7821 |
| sp P00966 ASSY_HUMAN           | 1324.583  |
| sp P62750 RL23A_HUMAN          | 2483.2908 |
| sp O14617 AP3D1_HUMAN          | 2657.3119 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp Q06830 PRDX1_HUMAN          | 3779.8254 |
| sp Q05639 EF1A2_HUMAN,sp P681! | 2362.2896 |
| sp P16403 H12_HUMAN            | 1065.6182 |
| sp P49327 FAS_HUMAN            | 1439.7872 |
| sp Q9BZE4 NOG1_HUMAN           | 1759.8278 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |

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| sp P23396 RS3_HUMAN            | 2196.0375 |
| sp P20908 CO5A1_HUMAN          | 1478.6902 |
| sp P17987 TCPA_HUMAN           | 1729.9251 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 1560.7573 |
| sp P09874 PARP1_HUMAN          | 1738.7798 |
| sp P19338 NUCL_HUMAN           | 1972.8578 |
| sp P10809 CH60_HUMAN           | 1382.7479 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P21333 FLNA_HUMAN           | 1653.7821 |
| sp P11387 TOP1_HUMAN           | 2405.2261 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1490.7075 |
| sp P14618 KPYM_HUMAN           | 1717.8127 |
| sp P50995 ANX11_HUMAN          | 2360.9856 |
| sp Q9Y4W6 AFG32_HUMAN          | 2248.0509 |
| sp P18669 PGAM1_HUMAN          | 2332.0033 |
| sp Q96FW1 OTUB1_HUMAN          | 2372.1285 |
| sp Q06830 PRDX1_HUMAN          | 2179.0433 |
| sp P27635 RL10_HUMAN           | 1372.583  |
| sp Q01082 SPTB2_HUMAN          | 1578.7103 |
| sp P13639 EF2_HUMAN            | 1470.7355 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 3923.7811 |
| sp P17844 DDX5_HUMAN           | 2881.4498 |
| sp Q9BQG0 MBB1A_HUMAN          | 1418.8133 |
| sp Q02878 RL6_HUMAN            | 1165.5298 |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp Q96E39 RMXL1_HUMAN,sp P381  | 2095.9487 |
| sp P50395 GDIB_HUMAN,sp P31150 | 2685.3115 |
| sp Q9HCU4 CELR2_HUMAN          | 2100.0099 |
| sp P62917 RL8_HUMAN            | 1515.7682 |
| sp P07900 HS90A_HUMAN          | 2286.1604 |
| sp P06733 ENOA_HUMAN           | 2505.1296 |
| sp O75369 FLNB_HUMAN           | 1340.6976 |
| sp P53621 COPA_HUMAN           | 1485.6922 |
| sp P11940 PABP1_HUMAN          | 2015.9986 |
| sp P78527 PRKDC_HUMAN          | 2994.5008 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P30101 PDIA3_HUMAN          | 1711.7842 |
| sp P18669 PGAM1_HUMAN          | 2311.1518 |
| sp P18124 RL7_HUMAN            | 2440.1003 |
| sp Q13151 ROA0_HUMAN           | 1655.8532 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp P43121 MUC18_HUMAN          | 1471.7783 |
| sp Q8TEM1 PO210_HUMAN          | 1851.8428 |
| sp O15031 PLXB2_HUMAN          | 2446.1435 |
| sp Q08945 SSRP1_HUMAN          | 1806.9    |

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| sp Q13263 TIF1B_HUMAN          | 1989.954  |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P08621 RU17_HUMAN           | 1555.6362 |
| sp Q96QK1 VPS35_HUMAN          | 2258.1583 |
| sp P06899 H2B1J_HUMAN,sp P5705 | 1164.5663 |
| sp Q8IWS0 PHF6_HUMAN           | 2561.0841 |
| sp P02786 TFR1_HUMAN           | 1410.7718 |
| sp P21333 FLNA_HUMAN           | 1390.7092 |
| sp P12956 XRCC6_HUMAN          | 1237.6303 |
| sp Q13838 DX39B_HUMAN          | 1834.8486 |
| sp Q96E39 RMXL1_HUMAN,sp P381  | 1676.6438 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 3320.5296 |
| sp Q00610 CLH1_HUMAN           | 1547.8712 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P23284 PPIB_HUMAN           | 1767.8713 |
| sp Q9UHX1 PUF60_HUMAN          | 2913.4944 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1384.6735 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1614.8175 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp Q15149 PLEC_HUMAN           | 1640.8621 |
| sp O15031 PLXB2_HUMAN          | 2207.0681 |
| sp P00966 ASSY_HUMAN           | 2347.1518 |
| sp P63244 RACK1_HUMAN          | 3222.5768 |
| sp Q6P2Q9 PRP8_HUMAN           | 1617.8726 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P40926 MDHM_HUMAN           | 2695.4367 |
| sp Q5JTH9 RRP12_HUMAN          | 3013.5338 |
| sp Q8NC51 PAIRB_HUMAN          | 1948.9603 |
| sp P23921 RIR1_HUMAN           | 2504.2911 |
| sp P32969 RL9_HUMAN            | 2257.0984 |
| sp Q15149 PLEC_HUMAN           | 1467.6049 |
| sp Q9UHB6 LIMA1_HUMAN          | 2097.0127 |
| sp O43390 HNRPR_HUMAN          | 3197.6033 |
| sp P63244 RACK1_HUMAN          | 1600.8283 |
| sp Q01082 SPTB2_HUMAN          | 2121.0048 |
| sp P17987 TCPA_HUMAN           | 2818.5076 |
| sp P46060 RAGP1_HUMAN          | 2772.4157 |
| sp Q8N1F7 NUP93_HUMAN          | 2197.163  |
| sp P55145 MANF_HUMAN           | 2120.1266 |
| sp Q13263 TIF1B_HUMAN          | 1413.7405 |
| sp P17812 PYRG1_HUMAN          | 1457.6721 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp Q6UVK1 CSPG4_HUMAN          | 2933.6087 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P05783 K1C18_HUMAN          | 1440.7209 |

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| sp P23284 PPIB_HUMAN           | 1653.8151 |
| sp P61247 RS3A_HUMAN           | 2101.9626 |
| sp P31327 CPSM_HUMAN           | 1575.7682 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp P04843 RPN1_HUMAN           | 2322.1703 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp Q86VP6 CAND1_HUMAN          | 2366.1788 |
| sp P34897 GLYM_HUMAN           | 2183.0528 |
| sp P62081 RS7_HUMAN            | 1161.6394 |
| sp P05141 ADT2_HUMAN           | 1619.8308 |
| sp P62805 H4_HUMAN             | 1790.9237 |
| sp P09429 HMGB1_HUMAN          | 1788.7955 |
| sp P07737 PROF1_HUMAN          | 2282.1001 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P06748 NPM_HUMAN            | 3141.4812 |
| sp Q14980 NUMA1_HUMAN          | 1995.8882 |
| sp P26639 SYTC_HUMAN           | 1645.7372 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 1761.8646 |
| sp P26641 EF1G_HUMAN           | 1319.651  |
| sp Q06830 PRDX1_HUMAN          | 2103.0783 |
| sp P13639 EF2_HUMAN            | 2673.3472 |
| sp P50238 CRIP1_HUMAN          | 1724.7399 |
| sp Q14204 DYHC1_HUMAN          | 2240.0532 |
| sp Q7KZF4 SND1_HUMAN           | 2228.9949 |
| sp Q7KZF4 SND1_HUMAN           | 2228.9949 |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1370.7082 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1461.6664 |
| sp P23284 PPIB_HUMAN           | 2425.1438 |
| sp Q13310 PABP4_HUMAN          | 1601.7256 |
| sp O00571 DDX3X_HUMAN          | 2008.0728 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp P53396 ACLY_HUMAN           | 1715.873  |
| sp P62829 RL23_HUMAN           | 2123.9946 |
| sp P07195 LDHB_HUMAN           | 1704.8644 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3923.7811 |
| sp Q13263 TIF1B_HUMAN          | 2005.9489 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp P07910 HNRPC_HUMAN,sp PODN  | 1640.9138 |
| sp O00231 PSD11_HUMAN          | 1676.8734 |
| sp P55072 TERA_HUMAN           | 1825.8305 |
| sp P62851 RS25_HUMAN           | 2011.0262 |
| sp P12268 IMDH2_HUMAN          | 2042.8786 |
| sp Q02878 RL6_HUMAN            | 1556.7835 |



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| sp P41091 IF2G_HUMAN,sp Q2VIR3 | 3621.8137 |
| sp P49327 FAS_HUMAN            | 3666.8134 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P55795 HNRH2_HUMAN,sp P319  | 2350.1329 |
| sp Q92841 DDX17_HUMAN          | 2179.9051 |
| sp P31943 HNRH1_HUMAN          | 3196.4156 |
| sp P04350 TBB4A_HUMAN,sp Q3ZCI | 3776.7444 |
| sp Q6FI13 H2A2A_HUMAN,sp P2067 | 2538.4785 |
| sp O00505 IMA4_HUMAN           | 4055.9899 |
| sp P21796 VDAC1_HUMAN          | 1724.7893 |
| sp P04843 RPN1_HUMAN           | 1940.0037 |
| sp P51991 ROA3_HUMAN           | 1576.7733 |
| sp Q9P2B2 FPRP_HUMAN           | 1793.92   |
| sp P08758 ANXA5_HUMAN          | 1659.8144 |
| sp P08708 RS17_HUMAN           | 1380.6925 |
| sp P62424 RL7A_HUMAN           | 2337.0795 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P43121 MUC18_HUMAN          | 2985.5086 |
| sp Q99714 HCD2_HUMAN           | 3883.9893 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp Q9Y624 JAM1_HUMAN           | 2569.4116 |
| sp Q07065 CKAP4_HUMAN          | 1850.9989 |
| sp P36776 LONM_HUMAN           | 2005.019  |
| sp P08758 ANXA5_HUMAN          | 3066.4645 |
| sp P61313 RL15_HUMAN           | 1915.9541 |
| sp P00558 PGK1_HUMAN           | 1927.8548 |
| sp P78371 TCPB_HUMAN           | 1680.8406 |
| sp P06748 NPM_HUMAN            | 1541.7396 |
| sp P27824 CALX_HUMAN           | 2425.1525 |
| sp P62280 RS11_HUMAN           | 2538.2748 |
| sp Q15392 DHC24_HUMAN          | 1942.8843 |
| sp P00338 LDHA_HUMAN           | 2270.1067 |
| sp Q92499 DDX1_HUMAN           | 2012.0037 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P31327 CPSM_HUMAN           | 2970.4215 |
| sp P78347 GTF2I_HUMAN          | 3221.5881 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp P62263 RS14_HUMAN           | 1559.8671 |
| sp P38646 GRP75_HUMAN          | 3072.4651 |
| sp P12956 XRCC6_HUMAN          | 2230.1418 |
| sp P62424 RL7A_HUMAN           | 1793.906  |
| sp P60174 TPIS_HUMAN           | 3443.7031 |
| sp Q14974 IMB1_HUMAN           | 2194.1481 |
| sp O75533 SF3B1_HUMAN          | 1995.9286 |
| sp P09874 PARP1_HUMAN          | 1561.8716 |
| sp Q24JP5 T132A_HUMAN          | 2518.2063 |
| sp P62851 RS25_HUMAN           | 1579.8821 |

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| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp P08133 ANXA6_HUMAN          | 2295.1053 |
| sp Q13151 ROA0_HUMAN           | 1655.8532 |
| sp P02786 TFR1_HUMAN           | 1663.7326 |
| sp P07814 SYEP_HUMAN           | 2075.0245 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q9BY67 CADM1_HUMAN          | 3001.5008 |
| sp P10809 CH60_HUMAN           | 2243.191  |
| sp P83881 RL36A_HUMAN,sp Q969C | 1461.7001 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P14618 KPYM_HUMAN           | 1863.8924 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P47897 SYQ_HUMAN            | 2051.0324 |
| sp O00231 PSD11_HUMAN          | 3359.7361 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q12931 TRAP1_HUMAN          | 1900.9319 |
| sp Q16630 CPSF6_HUMAN          | 3170.455  |
| sp P09622 DLDH_HUMAN           | 2393.2227 |
| sp P62829 RL23_HUMAN           | 1443.7973 |
| sp P09382 LEG1_HUMAN           | 1678.7627 |
| sp P63244 RACK1_HUMAN          | 2175.0233 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp P62424 RL7A_HUMAN           | 2465.1744 |
| sp P26447 S10A4_HUMAN          | 1878.8822 |
| sp P50991 TCPD_HUMAN           | 1729.8635 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp P06748 NPM_HUMAN            | 3141.4812 |
| sp Q71U36 TBA1A_HUMAN,sp P0DP  | 2611.2303 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2768.3367 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp P62937 PPIA_HUMAN           | 1109.5869 |
| sp P55884 EIF3B_HUMAN          | 1996.9465 |
| sp P49327 FAS_HUMAN            | 3666.8134 |
| sp P11586 C1TC_HUMAN           | 1832.9381 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp Q14978 NOLC1_HUMAN          | 2360.2336 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18I  | 1419.6895 |
| sp Q9ULF5 S39AA_HUMAN          | 1456.6874 |
| sp Q6YHK3 CD109_HUMAN          | 1810.7659 |
| sp P21796 VDAC1_HUMAN          | 2142.0342 |
| sp P14174 MIF_HUMAN            | 6700.2789 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp P62805 H4_HUMAN             | 1806.9186 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1752.9192 |
| sp Q9BZE4 NOG1_HUMAN           | 1759.8278 |

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| sp Q16891 MIC60_HUMAN          | 1747.8278 |
| sp P00533 EGFR_HUMAN           | 2975.4083 |
| sp P61020 RAB5B_HUMAN,sp P2033 | 1958.0183 |
| sp P00558 PGK1_HUMAN           | 2500.2175 |
| sp P13639 EF2_HUMAN            | 1048.4686 |
| sp P23284 PIIB_HUMAN           | 1346.6314 |
| sp P13639 EF2_HUMAN            | 1626.7638 |
| sp P13010 XRCC5_HUMAN          | 2090.0433 |
| sp Q8NBS9 TXND5_HUMAN          | 1913.9636 |
| sp P14649 MYL6B_HUMAN,sp P6061 | 2159.1222 |
| sp P62750 RL23A_HUMAN          | 1147.5986 |
| sp P62750 RL23A_HUMAN          | 1147.5986 |
| sp Q13283 G3BP1_HUMAN          | 3126.4909 |
| sp P49915 GUAA_HUMAN           | 2206.1746 |
| sp P20700 LMNB1_HUMAN          | 2014.9807 |
| sp P19338 NUCL_HUMAN           | 1351.666  |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P23396 RS3_HUMAN            | 2166.0633 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1446.7355 |
| sp Q13435 SF3B2_HUMAN          | 2194.1052 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |
| sp Q02790 FKBP4_HUMAN          | 1380.6561 |
| sp Q6P2Q9 PRP8_HUMAN           | 1770.8325 |
| sp P10586 PTPRF_HUMAN          | 1762.8349 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp P10586 PTPRF_HUMAN          | 2457.2176 |
| sp Q9P2B2 FPRP_HUMAN           | 2471.0666 |
| sp P31040 SDHA_HUMAN           | 3137.5703 |
| sp Q9Y3U8 RL36_HUMAN           | 1510.7238 |
| sp Q14126 DSG2_HUMAN           | 1916.9592 |
| sp Q13263 TIF1B_HUMAN          | 1413.7405 |
| sp P08195 4F2_HUMAN            | 2518.1864 |
| sp P16403 H12_HUMAN            | 1210.6558 |
| sp Q15149 PLEC_HUMAN           | 1416.6997 |
| sp P46940 IQGA1_HUMAN          | 1878.9258 |
| sp Q06830 PRDX1_HUMAN          | 3779.8254 |
| sp Q06830 PRDX1_HUMAN          | 2338.1052 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp Q7KZF4 SND1_HUMAN           | 2451.0979 |
| sp O75367 H2AY_HUMAN           | 1397.7303 |
| sp P62258 1433E_HUMAN          | 2891.4045 |
| sp P84098 RL19_HUMAN           | 1119.5673 |
| sp O75369 FLNB_HUMAN           | 2072.999  |

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| sp P26038 MOES_HUMAN           | 1619.8267 |
| sp P36578 RL4_HUMAN            | 1435.7671 |
| sp P39023 RL3_HUMAN            | 1619.8923 |
| sp Q14566 MCM6_HUMAN           | 1863.7702 |
| sp P23284 PPIB_HUMAN           | 1492.643  |
| sp P04406 G3P_HUMAN            | 1420.7562 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp P20908 CO5A1_HUMAN          | 1091.5975 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P05783 K1C18_HUMAN          | 2389.1974 |
| sp P42704 LPPRC_HUMAN          | 2608.1978 |
| sp P04083 ANXA1_HUMAN          | 2101.0579 |
| sp Q5JTH9 RRP12_HUMAN          | 3013.5338 |
| sp P62244 RS15A_HUMAN          | 1323.7147 |
| sp Q15149 PLEC_HUMAN           | 2859.3093 |
| sp P21333 FLNA_HUMAN           | 2222.1331 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp P29692 EF1D_HUMAN,sp P24534 | 1249.7394 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp Q09666 AHNK_HUMAN           | 1365.6097 |
| sp Q15149 PLEC_HUMAN           | 1467.6049 |
| sp P08195 4F2_HUMAN            | 2276.278  |
| sp P25705 ATPA_HUMAN           | 2905.5086 |
| sp P27105 STOM_HUMAN           | 2854.4688 |
| sp P13639 EF2_HUMAN            | 4552.2043 |
| sp P08865 RSSA_HUMAN           | 1810.9577 |
| sp P29401 TKT_HUMAN            | 1374.6568 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 2350.1957 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P31327 CPSM_HUMAN           | 1908.904  |
| sp P08758 ANXA5_HUMAN          | 2247.094  |
| sp Q8NC51 PAIRB_HUMAN          | 1553.711  |
| sp P04080 CYTB_HUMAN           | 2654.2976 |
| sp P12277 KCRB_HUMAN           | 3783.8124 |
| sp P13639 EF2_HUMAN            | 2743.3229 |
| sp P26599 PTBP1_HUMAN          | 1729.9111 |
| sp P07900 HS90A_HUMAN          | 2260.1164 |
| sp P07900 HS90A_HUMAN          | 2901.3929 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2547.1006 |
| sp O94776 MTA2_HUMAN           | 2240.1008 |
| sp P84098 RL19_HUMAN           | 1614.7864 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1651.9145 |
| sp Q15233 NONO_HUMAN           | 1680.7856 |
| sp P18077 RL35A_HUMAN          | 1795.9105 |
| sp P23246 SFPQ_HUMAN           | 2160.0375 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp Q16666 IF16_HUMAN           | 2776.3299 |

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| sp P62701 RS4X_HUMAN,sp Q8TD4: | 1491.718  |
| sp Q08211 DHX9_HUMAN           | 1540.7093 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1467.7544 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P62277 RS13_HUMAN           | 1577.8777 |
| sp O75643 U520_HUMAN           | 2130.0269 |
| sp Q15149 PLEC_HUMAN           | 3067.623  |
| sp P40227 TCPZ_HUMAN           | 1621.7195 |
| sp P27816 MAP4_HUMAN           | 1516.7634 |
| sp Q96QK1 VPS35_HUMAN          | 1994.9554 |
| sp P30044 PRDX5_HUMAN          | 3310.6332 |
| sp P31327 CPSM_HUMAN           | 2147.1851 |
| sp P68371 TBB4B_HUMAN          | 2039.9589 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P15121 ALDR_HUMAN           | 3458.6994 |
| sp P78527 PRKDC_HUMAN          | 1508.7875 |
| sp Q13310 PABP4_HUMAN          | 1585.7307 |
| sp P22102 PUR2_HUMAN           | 1331.647  |
| sp Q15149 PLEC_HUMAN           | 1404.7071 |
| sp P78527 PRKDC_HUMAN          | 1725.8839 |
| sp Q96E39 RMXL1_HUMAN,sp P381  | 1676.6438 |
| sp P06748 NPM_HUMAN            | 1234.583  |
| sp Q15233 NONO_HUMAN           | 1736.7788 |
| sp P16066 ANPRA_HUMAN          | 2663.3371 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp Q9NZB2 F120A_HUMAN          | 2559.3155 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp Q00839 HNRPU_HUMAN          | 1893.8057 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp P00491 PNPH_HUMAN           | 2382.1143 |
| sp P05787 K2C8_HUMAN           | 1824.8854 |
| sp P61247 RS3A_HUMAN           | 2358.0281 |
| sp P61247 RS3A_HUMAN           | 2358.0281 |
| sp Q8NF37 PCAT1_HUMAN          | 2677.4302 |
| sp Q15365 PCBP1_HUMAN          | 2040.9972 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1815.9295 |
| sp Q13332 PTPRS_HUMAN          | 3577.7424 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 2611.2303 |
| sp Q63HN8 RN213_HUMAN          | 2562.3152 |
| sp P62987 RL40_HUMAN,sp P62979 | 2484.2483 |
| sp P53396 ACLY_HUMAN           | 1406.6976 |
| sp Q9BQG0 MBB1A_HUMAN          | 1592.8886 |
| sp P04075 ALDOA_HUMAN          | 3537.6107 |
| sp Q15029 U5S1_HUMAN           | 3869.9152 |
| sp Q86VP6 CAND1_HUMAN          | 1610.794  |

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| sp P08729 K2C7_HUMAN           | 1596.7631 |
| sp P07195 LDHB_HUMAN           | 2295.1958 |
| sp P49327 FAS_HUMAN            | 1775.9669 |
| sp Q13200 PSMD2_HUMAN          | 2539.3257 |
| sp P53621 COPA_HUMAN           | 1874.9738 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P15170 ERF3A_HUMAN,sp Q8IYD | 1451.7079 |
| sp Q9HB71 CYBP_HUMAN           | 1641.876  |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2404.2387 |
| sp Q9Y6N7 ROBO1_HUMAN          | 1193.5677 |
| sp Q15149 PLEC_HUMAN           | 2456.2799 |
| sp Q15149 PLEC_HUMAN           | 1908.929  |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P52597 HNRPF_HUMAN          | 1698.9053 |
| sp O43707 ACTN4_HUMAN          | 2841.3868 |
| sp P22234 PUR6_HUMAN           | 1605.8111 |
| sp P61313 RL15_HUMAN           | 1529.7124 |
| sp Q9HCU4 CELR2_HUMAN          | 3678.7438 |
| sp P10412 H14_HUMAN            | 1390.7932 |
| sp P26599 PTBP1_HUMAN,sp O9575 | 1604.7682 |
| sp Q06323 PSME1_HUMAN          | 2827.3375 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp Q9NZB2 F120A_HUMAN          | 1905.9699 |
| sp Q96MU7 YTDC1_HUMAN          | 2280.14   |
| sp P10586 PTPRF_HUMAN          | 1778.8298 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P16401 H15_HUMAN,sp P10412  | 1381.7201 |
| sp P08581 MET_HUMAN            | 3111.381  |
| sp O14617 AP3D1_HUMAN          | 2315.0926 |
| sp O60506 HNRPQ_HUMAN          | 1749.7999 |
| sp P43243 MATR3_HUMAN          | 2921.431  |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P46776 RL27A_HUMAN          | 2832.3389 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1239.5594 |
| sp P35579 MYH9_HUMAN           | 1996.9643 |
| sp P26641 EF1G_HUMAN           | 1319.651  |
| sp P16401 H15_HUMAN,rev_sp P16 | 1205.6768 |
| sp P36578 RL4_HUMAN            | 1418.7405 |
| sp O75643 U520_HUMAN           | 1366.7245 |
| sp Q96QK1 VPS35_HUMAN          | 2229.1464 |
| sp Q9Y490 TLN1_HUMAN           | 2349.0292 |
| sp Q9Y490 TLN1_HUMAN           | 2349.0292 |
| sp Q9Y490 TLN1_HUMAN           | 2349.0292 |
| sp P22314 UBA1_HUMAN           | 3250.559  |
| sp O75369 FLNB_HUMAN           | 2484.2537 |
| sp P14735 IDE_HUMAN            | 2982.4896 |
| sp P21266 GSTM3_HUMAN          | 2790.4302 |

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| sp P39023 RL3_HUMAN            | 2163.9895 |
| sp P49411 EFTU_HUMAN           | 1873.9058 |
| sp P02786 TFR1_HUMAN           | 1410.7718 |
| sp P40227 TCPZ_HUMAN           | 2344.1951 |
| sp P32004 L1CAM_HUMAN          | 2017.8986 |
| sp P14923 PLAK_HUMAN           | 2714.4796 |
| sp P35232 PHB_HUMAN            | 3319.67   |
| sp P62263 RS14_HUMAN           | 2688.245  |
| sp P12814 ACTN1_HUMAN          | 2816.3756 |
| sp Q9ULF5 S39AA_HUMAN          | 1456.6874 |
| sp P20700 LMNB1_HUMAN          | 2089.0215 |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp P78347 GTF2I_HUMAN          | 1912.0458 |
| sp P26641 EF1G_HUMAN           | 1571.8559 |
| sp Q9Y3F4 STRAP_HUMAN          | 2622.2813 |
| sp P52597 HNRPF_HUMAN          | 2845.2249 |
| sp Q15149 PLEC_HUMAN           | 3300.699  |
| sp P14174 MIF_HUMAN            | 6019.9071 |
| sp P05783 K1C18_HUMAN          | 1370.6678 |
| sp P61978 HNRPK_HUMAN          | 2265.0033 |
| sp Q15233 NONO_HUMAN           | 1444.6987 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P04843 RPN1_HUMAN           | 1798.9505 |
| sp P78527 PRKDC_HUMAN          | 2460.1591 |
| sp P38919 IF4A3_HUMAN          | 2190.0845 |
| sp P50990 TCPQ_HUMAN           | 2191.0514 |
| sp P61247 RS3A_HUMAN           | 2049.9618 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P21333 FLNA_HUMAN           | 1852.9068 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1419.6895 |
| sp P48643 TCPE_HUMAN           | 2248.1562 |
| sp P60174 TPIS_HUMAN           | 1914.9072 |
| sp P62424 RL7A_HUMAN           | 2465.1744 |
| sp P15121 ALDR_HUMAN           | 2414.1213 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1467.7544 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp P37837 TALDO_HUMAN          | 1936.0153 |
| sp O75475 PSIP1_HUMAN,sp Q7Z4V | 1438.6452 |
| sp Q9Y5B9 SP16H_HUMAN          | 1993.9455 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P62805 H4_HUMAN             | 1790.9237 |
| sp P68032 ACTC_HUMAN,sp P68132 | 3669.6623 |
| sp Q15717 ELAV1_HUMAN          | 2450.1503 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P07814 SYEP_HUMAN           | 2075.0245 |
| sp P47897 SYQ_HUMAN            | 3073.5568 |
| sp Q9P2J5 SYLC_HUMAN           | 2278.9259 |

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| sp Q9P2J5 SYLC_HUMAN           | 2679.2857 |
| sp Q00610 CLH1_HUMAN           | 1547.8712 |
| sp P53396 ACLY_HUMAN           | 1973.0087 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp Q00341 VIGLN_HUMAN          | 1475.7481 |
| sp Q9Y3F4 STRAP_HUMAN          | 2953.2613 |
| sp Q9NVP1 DDX18_HUMAN          | 3317.5155 |
| sp Q13283 G3BP1_HUMAN          | 3126.4909 |
| sp P30043 BLVRB_HUMAN          | 2353.1777 |
| sp P42704 LPPRC_HUMAN          | 2794.4218 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp Q14152 EIF3A_HUMAN          | 1719.8654 |
| sp Q9BQG0 MBB1A_HUMAN          | 1169.5829 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1900.0094 |
| sp P00491 PNPH_HUMAN           | 2382.1143 |
| sp P56192 SYMC_HUMAN           | 2887.3197 |
| sp Q9Y224 RTRAF_HUMAN          | 1830.8213 |
| sp P35998 PRS7_HUMAN           | 1318.6782 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp O95782 AP2A1_HUMAN          | 3322.6582 |
| sp O14745 NHRF1_HUMAN          | 2412.0627 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp Q9UQ80 PA2G4_HUMAN          | 2861.3912 |
| sp P23284 PPIB_HUMAN           | 1911.8938 |
| sp O14980 XPO1_HUMAN           | 2358.1063 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P61086 UBE2K_HUMAN          | 2300.1113 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P28288 ABCD3_HUMAN          | 1553.8202 |
| sp Q14118 DAG1_HUMAN           | 2055.9722 |
| sp O75694 NU155_HUMAN          | 2246.1253 |
| sp Q05639 EF1A2_HUMAN,sp P6810 | 2178.1685 |
| sp P00558 PGK1_HUMAN           | 2500.2175 |
| sp P32969 RL9_HUMAN            | 2257.0984 |
| sp P28288 ABCD3_HUMAN          | 2575.0921 |
| sp P11717 MPRI_HUMAN           | 2314.1151 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P54709 AT1B3_HUMAN          | 1374.7507 |
| sp Q00839 HNRPU_HUMAN          | 1453.6482 |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp P22102 PUR2_HUMAN           | 1331.647  |
| sp P50990 TCPQ_HUMAN           | 2494.289  |
| sp P27797 CALR_HUMAN           | 1996.865  |
| sp P05787 K2C8_HUMAN           | 2727.2698 |



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| sp P68032 ACTC_HUMAN,sp P68133 | 3653.6674 |
| sp P52272 HNRPM_HUMAN          | 2092.0185 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp Q06830 PRDX1_HUMAN          | 3779.8254 |
| sp P17812 PYRG1_HUMAN          | 3079.5437 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3535.7154 |
| sp P34897 GLYM_HUMAN           | 1606.7475 |
| sp P04406 G3P_HUMAN            | 1420.7562 |
| sp P62280 RS11_HUMAN           | 1398.682  |
| sp Q06830 PRDX1_HUMAN          | 2338.1052 |
| sp Q13148 TADBP_HUMAN          | 2055.9722 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P08238 HS90B_HUMAN          | 3220.4257 |
| sp P05787 K2C8_HUMAN           | 2577.1905 |
| sp P42704 LPPRC_HUMAN          | 2743.3857 |
| sp P35637 FUS_HUMAN            | 1732.809  |
| sp P35637 FUS_HUMAN            | 1732.809  |
| sp P62258 1433E_HUMAN          | 1713.905  |
| sp P45880 VDAC2_HUMAN          | 1475.766  |
| sp Q92598 HS105_HUMAN          | 1796.921  |
| sp P26641 EF1G_HUMAN           | 1571.8559 |
| sp P38919 IF4A3_HUMAN          | 4038.9238 |
| sp Q8WW12 PCNP_HUMAN           | 1786.7871 |
| sp P10586 PTPRF_HUMAN          | 3515.6377 |
| sp P26599 PTBP1_HUMAN          | 3687.8421 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P16402 H13_HUMAN,sp P10412  | 1921.9997 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P42704 LPPRC_HUMAN          | 1549.781  |
| sp Q15369 ELOC_HUMAN           | 2298.0701 |
| sp P29401 TKT_HUMAN            | 4178.063  |
| sp P04792 HSPB1_HUMAN          | 1664.7642 |
| sp Q9Y3I0 RTCB_HUMAN           | 2166.0449 |
| sp P21333 FLNA_HUMAN           | 1472.726  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2711.4092 |
| sp Q7KZF4 SND1_HUMAN           | 2108.0401 |
| sp P54886 P5CS_HUMAN           | 1949.0622 |
| sp Q9BSJ8 ESYT1_HUMAN          | 1816.9319 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P49327 FAS_HUMAN            | 1344.6132 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp P10586 PTPRF_HUMAN          | 2448.1995 |
| sp P08670 VIME_HUMAN           | 1768.8778 |
| sp Q8NC51 PAIRB_HUMAN          | 1111.5662 |
| sp O94776 MTA2_HUMAN           | 1369.7718 |
| sp P18669 PGAM1_HUMAN          | 2332.0033 |
| sp Q9UHX1 PUF60_HUMAN          | 2913.4944 |

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| sp P62829 RL23_HUMAN           | 2494.2129 |
| sp P30101 PDIA3_HUMAN          | 1841.906  |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp P05787 K2C8_HUMAN           | 1844.8978 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1989.9643 |
| sp Q13813 SPTN1_HUMAN          | 2138.9981 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp P62826 RAN_HUMAN            | 2376.2226 |
| sp P02786 TFR1_HUMAN           | 2596.3061 |
| sp P38159 RBMX_HUMAN           | 2447.222  |
| sp Q7KZF4 SND1_HUMAN           | 1443.751  |
| sp P21333 FLNA_HUMAN           | 1766.7748 |
| sp P32004 L1CAM_HUMAN          | 2931.4324 |
| sp P00966 ASSY_HUMAN           | 1784.8078 |
| sp P62807 H2B1C_HUMAN,sp P588; | 1801.9138 |
| sp P46060 RAGP1_HUMAN          | 2772.4157 |
| sp Q9BQG0 MBB1A_HUMAN          | 1412.73   |
| sp P11021 BIP_HUMAN            | 2259.0848 |
| sp Q92841 DDX17_HUMAN          | 2179.9051 |
| sp O75691 UTP20_HUMAN          | 2496.3087 |
| sp Q15149 PLEC_HUMAN           | 1248.6826 |
| sp P26373 RL13_HUMAN           | 1169.6445 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp P11387 TOP1_HUMAN           | 1953.9618 |
| sp P06899 H2B1J_HUMAN,sp P5705 | 1973.9694 |
| sp P31327 CPSM_HUMAN           | 3066.5047 |
| sp O43707 ACTN4_HUMAN          | 2700.2701 |
| sp P07195 LDHB_HUMAN           | 1855.0244 |
| sp Q6YHK3 CD109_HUMAN          | 2762.2824 |
| sp Q13813 SPTN1_HUMAN          | 1424.7048 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1261.6051 |
| sp Q9UHD8 SEPT9_HUMAN          | 2577.2057 |
| sp P62917 RL8_HUMAN            | 2721.3221 |
| sp Q9NR30 DDX21_HUMAN          | 2264.1325 |
| sp P49327 FAS_HUMAN            | 1356.6826 |
| sp Q14240 IF4A2_HUMAN          | 2371.159  |
| sp O14880 MGST3_HUMAN          | 1962.9    |
| sp Q9NZ01 TECR_HUMAN           | 1669.7948 |
| sp Q9HCU4 CELR2_HUMAN          | 3678.7438 |
| sp P16403 H12_HUMAN            | 1219.6925 |
| sp P00491 PNPH_HUMAN           | 2382.1143 |
| sp Q92945 FUBP2_HUMAN          | 2305.0975 |
| sp P27816 MAP4_HUMAN           | 1804.8414 |
| sp P16403 H12_HUMAN            | 1065.6182 |
| sp P62807 H2B1C_HUMAN,sp P588; | 1704.7995 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P62805 H4_HUMAN             | 1790.9237 |

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| sp P31327 CPSM_HUMAN           | 2274.2412 |
| sp P26639 SYTC_HUMAN           | 1944.9793 |
| sp P04083 ANXA1_HUMAN          | 2300.1206 |
| sp P06899 H2B1J_HUMAN,sp P5705 | 1973.9694 |
| sp Q15233 NONO_HUMAN           | 1424.6684 |
| sp O43707 ACTN4_HUMAN,sp P128  | 1324.6412 |
| sp Q96DG6 CMBL_HUMAN           | 2330.108  |
| sp P19338 NUCL_HUMAN           | 2005.8945 |
| sp P62750 RL23A_HUMAN          | 1410.7143 |
| sp P55884 EIF3B_HUMAN          | 1281.6717 |
| sp Q9Y383 LC7L2_HUMAN          | 2449.0937 |
| sp P78347 GTF2I_HUMAN          | 2430.1339 |
| sp Q13813 SPTN1_HUMAN          | 1880.9129 |
| sp Q16891 MIC60_HUMAN          | 1802.9163 |
| sp P46940 IQGA1_HUMAN          | 2360.1285 |
| sp P15880 RS2_HUMAN            | 1855.8774 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3246.5901 |
| sp P14625 ENPL_HUMAN           | 3272.5111 |
| sp P31327 CPSM_HUMAN           | 2147.1851 |
| sp P07910 HNRPC_HUMAN          | 2264.1471 |
| sp P63010 AP2B1_HUMAN          | 2589.4054 |
| sp P62424 RL7A_HUMAN           | 1650.9093 |
| sp P09874 PARP1_HUMAN          | 1758.7849 |
| sp P05141 ADT2_HUMAN,sp P12235 | 1559.8671 |
| sp P47914 RL29_HUMAN           | 2245.1339 |
| sp P10586 PTPRF_HUMAN          | 2164.1052 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |
| sp Q15149 PLEC_HUMAN           | 1416.6997 |
| sp P05556 ITB1_HUMAN           | 1830.8346 |
| sp Q14247 SRC8_HUMAN           | 1494.6562 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q01082 SPTB2_HUMAN          | 2437.1121 |
| sp Q71RC2 LARP4_HUMAN          | 1999.9963 |
| sp P06748 NPM_HUMAN            | 1798.8082 |
| sp O75369 FLNB_HUMAN           | 2797.4399 |
| sp P30153 2AAA_HUMAN,sp P30154 | 2463.2646 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1704.7811 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2332.2023 |
| sp P35052 GPC1_HUMAN           | 2798.3511 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp Q13435 SF3B2_HUMAN          | 2194.1052 |
| sp P23284 PIIB_HUMAN           | 1501.8181 |
| sp P61247 RS3A_HUMAN           | 1921.8669 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P13010 XRCC5_HUMAN          | 1824.9622 |
| sp P31948 STIP1_HUMAN          | 2455.0672 |
| sp P23526 SAHH_HUMAN           | 3501.745  |

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| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P40227 TCPZ_HUMAN           | 1621.7195 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1801.9138 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q15477 SKIV2_HUMAN          | 2060.9949 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P05026 AT1B1_HUMAN          | 1956.8411 |
| sp P13010 XRCC5_HUMAN          | 2005.8914 |
| sp Q3ZCQ8 TIM50_HUMAN          | 2412.1598 |
| sp P23396 RS3_HUMAN            | 2294.1583 |
| sp Q96KR1 ZFR_HUMAN,sp Q96SI9  | 1239.5785 |
| sp P14625 ENPL_HUMAN           | 2556.1705 |
| sp Q14847 LASP1_HUMAN          | 2006.7862 |
| sp Q15185 TEBP_HUMAN           | 2684.2401 |
| sp P27824 CALX_HUMAN           | 1765.8159 |
| sp Q7KZF4 SND1_HUMAN           | 2204.0538 |
| sp O00231 PSD11_HUMAN          | 2890.4713 |
| sp P50454 SERPH_HUMAN          | 2739.4079 |
| sp Q00796 DHSO_HUMAN           | 1865.9087 |
| sp Q15181 IPYR_HUMAN           | 1618.774  |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp Q8TDN6 BRX1_HUMAN           | 2526.2611 |
| sp Q9H361 PABP3_HUMAN,sp P119  | 1889.9483 |
| sp P13639 EF2_HUMAN            | 1558.8355 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P26599 PTBP1_HUMAN          | 3963.0054 |
| sp P49411 EFTU_HUMAN           | 2325.1893 |
| sp Q06830 PRDX1_HUMAN          | 2602.2122 |
| sp Q15149 PLEC_HUMAN           | 2252.1437 |
| sp P16403 H12_HUMAN            | 1065.6182 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P14618 KPYM_HUMAN           | 1991.9874 |
| sp Q9NZN4 EHD2_HUMAN           | 4240.0383 |
| sp P62805 H4_HUMAN             | 1521.7787 |
| sp P07737 PROF1_HUMAN          | 1414.7378 |
| sp O76021 RL1D1_HUMAN          | 1576.7773 |
| sp Q9Y490 TLN1_HUMAN           | 1859.9564 |
| sp P60842 IF4A1_HUMAN          | 1837.0197 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp O15031 PLXB2_HUMAN          | 3672.6858 |
| sp Q08211 DHX9_HUMAN           | 2398.3182 |
| sp P00558 PGK1_HUMAN           | 2378.2482 |
| sp Q07020 RL18_HUMAN           | 1969.9997 |
| sp Q14974 IMB1_HUMAN           | 2298.1492 |

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| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp Q9Y2Q3 GSTK1_HUMAN          | 2739.3877 |
| sp Q9Y3F4 STRAP_HUMAN          | 2675.2715 |
| sp P62753 RS6_HUMAN            | 2501.1744 |
| sp Q9P289 STK26_HUMAN          | 2309.2307 |
| sp P15121 ALDR_HUMAN           | 1729.8134 |
| sp P08069 IGF1R_HUMAN          | 1918.0061 |
| sp P62937 PPIA_HUMAN           | 3816.7512 |
| sp P51991 ROA3_HUMAN           | 2095.011  |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P21333 FLNA_HUMAN           | 3297.6056 |
| sp P05787 K2C8_HUMAN           | 1404.6191 |
| sp P08195 4F2_HUMAN            | 2518.1864 |
| sp Q13263 TIF1B_HUMAN          | 2921.3978 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2703.2017 |
| sp O75153 CLU_HUMAN            | 2279.1474 |
| sp P31327 CPSM_HUMAN           | 2198.1259 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp O00425 IF2B3_HUMAN          | 2279.2525 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q04637 IF4G1_HUMAN          | 2845.3447 |
| sp P14923 PLAK_HUMAN           | 1814.9639 |
| sp Q9UHB9 SRP68_HUMAN          | 2651.3847 |
| sp P48509 CD151_HUMAN          | 2144.9653 |
| sp P60660 MYL6_HUMAN           | 2887.3772 |
| sp P60660 MYL6_HUMAN           | 2887.3772 |
| sp P26038 MOES_HUMAN           | 1304.6725 |
| sp P14735 IDE_HUMAN            | 2998.4845 |
| sp P36578 RL4_HUMAN            | 1221.7081 |
| sp Q99798 ACON_HUMAN           | 2942.4846 |
| sp P17987 TCPA_HUMAN           | 1729.9251 |
| sp Q9Y490 TLN1_HUMAN           | 2349.0292 |
| sp P05141 ADT2_HUMAN           | 1619.8308 |
| sp Q13263 TIF1B_HUMAN          | 1627.8313 |
| sp P31327 CPSM_HUMAN           | 1944.0932 |
| sp P08758 ANXA5_HUMAN          | 1642.7938 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1704.7995 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp P53396 ACLY_HUMAN           | 2153.0463 |
| sp P61247 RS3A_HUMAN           | 2386.1263 |
| sp Q96AG4 LRC59_HUMAN          | 1848.8788 |
| sp Q9HCU4 CELR2_HUMAN          | 1905.9221 |
| sp P07900 HS90A_HUMAN          | 2179.0256 |
| sp P39748 FEN1_HUMAN           | 1563.8045 |
| sp P09874 PARP1_HUMAN          | 2024.0215 |
| sp P11586 C1TC_HUMAN           | 1832.9381 |

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| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp Q15366 PCBP2_HUMAN          | 2026.9816 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P08708 RS17_HUMAN           | 1397.6324 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp Q15233 NONO_HUMAN           | 1424.6684 |
| sp O75369 FLNB_HUMAN           | 2797.4399 |
| sp Q9NR30 DDX21_HUMAN          | 2473.243  |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp Q9UHD1 CHRD1_HUMAN          | 2099.947  |
| sp Q08211 DHX9_HUMAN           | 2056.1278 |
| sp P46781 RS9_HUMAN            | 1654.7951 |
| sp Q00341 VIGLN_HUMAN          | 1475.7481 |
| sp P28288 ABCD3_HUMAN          | 1934.9772 |
| sp P46777 RL5_HUMAN            | 1690.8275 |
| sp Q12788 TBL3_HUMAN           | 2119.9382 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P26641 EF1G_HUMAN           | 1319.651  |
| sp P31327 CPSM_HUMAN           | 1833.8601 |
| sp Q13162 PRDX4_HUMAN          | 2304.095  |
| sp O14980 XPO1_HUMAN           | 1125.5607 |
| sp P48637 GSHB_HUMAN           | 1713.8985 |
| sp O00571 DDX3X_HUMAN          | 2008.0728 |
| sp O76094 SRP72_HUMAN          | 1301.6364 |
| sp P43121 MUC18_HUMAN          | 2985.5086 |
| sp P21333 FLNA_HUMAN           | 1775.8578 |
| sp A5YKK6 CNOT1_HUMAN          | 2942.4087 |
| sp P16403 H12_HUMAN            | 1065.6182 |
| sp Q12906 ILF3_HUMAN           | 2612.3374 |
| sp Q8N3U4 STAG2_HUMAN          | 1403.7409 |
| sp P36578 RL4_HUMAN            | 2332.127  |
| sp P07814 SYEP_HUMAN           | 1437.6565 |
| sp Q15436 SC23A_HUMAN          | 2667.3578 |
| sp P06899 H2B1J_HUMAN,sp P5705 | 1973.9694 |
| sp Q14137 BOP1_HUMAN           | 1971.9374 |
| sp P55072 TERA_HUMAN           | 1825.8305 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp Q92616 GCN1_HUMAN           | 3849.1325 |
| sp P06576 ATPB_HUMAN           | 2428.2962 |
| sp O43390 HNRPR_HUMAN          | 3197.6033 |
| sp P16401 H15_HUMAN            | 1264.7139 |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 3474.5279 |
| sp P30044 PRDX5_HUMAN          | 3310.6332 |
| sp P08670 VIME_HUMAN,sp P41215 | 1720.758  |
| sp O75369 FLNB_HUMAN           | 2368.1329 |
| sp P62917 RL8_HUMAN            | 1253.6768 |

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| sp P10586 PTPRF_HUMAN          | 2432.1397 |
| sp P21333 FLNA_HUMAN           | 2742.2926 |
| sp O75369 FLNB_HUMAN           | 2088.9939 |
| sp P18077 RL35A_HUMAN          | 1795.9105 |
| sp P49207 RL34_HUMAN           | 1555.6218 |
| sp P62753 RS6_HUMAN            | 1773.8785 |
| sp Q15149 PLEC_HUMAN           | 2252.1437 |
| sp P62750 RL23A_HUMAN          | 1566.8154 |
| sp P62937 PIIA_HUMAN           | 1575.7821 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp O43390 HNRPR_HUMAN          | 1735.7842 |
| sp P61313 RL15_HUMAN           | 2041.0673 |
| sp P36871 PGM1_HUMAN           | 1998.9898 |
| sp P53396 ACLY_HUMAN           | 1933.9898 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp Q8WUM4 PDC6I_HUMAN          | 2338.1117 |
| sp Q8NF37 PCAT1_HUMAN          | 2677.4302 |
| sp P11142 HSP7C_HUMAN          | 2348.1972 |
| sp P10586 PTPRF_HUMAN          | 2717.2459 |
| sp Q96HS1 PGAM5_HUMAN          | 3233.4578 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P29401 TKT_HUMAN            | 1550.8093 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P45880 VDAC2_HUMAN          | 1977.0167 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1461.6664 |
| sp P06748 NPM_HUMAN            | 1798.8082 |
| sp P15880 RS2_HUMAN            | 1745.8883 |
| sp P55884 EIF3B_HUMAN          | 1281.6717 |
| sp O75369 FLNB_HUMAN           | 2484.2537 |
| sp P33992 MCM5_HUMAN           | 2203.0797 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P13639 EF2_HUMAN            | 3856.8685 |
| sp P62987 RL40_HUMAN           | 1520.7154 |
| sp P43121 MUC18_HUMAN          | 2046.8265 |
| sp P16403 H12_HUMAN            | 1095.5924 |
| sp Q15149 PLEC_HUMAN           | 2841.3504 |
| sp Q15366 PCBP2_HUMAN          | 2625.3187 |
| sp P34897 GLYM_HUMAN           | 2197.1379 |
| sp Q9BT22 ALG1_HUMAN           | 2960.5066 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1673.8189 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp Q13505 MTX1_HUMAN           | 2284.16   |
| sp P30153 2AAA_HUMAN           | 2961.4576 |
| sp P52597 HNRPF_HUMAN          | 2829.23   |
| sp P11586 C1TC_HUMAN           | 2028.9905 |

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| sp P84243 H33_HUMAN            | 1517.7587 |
| sp P19338 NUCL_HUMAN           | 2542.1533 |
| sp O95573 ACSL3_HUMAN          | 2148.0528 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3595.6673 |
| sp P23497 SP100_HUMAN,sp P0942 | 1240.6088 |
| sp P00966 ASSY_HUMAN           | 2854.2933 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P78347 GTF2I_HUMAN          | 3239.5564 |
| sp P62136 PP1A_HUMAN,sp P6214C | 1991.9014 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P31327 CPSM_HUMAN           | 2254.1845 |
| sp Q13813 SPTN1_HUMAN          | 2242.0828 |
| sp Q9HB71 CYBP_HUMAN           | 1641.876  |
| sp P78527 PRKDC_HUMAN          | 1921.8451 |
| sp Q15185 TEBP_HUMAN           | 1930.9214 |
| sp Q15185 TEBP_HUMAN           | 1930.9214 |
| sp P58107 EPIPL_HUMAN          | 3328.5306 |
| sp P07737 PROF1_HUMAN          | 2075.1085 |
| sp P20700 LMNB1_HUMAN          | 2014.9807 |
| sp P13639 EF2_HUMAN            | 1048.4686 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp Q14258 TRI25_HUMAN          | 1877.9775 |
| sp Q16832 DDR2_HUMAN           | 2241.0702 |
| sp Q92804 RBP56_HUMAN          | 2157.0167 |
| sp P15880 RS2_HUMAN            | 1745.8883 |
| sp P38646 GRP75_HUMAN          | 2534.2839 |
| sp P14923 PLAK_HUMAN           | 1814.9639 |
| sp Q8NBS9 TXND5_HUMAN          | 2777.2254 |
| sp P21333 FLNA_HUMAN           | 1390.7092 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P18206 VINC_HUMAN           | 2026.0695 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2603.265  |
| sp Q13435 SF3B2_HUMAN          | 1948.9207 |
| sp P07814 SYEP_HUMAN           | 1926.9588 |
| sp P62851 RS25_HUMAN           | 2093.0317 |
| sp Q6DD88 ATLA3_HUMAN          | 2083.0083 |
| sp P41252 SYIC_HUMAN           | 1845.876  |
| sp Q08945 SSRP1_HUMAN          | 1758.9206 |
| sp P19338 NUCL_HUMAN           | 2005.8945 |
| sp Q86VP6 CAND1_HUMAN          | 1822.0452 |
| sp Q13263 TIF1B_HUMAN          | 2572.2082 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P42704 LPPRC_HUMAN          | 1549.781  |
| sp Q6UVK1 CSPG4_HUMAN          | 3838.953  |
| sp Q6UVK1 CSPG4_HUMAN          | 1547.7654 |



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| sp P17301 ITA2_HUMAN           | 2002.0048 |
| sp Q8TCS8 PNPT1_HUMAN          | 2302.2607 |
| sp P13010 XRCC5_HUMAN          | 2090.0433 |
| sp P33316 DUT_HUMAN            | 2144.0572 |
| sp Q14847 LASP1_HUMAN          | 1473.6347 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |
| sp P52272 HNRPM_HUMAN          | 1466.7729 |
| sp O43707 ACTN4_HUMAN          | 1450.7456 |
| sp P84098 RL19_HUMAN           | 2267.0455 |
| sp P08865 RSSA_HUMAN           | 1810.9577 |
| sp P62917 RL8_HUMAN            | 1139.6186 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2332.2023 |
| sp P62750 RL23A_HUMAN          | 1271.6622 |
| sp Q9HB71 CYBP_HUMAN           | 1513.781  |
| sp Q06830 PRDX1_HUMAN          | 1946.9772 |
| sp Q07065 CKAP4_HUMAN          | 1620.7744 |
| sp P21333 FLNA_HUMAN           | 1531.7743 |
| sp P49327 FAS_HUMAN            | 1797.9369 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 2255.2889 |
| sp P36871 PGM1_HUMAN           | 1725.8396 |
| sp P62841 RS15_HUMAN           | 3364.669  |
| sp P18621 RL17_HUMAN           | 1512.7647 |
| sp P29401 TKT_HUMAN            | 3284.7868 |
| sp P19338 NUCL_HUMAN           | 2217.9815 |
| sp Q15149 PLEC_HUMAN           | 2456.2799 |
| sp Q14315 FLNC_HUMAN,sp O7536  | 1578.8981 |
| sp Q13619 CUL4A_HUMAN          | 2166.1321 |
| sp P08708 RS17_HUMAN           | 1397.6324 |
| sp P43121 MUC18_HUMAN          | 2519.1499 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2886.4876 |
| sp P31040 SDHA_HUMAN           | 2991.4297 |
| sp P23284 PPIB_HUMAN           | 1501.8181 |
| sp P46781 RS9_HUMAN            | 1654.7951 |
| sp O43707 ACTN4_HUMAN          | 1764.8795 |
| sp P26447 S10A4_HUMAN          | 2135.943  |
| sp P40227 TCPZ_HUMAN           | 1621.7195 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P62081 RS7_HUMAN            | 1584.8049 |
| sp P17812 PYRG1_HUMAN          | 3258.4784 |
| sp P78527 PRKDC_HUMAN          | 1970.0374 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp P46013 KI67_HUMAN           | 1575.8257 |
| sp P39019 RS19_HUMAN           | 1606.741  |
| sp P15311 EZRI_HUMAN,sp P26038 | 1283.7125 |
| sp Q14240 IF4A2_HUMAN          | 1801.8846 |

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| sp Q15233 NONO_HUMAN           | 1892.8799 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp Q09161 NCBP1_HUMAN          | 1672.6826 |
| sp P50238 CRIP1_HUMAN          | 1724.7399 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P07900 HS90A_HUMAN,sp Q58F6 | 1126.5805 |
| sp P22392 NDKB_HUMAN           | 1906.9061 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P36871 PGM1_HUMAN           | 2350.1403 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp P10599 THIO_HUMAN           | 1659.7967 |
| sp Q12905 ILF2_HUMAN           | 2084.0426 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp P61160 ARP2_HUMAN           | 2622.2424 |
| sp P50991 TCPD_HUMAN           | 1576.7594 |
| sp P16403 H12_HUMAN            | 1219.6925 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18I  | 2884.265  |
| sp P08581 MET_HUMAN            | 3111.381  |
| sp Q9Y520 PRC2C_HUMAN          | 1547.8056 |
| sp P04843 RPN1_HUMAN           | 2521.2601 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2018.0433 |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp P41252 SYIC_HUMAN           | 1176.5815 |
| sp O00567 NOP56_HUMAN          | 2060.0579 |
| sp Q86VP6 CAND1_HUMAN          | 2314.1304 |
| sp P84098 RL19_HUMAN           | 1457.7701 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp Q9NR30 DDX21_HUMAN          | 3100.4237 |
| sp P62081 RS7_HUMAN            | 1981.0116 |
| sp P17301 ITA2_HUMAN           | 3283.6877 |
| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp Q14690 RRP5_HUMAN           | 2326.2031 |
| sp O00571 DDX3X_HUMAN          | 2349.9622 |
| sp P04075 ALDOA_HUMAN          | 1753.8635 |
| sp P04406 G3P_HUMAN            | 3129.4787 |
| sp Q9GZT3 SLIRP_HUMAN          | 2495.2517 |
| sp P08195 4F2_HUMAN            | 2051.9854 |
| sp P16066 ANPRA_HUMAN          | 2852.5549 |
| sp P28288 ABCD3_HUMAN          | 2575.0921 |
| sp Q9BS26 ERP44_HUMAN          | 2757.2704 |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P07205 PGK2_HUMAN,sp P00558 | 2317.0975 |
| sp Q13310 PABP4_HUMAN,sp P1194 | 2560.1792 |
| sp Q13813 SPTN1_HUMAN          | 2138.9981 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2404.2387 |
| sp Q00341 VIGLN_HUMAN          | 1404.7249 |

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| sp P10809 CH60_HUMAN           | 1868.952  |
| sp P14923 PLAK_HUMAN           | 1814.9639 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp Q9Y490 TLN1_HUMAN           | 4599.1033 |
| sp Q96MU7 YTDC1_HUMAN          | 2057.0218 |
| sp Q9H0U4 RAB1B_HUMAN,sp Q925  | 1854.9112 |
| sp P00533 EGFR_HUMAN           | 3240.3118 |
| sp Q9UMS4 PRP19_HUMAN          | 2797.3923 |
| sp P62847 RS24_HUMAN           | 2578.1322 |
| sp Q6UB35 C1TM_HUMAN           | 2011.9599 |
| sp Q16531 DDB1_HUMAN           | 1800.908  |
| sp Q13435 SF3B2_HUMAN          | 1246.7034 |
| sp P07237 PDIA1_HUMAN          | 2015.9741 |
| sp P46783 RS10_HUMAN,sp Q9NQ3  | 1765.7907 |
| sp P06733 ENOA_HUMAN           | 1377.6888 |
| sp O00231 PSD11_HUMAN          | 1790.9778 |
| sp Q99623 PHB2_HUMAN           | 1857.9585 |
| sp Q08945 SSRP1_HUMAN          | 1462.7569 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp Q96AE4 FUBP1_HUMAN          | 2522.2257 |
| sp P78527 PRKDC_HUMAN          | 1796.9672 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp Q14974 IMB1_HUMAN           | 1390.6266 |
| sp P50990 TCPQ_HUMAN           | 2191.0514 |
| sp P04843 RPN1_HUMAN           | 1465.7314 |
| sp P49411 EFTU_HUMAN           | 1958.9408 |
| sp P30041 PRDX6_HUMAN          | 2434.238  |
| sp Q9P035 HACD3_HUMAN          | 1927.9428 |
| sp P11142 HSP7C_HUMAN          | 3085.4062 |
| sp P61247 RS3A_HUMAN           | 3209.6067 |
| sp Q99497 PARK7_HUMAN          | 1998.7836 |
| sp Q00796 DHSD_HUMAN           | 1865.9087 |
| sp P26038 MOES_HUMAN           | 2154.0189 |
| sp P78527 PRKDC_HUMAN          | 4134.1022 |
| sp P27816 MAP4_HUMAN           | 1804.8414 |
| sp P16402 H13_HUMAN,sp P16401  | 1456.7773 |
| sp P61247 RS3A_HUMAN           | 1541.7223 |
| sp P49327 FAS_HUMAN            | 3832.8189 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 1761.8646 |
| sp Q00610 CLH1_HUMAN           | 1462.7205 |
| sp P07900 HS90A_HUMAN,sp Q1451 | 1886.9738 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 1761.8646 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp P02786 TFR1_HUMAN           | 2331.2032 |
| sp Q15149 PLEC_HUMAN           | 1454.675  |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |

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| sp Q14978 NOLC1_HUMAN          | 1360.7099 |
| sp P50914 RL14_HUMAN           | 2764.4184 |
| sp Q14980 NUMA1_HUMAN          | 2353.2206 |
| sp P07900 HS90A_HUMAN          | 1499.6933 |
| sp O75369 FLNB_HUMAN           | 1725.8322 |
| sp P35579 MYH9_HUMAN           | 1872.904  |
| sp P22392 NDKB_HUMAN           | 2092.0041 |
| sp P02786 TFR1_HUMAN           | 2331.2032 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1783.748  |
| sp P16402 H13_HUMAN,sp P16401  | 1140.639  |
| sp Q12905 ILF2_HUMAN           | 1516.7773 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P37837 TALDO_HUMAN          | 2783.4051 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P07900 HS90A_HUMAN,sp Q1451 | 1204.6816 |
| sp P62906 RL10A_HUMAN          | 1589.8599 |
| sp P62701 RS4X_HUMAN           | 2335.2689 |
| sp P11021 BIP_HUMAN            | 1708.7767 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1870.8275 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1716.7678 |
| sp Q92499 DDX1_HUMAN           | 2012.0037 |
| sp P25705 ATPA_HUMAN           | 1897.9058 |
| sp P00505 AATM_HUMAN           | 2221.0956 |
| sp P08758 ANXA5_HUMAN          | 2231.0991 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P05787 K2C8_HUMAN           | 1325.6463 |
| sp P46777 RL5_HUMAN            | 2570.2839 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp Q99623 PHB2_HUMAN           | 2270.1576 |
| sp P21333 FLNA_HUMAN           | 1390.7092 |
| sp P35579 MYH9_HUMAN           | 1965.8738 |
| sp P02786 TFR1_HUMAN           | 2173.13   |
| sp Q6YHK3 CD109_HUMAN          | 2760.3858 |
| sp P40429 RL13A_HUMAN,sp Q6NV  | 1732.8632 |
| sp P51610 HCFC1_HUMAN          | 2390.139  |
| sp O75533 SF3B1_HUMAN          | 1809.9335 |
| sp P35637 FUS_HUMAN            | 1748.8039 |
| sp P35637 FUS_HUMAN            | 1748.8039 |
| sp P49748 ACADV_HUMAN          | 1520.726  |
| sp Q16531 DDB1_HUMAN           | 1800.908  |
| sp P08195 4F2_HUMAN            | 1613.8777 |
| sp P10586 PTPRF_HUMAN          | 2657.2385 |
| sp P02786 TFR1_HUMAN           | 1437.7252 |
| sp P12270 TPR_HUMAN            | 1589.8413 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |

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| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P33991 MCM4_HUMAN           | 2103.0637 |
| sp Q96A72 MGN2_HUMAN,sp P613   | 2037.0015 |
| sp P00966 ASSY_HUMAN           | 1324.583  |
| sp Q08945 SSRP1_HUMAN          | 1758.9206 |
| sp Q9Y2Q3 GSTK1_HUMAN          | 2281.1049 |
| sp P20810 ICAL_HUMAN           | 2161.1267 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P29692 EF1D_HUMAN           | 1928.8581 |
| sp P55265 DSRAD_HUMAN          | 3058.4818 |
| sp P08195 4F2_HUMAN            | 2542.1823 |
| sp Q9BQG0 MBB1A_HUMAN          | 1169.5829 |
| sp Q24JP5 T132A_HUMAN          | 2518.2063 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp Q99808 S29A1_HUMAN          | 1991.1278 |
| sp Q92804 RBP56_HUMAN          | 2157.0167 |
| sp P22234 PUR6_HUMAN           | 2297.1396 |
| sp P16402 H13_HUMAN,sp P10412  | 1191.6612 |
| sp Q16891 MIC60_HUMAN          | 3165.6128 |
| sp P04075 ALDOA_HUMAN          | 1496.7623 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P02545 LMNA_HUMAN           | 2540.3221 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp P06744 G6PI_HUMAN           | 1856.8945 |
| sp P49327 FAS_HUMAN            | 2633.2003 |
| sp Q8NC51 PAIRB_HUMAN          | 1948.9603 |
| sp P06748 NPM_HUMAN            | 1308.631  |
| sp P16403 H12_HUMAN            | 1261.7394 |
| sp P06744 G6PI_HUMAN           | 3611.8512 |
| sp P15531 NDKA_HUMAN,sp P2239  | 1540.7886 |
| sp P13639 EF2_HUMAN            | 2429.1573 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2282.1729 |
| sp Q13263 TIF1B_HUMAN          | 2005.9489 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp P06213 INSR_HUMAN           | 1962.8643 |
| sp O94979 SC31A_HUMAN          | 2920.4164 |
| sp P21333 FLNA_HUMAN           | 2222.1331 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P04080 CYTB_HUMAN           | 2654.2976 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P08758 ANXA5_HUMAN          | 2422.0999 |
| sp P08729 K2C7_HUMAN           | 1825.9462 |
| sp Q01082 SPTB2_HUMAN          | 2437.1121 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P17987 TCPA_HUMAN           | 1729.9251 |
| sp Q16881 TRXR1_HUMAN          | 1891.8887 |
| sp P84098 RL19_HUMAN           | 2395.1404 |

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| sp Q09666 AHNK_HUMAN           | 1759.8815 |
| sp P11142 HSP7C_HUMAN          | 3257.5022 |
| sp Q9HAV4 XPO5_HUMAN           | 2945.575  |
| sp Q14166 TTL12_HUMAN          | 3020.4048 |
| sp P08238 HS90B_HUMAN          | 1570.7668 |
| sp P26640 SYVC_HUMAN           | 2806.3232 |
| sp P53680 AP2S1_HUMAN          | 1559.7005 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3080.4338 |
| sp P12956 XRCC6_HUMAN          | 2386.2429 |
| sp P30613 KPYP_HUMAN,sp P14618 | 2024.0466 |
| sp P36578 RL4_HUMAN            | 2332.127  |
| sp P35579 MYH9_HUMAN           | 1408.6947 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1461.6664 |
| sp P25685 DNJB1_HUMAN          | 1837.8119 |
| sp P62937 PPIA_HUMAN           | 1109.5869 |
| sp Q9BVL2 NUP58_HUMAN          | 2486.1503 |
| sp P04908 H2A1B_HUMAN,sp Q930  | 1496.7107 |
| sp Q86VP6 CAND1_HUMAN          | 2864.4055 |
| sp P07910 HNRPC_HUMAN          | 2264.1471 |
| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp P62851 RS25_HUMAN           | 1769.9312 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp P23396 RS3_HUMAN            | 1654.8566 |
| sp P04792 HSPB1_HUMAN          | 1664.7642 |
| sp O75955 FLOT1_HUMAN          | 1844.9745 |
| sp P36578 RL4_HUMAN            | 2499.225  |
| sp O75369 FLNB_HUMAN           | 1443.8449 |
| sp P99999 CYC_HUMAN            | 1752.7955 |
| sp P60174 TPIS_HUMAN           | 1470.6991 |
| sp P46781 RS9_HUMAN            | 1842.9363 |
| sp P55072 TERA_HUMAN           | 1996.0153 |
| sp P14625 ENPL_HUMAN           | 1875.9214 |
| sp P38646 GRP75_HUMAN          | 2534.2839 |
| sp P58107 EPIPL_HUMAN          | 2530.2591 |
| sp Q9UH65 SWP70_HUMAN          | 3315.6048 |
| sp Q9UMS4 PRP19_HUMAN          | 2797.3923 |
| sp Q8NFJ5 RAI3_HUMAN           | 1886.8475 |
| sp P62805 H4_HUMAN             | 2018.1273 |
| sp Q9Y624 JAM1_HUMAN           | 2796.5749 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P51571 SSRD_HUMAN           | 2530.1513 |
| sp P07900 HS90A_HUMAN          | 1499.6933 |
| sp P04075 ALDOA_HUMAN          | 1753.8635 |
| sp O95340 PAPS2_HUMAN          | 2112.1156 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P05141 ADT2_HUMAN,sp P12236 | 1655.8308 |

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| sp P23381 SYWC_HUMAN           | 2125.1532 |
| sp P62750 RL23A_HUMAN          | 2355.1958 |
| sp P10586 PTPRF_HUMAN          | 3515.6377 |
| sp P18621 RL17_HUMAN           | 1550.7511 |
| sp P08670 VIME_HUMAN,sp P08725 | 1256.5885 |
| sp P31327 CPSM_HUMAN           | 2146.1463 |
| sp P25786 PSA1_HUMAN           | 1362.7507 |
| sp P34897 GLYM_HUMAN           | 2188.1164 |
| sp P51610 HCFC1_HUMAN          | 2390.139  |
| sp P21333 FLNA_HUMAN           | 3685.8873 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1800.8465 |
| sp P28066 PSA5_HUMAN           | 3692.7987 |
| sp P06576 ATPB_HUMAN           | 3860.8244 |
| sp Q9Y653 AGRG1_HUMAN          | 2550.3038 |
| sp P35579 MYH9_HUMAN           | 1724.9825 |
| sp P51397 DAP1_HUMAN           | 1942.9385 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P02786 TFR1_HUMAN           | 2530.1765 |
| sp P06733 ENOA_HUMAN           | 3181.4193 |
| sp Q15029 U5S1_HUMAN           | 2258.1331 |
| sp Q14204 DYHC1_HUMAN          | 3084.588  |
| sp Q9H0A0 NAT10_HUMAN          | 2210.0103 |
| sp P62266 RS23_HUMAN           | 1712.9713 |
| sp P35613 BASI_HUMAN           | 4216.8783 |
| sp Q9NQC3 RTN4_HUMAN           | 3467.7184 |
| sp P60842 IF4A1_HUMAN          | 1697.7937 |
| sp P10412 H14_HUMAN            | 1134.6397 |
| sp P29401 TKT_HUMAN            | 1609.8352 |
| sp P32322 P5CR1_HUMAN          | 3097.5213 |
| sp Q9BXP5 SRRT_HUMAN           | 2638.265  |
| sp P78527 PRKDC_HUMAN          | 1032.5968 |
| sp P07900 HS90A_HUMAN,sp Q1451 | 2487.2282 |
| sp Q14103 HNRPD_HUMAN          | 1771.8563 |
| sp O75369 FLNB_HUMAN           | 2072.999  |
| sp P35221 CTNA1_HUMAN          | 1692.8471 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp P16401 H15_HUMAN            | 1264.7139 |
| sp P06733 ENOA_HUMAN           | 2097.0306 |
| sp P62805 H4_HUMAN             | 1634.8226 |
| sp O43390 HNRPR_HUMAN          | 2714.3116 |
| sp P10599 THIO_HUMAN           | 1659.7967 |
| sp Q96QK1 VPS35_HUMAN          | 2040.1143 |
| sp Q12905 ILF2_HUMAN           | 2084.0426 |
| sp Q96AY3 FKB10_HUMAN          | 1684.9076 |
| sp Q9UNX3 RL26L_HUMAN,sp P6121 | 1311.6208 |
| sp P62826 RAN_HUMAN            | 3176.5244 |
| sp P43243 MATR3_HUMAN          | 1908.8788 |

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| sp P20908 CO5A1_HUMAN          | 1478.6902 |
| sp P20908 CO5A1_HUMAN          | 1478.6902 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp P46777 RL5_HUMAN            | 1758.7818 |
| sp P46777 RL5_HUMAN            | 1758.7818 |
| sp O60832 DKC1_HUMAN           | 2461.3693 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp P13639 EF2_HUMAN            | 2059.0256 |
| sp P06748 NPM_HUMAN            | 2240.0418 |
| sp O43592 XPOT_HUMAN           | 2857.4149 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp Q14974 IMB1_HUMAN           | 2194.1481 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp P31327 CPSM_HUMAN           | 3339.6697 |
| sp Q02790 FKBP4_HUMAN          | 2881.3406 |
| sp Q9P0L0 VAPA_HUMAN           | 3085.4775 |
| sp P07814 SYEP_HUMAN           | 2943.4192 |
| sp Q14137 BOP1_HUMAN           | 1971.9374 |
| sp O00159 MYO1C_HUMAN          | 1778.9315 |
| sp P42126 ECI1_HUMAN           | 2371.1386 |
| sp P04083 ANXA1_HUMAN          | 1393.6772 |
| sp P25789 PSA4_HUMAN           | 1551.6801 |
| sp P22314 UBA1_HUMAN           | 2876.3882 |
| sp P06493 CDK1_HUMAN           | 1594.7627 |
| sp Q15041 AR6P1_HUMAN          | 1918.881  |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1704.8683 |
| sp P32004 L1CAM_HUMAN          | 2041.0116 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp O95831 AIFM1_HUMAN          | 2162.0491 |
| sp P16403 H12_HUMAN            | 1065.6182 |
| sp P50990 TCPQ_HUMAN           | 2319.1464 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2075.9912 |
| sp P78527 PRKDC_HUMAN          | 4134.1022 |
| sp P35052 GPC1_HUMAN           | 1636.7879 |
| sp P16402 H13_HUMAN,sp Q02539  | 1431.6882 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp Q9BUJ2 HNRL1_HUMAN          | 1707.8216 |
| sp P23396 RS3_HUMAN            | 1285.703  |
| sp P17301 ITA2_HUMAN           | 1326.584  |
| sp P08729 K2C7_HUMAN           | 1637.8009 |
| sp Q14118 DAG1_HUMAN           | 3790.7744 |
| sp P04439 HLAA_HUMAN,sp P0188: | 2245.095  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P22626 ROA2_HUMAN           | 2473.1802 |
| sp P27797 CALR_HUMAN           | 1732.842  |
| sp Q15149 PLEC_HUMAN           | 1893.9221 |



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| sp P16403 H12_HUMAN            | 1505.8202 |
| sp O00232 PSD12_HUMAN          | 2420.0979 |
| sp P12277 KCRB_HUMAN           | 3799.8073 |
| sp P62847 RS24_HUMAN           | 2578.1322 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp P58107 EPIPL_HUMAN          | 1785.8356 |
| sp Q92616 GCN1_HUMAN           | 2221.1994 |
| sp P46783 RS10_HUMAN,sp Q9NQ3  | 1765.7907 |
| sp P05141 ADT2_HUMAN,sp Q9H0C  | 1885.8887 |
| sp P40429 RL13A_HUMAN          | 2369.1539 |
| sp Q9NX63 MIC19_HUMAN          | 2547.1522 |
| sp Q8NBS9 TXND5_HUMAN          | 2777.2254 |
| sp Q15233 NONO_HUMAN           | 2010.0283 |
| sp P05787 K2C8_HUMAN           | 1844.8978 |
| sp P40926 MDHM_HUMAN           | 2930.5026 |
| sp P36871 PGM1_HUMAN           | 2090.032  |
| sp Q9P2B2 FPRP_HUMAN           | 2660.2467 |
| sp P36578 RL4_HUMAN            | 2230.0147 |
| sp Q9NZB2 F120A_HUMAN          | 3665.5707 |
| sp P50990 TCPQ_HUMAN           | 2319.1464 |
| sp Q86V81 THOC4_HUMAN          | 1155.5309 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P08708 RS17_HUMAN           | 1397.6324 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2290.127  |
| sp P27824 CALX_HUMAN           | 1639.7842 |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 4134.8921 |
| sp P31947 1433S_HUMAN          | 3540.6276 |
| sp Q9BZE4 NOG1_HUMAN           | 1759.8278 |
| sp P21796 VDAC1_HUMAN          | 2299.206  |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P27824 CALX_HUMAN           | 2094.0269 |
| sp Q9NQC3 RTN4_HUMAN           | 2158.0113 |
| sp Q9BSY4 CHCH5_HUMAN          | 2613.1774 |
| sp Q9BV38 WDR18_HUMAN          | 3998.1339 |
| sp Q969H8 MYDGF_HUMAN          | 1366.7708 |
| sp P13861 KAP2_HUMAN,sp P31323 | 1888.9319 |
| sp Q8N4H5 TOM5_HUMAN           | 1921.9455 |
| sp P07195 LDHB_HUMAN           | 1704.8644 |
| sp P31327 CPSM_HUMAN           | 3073.5318 |
| sp P49327 FAS_HUMAN            | 2625.2071 |
| sp P05787 K2C8_HUMAN           | 1669.8047 |
| sp Q00610 CLH1_HUMAN           | 2391.2144 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 1761.8646 |
| sp P07437 TBB5_HUMAN           | 2012.948  |
| sp P20700 LMNB1_HUMAN          | 2431.1656 |
| sp P00387 NB5R3_HUMAN          | 4256.0882 |
| sp P05455 LA_HUMAN             | 2318.1358 |

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| sp Q03405 UPAR_HUMAN           | 2888.3644 |
| sp Q9UNX3 RL26L_HUMAN,sp P612! | 1311.6208 |
| sp P08238 HS90B_HUMAN          | 3220.4257 |
| sp Q24JP5 T132A_HUMAN          | 3029.655  |
| sp Q9UQ80 PA2G4_HUMAN          | 2033.0364 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P38646 GRP75_HUMAN          | 1096.5553 |
| sp Q15149 PLEC_HUMAN           | 1134.5782 |
| sp O15143 ARC1B_HUMAN          | 2601.2751 |
| sp O00567 NOP56_HUMAN          | 2330.0961 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp P04843 RPN1_HUMAN           | 2322.1703 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1613.7838 |
| sp P00338 LDHA_HUMAN           | 1874.9237 |
| sp P00558 PGK1_HUMAN           | 2617.2912 |
| sp Q07020 RL18_HUMAN           | 2754.3898 |
| sp P32320 CDD_HUMAN            | 2811.3354 |
| sp P63104 1433Z_HUMAN,sp P3194 | 1448.6718 |
| sp Q96DG6 CMBL_HUMAN           | 3010.5903 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P02786 TFR1_HUMAN           | 2596.3061 |
| sp Q1KMD3 HNRL2_HUMAN          | 2453.2584 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1411.8075 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P17813 EGLN_HUMAN           | 1894.9425 |
| sp P11021 BIP_HUMAN            | 1512.7168 |
| sp O00231 PSD11_HUMAN          | 2735.4593 |
| sp Q6PK04 CC137_HUMAN          | 2337.1536 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4302.2206 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp Q8NC51 PAIRB_HUMAN          | 1948.9603 |
| sp P35250 RFC2_HUMAN           | 2285.1288 |
| sp Q96KR1 ZFR_HUMAN,sp Q96SI9  | 1239.5785 |
| sp P26639 SYTC_HUMAN           | 1868.8792 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1704.7995 |
| sp P31327 CPSM_HUMAN           | 1908.904  |
| sp P02786 TFR1_HUMAN           | 2331.2032 |
| sp P62424 RL7A_HUMAN           | 1650.9093 |
| sp Q13148 TADBP_HUMAN          | 2055.9722 |
| sp P14174 MIF_HUMAN            | 6003.9122 |
| sp P78527 PRKDC_HUMAN          | 4134.1022 |
| sp P61020 RAB5B_HUMAN,sp P2033 | 1958.0183 |
| sp P62826 RAN_HUMAN            | 1980.937  |
| sp Q92499 DDX1_HUMAN           | 1396.583  |
| sp O75369 FLNB_HUMAN           | 2072.999  |
| sp Q9UHD1 CHRD1_HUMAN          | 2370.1703 |

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| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P61163 ACTZ_HUMAN           | 3797.8577 |
| sp P12814 ACTN1_HUMAN          | 1234.6306 |
| sp Q15149 PLEC_HUMAN           | 2841.3504 |
| sp O00534 VMA5A_HUMAN          | 1842.8973 |
| sp P30086 PEBP1_HUMAN          | 2767.3049 |
| sp P45880 VDAC2_HUMAN          | 1637.809  |
| sp P46777 RL5_HUMAN            | 1758.7818 |
| sp P16401 H15_HUMAN,sp P10412  | 1253.6252 |
| sp Q14847 LASP1_HUMAN          | 1950.857  |
| sp Q96N21 AP4AT_HUMAN          | 2594.2799 |
| sp P13639 EF2_HUMAN            | 1640.7934 |
| sp P19338 NUCL_HUMAN           | 2863.2759 |
| sp P21333 FLNA_HUMAN           | 1640.7651 |
| sp P33316 DUT_HUMAN            | 2144.0572 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q9NW13 RBM28_HUMAN          | 3140.4332 |
| sp P05141 ADT2_HUMAN,sp Q9H0C  | 1885.8887 |
| sp P51991 ROA3_HUMAN           | 1972.8875 |
| sp O60506 HNRPQ_HUMAN          | 3256.6041 |
| sp Q15029 U5S1_HUMAN           | 2258.1331 |
| sp P62913 RL11_HUMAN           | 2013.0419 |
| sp Q9BTW9 TBCD_HUMAN           | 3693.7951 |
| sp O94910 AGRL1_HUMAN          | 2462.135  |
| sp Q9BUZ4 TRAF4_HUMAN          | 1706.8046 |
| sp P35222 CTNB1_HUMAN          | 3409.6175 |
| sp Q00610 CLH1_HUMAN           | 2639.3344 |
| sp Q13671 RIN1_HUMAN           | 2494.1917 |
| sp P05787 K2C8_HUMAN           | 2436.2496 |
| sp P23921 RIR1_HUMAN           | 2768.3505 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4150.887  |
| sp P08708 RS17_HUMAN           | 1484.7446 |
| sp P08670 VIME_HUMAN           | 1930.8401 |
| sp P19338 NUCL_HUMAN           | 2027.8749 |
| sp Q13619 CUL4A_HUMAN          | 3124.4522 |
| sp P00558 PGK1_HUMAN           | 2830.4541 |
| sp P14618 KPYM_HUMAN           | 1863.8924 |
| sp O14979 HNRDL_HUMAN          | 1615.7301 |
| sp P62753 RS6_HUMAN            | 1659.8104 |
| sp O00159 MYO1C_HUMAN          | 1778.9315 |
| sp O00567 NOP56_HUMAN          | 2149.0626 |
| sp P14854 CX6B1_HUMAN          | 2167.9303 |
| sp O14617 AP3D1_HUMAN          | 2216.0995 |
| sp Q02790 FKBP4_HUMAN          | 2623.2628 |
| sp P14174 MIF_HUMAN            | 6003.9122 |
| sp Q14181 DPOA2_HUMAN          | 1579.6434 |
| sp P52597 HNRPF_HUMAN          | 2433.2064 |

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| sp P07205 PGK2_HUMAN,sp P00558 P07237 PDIA1_HUMAN                            | 1428.7864 |
| sp P07237 PDIA1_HUMAN                                                        | 1482.7103 |
| sp P42167 LAP2B_HUMAN                                                        | 2635.3282 |
| sp P62805 H4_HUMAN                                                           | 1634.8226 |
| sp Q09666 AHNK_HUMAN                                                         | 3183.5796 |
| sp P68032 ACTC_HUMAN,sp P63267 P62805 H4_HUMAN                               | 2938.4535 |
| sp P62805 H4_HUMAN                                                           | 1662.8287 |
| sp O60568 PLOD3_HUMAN                                                        | 2937.5084 |
| sp P62987 RL40_HUMAN                                                         | 1520.7154 |
| sp P36578 RL4_HUMAN                                                          | 1640.8998 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C Q14204 DYHC1_HUMAN                            | 1261.6051 |
| sp Q14204 DYHC1_HUMAN                                                        | 2440.0675 |
| sp Q9P2B2 FPRP_HUMAN                                                         | 2659.1609 |
| sp P15924 DESP_HUMAN                                                         | 1939.9276 |
| sp P41250 GARS_HUMAN                                                         | 1833.8242 |
| sp P26599 PTBP1_HUMAN,sp O9578 O95816 BAG2_HUMAN                             | 1604.7682 |
| sp O95816 BAG2_HUMAN                                                         | 1732.8129 |
| sp P09651 ROA1_HUMAN                                                         | 1824.8067 |
| sp P26038 MOES_HUMAN                                                         | 1332.6714 |
| sp Q06830 PRDX1_HUMAN                                                        | 2338.1052 |
| sp Q9ULW0 TPX2_HUMAN                                                         | 2327.1699 |
| sp Q15293 RCN1_HUMAN                                                         | 1800.8166 |
| sp A6NMY6 AXA2L_HUMAN,sp P073 P35221 CTNA1_HUMAN,sp P2623 P31943 HNRH1_HUMAN | 2391.0934 |
| sp P35221 CTNA1_HUMAN,sp P2623 P31943 HNRH1_HUMAN                            | 2042.9918 |
| sp P31943 HNRH1_HUMAN                                                        | 1936.8738 |
| sp P31943 HNRH1_HUMAN                                                        | 1936.8738 |
| sp P31943 HNRH1_HUMAN                                                        | 1936.8738 |
| sp P43243 MATR3_HUMAN                                                        | 1972.0993 |
| sp P16435 NCPR_HUMAN                                                         | 1804.9108 |
| sp Q14204 DYHC1_HUMAN                                                        | 3084.588  |
| sp O15371 EIF3D_HUMAN                                                        | 1706.7536 |
| sp Q9Y624 JAM1_HUMAN                                                         | 2041.9051 |
| sp P54851 EMP2_HUMAN                                                         | 1291.6197 |
| sp P06748 NPM_HUMAN                                                          | 2769.2267 |
| sp Q00610 CLH1_HUMAN                                                         | 2639.3344 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI P09429 HMGB1_HUMAN                            | 4150.887  |
| sp P09429 HMGB1_HUMAN                                                        | 1788.7955 |
| sp O60264 SMCA5_HUMAN                                                        | 3602.5541 |
| sp P62937 PPIA_HUMAN                                                         | 1543.6903 |
| sp P55795 HNRH2_HUMAN,sp P319 Q99729 ROAA_HUMAN                              | 2350.1329 |
| sp Q99729 ROAA_HUMAN                                                         | 1716.8141 |
| sp P08670 VIME_HUMAN                                                         | 1321.6303 |
| sp P26640 SYVC_HUMAN                                                         | 1069.5193 |
| sp P00491 PNPH_HUMAN                                                         | 2366.1194 |
| sp P05362 ICAM1_HUMAN                                                        | 1813.9686 |
| sp P38919 IF4A3_HUMAN                                                        | 2259.9525 |
| sp P62937 PPIA_HUMAN                                                         | 3832.7461 |

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| sp P52272 HNRPM_HUMAN          | 1802.8336 |
| sp P31040 SDHA_HUMAN           | 2914.5076 |
| sp P13693 TCTP_HUMAN           | 2177.9939 |
| sp P38646 GRP75_HUMAN          | 3887.7176 |
| sp P28288 ABCD3_HUMAN          | 1553.8202 |
| sp P36578 RL4_HUMAN            | 2499.225  |
| sp Q9GZT3 SLIRP_HUMAN          | 2495.2517 |
| sp O75874 IDHC_HUMAN           | 2625.217  |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp P16401 H15_HUMAN            | 1264.7139 |
| sp P23284 PPIB_HUMAN           | 1985.9946 |
| sp O95373 IPO7_HUMAN           | 2263.2253 |
| sp P08238 HS90B_HUMAN          | 3552.5481 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp P28288 ABCD3_HUMAN          | 1934.9772 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4174.1256 |
| sp P54819 KAD2_HUMAN           | 1103.5724 |
| sp P60900 PSA6_HUMAN           | 2623.3282 |
| sp O00567 NOP56_HUMAN          | 2104.0378 |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp P09382 LEG1_HUMAN           | 1678.7627 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2583.287  |
| sp P02545 LMNA_HUMAN           | 1334.6103 |
| sp P26447 S10A4_HUMAN          | 2135.943  |
| sp P15121 ALDR_HUMAN           | 2414.1213 |
| sp Q02543 RL18A_HUMAN          | 1534.7892 |
| sp P23396 RS3_HUMAN            | 2166.0633 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P61978 HNRPK_HUMAN          | 2265.0033 |
| sp Q9Y3E5 PTH2_HUMAN           | 3079.619  |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp Q13057 COASY_HUMAN          | 3265.6044 |
| sp P07900 HS90A_HUMAN,sp P0823 | 2497.2336 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2932.3702 |
| sp Q86V81 THOC4_HUMAN          | 2560.1678 |
| sp Q14240 IF4A2_HUMAN          | 2044.8796 |
| sp P15121 ALDR_HUMAN           | 2405.2301 |
| sp P50990 TCPQ_HUMAN           | 2191.0514 |
| sp Q13573 SNW1_HUMAN           | 2782.3926 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1947.856  |
| sp P51991 ROA3_HUMAN           | 2078.9797 |
| sp P51610 HCFC1_HUMAN          | 2390.139  |
| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp P47914 RL29_HUMAN           | 1406.7558 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P14174 MIF_HUMAN            | 1705.8345 |

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| sp P62899 RL31_HUMAN           | 1369.6626 |
| sp P61201 CSN2_HUMAN           | 2110.0153 |
| sp P09429 HMGB1_HUMAN          | 1916.8905 |
| sp P08195 4F2_HUMAN            | 2051.9854 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P19075 TSN8_HUMAN           | 2967.439  |
| sp P30153 2AAA_HUMAN           | 1770.904  |
| sp Q15717 ELAV1_HUMAN          | 1931.984  |
| sp P42704 LPPRC_HUMAN          | 2259.0556 |
| sp Q9HAV4 XPO5_HUMAN           | 1720.9764 |
| sp P30101 PDIA3_HUMAN          | 1711.7842 |
| sp P46060 RAGP1_HUMAN          | 2772.4157 |
| sp P32004 L1CAM_HUMAN          | 2033.8935 |
| sp P08729 K2C7_HUMAN           | 1825.9462 |
| sp P02786 TFR1_HUMAN           | 2177.0463 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2409.254  |
| sp P49368 TCPG_HUMAN           | 2133.0525 |
| sp P07437 TBB5_HUMAN           | 2902.3299 |
| sp P04083 ANXA1_HUMAN          | 3094.507  |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp P50895 BCAM_HUMAN           | 2579.2405 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp Q86VP6 CAND1_HUMAN          | 1610.794  |
| sp Q7KZF4 SND1_HUMAN           | 2866.4649 |
| sp O75153 CLU_HUMAN            | 2397.258  |
| sp Q6PD62 CTR9_HUMAN           | 3622.809  |
| sp P07900 HS90A_HUMAN,sp Q145i | 2487.2282 |
| sp P61927 RL37_HUMAN           | 1124.5978 |
| sp Q9UIG0 BAZ1B_HUMAN          | 3184.6597 |
| sp P39023 RL3_HUMAN            | 1491.7973 |
| sp Q16881 TRXR1_HUMAN          | 3190.4151 |
| sp O94776 MTA2_HUMAN           | 1631.725  |
| sp P11142 HSP7C_HUMAN          | 2034.0382 |
| sp O94776 MTA2_HUMAN           | 1369.7718 |
| sp O00303 EIF3F_HUMAN          | 2582.1709 |
| sp P33240 CSTF2_HUMAN          | 1712.9461 |
| sp Q6UVK1 CSPG4_HUMAN          | 2353.0744 |
| sp P41252 SYIC_HUMAN           | 2075.0364 |
| sp P26006 ITA3_HUMAN           | 1718.8628 |
| sp P15924 DESP_HUMAN           | 1453.7777 |
| sp P11413 G6PD_HUMAN           | 1989.9684 |
| sp Q8WW12 PCNP_HUMAN           | 1712.7543 |
| sp Q53EL6 PDCD4_HUMAN          | 2179.0294 |
| sp Q9Y277 VDAC3_HUMAN          | 2025.0167 |
| sp Q00839 HNRPU_HUMAN          | 1476.7283 |
| sp P62805 H4_HUMAN             | 1486.6688 |

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| sp Q14839 CHD4_HUMAN           | 2364.2478 |
| sp Q14839 CHD4_HUMAN           | 2364.2478 |
| sp Q09666 AHNK_HUMAN           | 2602.2697 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2583.287  |
| sp P62266 RS23_HUMAN           | 2044.0126 |
| sp O60841 IF2P_HUMAN           | 1650.7962 |
| sp P05783 K1C18_HUMAN          | 3551.6322 |
| sp Q8WW12 PCNP_HUMAN           | 1786.7871 |
| sp Q92900 RENT1_HUMAN          | 2184.1004 |
| sp P07910 HNRPC_HUMAN          | 2264.1471 |
| sp O60361 NDK8_HUMAN,sp P2239  | 2603.2512 |
| sp Q6NUQ4 TM214_HUMAN          | 2650.3068 |
| sp P09429 HMGB1_HUMAN          | 2439.2045 |
| sp P05023 AT1A1_HUMAN          | 2327.1798 |
| sp A1L0T0 ILVBL_HUMAN          | 3232.4917 |
| sp P49257 LMAN1_HUMAN          | 3799.7721 |
| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp O95347 SMC2_HUMAN           | 2737.403  |
| sp P21333 FLNA_HUMAN           | 1471.8511 |
| sp P21333 FLNA_HUMAN           | 1775.8578 |
| sp P04350 TBB4A_HUMAN,sp P6837 | 2934.302  |
| sp P29692 EF1D_HUMAN           | 1532.7583 |
| sp P33991 MCM4_HUMAN           | 1917.9472 |
| sp P05783 K1C18_HUMAN          | 2389.1974 |
| sp P29401 TKT_HUMAN            | 3378.6554 |
| sp P05386 RLA1_HUMAN           | 2551.3475 |
| sp P05386 RLA1_HUMAN           | 2551.3475 |
| sp O75643 U520_HUMAN           | 2644.2592 |
| sp Q9NZ01 TECR_HUMAN           | 1671.7814 |
| sp O43707 ACTN4_HUMAN          | 3008.5091 |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp P43243 MATR3_HUMAN          | 1908.8788 |
| sp Q24JP5 T132A_HUMAN          | 2518.2063 |
| sp Q24JP5 T132A_HUMAN          | 2518.2063 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1261.6051 |
| sp Q08945 SSRP1_HUMAN          | 1462.7569 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P00367 DHE3_HUMAN           | 2266.1018 |
| sp P41252 SYIC_HUMAN           | 1176.5815 |
| sp P22695 QCR2_HUMAN           | 2847.4775 |
| sp P60174 TPIS_HUMAN           | 1470.6991 |
| sp O95831 AIFM1_HUMAN          | 2016.9429 |
| sp P21333 FLNA_HUMAN           | 4965.3365 |
| sp Q14103 HNRPD_HUMAN          | 1241.6041 |
| sp P50995 ANX11_HUMAN          | 2304.2327 |
| sp P00533 EGFR_HUMAN           | 2127.9314 |
| sp P07237 PDIA1_HUMAN          | 2206.043  |

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| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp Q92901 RL3L_HUMAN,sp P39023 | 1561.7161 |
| sp P62266 RS23_HUMAN           | 1134.6033 |
| sp P26639 SYTC_HUMAN           | 1681.8385 |
| sp P62937 PPIA_HUMAN           | 4138.9041 |
| sp Q9UBQ5 EIF3K_HUMAN          | 2182.063  |
| sp Q14118 DAG1_HUMAN           | 1861.9574 |
| sp P68371 TBB4B_HUMAN          | 2039.9589 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1461.6664 |
| sp Q9P0L0 VAPA_HUMAN           | 1971.9286 |
| sp O00264 PGRC1_HUMAN          | 1840.842  |
| sp Q86YQ8 CPNE8_HUMAN          | 2607.3445 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3579.6724 |
| sp Q15262 PTPRK_HUMAN          | 2990.412  |
| sp Q15067 ACOX1_HUMAN          | 1735.7876 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 3714.7447 |
| sp Q13283 G3BP1_HUMAN          | 1947.8567 |
| sp P78527 PRKDC_HUMAN          | 1122.5054 |
| sp Q92598 HS105_HUMAN          | 1704.7818 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P04792 HSPB1_HUMAN          | 3422.6803 |
| sp Q01650 LAT1_HUMAN           | 1651.7689 |
| sp Q14204 DYHC1_HUMAN          | 3592.7281 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp Q969P0 IGSF8_HUMAN          | 1478.8093 |
| sp P07205 PGK2_HUMAN,sp P00558 | 2317.0975 |
| sp O00571 DDX3X_HUMAN,sp O155  | 1838.005  |
| sp P84077 ARF1_HUMAN,sp P61204 | 2583.287  |
| sp P13639 EF2_HUMAN            | 3856.8685 |
| sp P50990 TCPQ_HUMAN           | 1730.8475 |
| sp P23528 COF1_HUMAN           | 1633.8022 |
| sp P06730 IF4E_HUMAN           | 2305.1954 |
| sp P06730 IF4E_HUMAN           | 2305.1954 |
| sp Q9BYX7 ACTBM_HUMAN,sp POC   | 1820.8866 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P63244 RACK1_HUMAN          | 2826.4539 |
| sp P08195 4F2_HUMAN            | 1361.7078 |
| sp Q14061 COX17_HUMAN          | 1912.8845 |
| sp Q14061 COX17_HUMAN          | 1912.8845 |
| sp P07195 LDHB_HUMAN           | 2295.1958 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P08670 VIME_HUMAN           | 1784.8727 |
| sp P19338 NUCL_HUMAN           | 1351.666  |
| sp Q13310 PABP4_HUMAN          | 1601.7256 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2383.1954 |
| sp P08195 4F2_HUMAN            | 2542.1823 |



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| sp P18124 RL7_HUMAN            | 2735.3186 |
| sp P06756 ITAV_HUMAN           | 2255.0495 |
| sp P06756 ITAV_HUMAN           | 2255.0495 |
| sp Q09666 AHNK_HUMAN           | 1390.605  |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp Q9BT78 CSN4_HUMAN           | 2743.3956 |
| sp P23396 RS3_HUMAN            | 1285.703  |
| sp P62701 RS4X_HUMAN           | 2185.1644 |
| sp P49327 FAS_HUMAN            | 2875.3925 |
| sp P54709 AT1B3_HUMAN          | 1857.8341 |
| sp P25205 MCM3_HUMAN           | 1332.715  |
| sp Q9Y262 EIF3L_HUMAN          | 3319.6302 |
| sp P06576 ATPB_HUMAN           | 3016.4084 |
| sp O75369 FLNB_HUMAN           | 1340.6976 |
| sp P12956 XRCC6_HUMAN          | 2344.1434 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp Q9ULF5 S39AA_HUMAN          | 2182.0616 |
| sp P62750 RL23A_HUMAN          | 1566.8154 |
| sp P02786 TFR1_HUMAN           | 2596.3061 |
| sp P62854 RS26_HUMAN,sp Q5JNZ5 | 2024.9561 |
| sp P53597 SUCA_HUMAN           | 2574.3442 |
| sp Q02750 MP2K1_HUMAN          | 1709.8811 |
| sp P36578 RL4_HUMAN            | 3027.6294 |
| sp Q14254 FLOT2_HUMAN          | 2272.1812 |
| sp P41091 IF2G_HUMAN,sp Q2VIR3 | 1415.8137 |
| sp P35579 MYH9_HUMAN           | 1811.0193 |
| sp Q6DD87 ZN787_HUMAN          | 2168.159  |
| sp Q13283 G3BP1_HUMAN          | 3169.6448 |
| sp P14618 KPYM_HUMAN           | 2587.2853 |
| sp Q9H8H0 NOL11_HUMAN          | 2867.4705 |
| sp P09012 SNRPA_HUMAN          | 2134.0695 |
| sp P12956 XRCC6_HUMAN          | 1491.8449 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp O00231 PSD11_HUMAN          | 3359.7361 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P30050 RL12_HUMAN           | 2237.1077 |
| sp P63244 RACK1_HUMAN          | 1600.8283 |
| sp P19338 NUCL_HUMAN           | 1597.8352 |
| sp Q14978 NOLC1_HUMAN          | 2017.0956 |
| sp Q9H9B4 SFXN1_HUMAN          | 2866.3655 |
| sp P09429 HMGB1_HUMAN          | 2434.0747 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp Q09666 AHNK_HUMAN           | 1669.9039 |
| sp Q9UKG1 DP13A_HUMAN          | 2693.3297 |
| sp P68366 TBA4A_HUMAN          | 2022.0058 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |

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| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp P62826 RAN_HUMAN            | 1666.8203 |
| sp P07737 PROF1_HUMAN          | 2075.1085 |
| sp P26373 RL13_HUMAN           | 1867.9163 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P21964 COMT_HUMAN           | 2221.0038 |
| sp P06733 ENOA_HUMAN           | 2076.0164 |
| sp P17813 EGLN_HUMAN           | 1894.9425 |
| sp Q13442 HAP28_HUMAN          | 1409.6609 |
| sp Q14103 HNRPD_HUMAN          | 1771.8563 |
| sp O00571 DDX3X_HUMAN,sp O155  | 2937.2512 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3217.5925 |
| sp Q15149 PLEC_HUMAN           | 3544.6634 |
| sp P14174 MIF_HUMAN            | 6003.9122 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 3040.3661 |
| sp P05388 RLA0_HUMAN           | 2020.9742 |
| sp Q13838 DX39B_HUMAN          | 1834.8486 |
| sp P30622 CLIP1_HUMAN          | 1555.8035 |
| sp P46781 RS9_HUMAN            | 2086.0695 |
| sp P55265 DSRAD_HUMAN          | 1596.8161 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp P45880 VDAC2_HUMAN          | 1637.809  |
| sp Q13421 MSLN_HUMAN           | 2723.4745 |
| sp Q13428 TCOF_HUMAN           | 1713.905  |
| sp P52272 HNRPM_HUMAN          | 1758.9338 |
| sp O00571 DDX3X_HUMAN,sp O155  | 1636.8784 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp Q99729 ROAA_HUMAN           | 2134.93   |
| sp P06756 ITAV_HUMAN           | 2105.9874 |
| sp Q14258 TRI25_HUMAN          | 2020.9854 |
| sp Q9Y3T9 NOC2L_HUMAN          | 2240.1187 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1704.7811 |
| sp Q15019 SEPT2_HUMAN          | 2750.334  |
| sp Q15019 SEPT2_HUMAN          | 2750.334  |
| sp P60709 ACTB_HUMAN,sp P6803z | 2375.277  |
| sp P31327 CPSM_HUMAN           | 2198.1259 |
| sp Q8NC51 PAIRB_HUMAN          | 2814.3097 |
| sp P34897 GLYM_HUMAN           | 2188.1164 |
| sp P08670 VIME_HUMAN,sp P0872c | 1256.5885 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P12268 IMDH2_HUMAN          | 2835.4014 |
| sp P11021 BIP_HUMAN            | 1512.7168 |
| sp P00505 AATM_HUMAN           | 2221.0956 |
| sp P50454 SERPH_HUMAN          | 2739.4079 |

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| sp O96008 TOM40_HUMAN          | 2167.2154 |
| sp P49748 ACADV_HUMAN          | 1561.7849 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 1761.8646 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P0DMV8 HS71A_HUMAN,sp P34C  | 2970.4281 |
| sp P62987 RL40_HUMAN,sp P62979 | 1461.7538 |
| sp Q9HCU4 CELR2_HUMAN          | 2731.262  |
| sp P13639 EF2_HUMAN            | 1598.8304 |
| sp O75533 SF3B1_HUMAN          | 2585.189  |
| sp Q14C86 GAPD1_HUMAN          | 2468.1794 |
| sp Q9Y624 JAM1_HUMAN           | 2041.9051 |
| sp P02786 TFR1_HUMAN           | 2321.9569 |
| sp Q7KZF4 SND1_HUMAN           | 3240.619  |
| sp Q5JVF3 PCID2_HUMAN          | 2868.3905 |
| sp Q16630 CPSF6_HUMAN          | 2991.4924 |
| sp O14617 AP3D1_HUMAN          | 2216.0995 |
| sp P10809 CH60_HUMAN           | 3003.4561 |
| sp Q12931 TRAP1_HUMAN          | 1319.7449 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp Q6YHK3 CD109_HUMAN          | 2760.3858 |
| sp Q15067 ACOX1_HUMAN          | 1751.7825 |
| sp Q9Y490 TLN1_HUMAN           | 1859.9564 |
| sp Q01650 LAT1_HUMAN           | 2457.2726 |
| sp P26641 EF1G_HUMAN           | 2386.1845 |
| sp P16402 H13_HUMAN,sp Q02539  | 1431.6882 |
| sp Q13310 PABP4_HUMAN          | 1710.9305 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp Q14847 LASP1_HUMAN          | 1950.857  |
| sp P49327 FAS_HUMAN            | 2633.2003 |
| sp P40926 MDHM_HUMAN           | 2930.5026 |
| sp P11021 BIP_HUMAN            | 2116.0589 |
| sp P49257 LMAN1_HUMAN          | 1459.7783 |
| sp P15328 FOLR1_HUMAN          | 1890.8717 |
| sp Q9BYX7 ACTBM_HUMAN,sp POCC  | 1820.8866 |
| sp Q9BYX7 ACTBM_HUMAN,sp POCC  | 1820.8866 |
| sp P04083 ANXA1_HUMAN          | 1409.6721 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P53675 CLH2_HUMAN           | 2242.1746 |
| sp Q9NQR4 NIT2_HUMAN           | 2283.1423 |
| sp O15067 PUR4_HUMAN           | 1922.9064 |
| sp Q9Y3U8 RL36_HUMAN           | 1510.7238 |
| sp P22102 PUR2_HUMAN           | 2261.1077 |
| sp P51970 NDUA8_HUMAN          | 2672.2792 |
| sp Q8TDD1 DDX54_HUMAN          | 2166.0779 |
| sp Q01082 SPTB2_HUMAN          | 2266.1117 |
| sp P04843 RPN1_HUMAN           | 1674.7849 |
| sp Q9UQE7 SMC3_HUMAN           | 2121.0855 |

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| sp Q02878 RL6_HUMAN            | 2705.2093 |
| sp P21333 FLNA_HUMAN           | 4166.9604 |
| sp P06748 NPM_HUMAN            | 2240.0418 |
| sp Q16576 RBBP7_HUMAN          | 1985.8538 |
| sp O95757 HS74L_HUMAN,sp P3493 | 1986.9656 |
| sp P29401 TKT_HUMAN            | 2347.1366 |
| sp P06213 INSR_HUMAN           | 2273.1944 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P12956 XRCC6_HUMAN          | 2230.1418 |
| sp P30622 CLIP1_HUMAN          | 2330.0597 |
| sp P62424 RL7A_HUMAN           | 2007.0425 |
| sp P18124 RL7_HUMAN            | 2506.1872 |
| sp Q01105 SET_HUMAN            | 2424.2649 |
| sp P09622 DLDH_HUMAN           | 2679.3731 |
| sp Q15149 PLEC_HUMAN           | 1724.8078 |
| sp O95340 PAPS2_HUMAN          | 2635.1926 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P15:  | 1826.8799 |
| sp Q09666 AHNK_HUMAN           | 1345.67   |
| sp P09429 HMGB1_HUMAN          | 1788.7955 |
| sp Q07955 SRSF1_HUMAN          | 2404.1481 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp Q03405 UPAR_HUMAN           | 2888.3644 |
| sp Q09666 AHNK_HUMAN           | 1365.6097 |
| sp P26038 MOES_HUMAN           | 2148.0236 |
| sp Q08J23 NSUN2_HUMAN          | 1541.766  |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp Q8NCA5 FA98A_HUMAN,sp Q52L  | 2508.1856 |
| sp Q8NCA5 FA98A_HUMAN,sp Q52L  | 2508.1856 |
| sp Q15181 IPYR_HUMAN           | 1618.774  |
| sp O75694 NU155_HUMAN          | 2381.136  |
| sp P26641 EF1G_HUMAN           | 1571.8559 |
| sp P22314 UBA1_HUMAN           | 2805.3908 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp Q9UMS4 PRP19_HUMAN          | 1771.8992 |
| sp P07355 ANXA2_HUMAN          | 3390.6554 |
| sp Q9NZ45 CISD1_HUMAN          | 2139.9419 |
| sp P11142 HSP7C_HUMAN          | 1587.7504 |
| sp P83881 RL36A_HUMAN,sp Q969C | 1461.7001 |
| sp P78371 TCPB_HUMAN           | 2289.1675 |
| sp O75369 FLNB_HUMAN           | 4083.7857 |
| sp Q9BQG0 MBB1A_HUMAN          | 2824.5521 |
| sp Q96AE4 FUBP1_HUMAN          | 1752.908  |
| sp Q6NUQ4 TM214_HUMAN          | 2650.3068 |
| sp Q12788 TBL3_HUMAN           | 2478.2478 |
| sp P18669 PGAM1_HUMAN          | 2439.2468 |
| sp P62937 PPIA_HUMAN           | 1109.5869 |

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| sp P60981 DEST_HUMAN           | 1684.7338 |
| sp P05388 RLA0_HUMAN           | 2020.9742 |
| sp P02786 TFR1_HUMAN           | 1582.897  |
| sp O75955 FLOT1_HUMAN          | 1844.9745 |
| sp O95573 ACSL3_HUMAN          | 2148.0528 |
| sp Q12931 TRAP1_HUMAN          | 1380.6422 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3080.4338 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1965.8996 |
| sp Q96AE4 FUBP1_HUMAN          | 1664.7642 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp Q96T88 UHRF1_HUMAN          | 2999.5393 |
| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp P26368 U2AF2_HUMAN          | 1362.6528 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1613.7838 |
| sp Q08J23 NSUN2_HUMAN          | 1483.7242 |
| sp P04406 G3P_HUMAN            | 1526.6745 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q14258 TRI25_HUMAN          | 1877.9775 |
| sp P62805 H4_HUMAN             | 1650.8175 |
| sp P18084 ITB5_HUMAN           | 1830.8788 |
| sp Q12905 ILF2_HUMAN           | 2289.258  |
| sp P62633 CNBP_HUMAN           | 2045.8142 |
| sp P07437 TBB5_HUMAN           | 2380.1984 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1239.5594 |
| sp P00558 PGK1_HUMAN           | 2958.5491 |
| sp P27816 MAP4_HUMAN           | 1090.5043 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1576.7232 |
| sp P62851 RS25_HUMAN           | 1849.9098 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp Q00839 HNRPU_HUMAN          | 1476.7283 |
| sp P08758 ANXA5_HUMAN          | 2422.0999 |
| sp Q16719 KYNU_HUMAN           | 2285.2016 |
| sp Q96ER9 MITOK_HUMAN          | 2335.1404 |
| sp A0AVT1 UBA6_HUMAN           | 2018.0684 |
| sp P61247 RS3A_HUMAN           | 1295.622  |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2611.2303 |
| sp P50990 TCPQ_HUMAN           | 2319.1464 |
| sp P22695 QCR2_HUMAN           | 2659.2667 |
| sp P62266 RS23_HUMAN           | 1200.52   |
| sp P62826 RAN_HUMAN            | 1284.5986 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P49368 TCPG_HUMAN           | 2015.0939 |
| sp P20042 IF2B_HUMAN           | 2046.9833 |
| sp P06733 ENOA_HUMAN           | 1377.6888 |
| sp P10809 CH60_HUMAN           | 2538.2822 |
| sp P62266 RS23_HUMAN           | 1134.6033 |
| sp Q14204 DYHC1_HUMAN          | 1204.62   |

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| sp P31930 QCR1_HUMAN           | 4623.289  |
| sp P23396 RS3_HUMAN            | 1285.703  |
| sp P31327 CPSM_HUMAN           | 1908.904  |
| sp Q8WUM4 PDC6I_HUMAN          | 1732.9108 |
| sp Q13421 MSLN_HUMAN           | 4011.9717 |
| sp O95372 LYPA2_HUMAN          | 1301.6616 |
| sp P42166 LAP2A_HUMAN          | 1637.7645 |
| sp O14579 COPE_HUMAN           | 2479.2959 |
| sp P61927 RL37_HUMAN           | 1225.551  |
| sp P60174 TPIS_HUMAN           | 3911.9615 |
| sp Q10713 MPPA_HUMAN           | 1964.952  |
| sp P07900 HS90A_HUMAN,sp Q145i | 1886.9738 |
| sp P56192 SYMC_HUMAN           | 1964.9129 |
| sp P23381 SYWC_HUMAN           | 2681.3853 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3535.7154 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp Q02543 RL18A_HUMAN          | 1534.7892 |
| sp Q14690 RRP5_HUMAN           | 1857.9585 |
| sp P07900 HS90A_HUMAN,sp Q145i | 1204.6816 |
| sp Q9NZ01 TECR_HUMAN           | 1954.9326 |
| sp P19338 NUCL_HUMAN           | 2115.0484 |
| sp P14384 CBPM_HUMAN           | 3410.689  |
| sp P84077 ARF1_HUMAN,sp P61204 | 2583.287  |
| sp P52597 HNRPF_HUMAN          | 1542.8042 |
| sp P78371 TCPB_HUMAN           | 1680.8406 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3246.5901 |
| sp P14866 HNRPL_HUMAN          | 1387.7096 |
| sp Q15717 ELAV1_HUMAN          | 2222.0644 |
| sp P40227 TCPZ_HUMAN           | 1959.8487 |
| sp Q9NYF8 BCLF1_HUMAN          | 1880.8177 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1467.7544 |
| sp O43390 HNRPR_HUMAN,sp O605  | 1628.7327 |
| sp P47914 RL29_HUMAN           | 1432.829  |
| sp Q16630 CPSF6_HUMAN          | 2991.4924 |
| sp Q6PL18 ATAD2_HUMAN          | 1425.7504 |
| sp Q9H2P0 ADNP_HUMAN           | 1908.8247 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3207.4199 |
| sp P31153 METK2_HUMAN          | 2568.2496 |
| sp P83731 RL24_HUMAN           | 2084.9877 |
| sp P61313 RL15_HUMAN           | 2041.0673 |
| sp Q01082 SPTB2_HUMAN          | 1958.9334 |
| sp P23284 PIIB_HUMAN           | 1767.8713 |
| sp P50454 SERPH_HUMAN          | 1700.6849 |
| sp P40227 TCPZ_HUMAN           | 1482.6951 |
| sp P35613 BASI_HUMAN           | 1195.6601 |
| sp P23396 RS3_HUMAN            | 2196.0375 |

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| sp P36578 RL4_HUMAN            | 1418.7405 |
| sp O14980 XPO1_HUMAN           | 1125.5607 |
| sp P04083 ANXA1_HUMAN          | 2101.0579 |
| sp Q9BZE4 NOG1_HUMAN           | 1824.8505 |
| sp Q00610 CLH1_HUMAN           | 1547.8712 |
| sp Q04637 IF4G1_HUMAN          | 2383.1074 |
| sp P54851 EMP2_HUMAN           | 1291.6197 |
| sp P62241 RS8_HUMAN            | 1838.9275 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1531.7155 |
| sp P08670 VIME_HUMAN           | 1729.8774 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P62937 PPIA_HUMAN           | 1701.7702 |
| sp P31327 CPSM_HUMAN           | 2579.2499 |
| sp P21796 VDAC1_HUMAN          | 1640.8086 |
| sp P78527 PRKDC_HUMAN          | 2994.5008 |
| sp Q96HS1 PGAM5_HUMAN          | 1866.8133 |
| sp P62937 PPIA_HUMAN           | 1109.5869 |
| sp P23396 RS3_HUMAN            | 2294.1583 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp P17301 ITA2_HUMAN           | 3283.6877 |
| sp P21964 COMT_HUMAN           | 2221.0038 |
| sp P11388 TOP2A_HUMAN          | 1123.6026 |
| sp P27824 CALX_HUMAN           | 3584.622  |
| sp Q14980 NUMA1_HUMAN          | 2381.1751 |
| sp Q14980 NUMA1_HUMAN          | 1995.8882 |
| sp P17813 EGLN_HUMAN           | 1894.9425 |
| sp P84098 RL19_HUMAN           | 1119.5673 |
| sp Q1KMD3 HNRL2_HUMAN          | 2337.1066 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1651.9145 |
| sp P15880 RS2_HUMAN            | 1745.8883 |
| sp P19338 NUCL_HUMAN           | 1095.5924 |
| sp Q53LP3 SWAHC_HUMAN          | 1750.9002 |
| sp P32004 L1CAM_HUMAN          | 3537.6742 |
| sp P62987 RL40_HUMAN,sp P62979 | 1477.7487 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P50213 IDH3A_HUMAN          | 2182.1569 |
| sp P16401 H15_HUMAN,sp P10412  | 1233.7081 |
| sp O75643 U520_HUMAN           | 1930.9775 |
| sp P46940 IQGA1_HUMAN          | 2079.0347 |
| sp Q09666 AHNK_HUMAN           | 2373.1747 |
| sp P61020 RAB5B_HUMAN,sp P203: | 1958.0183 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp Q8IZ83 A16A1_HUMAN          | 1738.825  |
| sp P62244 RS15A_HUMAN          | 1419.6823 |
| sp P62424 RL7A_HUMAN           | 1793.906  |
| sp P27824 CALX_HUMAN           | 1158.5782 |

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| sp P11940 PABP1_HUMAN          | 1608.7672 |
| sp Q15437 SC23B_HUMAN          | 1566.6699 |
| sp P02786 TFR1_HUMAN           | 2530.1765 |
| sp Q5VTL8 PR38B_HUMAN          | 2055.0095 |
| sp Q9Y262 EIF3L_HUMAN          | 2595.3445 |
| sp Q9NR30 DDX21_HUMAN          | 2333.0423 |
| sp P46776 RL27A_HUMAN          | 1579.7129 |
| sp P15924 DESP_HUMAN           | 2339.2009 |
| sp P50990 TCPQ_HUMAN           | 1976.9765 |
| sp Q9UKM9 RALY_HUMAN           | 2368.0542 |
| sp P31930 QCR1_HUMAN           | 1960.9167 |
| sp P00558 PGK1_HUMAN           | 4677.1891 |
| sp O75643 U520_HUMAN           | 3145.7063 |
| sp P07954 FUMH_HUMAN           | 1610.8742 |
| sp Q9Y3D3 RT16_HUMAN           | 1361.651  |
| sp Q00610 CLH1_HUMAN,sp P5367  | 1892.0367 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp Q86V81 THOC4_HUMAN          | 2899.3049 |
| sp P35579 MYH9_HUMAN           | 1811.0193 |
| sp P08240 SRPRA_HUMAN          | 1848.9114 |
| sp Q15262 PTPRK_HUMAN          | 1575.7794 |
| sp Q9NQR4 NIT2_HUMAN           | 2283.1423 |
| sp O15031 PLXB2_HUMAN          | 2462.1384 |
| sp P02786 TFR1_HUMAN           | 1437.7252 |
| sp Q00610 CLH1_HUMAN           | 1251.6136 |
| sp Q06830 PRDX1_HUMAN          | 3077.4488 |
| sp P50238 CRIP1_HUMAN          | 1892.9203 |
| sp P05362 ICAM1_HUMAN          | 1308.7038 |
| sp P62937 PPIA_HUMAN           | 2027.9364 |
| sp O14980 XPO1_HUMAN           | 2450.1655 |
| sp P36871 PGM1_HUMAN           | 1523.6892 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4150.887  |
| sp P62753 RS6_HUMAN            | 1782.8835 |
| sp Q00610 CLH1_HUMAN           | 1462.7205 |
| sp Q9NRJ5 PAPOB_HUMAN,sp P510  | 3045.5811 |
| sp Q00796 DHSO_HUMAN           | 2550.3152 |
| sp Q16695 H31T_HUMAN,sp Q71DI  | 1501.7637 |
| sp Q8WXF1 PSPC1_HUMAN          | 1485.7252 |
| sp O00264 PGRC1_HUMAN          | 1840.842  |
| sp P22234 PUR6_HUMAN           | 1343.647  |
| sp Q01105 SET_HUMAN            | 2464.1111 |
| sp Q16695 H31T_HUMAN,sp Q71DI  | 1629.8587 |
| sp P06733 ENOA_HUMAN           | 1377.6888 |
| sp Q14789 GOGB1_HUMAN          | 1979.98   |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp P16402 H13_HUMAN,sp P16401  | 1734.8424 |
| sp Q96AE4 FUBP1_HUMAN          | 1752.908  |



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| sp Q9GZL7 WDR12_HUMAN          | 2409.225  |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp P10809 CH60_HUMAN           | 1969.9745 |
| sp P30086 PEBP1_HUMAN          | 2695.3453 |
| sp P23284 PPIB_HUMAN           | 1501.8181 |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P49588 SYAC_HUMAN           | 2366.1866 |
| sp Q9Y6X3 SCC4_HUMAN           | 2111.9847 |
| sp O60784 TOM1_HUMAN           | 2622.2458 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1736.9243 |
| sp Q02878 RL6_HUMAN            | 1556.7835 |
| sp P62906 RL10A_HUMAN          | 1589.8599 |
| sp P18887 XRCC1_HUMAN          | 1438.6299 |
| sp Q9UHX1 PUF60_HUMAN          | 3517.6646 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3891.7913 |
| sp P99999 CYC_HUMAN            | 1994.9334 |
| sp P00505 AATM_HUMAN           | 2221.0956 |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp O75976 CBPD_HUMAN           | 1753.7948 |
| sp P17301 ITA2_HUMAN           | 1326.584  |
| sp P02786 TFR1_HUMAN           | 2530.1765 |
| sp P30044 PRDX5_HUMAN          | 3310.6332 |
| sp P08069 IGF1R_HUMAN          | 1918.0061 |
| sp P09661 RU2A_HUMAN           | 1562.8417 |
| sp P05783 K1C18_HUMAN          | 3411.526  |
| sp Q14839 CHD4_HUMAN           | 2451.2282 |
| sp Q08J23 NSUN2_HUMAN          | 2472.0805 |
| sp Q14738 2A5D_HUMAN,sp Q1336  | 2704.3571 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P62826 RAN_HUMAN            | 1666.8203 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P57081 WDR4_HUMAN           | 2688.249  |
| sp P10586 PTPRF_HUMAN          | 1762.8349 |
| sp P10586 PTPRF_HUMAN          | 2331.0444 |
| sp P07237 PDIA1_HUMAN          | 1324.6452 |
| sp O60684 IMA7_HUMAN           | 2389.21   |
| sp P30405 PPIF_HUMAN           | 1933.9323 |
| sp P83731 RL24_HUMAN           | 2084.9877 |
| sp Q04637 IF4G1_HUMAN          | 2845.3447 |
| sp Q15019 SEPT2_HUMAN          | 2259.9994 |
| sp P14618 KPYM_HUMAN           | 2449.1411 |
| sp P50914 RL14_HUMAN           | 1235.6146 |
| sp O43175 SERA_HUMAN           | 3733.9138 |
| sp P08670 VIME_HUMAN,sp P08725 | 1256.5885 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2208.9851 |
| sp P62249 RS16_HUMAN           | 1410.6925 |
| sp P50991 TCPD_HUMAN           | 1729.8635 |

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| sp P46783 RS10_HUMAN,sp Q9NQ3  | 1905.9441 |
| sp P11142 HSP7C_HUMAN          | 2348.1972 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1322.5999 |
| sp P62937 PIIA_HUMAN           | 1543.6903 |
| sp P00387 NB5R3_HUMAN          | 4256.0882 |
| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp Q9Y3T9 NOC2L_HUMAN          | 2240.1187 |
| sp P68431 H31_HUMAN            | 3938.8277 |
| sp Q15459 SF3A1_HUMAN          | 1516.7522 |
| sp Q9UDY4 DNJB4_HUMAN          | 1850.8435 |
| sp P00558 PGK1_HUMAN           | 1425.7715 |
| sp P43121 MUC18_HUMAN          | 3829.8833 |
| sp Q15149 PLEC_HUMAN           | 2644.3425 |
| sp P08174 DAF_HUMAN            | 1554.76   |
| sp P38606 VATA_HUMAN           | 2238.0263 |
| sp P02786 TFR1_HUMAN           | 2266.0398 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1796.872  |
| sp P09622 DLDH_HUMAN           | 2393.2227 |
| sp P78371 TCPB_HUMAN           | 1680.8406 |
| sp Q9UMS4 PRP19_HUMAN          | 1771.8992 |
| sp Q14160 SCRIB_HUMAN          | 1763.8479 |
| sp Q6PD62 CTR9_HUMAN           | 1370.7558 |
| sp Q96HS1 PGAM5_HUMAN          | 1515.714  |
| sp P14866 HNRPL_HUMAN          | 1387.7096 |
| sp Q99808 S29A1_HUMAN          | 1991.1278 |
| sp Q13263 TIF1B_HUMAN          | 1306.6517 |
| sp P21796 VDAC1_HUMAN          | 1724.7893 |
| sp Q9BUJ2 HNRL1_HUMAN          | 1707.8216 |
| sp Q92616 GCN1_HUMAN           | 2228.2304 |
| sp P16152 CBR1_HUMAN           | 2026.9385 |
| sp P54577 SYYC_HUMAN           | 2146.9695 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q00610 CLH1_HUMAN           | 2040.9905 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp P15170 ERF3A_HUMAN,sp Q8IYD | 1601.9141 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P78527 PRKDC_HUMAN          | 1692.8107 |
| sp Q9HD20 AT131_HUMAN          | 1742.8951 |
| sp Q5JVF3 PCID2_HUMAN          | 1819.9217 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P53396 ACLY_HUMAN           | 2697.3538 |
| sp Q16832 DDR2_HUMAN           | 2241.0702 |
| sp Q9UHB9 SRP68_HUMAN          | 2043.9327 |
| sp Q9Y3T9 NOC2L_HUMAN          | 1880.9785 |
| sp P25685 DNJB1_HUMAN,sp Q9UD  | 1129.5404 |

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| sp P07737 PROF1_HUMAN          | 1430.7327 |
| sp P53621 COPA_HUMAN           | 1583.7984 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp Q9UQ80 PA2G4_HUMAN          | 2716.2877 |
| sp P27816 MAP4_HUMAN           | 1516.7634 |
| sp P14923 PLAK_HUMAN           | 1937.0622 |
| sp Q15067 ACOX1_HUMAN          | 1751.7825 |
| sp P17301 ITA2_HUMAN           | 1326.584  |
| sp P54819 KAD2_HUMAN           | 1785.9373 |
| sp P15121 ALDR_HUMAN           | 3129.6063 |
| sp O15173 PGRC2_HUMAN          | 1940.9057 |
| sp P35052 GPC1_HUMAN           | 2798.3511 |
| sp P49720 PSB3_HUMAN           | 2006.9983 |
| sp P16403 H12_HUMAN            | 1219.6925 |
| sp P50238 CRIP1_HUMAN          | 1724.7399 |
| sp Q00796 DHSD_HUMAN           | 2550.3152 |
| sp P27824 CALX_HUMAN           | 2094.0269 |
| sp Q13263 TIF1B_HUMAN          | 1306.6517 |
| sp P21796 VDAC1_HUMAN          | 2004.0276 |
| sp P08621 RU17_HUMAN           | 1555.6362 |
| sp P51991 ROA3_HUMAN           | 1576.7733 |
| sp P61978 HNRPK_HUMAN          | 1249.6667 |
| sp P43243 MATR3_HUMAN          | 2806.1055 |
| sp O60568 PLOD3_HUMAN          | 1378.6841 |
| sp P26641 EF1G_HUMAN           | 1319.651  |
| sp Q13283 G3BP1_HUMAN          | 1931.8618 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3089.4223 |
| sp P09622 DLDH_HUMAN           | 2695.368  |
| sp Q96AG4 LRC59_HUMAN          | 3113.5413 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp Q9NQC3 RTN4_HUMAN           | 2158.0113 |
| sp Q9NQC3 RTN4_HUMAN           | 2158.0113 |
| sp P33176 KINH_HUMAN           | 1565.7508 |
| sp Q9Y5Y5 PEX16_HUMAN          | 2830.2179 |
| sp P49184 DNSL1_HUMAN          | 3553.9072 |
| sp Q9H4M9 EHD1_HUMAN           | 2469.2904 |
| sp P27797 CALR_HUMAN           | 1996.865  |
| sp P63244 RACK1_HUMAN          | 2175.0233 |
| sp O43390 HNRPR_HUMAN          | 2439.1693 |
| sp P26640 SYVC_HUMAN           | 1322.7558 |
| sp P62937 PPIA_HUMAN           | 1711.8206 |
| sp Q12788 TBL3_HUMAN           | 3115.3151 |
| sp P14866 HNRPL_HUMAN          | 1444.6583 |
| sp Q14118 DAG1_HUMAN           | 2055.9722 |
| sp P04792 HSPB1_HUMAN          | 2209.0903 |
| sp P52272 HNRPM_HUMAN          | 1916.0116 |

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| sp P49327 FAS_HUMAN           | 1922.9659 |
| sp P11021 BIP_HUMAN           | 2116.0589 |
| sp O75367 H2AY_HUMAN          | 2727.2309 |
| sp P0DMV8 HS71A_HUMAN,sp PODI | 1613.7838 |
| sp P41252 SYIC_HUMAN          | 1845.876  |
| sp P05023 AT1A1_HUMAN         | 1937.0007 |
| sp P62424 RL7A_HUMAN          | 1522.8144 |
| sp P10809 CH60_HUMAN          | 2051.08   |
| sp Q15365 PCBP1_HUMAN         | 3809.9002 |
| sp P06748 NPM_HUMAN           | 1234.583  |
| sp Q14677 EPN4_HUMAN          | 2567.1677 |
| sp P11142 HSP7C_HUMAN         | 1603.7453 |
| sp P32320 CDD_HUMAN           | 2811.3354 |
| sp P40429 RL13A_HUMAN,sp Q6NV | 1732.8632 |
| sp Q9H0X4 F234A_HUMAN         | 3014.3613 |
| sp P22626 ROA2_HUMAN          | 2123.0423 |
| sp P14923 PLAK_HUMAN          | 1814.9639 |
| sp O75694 NU155_HUMAN         | 1901.971  |
| sp P15121 ALDR_HUMAN          | 2135.1449 |
| sp P56378 ATP68_HUMAN         | 1352.6473 |
| sp P21333 FLNA_HUMAN          | 5144.2492 |
| sp P27694 RFA1_HUMAN          | 2114.9869 |
| sp Q02543 RL18A_HUMAN         | 1935.8971 |
| sp P05787 K2C8_HUMAN          | 1537.7736 |
| sp Q86V81 THOC4_HUMAN         | 3339.634  |
| sp P26368 U2AF2_HUMAN         | 1934.8469 |
| sp Q9NQR4 NIT2_HUMAN          | 2283.1423 |
| sp P62805 H4_HUMAN            | 1614.7638 |
| sp P39748 FEN1_HUMAN          | 2202.0858 |
| sp P08865 RSSA_HUMAN          | 1487.762  |
| sp P17813 EGLN_HUMAN          | 2737.309  |
| sp Q16658 FSCN1_HUMAN         | 2478.1663 |
| sp Q7Z794 K2C1B_HUMAN,sp O956 | 1278.6245 |
| sp Q71UM5 RS27L_HUMAN         | 1761.8785 |
| sp P54136 SYRC_HUMAN          | 2087.9146 |
| sp P46781 RS9_HUMAN           | 1595.8671 |
| sp P43243 MATR3_HUMAN         | 2526.1083 |
| sp P50914 RL14_HUMAN          | 1235.6146 |
| sp P62805 H4_HUMAN            | 1486.6688 |
| sp P02786 TFR1_HUMAN          | 2997.472  |
| sp Q9NZB2 F120A_HUMAN         | 1905.9699 |
| sp P32004 L1CAM_HUMAN         | 3537.6742 |
| sp Q5VZK9 CARL1_HUMAN         | 1777.8781 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3429.6697 |
| sp P05783 K1C18_HUMAN         | 1700.8105 |
| sp Q9BQG0 MBB1A_HUMAN         | 1418.8133 |
| sp P14866 HNRPL_HUMAN         | 2190.0011 |

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| sp P17987 TCPA_HUMAN           | 2119.1161 |
| sp Q12904 AIMP1_HUMAN          | 1882.9831 |
| sp Q12904 AIMP1_HUMAN          | 1882.9831 |
| sp P06748 NPM_HUMAN            | 1798.8082 |
| sp P15151 PVR_HUMAN            | 2719.1569 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P07195 LDHB_HUMAN           | 1500.7096 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp Q15233 NONO_HUMAN           | 1892.8799 |
| sp O95292 VAPB_HUMAN           | 2782.2077 |
| sp P27816 MAP4_HUMAN           | 1804.8414 |
| sp P18077 RL35A_HUMAN          | 1359.6895 |
| sp Q16531 DDB1_HUMAN           | 1541.7263 |
| sp P02786 TFR1_HUMAN           | 2321.9569 |
| sp P49207 RL34_HUMAN           | 1455.6235 |
| sp Q15046 SYK_HUMAN            | 1733.8117 |
| sp P31327 CPSM_HUMAN           | 3323.6748 |
| sp P67936 TPM4_HUMAN,sp P0795  | 1494.793  |
| sp P30048 PRDX3_HUMAN          | 4276.9688 |
| sp P13639 EF2_HUMAN            | 1558.8355 |
| sp P63173 RL38_HUMAN           | 1681.8451 |
| sp P00558 PGK1_HUMAN           | 3015.5401 |
| sp P62258 1433E_HUMAN          | 2596.2068 |
| sp Q9Y3T9 NOC2L_HUMAN          | 2240.1187 |
| sp P26599 PTBP1_HUMAN          | 2308.2202 |
| sp O60361 NDK8_HUMAN,sp P2239  | 1680.7955 |
| sp Q14203 DCTN1_HUMAN          | 1924.8414 |
| sp P11586 C1TC_HUMAN           | 3158.545  |
| sp P61158 ARP3_HUMAN           | 2724.1901 |
| sp P62263 RS14_HUMAN           | 2688.245  |
| sp Q99832 TCPH_HUMAN           | 3087.4713 |
| sp Q16531 DDB1_HUMAN           | 2390.2417 |
| sp P22626 ROA2_HUMAN           | 2257.9772 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp Q9NQ29 LUC7L_HUMAN          | 2118.1011 |
| sp Q15041 AR6P1_HUMAN          | 1918.881  |
| sp Q9BQA1 MEP50_HUMAN          | 3153.388  |
| sp Q9NQ55 SSF1_HUMAN           | 1608.826  |
| sp O14929 HAT1_HUMAN           | 3007.3552 |
| sp P08729 K2C7_HUMAN           | 2466.1339 |
| sp P29401 TKT_HUMAN            | 3284.7868 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp P60842 IF4A1_HUMAN          | 1837.0197 |
| sp Q06830 PRDX1_HUMAN          | 1946.9772 |
| sp P31949 S10AB_HUMAN          | 2416.1257 |
| sp P60981 DEST_HUMAN           | 1875.8163 |
| sp P20042 IF2B_HUMAN           | 1825.7764 |

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| sp O60313 OPA1_HUMAN            | 2338.123  |
| sp Q14980 NUMA1_HUMAN           | 2353.2206 |
| sp P08754 GNAI3_HUMAN,sp P0947  | 1803.9043 |
| sp Q9UHB6 LIMA1_HUMAN           | 2055.8869 |
| sp Q15366 PCBP2_HUMAN           | 2198.0274 |
| sp P62424 RL7A_HUMAN            | 3018.4968 |
| sp P48668 K2C6C_HUMAN,sp P0426  | 1504.6794 |
| sp Q7L1Q6 BZW1_HUMAN            | 1551.7205 |
| sp P05362 ICAM1_HUMAN           | 1813.9686 |
| sp Q14118 DAG1_HUMAN            | 3790.7744 |
| sp Q8N257 H2B3B_HUMAN,sp P628   | 1097.5254 |
| sp Q99798 ACON_HUMAN            | 2942.4846 |
| sp P43121 MUC18_HUMAN           | 1467.6412 |
| sp P53621 COPA_HUMAN            | 2031.0749 |
| sp P58107 EPIPL_HUMAN           | 2812.3702 |
| sp P07737 PROF1_HUMAN           | 2282.1001 |
| sp P13639 EF2_HUMAN             | 1626.7638 |
| sp P31930 QCR1_HUMAN            | 1960.9167 |
| sp P62424 RL7A_HUMAN            | 2007.0425 |
| sp P30740 ILEU_HUMAN            | 1395.7398 |
| sp O76021 RL1D1_HUMAN           | 1377.6525 |
| sp P63244 RACK1_HUMAN           | 3222.5768 |
| sp Q96L21 RL10L_HUMAN,sp P2763  | 1531.6759 |
| sp P16402 H13_HUMAN,sp P10412   | 2050.0946 |
| sp P40429 RL13A_HUMAN           | 1547.9035 |
| sp P10586 PTPRF_HUMAN           | 2733.2408 |
| sp P62937 PPIA_HUMAN            | 1543.6903 |
| sp P49736 MCM2_HUMAN            | 1858.8347 |
| sp P62854 RS26_HUMAN,sp Q5JNZ5  | 1785.8985 |
| sp P36952 SPB5_HUMAN            | 2775.3279 |
| sp Q08945 SSRP1_HUMAN           | 4477.1424 |
| sp Q96HY6 DDR GK_HUMAN          | 2348.2052 |
| sp P05387 RLA2_HUMAN            | 2421.2064 |
| sp P62805 H4_HUMAN              | 1614.7638 |
| sp Q9HB71 CYBP_HUMAN            | 2490.2676 |
| sp P22102 PUR2_HUMAN            | 3754.8705 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 2513.1315 |
| sp Q9Y6N7 ROBO1_HUMAN           | 1335.6493 |
| sp Q9HCS7 SYF1_HUMAN            | 2024.9803 |
| sp Q9UBQ0 VPS29_HUMAN           | 2361.2185 |
| sp Q96ER9 MITOK_HUMAN           | 2335.1404 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI  | 3907.7862 |
| sp P62266 RS23_HUMAN            | 1891.9428 |
| sp P62258 1433E_HUMAN           | 2134.0371 |
| sp P27635 RL10_HUMAN            | 1797.872  |
| sp P04406 G3P_HUMAN             | 1411.6732 |
| sp Q14118 DAG1_HUMAN            | 2055.9722 |

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| sp P00533 EGFR_HUMAN           | 1750.889  |
| sp P26641 EF1G_HUMAN           | 1571.8559 |
| sp O75369 FLNB_HUMAN           | 1725.8322 |
| sp O95816 BAG2_HUMAN           | 1322.6466 |
| sp P09429 HMGB1_HUMAN          | 2450.0696 |
| sp P61604 CH10_HUMAN           | 2783.4058 |
| sp P36578 RL4_HUMAN            | 2499.225  |
| sp Q9UI26 IPO11_HUMAN          | 2556.2934 |
| sp Q9UBS4 DJB11_HUMAN          | 2509.2197 |
| sp Q9BYT8 NEUL_HUMAN           | 1505.7013 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp O43809 CPSF5_HUMAN          | 2517.2864 |
| sp Q15084 PDIA6_HUMAN          | 2252.1113 |
| sp Q99873 ANM1_HUMAN           | 2973.5733 |
| sp Q6Y1H2 HACD2_HUMAN          | 1417.6838 |
| sp Q6Y1H2 HACD2_HUMAN          | 1417.6838 |
| sp P09874 PARP1_HUMAN          | 1738.7798 |
| sp P43243 MATR3_HUMAN          | 1463.762  |
| sp P16401 H15_HUMAN            | 1108.6241 |
| sp Q08211 DHX9_HUMAN           | 2100.9501 |
| sp O75396 SC22B_HUMAN          | 2598.3006 |
| sp P23396 RS3_HUMAN            | 3010.3841 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1535.7216 |
| sp P30740 ILEU_HUMAN           | 1812.9006 |
| sp P08729 K2C7_HUMAN           | 1981.913  |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1531.6759 |
| sp Q06323 PSME1_HUMAN          | 2429.1533 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P62910 RL32_HUMAN           | 2091.0459 |
| sp Q5BKZ1 ZN326_HUMAN          | 2106.9577 |
| sp P30041 PRDX6_HUMAN          | 2793.3929 |
| sp P16403 H12_HUMAN            | 1505.8202 |
| sp P31327 CPSM_HUMAN           | 2886.5015 |
| sp P36871 PGM1_HUMAN           | 3222.5833 |
| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q9H0X4 F234A_HUMAN          | 3014.3613 |
| sp Q10471 GALT2_HUMAN          | 2045.9595 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 2401.2206 |
| sp P07900 HS90A_HUMAN          | 3538.5325 |
| sp Q08945 SSRP1_HUMAN          | 1430.6864 |
| sp Q969P0 IGSF8_HUMAN          | 1337.6398 |
| sp P49750 YLPM1_HUMAN          | 2375.1632 |
| sp P05783 K1C18_HUMAN          | 2069.0641 |
| sp O75794 CD123_HUMAN          | 1701.7821 |
| sp P08069 IGF1R_HUMAN          | 2337.0179 |
| sp Q92499 DDX1_HUMAN           | 1396.583  |
| sp Q14118 DAG1_HUMAN           | 2055.9722 |

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| sp P08195 4F2_HUMAN            | 2276.1298 |
| sp Q13616 CUL1_HUMAN           | 2529.2248 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp Q13838 DX39B_HUMAN          | 1834.8486 |
| sp Q9UKV3 ACINU_HUMAN          | 1961.9555 |
| sp Q02790 FKBP4_HUMAN          | 1489.7089 |
| sp P35637 FUS_HUMAN            | 2090.9585 |
| sp P15880 RS2_HUMAN            | 1871.8723 |
| sp P48556 PSMD8_HUMAN          | 4525.1714 |
| sp Q687X5 STEA4_HUMAN          | 2198.05   |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp Q9Y490 TLN1_HUMAN           | 1479.8297 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp Q16666 IF16_HUMAN           | 2230.0762 |
| sp Q06830 PRDX1_HUMAN          | 2817.3392 |
| sp P27816 MAP4_HUMAN           | 1676.7464 |
| sp Q58FG0 HS905_HUMAN,sp P0790 | 1363.6442 |
| sp Q15149 PLEC_HUMAN           | 1640.8621 |
| sp Q99873 ANM1_HUMAN           | 2389.177  |
| sp P42677 RS27_HUMAN           | 1773.8533 |
| sp P14618 KPYM_HUMAN           | 2808.4449 |
| sp P26373 RL13_HUMAN           | 1867.9163 |
| sp P60866 RS20_HUMAN           | 1717.7366 |
| sp Q9P0L0 VAPA_HUMAN           | 1971.9286 |
| sp Q08211 DHX9_HUMAN           | 3151.6554 |
| sp P61513 RL37A_HUMAN          | 2124.9245 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp P08758 ANXA5_HUMAN          | 1727.928  |
| sp P15924 DESP_HUMAN           | 2943.5012 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1614.8175 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P35573 GDE_HUMAN            | 2689.2265 |
| sp P35613 BASI_HUMAN           | 4232.8732 |
| sp P04406 G3P_HUMAN            | 3129.4787 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P04040 CATA_HUMAN           | 1844.9461 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp Q13740 CD166_HUMAN          | 1821.8574 |
| sp P19338 NUCL_HUMAN           | 1758.8676 |
| sp Q15631 TSN_HUMAN            | 2516.3023 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2386.1839 |
| sp O43776 SYNC_HUMAN           | 1736.8257 |
| sp Q5JVF3 PCID2_HUMAN          | 2774.4392 |
| sp P40937 RFC5_HUMAN           | 3453.7165 |



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| sp Q8WWM7 ATX2L_HUMAN          | 2201.0861 |
| sp P49368 TCPG_HUMAN           | 2015.0939 |
| sp P62266 RS23_HUMAN           | 1200.52   |
| sp Q96T37 RBM15_HUMAN          | 3144.5251 |
| sp Q9UQE7 SMC3_HUMAN           | 1878.9727 |
| sp P14384 CBPM_HUMAN           | 3221.462  |
| sp P32119 PRDX2_HUMAN          | 1483.8035 |
| sp P45880 VDAC2_HUMAN          | 1637.809  |
| sp P06730 IF4E_HUMAN           | 2087.9582 |
| sp Q00341 VIGLN_HUMAN          | 1373.6939 |
| sp P41091 IF2G_HUMAN,sp Q2VIR3 | 1415.8137 |
| sp P21796 VDAC1_HUMAN          | 2004.0276 |
| sp P19338 NUCL_HUMAN           | 1253.6292 |
| sp P36542 ATPG_HUMAN           | 1420.731  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q92499 DDX1_HUMAN           | 1896.7995 |
| sp Q9UMS4 PRP19_HUMAN          | 1708.8632 |
| sp P30043 BLVRB_HUMAN          | 2353.1777 |
| sp O76021 RL1D1_HUMAN          | 2647.2218 |
| sp P63244 RACK1_HUMAN          | 2826.4539 |
| sp P15880 RS2_HUMAN            | 2169.0048 |
| sp P69849 NOMO3_HUMAN,sp Q15   | 1847.924  |
| sp Q14152 EIF3A_HUMAN          | 1887.9189 |
| sp Q6P2Q9 PRP8_HUMAN           | 1617.8726 |
| sp P49773 HINT1_HUMAN          | 1995.0538 |
| sp Q10567 AP1B1_HUMAN          | 2617.4367 |
| sp Q13813 SPTN1_HUMAN          | 1506.7606 |
| sp Q14847 LASP1_HUMAN          | 1799.869  |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P22626 ROA2_HUMAN           | 2473.1802 |
| sp P40926 MDHM_HUMAN           | 3005.4627 |
| sp P05141 ADT2_HUMAN,sp P12235 | 1591.7783 |
| sp Q00610 CLH1_HUMAN           | 2355.1495 |
| sp Q9NYF8 BCLF1_HUMAN          | 1806.8934 |
| sp Q9Y624 JAM1_HUMAN           | 2796.5749 |
| sp P06756 ITAV_HUMAN           | 2624.1523 |
| sp P05556 ITB1_HUMAN           | 2040.9575 |
| sp Q8TEM1 PO210_HUMAN          | 2069.0793 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp O76094 SRP72_HUMAN          | 1782.9152 |
| sp P41252 SYIC_HUMAN           | 1176.5815 |
| sp Q9BQG0 MBB1A_HUMAN          | 2038.963  |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp O94925 GLSK_HUMAN           | 2800.2942 |
| sp P13797 PLST_HUMAN           | 1940.9632 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |

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| sp P62277 RS13_HUMAN           | 1577.8777 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1062.473  |
| sp P32004 L1CAM_HUMAN          | 1627.8246 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp P23396 RS3_HUMAN            | 1748.8807 |
| sp P21333 FLNA_HUMAN           | 1416.7249 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp P07237 PDIA1_HUMAN          | 3188.5852 |
| sp O43776 SYNC_HUMAN           | 1960.8738 |
| sp O75436 VP26A_HUMAN          | 1689.9124 |
| sp Q9NTK5 OLA1_HUMAN           | 2884.4899 |
| sp Q08380 LG3BP_HUMAN          | 2445.1237 |
| sp P04406 G3P_HUMAN            | 2478.3118 |
| sp P06576 ATPB_HUMAN           | 3860.8244 |
| sp P15311 EZRI_HUMAN,sp P35241 | 1502.7518 |
| sp P32004 L1CAM_HUMAN          | 1627.8246 |
| sp Q12792 TWF1_HUMAN           | 2399.1856 |
| sp Q9NR30 DDX21_HUMAN          | 3100.4237 |
| sp Q6IAA8 LTOR1_HUMAN          | 4233.9318 |
| sp Q53H96 P5CR3_HUMAN          | 1959.965  |
| sp Q9NR30 DDX21_HUMAN          | 1818.9476 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp O95782 AP2A1_HUMAN          | 1779.8792 |
| sp P78371 TCPB_HUMAN           | 1694.8628 |
| sp P52272 HNRPM_HUMAN          | 1312.6663 |
| sp Q13813 SPTN1_HUMAN          | 1563.7641 |
| sp Q5VTR2 BRE1A_HUMAN          | 2190.0917 |
| sp Q96I24 FUBP3_HUMAN          | 2475.2719 |
| sp O14980 XPO1_HUMAN           | 2374.1012 |
| sp P05388 RLA0_HUMAN           | 2319.1886 |
| sp P61978 HNRPK_HUMAN          | 1971.1153 |
| sp Q92538 GBF1_HUMAN           | 1736.7966 |
| sp O95373 IPO7_HUMAN           | 2414.1801 |
| sp Q16891 MIC60_HUMAN          | 1931.0112 |
| sp Q12788 TBL3_HUMAN           | 2478.2478 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp P62753 RS6_HUMAN            | 2407.1002 |
| sp Q14320 FA50A_HUMAN          | 1998.9072 |
| sp P84098 RL19_HUMAN           | 1630.7813 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1506.8406 |
| sp Q15149 PLEC_HUMAN           | 2021.0106 |
| sp P02545 LMNA_HUMAN           | 1974.9171 |
| sp P62633 CNBP_HUMAN           | 2045.8142 |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp P16152 CBR1_HUMAN           | 2026.9385 |
| sp Q9BUJ2 HNRL1_HUMAN          | 1968.9463 |

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| sp Q9BZE4 NOG1_HUMAN           | 1631.7328 |
| sp P05783 K1C18_HUMAN          | 1370.6678 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P02786 TFR1_HUMAN           | 1810.9214 |
| sp Q14847 LASP1_HUMAN          | 1950.857  |
| sp O14579 COPE_HUMAN           | 1426.6841 |
| sp O75369 FLNB_HUMAN           | 2072.999  |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp Q14978 NOLC1_HUMAN          | 1984.0378 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2559.416  |
| sp P62805 H4_HUMAN             | 1806.9186 |
| sp Q99714 HCD2_HUMAN           | 1655.754  |
| sp P78417 GSTO1_HUMAN          | 2352.1903 |
| sp Q8NC51 PAIRB_HUMAN          | 1172.5826 |
| sp Q8TEM1 PO210_HUMAN          | 2069.0793 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp Q93052 LPP_HUMAN            | 2296.9734 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P36578 RL4_HUMAN            | 1221.7081 |
| sp P43121 MUC18_HUMAN          | 2985.5086 |
| sp Q8WUM0 NU133_HUMAN          | 2164.1528 |
| sp Q9NR31 SAR1A_HUMAN,sp Q9Y6  | 1538.7399 |
| sp Q16666 IF16_HUMAN           | 2776.3299 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P17987 TCPA_HUMAN           | 1763.8955 |
| sp P11388 TOP2A_HUMAN          | 1320.6058 |
| sp P05787 K2C8_HUMAN           | 2484.1366 |
| sp P61604 CH10_HUMAN           | 1231.6237 |
| sp P62263 RS14_HUMAN           | 1578.8076 |
| sp P50570 DYN2_HUMAN,sp Q9UQ1  | 1461.7041 |
| sp Q5SRE5 NU188_HUMAN          | 1858.9533 |
| sp P53999 TCP4_HUMAN           | 1823.9054 |
| sp Q9Y678 COPG1_HUMAN,sp Q9UI  | 2027.051  |
| sp P31327 CPSM_HUMAN           | 2970.4215 |
| sp P41091 IF2G_HUMAN,sp Q2VIR3 | 2295.178  |
| sp Q9H4A4 AMPB_HUMAN           | 1945.0058 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp P62913 RL11_HUMAN           | 1522.7198 |
| sp O75054 IGSF3_HUMAN          | 2179.948  |
| sp Q9BTV4 TMM43_HUMAN          | 2135.0899 |
| sp Q92979 NEP1_HUMAN           | 1138.5731 |
| sp Q13573 SNW1_HUMAN           | 2782.3926 |
| sp P23284 PIIB_HUMAN           | 1894.9611 |
| sp Q9P2E9 RRBP1_HUMAN          | 1354.6477 |
| sp Q92859 NEO1_HUMAN           | 2774.3915 |
| sp O15371 EIF3D_HUMAN          | 1187.5207 |
| sp Q07065 CKAP4_HUMAN          | 3672.8231 |

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| sp Q92616 GCN1_HUMAN           | 2670.3245 |
| sp Q16891 MIC60_HUMAN          | 2764.4144 |
| sp Q16891 MIC60_HUMAN          | 1718.8992 |
| sp Q16891 MIC60_HUMAN          | 4555.1912 |
| sp P32004 L1CAM_HUMAN          | 3665.7923 |
| sp P46940 IQGA1_HUMAN          | 1976.0942 |
| sp P25788 PSA3_HUMAN           | 1831.9316 |
| sp Q8NCA5 FA98A_HUMAN,sp Q52L  | 2508.1856 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2075.9912 |
| sp Q9BT78 CSN4_HUMAN           | 1869.9261 |
| sp P43243 MATR3_HUMAN          | 2991.4978 |
| sp Q9BQ04 RBM4B_HUMAN,sp Q9B   | 2269.124  |
| sp Q00839 HNRPU_HUMAN          | 2383.1114 |
| sp Q9Y314 NOSIP_HUMAN          | 2031.8745 |
| sp Q9H0S4 DDX47_HUMAN          | 2181.0637 |
| sp P40925 MDHC_HUMAN           | 2374.1693 |
| sp Q15067 ACOX1_HUMAN          | 1735.7876 |
| sp Q10567 AP1B1_HUMAN          | 1285.6779 |
| sp P41250 GARS_HUMAN           | 1833.8242 |
| sp P15927 RFA2_HUMAN           | 2324.1219 |
| sp P07900 HS90A_HUMAN,sp Q145i | 1204.6816 |
| sp Q8N163 CCAR2_HUMAN          | 1449.7001 |
| sp Q9UHB6 LIMA1_HUMAN          | 2906.4372 |
| sp P13639 EF2_HUMAN            | 1453.7599 |
| sp Q96RU2 UBP28_HUMAN          | 1915.968  |
| sp P49321 NASP_HUMAN           | 2340.0652 |
| sp Q15005 SPCS2_HUMAN          | 2809.2905 |
| sp P16401 H15_HUMAN            | 1108.6241 |
| sp P05783 K1C18_HUMAN          | 1440.7209 |
| sp Q96KB5 TOPK_HUMAN           | 1842.9741 |
| sp Q16513 PKN2_HUMAN           | 1762.885  |
| sp O00193 SMAP_HUMAN           | 1692.822  |
| sp Q9UHB9 SRP68_HUMAN          | 2670.2813 |
| sp Q8IWS0 PHF6_HUMAN           | 2061.8673 |
| sp P61764 STXB1_HUMAN          | 2720.2541 |
| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp Q14527 HLTF_HUMAN           | 3298.7085 |
| sp P61313 RL15_HUMAN           | 1901.9384 |
| sp Q12906 ILF3_HUMAN           | 2612.3374 |
| sp Q9UPN9 TRI33_HUMAN          | 1871.8915 |
| sp Q9P289 STK26_HUMAN          | 2309.2307 |
| sp P29401 TKT_HUMAN            | 1145.5717 |
| sp P00966 ASSY_HUMAN           | 1324.583  |
| sp Q13547 HDAC1_HUMAN          | 1652.7471 |
| sp P11142 HSP7C_HUMAN          | 3085.4062 |
| sp Q969X5 ERGI1_HUMAN          | 2596.1506 |
| sp P06493 CDK1_HUMAN           | 2514.1849 |

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| sp P05787 K2C8_HUMAN           | 1277.5888 |
| sp P31949 S10AB_HUMAN          | 1675.7366 |
| sp P20700 LMNB1_HUMAN          | 1672.758  |
| sp Q9Y2X3 NOP58_HUMAN          | 2008.0378 |
| sp P11586 C1TC_HUMAN           | 1832.9381 |
| sp P27824 CALX_HUMAN           | 2458.1329 |
| sp Q14152 EIF3A_HUMAN          | 1350.6317 |
| sp P06733 ENOA_HUMAN           | 4588.1275 |
| sp P14618 KPYM_HUMAN           | 2753.3007 |
| sp P06733 ENOA_HUMAN           | 1268.5561 |
| sp P78527 PRKDC_HUMAN          | 2343.092  |
| sp Q9Y2Z4 SYYM_HUMAN           | 1489.7889 |
| sp P31939 PUR9_HUMAN           | 1495.7783 |
| sp P62937 PIIA_HUMAN           | 3816.7512 |
| sp P78371 TCPB_HUMAN           | 2404.2057 |
| sp P10586 PTPRF_HUMAN          | 1778.8298 |
| sp Q9HCU4 CELR2_HUMAN          | 2100.0099 |
| sp Q9Y2R4 DDX52_HUMAN          | 2041.9891 |
| sp P22314 UBA1_HUMAN           | 2805.3908 |
| sp P61981 1433G_HUMAN,sp P631C | 1699.8893 |
| sp P62753 RS6_HUMAN            | 1659.8104 |
| sp Q9NRX1 PNO1_HUMAN           | 2983.4815 |
| sp P05141 ADT2_HUMAN,sp P1223C | 1655.8308 |
| sp P20700 LMNB1_HUMAN          | 2218.0365 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P12956 XRCC6_HUMAN          | 1547.7112 |
| sp P17987 TCPA_HUMAN           | 1729.9251 |
| sp Q96AG4 LRC59_HUMAN          | 3113.5413 |
| sp O43390 HNRPR_HUMAN          | 3197.6033 |
| sp P35659 DEK_HUMAN            | 2136.1328 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P50914 RL14_HUMAN           | 1235.6146 |
| sp Q12965 MYO1E_HUMAN          | 1261.6415 |
| sp P00390 GSHR_HUMAN           | 2336.2125 |
| sp Q01082 SPTB2_HUMAN          | 2904.3348 |
| sp P62269 RS18_HUMAN           | 1675.7995 |
| sp P08621 RU17_HUMAN           | 1229.5863 |
| sp P35579 MYH9_HUMAN           | 1408.6947 |
| sp P30101 PDIA3_HUMAN          | 1696.8461 |
| sp P29401 TKT_HUMAN            | 1517.7072 |
| sp P12814 ACTN1_HUMAN          | 1234.6306 |
| sp P08670 VIME_HUMAN           | 2020.9702 |
| sp O00567 NOP56_HUMAN          | 1474.8031 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp P51398 RT29_HUMAN           | 1520.8239 |
| sp P00966 ASSY_HUMAN           | 1324.583  |
| sp Q14152 EIF3A_HUMAN          | 1461.7464 |

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| sp P04406 G3P_HUMAN            | 3548.7457 |
| sp P58107 EPIPL_HUMAN          | 2427.174  |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp P30086 PEBP1_HUMAN          | 2695.3453 |
| sp Q12906 ILF3_HUMAN           | 4040.8554 |
| sp P63104 1433Z_HUMAN,sp P3194 | 1448.6718 |
| sp Q9HB71 CYBP_HUMAN           | 1641.876  |
| sp Q06830 PRDX1_HUMAN          | 1321.6038 |
| sp P46781 RS9_HUMAN            | 1398.7368 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp O60888 CUTA_HUMAN           | 2500.2672 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp Q9BY67 CADM1_HUMAN          | 1329.6313 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P10809 CH60_HUMAN           | 3904.9153 |
| sp Q9Y4D7 PLXD1_HUMAN          | 2149.0593 |
| sp P53701 CCHL_HUMAN           | 2646.257  |
| sp P10412 H14_HUMAN            | 1390.7932 |
| sp P31947 1433S_HUMAN          | 1813.9323 |
| sp Q9HD20 AT131_HUMAN          | 2404.2387 |
| sp P51991 ROA3_HUMAN           | 2207.0746 |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp P51659 DHB4_HUMAN           | 1667.8308 |
| sp O75821 EIF3G_HUMAN          | 1469.6358 |
| sp P08670 VIME_HUMAN           | 1504.6794 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp Q969P0 IGSF8_HUMAN          | 1337.6398 |
| sp Q01433 AMPD2_HUMAN          | 2114.0619 |
| sp P40938 RFC3_HUMAN           | 2084.0942 |
| sp P23284 PPIB_HUMAN           | 1501.8181 |
| sp O60216 RAD21_HUMAN,sp Q9H4  | 1809.9665 |
| sp P46776 RL27A_HUMAN          | 1781.8049 |
| sp P61313 RL15_HUMAN           | 2209.1141 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P31943 HNRH1_HUMAN          | 1936.8738 |
| sp P16401 H15_HUMAN,sp P10412  | 1233.7081 |
| sp P53396 ACLY_HUMAN           | 1610.8417 |
| sp Q99729 ROAA_HUMAN           | 1588.7192 |
| sp P29401 TKT_HUMAN            | 2421.1383 |
| sp P27797 CALR_HUMAN           | 3052.4124 |
| sp Q14152 EIF3A_HUMAN          | 1350.6317 |
| sp P35232 PHB_HUMAN            | 3319.67   |
| sp Q9P244 LRFN1_HUMAN          | 3629.7395 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1467.7544 |
| sp P22626 ROA2_HUMAN           | 2123.0423 |

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| sp Q15041 AR6P1_HUMAN          | 1699.7988 |
| sp P63244 RACK1_HUMAN          | 2444.1682 |
| sp P62995 TRA2B_HUMAN          | 2145.9531 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P21291 CSRP1_HUMAN          | 2675.1731 |
| sp Q96EX1 SIM12_HUMAN          | 1696.8784 |
| sp P26641 EF1G_HUMAN           | 2785.2548 |
| sp O43707 ACTN4_HUMAN          | 3520.7726 |
| sp P62913 RL11_HUMAN           | 2747.2827 |
| sp Q08J23 NSUN2_HUMAN          | 1541.766  |
| sp P60900 PSA6_HUMAN           | 2124.1103 |
| sp Q96A72 MGN2_HUMAN,sp P613:  | 1147.5298 |
| sp Q92621 NU205_HUMAN          | 1620.8042 |
| sp Q96ER9 MITOK_HUMAN          | 2335.1404 |
| sp P62081 RS7_HUMAN            | 1161.6394 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1783.748  |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3535.7154 |
| sp P07814 SYEP_HUMAN           | 3496.6245 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P19338 NUCL_HUMAN           | 2863.2759 |
| sp Q06830 PRDX1_HUMAN          | 2179.0433 |
| sp P11413 G6PD_HUMAN           | 1989.9684 |
| sp P49411 EFTU_HUMAN           | 1958.9408 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P39023 RL3_HUMAN            | 2007.8884 |
| sp O00159 MYO1C_HUMAN          | 1932.9469 |
| sp P39023 RL3_HUMAN            | 2163.9895 |
| sp P22626 ROA2_HUMAN           | 2257.9772 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1592.7181 |
| sp P61313 RL15_HUMAN           | 1915.9541 |
| sp P53621 COPA_HUMAN           | 2128.9194 |
| sp P60891 PRPS1_HUMAN,sp P2110 | 2084.9763 |
| sp P63162 RSMN_HUMAN,sp P1467  | 2508.0872 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2409.254  |
| sp P35232 PHB_HUMAN            | 3319.67   |
| sp Q15149 PLEC_HUMAN           | 1270.6558 |
| sp Q9BUJ2 HNRL1_HUMAN          | 2592.282  |
| sp P12956 XRCC6_HUMAN          | 1237.6303 |
| sp P63104 1433Z_HUMAN,sp P3194 | 1432.6769 |
| sp P09874 PARP1_HUMAN          | 2640.3031 |
| sp P13639 EF2_HUMAN            | 1334.599  |
| sp Q9Y3U8 RL36_HUMAN           | 1510.7238 |
| sp P26640 SYVC_HUMAN           | 3109.4597 |
| sp P05783 K1C18_HUMAN          | 3531.6028 |
| sp P78527 PRKDC_HUMAN          | 1450.698  |

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| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp O15031 PLXB2_HUMAN          | 2524.2156 |
| sp Q13813 SPTN1_HUMAN          | 1563.7641 |
| sp Q6PJG9 LRFN4_HUMAN          | 4420.2526 |
| sp P35232 PHB_HUMAN            | 1922.0724 |
| sp P51991 ROA3_HUMAN           | 3254.422  |
| sp O14979 HNRDL_HUMAN          | 2089.9626 |
| sp P50995 ANX11_HUMAN          | 1975.019  |
| sp Q9Y262 EIF3L_HUMAN          | 3319.6302 |
| sp P62805 H4_HUMAN             | 1650.8175 |
| sp Q06830 PRDX1_HUMAN          | 2103.0783 |
| sp P31937 3HIDH_HUMAN          | 2590.2236 |
| sp Q00839 HNRPU_HUMAN          | 1572.7784 |
| sp Q9BQG0 MBB1A_HUMAN          | 3089.6146 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp O00534 VMA5A_HUMAN          | 1842.8973 |
| sp Q96I24 FUBP3_HUMAN          | 2475.2719 |
| sp P15880 RS2_HUMAN            | 2169.0048 |
| sp Q12906 ILF3_HUMAN           | 4604.0402 |
| sp Q13332 PTPRS_HUMAN          | 2703.2354 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4777.1899 |
| sp P31942 HNRH3_HUMAN          | 2393.1387 |
| sp P31327 CPSM_HUMAN           | 2518.2955 |
| sp P07900 HS90A_HUMAN,sp Q1451 | 2487.2282 |
| sp P21796 VDAC1_HUMAN          | 2483.2405 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp Q14320 FA50A_HUMAN          | 2363.1969 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P05556 ITB1_HUMAN           | 1578.7566 |
| sp Q96AE4 FUBP1_HUMAN          | 2522.2257 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1783.748  |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P46783 RS10_HUMAN,sp Q9NQ3  | 1712.7828 |
| sp Q13501 SQSTM_HUMAN          | 2592.2146 |
| sp P38646 GRP75_HUMAN          | 2534.2839 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp Q15758 AAAT_HUMAN           | 2810.4127 |
| sp Q14103 HNRPD_HUMAN          | 2116.0147 |
| sp P08729 K2C7_HUMAN           | 2419.1465 |
| sp P82930 RT34_HUMAN           | 2186.9269 |
| sp Q13228 SBP1_HUMAN           | 2743.397  |
| sp Q9NZN4 EHD2_HUMAN           | 4240.0383 |
| sp Q15042 RB3GP_HUMAN          | 2339.078  |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P46776 RL27A_HUMAN          | 1402.8184 |
| sp P46977 STT3A_HUMAN          | 2063.9701 |
| sp Q00610 CLH1_HUMAN           | 2473.1649 |



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| sp P45973 CBX5_HUMAN           | 2099.8861 |
| sp Q9HAV4 XPO5_HUMAN           | 1620.8512 |
| sp Q9UN86 G3BP2_HUMAN          | 2105.0218 |
| sp P23396 RS3_HUMAN            | 2294.1583 |
| sp P06733 ENOA_HUMAN           | 1068.5451 |
| sp Q92945 FUBP2_HUMAN          | 2575.2121 |
| sp P15880 RS2_HUMAN            | 2365.1114 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P63279 UBC9_HUMAN           | 2008.891  |
| sp Q8N3U4 STAG2_HUMAN          | 1403.7409 |
| sp Q9NR31 SAR1A_HUMAN,sp Q9Y6  | 1538.7399 |
| sp Q00341 VIGLN_HUMAN          | 1391.7157 |
| sp P58107 EPIPL_HUMAN          | 1850.0302 |
| sp Q92769 HDAC2_HUMAN,sp Q135  | 2165.947  |
| sp P14854 CX6B1_HUMAN          | 2167.9303 |
| sp Q12906 ILF3_HUMAN           | 2612.3374 |
| sp P11586 C1TC_HUMAN           | 2561.3013 |
| sp P20700 LMNB1_HUMAN          | 1847.8578 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp P61158 ARP3_HUMAN           | 3999.0412 |
| sp P28288 ABCD3_HUMAN          | 2359.0717 |
| sp P32004 L1CAM_HUMAN          | 4463.2029 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1688.7862 |
| sp P60900 PSA6_HUMAN           | 2623.3282 |
| sp Q9NV06 DCA13_HUMAN          | 1922.9486 |
| sp P00533 EGFR_HUMAN           | 2975.4083 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp Q14847 LASP1_HUMAN          | 1420.5895 |
| sp Q09666 AHNK_HUMAN           | 1787.9128 |
| sp P61513 RL37A_HUMAN          | 2124.9245 |
| sp P62913 RL11_HUMAN           | 2747.2827 |
| sp P16403 H12_HUMAN            | 1065.6182 |
| sp P52597 HNRPF_HUMAN          | 1374.6568 |
| sp P61619 S61A1_HUMAN          | 2651.4033 |
| sp Q15149 PLEC_HUMAN           | 2644.3425 |
| sp Q00610 CLH1_HUMAN           | 1954.9061 |
| sp P61513 RL37A_HUMAN          | 2450.2078 |
| sp P43121 MUC18_HUMAN          | 3829.8833 |
| sp O00566 MPP10_HUMAN          | 2851.4062 |
| sp P22695 QCR2_HUMAN           | 1459.7056 |
| sp P33991 MCM4_HUMAN           | 2103.0637 |
| sp Q9UNX3 RL26L_HUMAN,sp P6121 | 2182.1495 |
| sp Q8TDN6 BRX1_HUMAN           | 3720.8927 |
| sp Q9BQG0 MBB1A_HUMAN          | 2840.547  |
| sp Q96A72 MGN2_HUMAN,sp P6131  | 2037.0015 |
| sp P05787 K2C8_HUMAN           | 1560.7202 |

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| sp Q06830 PRDX1_HUMAN          | 3077.4488 |
| sp P43121 MUC18_HUMAN          | 1471.7783 |
| sp Q09666 AHNK_HUMAN           | 2122.0331 |
| sp Q09666 AHNK_HUMAN           | 2801.4018 |
| sp Q9Y3U8 RL36_HUMAN           | 1526.7187 |
| sp Q15149 PLEC_HUMAN           | 1134.5782 |
| sp P50416 CPT1A_HUMAN          | 1679.7732 |
| sp P38646 GRP75_HUMAN          | 1208.5972 |
| sp O60264 SMCA5_HUMAN,sp P283  | 1355.6622 |
| sp A6NIZ1 RP1BL_HUMAN,sp P6283 | 1905.9472 |
| sp O43169 CYB5B_HUMAN          | 1760.921  |
| sp Q12788 TBL3_HUMAN           | 4510.3159 |
| sp P49327 FAS_HUMAN            | 1775.9669 |
| sp P11142 HSP7C_HUMAN          | 2228.0195 |
| sp P68371 TBB4B_HUMAN          | 2039.9589 |
| sp P31947 1433S_HUMAN          | 1813.9323 |
| sp Q13619 CUL4A_HUMAN          | 2166.1321 |
| sp P07900 HS90A_HUMAN          | 2901.3929 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P78371 TCPB_HUMAN           | 2707.3752 |
| sp P30050 RL12_HUMAN           | 1699.8053 |
| sp Q99798 ACON_HUMAN           | 2149.0328 |
| sp P32119 PRDX2_HUMAN          | 2128.0841 |
| sp P00533 EGFR_HUMAN           | 2127.9314 |
| sp P31937 3HIDH_HUMAN          | 2590.2236 |
| sp P42704 LPPRC_HUMAN          | 2308.1699 |
| sp P62987 RL40_HUMAN,sp P62979 | 1461.7538 |
| sp P15924 DESP_HUMAN           | 2622.2847 |
| sp Q15287 RNPS1_HUMAN          | 2078.9619 |
| sp P62241 RS8_HUMAN            | 2088.0561 |
| sp Q14683 SMC1A_HUMAN          | 2291.1104 |
| sp Q96DG6 CMBL_HUMAN           | 2330.108  |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp O00148 DX39A_HUMAN          | 1976.9592 |
| sp Q15392 DHC24_HUMAN          | 1942.8843 |
| sp Q15042 RB3GP_HUMAN          | 2169.1106 |
| sp P26599 PTBP1_HUMAN          | 3687.8421 |
| sp P55327 TPD52_HUMAN          | 1993.0844 |
| sp P62491 RB11A_HUMAN,sp Q1591 | 2627.3231 |
| sp P35637 FUS_HUMAN            | 1748.8039 |
| sp Q5TFE4 NT5D1_HUMAN          | 2031.9724 |
| sp P35573 GDE_HUMAN            | 2932.4355 |
| sp P23528 COF1_HUMAN           | 1986.8378 |
| sp P52907 CAZA1_HUMAN          | 1358.6619 |
| sp P78371 TCPB_HUMAN           | 1341.5884 |
| sp P29692 EF1D_HUMAN           | 2524.3326 |
| sp P55265 DSRAD_HUMAN          | 1218.6649 |

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| sp P39019 RS19_HUMAN           | 2164.949  |
| sp P18084 ITB5_HUMAN           | 2861.2942 |
| sp Q15424 SAFB1_HUMAN,sp Q141! | 1309.699  |
| sp Q86VP6 CAND1_HUMAN          | 2314.1304 |
| sp P15559 NQO1_HUMAN           | 2250.0845 |
| sp P60174 TPIS_HUMAN           | 3911.9615 |
| sp P00533 EGFR_HUMAN           | 2975.4083 |
| sp Q15149 PLEC_HUMAN           | 2337.2216 |
| sp P55072 TERA_HUMAN           | 1996.0153 |
| sp Q9NZB2 F120A_HUMAN          | 1878.8497 |
| sp P35579 MYH9_HUMAN           | 1337.6034 |
| sp P18754 RCC1_HUMAN           | 3060.526  |
| sp P16403 H12_HUMAN            | 1261.7394 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp O00567 NOP56_HUMAN          | 3288.6878 |
| sp Q99797 MIPEP_HUMAN          | 2192.0902 |
| sp P00338 LDHA_HUMAN           | 2070.9867 |
| sp Q8WW12 PCNP_HUMAN           | 1712.7543 |
| sp P62495 ERF1_HUMAN           | 1621.8352 |
| sp P21796 VDAC1_HUMAN          | 1920.933  |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp P10412 H14_HUMAN            | 1307.7197 |
| sp P27635 RL10_HUMAN           | 1645.8424 |
| sp Q16630 CPSF6_HUMAN          | 3170.455  |
| sp P02786 TFR1_HUMAN           | 1310.6619 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp Q8WXH0 SYNE2_HUMAN          | 2098.0331 |
| sp O75794 CD123_HUMAN          | 1701.7821 |
| sp P43487 RANG_HUMAN           | 1816.7904 |
| sp P62847 RS24_HUMAN           | 1560.797  |
| sp P43121 MUC18_HUMAN          | 1470.7402 |
| sp Q15365 PCBP1_HUMAN          | 2040.9972 |
| sp P02786 TFR1_HUMAN           | 2891.3184 |
| sp O43175 SERA_HUMAN           | 3733.9138 |
| sp Q9Y696 CLIC4_HUMAN          | 1202.7023 |
| sp P54886 P5CS_HUMAN           | 2468.186  |
| sp Q92616 GCN1_HUMAN           | 1999.986  |
| sp P31930 QCR1_HUMAN           | 1960.9167 |
| sp Q13148 TADBP_HUMAN          | 1388.6473 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P54819 KAD2_HUMAN           | 2287.0943 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1261.6051 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1815.9295 |
| sp P62195 PRS8_HUMAN           | 1290.6932 |
| sp P23588 IF4B_HUMAN           | 2875.4168 |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |

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| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P17844 DDX5_HUMAN           | 3169.475  |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp P38919 IF4A3_HUMAN          | 1784.9057 |
| sp P11586 C1TC_HUMAN           | 2028.9905 |
| sp P16402 H13_HUMAN,sp P16401  | 1456.7773 |
| sp Q04637 IF4G1_HUMAN,sp O4343 | 2111.9252 |
| sp P60842 IF4A1_HUMAN          | 2370.2002 |
| sp Q96KB5 TOPK_HUMAN           | 1842.9741 |
| sp P62937 PPIA_HUMAN           | 1453.6725 |
| sp Q13057 COASY_HUMAN          | 2031.0174 |
| sp Q8NAV1 PR38A_HUMAN          | 2387.187  |
| sp O75643 U520_HUMAN           | 2130.0269 |
| sp P12236 ADT3_HUMAN           | 2027.9854 |
| sp P23528 COF1_HUMAN,sp Q9Y28  | 1877.8207 |
| sp P13984 T2FB_HUMAN           | 2074.967  |
| sp P50914 RL14_HUMAN           | 1208.7129 |
| sp P55795 HNRH2_HUMAN,sp P319  | 1338.6456 |
| sp Q6RFH5 WDR74_HUMAN          | 3381.6452 |
| sp O43242 PSMD3_HUMAN          | 1379.6834 |
| sp O60832 DKC1_HUMAN           | 2011.9422 |
| sp P23284 PPIB_HUMAN           | 1653.8151 |
| sp P62937 PPIA_HUMAN           | 4122.9092 |
| sp P23919 KTHY_HUMAN           | 1520.7406 |
| sp Q08211 DHX9_HUMAN           | 3904.8351 |
| sp P62829 RL23_HUMAN           | 2494.2129 |
| sp P62829 RL23_HUMAN           | 3096.6165 |
| sp O00303 EIF3F_HUMAN          | 2598.1658 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3595.6673 |
| sp Q13283 G3BP1_HUMAN          | 1947.8567 |
| sp P23396 RS3_HUMAN            | 1220.6077 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp P06748 NPM_HUMAN            | 1436.726  |
| sp P20042 IF2B_HUMAN           | 1825.7764 |
| sp P62140 PP1B_HUMAN           | 2026.9564 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp Q92804 RBP56_HUMAN          | 2331.178  |
| sp Q9ULF5 S39AA_HUMAN          | 2203.1525 |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp Q96I24 FUBP3_HUMAN          | 1529.7474 |
| sp P55884 EIF3B_HUMAN          | 1996.9465 |
| sp P62937 PPIA_HUMAN           | 4800.2476 |
| sp Q15149 PLEC_HUMAN           | 2054.0585 |
| sp P18621 RL17_HUMAN           | 1550.7511 |
| sp Q8WUM0 NU133_HUMAN          | 2164.1528 |
| sp Q9BQG0 MBB1A_HUMAN          | 2748.3507 |
| sp P52597 HNRPF_HUMAN          | 2433.2064 |

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| sp P17301 ITA2_HUMAN           | 2002.0048 |
| sp Q15149 PLEC_HUMAN           | 1404.7071 |
| sp P50395 GDIB_HUMAN           | 1494.7791 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P17844 DDX5_HUMAN           | 1568.726  |
| sp P34897 GLYM_HUMAN           | 1789.8959 |
| sp P06748 NPM_HUMAN            | 1234.583  |
| sp P58107 EPIPL_HUMAN          | 2427.174  |
| sp Q16881 TRXR1_HUMAN          | 1723.9356 |
| sp P09874 PARP1_HUMAN          | 1659.7252 |
| sp Q15149 PLEC_HUMAN           | 2670.2636 |
| sp Q53EL6 PDCD4_HUMAN          | 2179.0294 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1739.8883 |
| sp P62269 RS18_HUMAN           | 1181.5425 |
| sp O15260 SURF4_HUMAN          | 1507.7783 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2748.4083 |
| sp Q9HCU4 CELR2_HUMAN          | 2100.0099 |
| sp P05783 K1C18_HUMAN          | 2373.2025 |
| sp P31040 SDHA_HUMAN           | 1943.8982 |
| sp Q13283 G3BP1_HUMAN          | 2690.2864 |
| sp P15531 NDKA_HUMAN           | 2262.0514 |
| sp Q92688 AN32B_HUMAN          | 1857.9949 |
| sp P21926 CD9_HUMAN            | 1759.7577 |
| sp P14625 ENPL_HUMAN,sp Q58FF3 | 2125.0076 |
| sp Q2NL82 TSR1_HUMAN           | 2534.2839 |
| sp P31327 CPSM_HUMAN           | 1575.7682 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 2220.0771 |
| sp P05787 K2C8_HUMAN           | 1733.8584 |
| sp Q01974 ROR2_HUMAN           | 2407.2172 |
| sp Q15149 PLEC_HUMAN           | 2507.2366 |
| sp O75874 IDHC_HUMAN           | 1917.8646 |
| sp P62277 RS13_HUMAN           | 1243.6561 |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P15924 DESP_HUMAN           | 1313.698  |
| sp Q5SY16 NOL9_HUMAN           | 2618.3131 |
| sp Q92692 NECT2_HUMAN          | 3279.5969 |
| sp Q09666 AHNK_HUMAN           | 1803.8866 |
| sp P08648 ITA5_HUMAN           | 2765.3184 |
| sp P51151 RAB9A_HUMAN          | 2710.3279 |
| sp Q96QK1 VPS35_HUMAN          | 1267.5694 |
| sp Q09666 AHNK_HUMAN           | 1376.5893 |
| sp P43121 MUC18_HUMAN          | 1451.6463 |
| sp P27824 CALX_HUMAN           | 2409.1576 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp Q9BXP5 SRRT_HUMAN           | 2083.0157 |
| sp Q92598 HS105_HUMAN          | 3019.4352 |

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| sp P08758 ANXA5_HUMAN          | 1659.8144 |
| sp P31327 CPSM_HUMAN           | 2886.5015 |
| sp O43852 CALU_HUMAN           | 1748.8291 |
| sp P35237 SPB6_HUMAN           | 1421.6939 |
| sp Q9Y224 RTRAF_HUMAN          | 1830.8213 |
| sp P49327 FAS_HUMAN            | 1439.7872 |
| sp O00148 DX39A_HUMAN,sp Q138  | 4307.9418 |
| sp Q14118 DAG1_HUMAN           | 2055.9722 |
| sp Q8N5K1 CISD2_HUMAN          | 1943.9953 |
| sp P53618 COPB_HUMAN           | 1592.7583 |
| sp P62244 RS15A_HUMAN          | 1323.7147 |
| sp P14866 HNRPL_HUMAN          | 2697.2601 |
| sp P17812 PYRG1_HUMAN          | 1457.6721 |
| sp P52701 MSH6_HUMAN           | 1670.8053 |
| sp Q01105 SET_HUMAN            | 2424.2649 |
| sp Q3ZCQ8 TIM50_HUMAN          | 2412.1598 |
| sp P46063 RECQ1_HUMAN          | 1880.8727 |
| sp Q96KP4 CNDP2_HUMAN          | 2640.3184 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P49257 LMAN1_HUMAN          | 3678.7492 |
| sp Q9Y6M7 S4A7_HUMAN           | 1884.937  |
| sp P52888 THOP1_HUMAN          | 2062.012  |
| sp Q14320 FA50A_HUMAN          | 1998.9072 |
| sp Q9UHN6 CEIP2_HUMAN          | 1771.8992 |
| sp P04083 ANXA1_HUMAN          | 1393.6772 |
| sp Q96AG4 LRC59_HUMAN          | 3026.6805 |
| sp P61313 RL15_HUMAN           | 1529.7124 |
| sp P00558 PGK1_HUMAN           | 3475.7367 |
| sp Q7KZF4 SND1_HUMAN           | 2451.0979 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1687.8345 |
| sp P37802 TAGL2_HUMAN          | 2611.284  |
| sp Q9BSJ8 ESYT1_HUMAN          | 1364.6871 |
| sp Q92901 RL3L_HUMAN,sp P39023 | 1561.7161 |
| sp Q09666 AHNK_HUMAN           | 2258.0565 |
| sp P13639 EF2_HUMAN            | 1558.8355 |
| sp Q9HD20 AT131_HUMAN          | 1742.8951 |
| sp Q9BXP5 SRRT_HUMAN           | 1561.81   |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P60228 EIF3E_HUMAN          | 1808.8192 |
| sp P08195 4F2_HUMAN            | 1499.8096 |
| sp Q969P0 IGSF8_HUMAN          | 1865.902  |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp Q9NR31 SAR1A_HUMAN,sp Q9Y6  | 1538.7399 |
| sp Q9BYX7 ACTBM_HUMAN,sp POC   | 1820.8866 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp Q9UQ80 PA2G4_HUMAN          | 2716.2877 |
| sp P23921 RIR1_HUMAN           | 2024.0327 |

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| sp Q92616 GCN1_HUMAN           | 2176.1124 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp O75475 PSIP1_HUMAN          | 1348.6987 |
| sp Q5VYK3 ECM29_HUMAN          | 2080.1205 |
| sp Q9H910 JUPI2_HUMAN          | 1443.7106 |
| sp P07737 PROF1_HUMAN          | 2282.1001 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp Q04726 TLE3_HUMAN           | 4692.3071 |
| sp P18124 RL7_HUMAN            | 1736.8199 |
| sp P04406 G3P_HUMAN            | 3548.7457 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2295.9646 |
| sp P27816 MAP4_HUMAN           | 1090.5043 |
| sp P61604 CH10_HUMAN           | 2783.4058 |
| sp Q9UHB6 LIMA1_HUMAN          | 3045.3813 |
| sp Q96PD2 DCBD2_HUMAN          | 1815.8176 |
| sp P50238 CRIP1_HUMAN          | 1892.9203 |
| sp O75643 U520_HUMAN           | 3130.4805 |
| sp P02786 TFR1_HUMAN           | 1235.651  |
| sp Q9Y224 RTRAF_HUMAN          | 3271.6725 |
| sp P00747 PLMN_HUMAN           | 1700.7035 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1260.5523 |
| sp P36578 RL4_HUMAN            | 1581.7886 |
| sp O14646 CHD1_HUMAN           | 2382.0587 |
| sp P23528 COF1_HUMAN           | 1505.7072 |
| sp P00387 NB5R3_HUMAN          | 2097.063  |
| sp Q13162 PRDX4_HUMAN          | 1687.8529 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp P20700 LMNB1_HUMAN          | 2014.9807 |
| sp P42704 LPPRC_HUMAN          | 1584.7784 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P42695 CNDD3_HUMAN          | 1681.894  |
| sp Q969H8 MYDGF_HUMAN          | 1366.7708 |
| sp Q99733 NP1L4_HUMAN          | 2467.206  |
| sp Q14019 COTL1_HUMAN          | 2215.1273 |
| sp P49756 RBM25_HUMAN          | 1209.6969 |
| sp Q9NP81 SYSM_HUMAN           | 1350.6932 |
| sp Q9HA77 SYCM_HUMAN           | 1490.7478 |
| sp O75340 PDCD6_HUMAN          | 2539.1649 |
| sp O95298 NDUC2_HUMAN          | 1832.8734 |
| sp Q02790 FKBP4_HUMAN          | 1778.8727 |
| sp O14787 TNPO2_HUMAN          | 1594.749  |
| sp Q9Y624 JAM1_HUMAN           | 2796.5749 |
| sp P10606 COX5B_HUMAN          | 1817.8519 |
| sp P40222 TXLNA_HUMAN          | 1751.9054 |
| sp P62304 RUXE_HUMAN           | 1881.0182 |
| sp P43243 MATR3_HUMAN          | 2526.1083 |

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| sp P0DN76 U2AF5_HUMAN,sp Q010  | 2060.9084 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P27824 CALX_HUMAN           | 3584.622  |
| sp P32320 CDD_HUMAN            | 2581.14   |
| sp P20700 LMNB1_HUMAN          | 2218.0365 |
| sp P49327 FAS_HUMAN            | 2633.2003 |
| sp P15880 RS2_HUMAN            | 1332.6496 |
| sp P43243 MATR3_HUMAN          | 2806.1055 |
| sp Q14692 BMS1_HUMAN           | 1933.052  |
| sp P07237 PDIA1_HUMAN          | 3133.5972 |
| sp Q8WYA6 CTBL1_HUMAN          | 2581.3639 |
| sp Q9BWT3 PAPOG_HUMAN,sp P51   | 2089.0262 |
| sp P61769 B2MG_HUMAN           | 2116.1065 |
| sp Q9BU23 LMF2_HUMAN           | 1728.826  |
| sp Q15149 PLEC_HUMAN           | 2521.2999 |
| sp P00505 AATM_HUMAN           | 2221.0956 |
| sp O00541 PESC_HUMAN           | 1796.8298 |
| sp Q09161 NCBP1_HUMAN          | 1960.9863 |
| sp P52272 HNRPM_HUMAN          | 2393.1032 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3246.5901 |
| sp P16403 H12_HUMAN            | 1219.6925 |
| sp P0DPI2 GAL3A_HUMAN,sp A0A0E | 2938.3621 |
| sp Q16719 KYNU_HUMAN           | 1633.7948 |
| sp P23284 PPIB_HUMAN           | 2113.0004 |
| sp Q96E52 OMA1_HUMAN           | 1879.0302 |
| sp Q92575 UBXN4_HUMAN          | 2041.0455 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp P62424 RL7A_HUMAN           | 1547.8308 |
| sp Q04760 LGUL_HUMAN           | 2143.0157 |
| sp Q01433 AMPD2_HUMAN          | 1458.7507 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q10567 AP1B1_HUMAN,sp P630: | 1959.9612 |
| sp P11387 TOP1_HUMAN           | 1697.8777 |
| sp O60885 BRD4_HUMAN           | 2522.2383 |
| sp Q6YN16 HSDL2_HUMAN          | 2103.0888 |
| sp P41252 SYIC_HUMAN           | 2701.2483 |
| sp P15880 RS2_HUMAN            | 2154.997  |
| sp Q16836 HCDH_HUMAN           | 2481.313  |
| sp O15260 SURF4_HUMAN          | 1507.7783 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P35052 GPC1_HUMAN           | 1936.9742 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 3738.8417 |
| sp P05787 K2C8_HUMAN           | 1325.6463 |
| sp P10809 CH60_HUMAN           | 3904.9153 |
| sp P33993 MCM7_HUMAN           | 2021.9595 |
| sp P04040 CATA_HUMAN           | 1844.9461 |
| sp P15880 RS2_HUMAN            | 1745.8883 |



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| sp Q13242 SRSF9_HUMAN          | 1871.8578 |
| sp P00492 HPRT_HUMAN           | 1894.9465 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1613.7838 |
| sp Q9BXP5 SRRT_HUMAN           | 2083.0157 |
| sp P16402 H13_HUMAN,sp P10412  | 1191.6612 |
| sp Q99497 PARK7_HUMAN          | 1998.7836 |
| sp Q9NTK5 OLA1_HUMAN           | 2884.4899 |
| sp P09429 HMGB1_HUMAN,sp B2Rf  | 1716.8683 |
| sp P63244 RACK1_HUMAN          | 2175.0233 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp Q9ULV4 COR1C_HUMAN          | 2032.0629 |
| sp Q15149 PLEC_HUMAN           | 4160.1464 |
| sp P11142 HSP7C_HUMAN          | 2348.1972 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1531.7155 |
| sp Q9Y266 NUDC_HUMAN           | 2219.1083 |
| sp P40939 ECHA_HUMAN           | 1626.8465 |
| sp P07900 HS90A_HUMAN,sp P082: | 1343.7197 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp P49411 EFTU_HUMAN           | 1830.9662 |
| sp P43121 MUC18_HUMAN          | 3829.8833 |
| sp P21333 FLNA_HUMAN           | 2742.2926 |
| sp P61604 CH10_HUMAN           | 1231.6237 |
| sp P50454 SERPH_HUMAN          | 2146.0888 |
| sp Q9Y383 LC7L2_HUMAN          | 1965.9288 |
| sp Q00839 HNRPU_HUMAN          | 1784.8727 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P10586 PTPRF_HUMAN          | 1762.8349 |
| sp Q8NF37 PCAT1_HUMAN          | 2677.4302 |
| sp Q9UKL0 RCOR1_HUMAN          | 1795.8893 |
| sp P17844 DDX5_HUMAN           | 1568.726  |
| sp O95678 K2C75_HUMAN,sp P486t | 1593.7675 |
| sp P48163 MAOX_HUMAN           | 1915.8701 |
| sp Q9H361 PABP3_HUMAN,sp P119  | 1738.9618 |
| sp P50395 GDIB_HUMAN,sp P31150 | 2685.3115 |
| sp P21333 FLNA_HUMAN           | 4924.245  |
| sp O95218 ZRAB2_HUMAN          | 2610.1016 |
| sp P43243 MATR3_HUMAN          | 1198.5982 |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp P50395 GDIB_HUMAN           | 3555.7562 |
| sp P62140 PP1B_HUMAN           | 2026.9564 |
| sp Q9C0E2 XPO4_HUMAN           | 1812.8716 |
| sp Q8WXD5 GEMI6_HUMAN          | 1761.7702 |
| sp P57772 SELB_HUMAN           | 2487.2282 |
| sp P27816 MAP4_HUMAN           | 2185.1127 |
| sp P05783 K1C18_HUMAN          | 1440.7209 |
| sp P46060 RAGP1_HUMAN          | 3997.0725 |

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| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P17844 DDX5_HUMAN           | 2147.0859 |
| sp P07355 ANXA2_HUMAN          | 3518.7504 |
| sp P61086 UBE2K_HUMAN          | 1753.8675 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp Q15003 CND2_HUMAN           | 1987.0448 |
| sp P36871 PGM1_HUMAN           | 1998.9898 |
| sp O15143 ARC1B_HUMAN          | 2601.2751 |
| sp P09429 HMGB1_HUMAN          | 2434.0747 |
| sp P35579 MYH9_HUMAN           | 3206.4107 |
| sp P62854 RS26_HUMAN           | 2353.1729 |
| sp O75367 H2AY_HUMAN           | 2268.1862 |
| sp P30086 PEBP1_HUMAN          | 2695.3453 |
| sp P50990 TCPQ_HUMAN           | 1888.8592 |
| sp Q96RP9 EFGM_HUMAN           | 1935.9731 |
| sp Q96RP9 EFGM_HUMAN           | 1935.9731 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P50454 SERPH_HUMAN          | 3093.4641 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 3171.587  |
| sp P15880 RS2_HUMAN            | 2169.0048 |
| sp P52701 MSH6_HUMAN           | 1670.8053 |
| sp Q10589 BST2_HUMAN           | 3034.4731 |
| sp A5YKK6 CNOT1_HUMAN          | 1689.7569 |
| sp P43243 MATR3_HUMAN          | 1463.762  |
| sp P04792 HSPB1_HUMAN          | 5309.6541 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1704.7811 |
| sp Q12906 ILF3_HUMAN           | 2218.1456 |
| sp P62277 RS13_HUMAN           | 1784.8832 |
| sp O75691 UTP20_HUMAN          | 2496.3087 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp P61927 RL37_HUMAN           | 1124.5978 |
| sp O00592 PODXL_HUMAN          | 1673.7468 |
| sp P04075 ALDOA_HUMAN          | 1684.8268 |
| sp P35579 MYH9_HUMAN           | 2022.9681 |
| sp P62826 RAN_HUMAN            | 1980.937  |
| sp P39748 FEN1_HUMAN           | 1563.8045 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P34897 GLYM_HUMAN           | 1516.7522 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1261.6051 |
| sp P48668 K2C6C_HUMAN,sp P042E | 1504.6794 |
| sp P49327 FAS_HUMAN            | 1497.7398 |
| sp P23921 RIR1_HUMAN           | 1891.8927 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp Q09666 AHNK_HUMAN           | 1315.7136 |
| sp Q01974 ROR2_HUMAN           | 2407.2172 |
| sp P15880 RS2_HUMAN            | 1332.6496 |
| sp P11940 PABP1_HUMAN          | 1548.7573 |

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| sp Q9NTK5 OLA1_HUMAN           | 2884.4899 |
| sp P61247 RS3A_HUMAN           | 2358.0281 |
| sp O60568 PLOD3_HUMAN          | 2351.0892 |
| sp P38646 GRP75_HUMAN          | 3205.4952 |
| sp P11388 TOP2A_HUMAN          | 1320.6058 |
| sp Q9UKK9 NUDT5_HUMAN          | 1693.8464 |
| sp P10412 H14_HUMAN            | 1307.7197 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1673.8189 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2603.265  |
| sp Q14232 EI2BA_HUMAN          | 1655.7977 |
| sp P32119 PRDX2_HUMAN          | 1483.8035 |
| sp O15031 PLXB2_HUMAN          | 5121.4704 |
| sp P61604 CH10_HUMAN           | 1911.9902 |
| sp P07919 QCR6_HUMAN,sp A0A09  | 1791.8363 |
| sp P35237 SPB6_HUMAN           | 1421.6939 |
| sp P78527 PRKDC_HUMAN          | 1725.8839 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P16401 H15_HUMAN            | 1108.6241 |
| sp P06756 ITAV_HUMAN           | 2105.9874 |
| sp Q99627 CSN8_HUMAN           | 3836.0149 |
| sp O43707 ACTN4_HUMAN,sp P128  | 1324.6412 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 1560.7573 |
| sp O95249 GOSR1_HUMAN          | 2155.9844 |
| sp P54725 RD23A_HUMAN,sp P547: | 1773.8938 |
| sp P04632 CPNS1_HUMAN          | 1927.837  |
| sp P07919 QCR6_HUMAN,sp A0A09  | 1791.8363 |
| sp Q6UVK1 CSPG4_HUMAN          | 3667.808  |
| sp Q15020 SART3_HUMAN          | 2399.1944 |
| sp Q14258 TRI25_HUMAN          | 2020.9854 |
| sp P62701 RS4X_HUMAN,sp P22090 | 2736.2641 |
| sp P00966 ASSY_HUMAN           | 2474.2304 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp Q96KA5 CLP1L_HUMAN          | 2795.468  |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 3923.7811 |
| sp P35579 MYH9_HUMAN           | 3340.563  |
| sp P39748 FEN1_HUMAN           | 1563.8045 |
| sp P61604 CH10_HUMAN           | 1671.8356 |
| sp P06733 ENOA_HUMAN           | 1268.5561 |
| sp P83731 RL24_HUMAN           | 1563.7569 |
| sp Q9UHD8 SEPT9_HUMAN          | 1960.9967 |
| sp Q92466 DDB2_HUMAN           | 1571.7732 |
| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P52888 THOP1_HUMAN          | 2062.012  |
| sp P07195 LDHB_HUMAN           | 1704.8644 |
| sp Q06323 PSME1_HUMAN          | 2827.3375 |

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| sp P50454 SERPH_HUMAN          | 1700.6849 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp Q14204 DYHC1_HUMAN          | 2069.0528 |
| sp O60832 DKC1_HUMAN           | 2011.9422 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 1544.8273 |
| sp P18669 PGAM1_HUMAN          | 3632.8535 |
| sp P84098 RL19_HUMAN           | 1364.8028 |
| sp P04406 G3P_HUMAN            | 2714.2422 |
| sp P08670 VIME_HUMAN           | 1639.7914 |
| sp Q15084 PDIA6_HUMAN          | 2777.3409 |
| sp O00148 DX39A_HUMAN,sp Q138  | 4307.9418 |
| sp P27635 RL10_HUMAN           | 1896.7836 |
| sp O14737 PDCD5_HUMAN          | 1812.7776 |
| sp Q92879 CELF1_HUMAN,sp O9531 | 2373.0154 |
| sp Q92879 CELF1_HUMAN,sp O9531 | 2373.0154 |
| sp P11387 TOP1_HUMAN           | 2405.2261 |
| sp P62424 RL7A_HUMAN           | 1336.7351 |
| sp P05787 K2C8_HUMAN           | 1560.7202 |
| sp O43592 XPOT_HUMAN           | 1896.9503 |
| sp Q15393 SF3B3_HUMAN          | 2784.4851 |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp P42166 LAP2A_HUMAN,sp P4216 | 3998.8995 |
| sp P58107 EPIPL_HUMAN          | 3181.5754 |
| sp Q687X5 STEAA4_HUMAN         | 2198.05   |
| sp P11142 HSP7C_HUMAN          | 1893.8302 |
| sp Q9BXX1 KLF16_HUMAN          | 1487.7117 |
| sp P09622 DLDH_HUMAN           | 2679.3731 |
| sp P54886 P5CS_HUMAN           | 3298.6007 |
| sp Q16543 CDC37_HUMAN          | 1496.7722 |
| sp Q9HB71 CYBP_HUMAN           | 1513.781  |
| sp P12270 TPR_HUMAN            | 2137.0593 |
| sp Q9BSJ8 ESYT1_HUMAN          | 2138.028  |
| sp P13807 GYS1_HUMAN           | 2125.9956 |
| sp Q96AY3 FKB10_HUMAN          | 1684.9076 |
| sp O95758 PTBP3_HUMAN          | 4379.1784 |
| sp O94925 GLSK_HUMAN           | 2800.2942 |
| sp P06213 INSR_HUMAN           | 1962.8643 |
| sp P06756 ITAV_HUMAN           | 2105.9874 |
| sp P40925 MDHC_HUMAN           | 2004.9581 |
| sp Q969P0 IGSF8_HUMAN          | 1337.6398 |
| sp Q9NYL9 TMOD3_HUMAN          | 2115.0055 |
| sp P62987 RL40_HUMAN           | 1520.7154 |
| sp P61513 RL37A_HUMAN          | 2450.2078 |
| sp Q9BYX7 ACTBM_HUMAN,sp POC   | 1820.8866 |
| sp Q9HB90 RRAGC_HUMAN          | 1904.9381 |
| sp P31040 SDHA_HUMAN           | 1959.8931 |
| sp P35251 RFC1_HUMAN           | 1702.9254 |

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| sp Q12906 ILF3_HUMAN           | 2218.1456 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp Q13263 TIF1B_HUMAN          | 1783.9325 |
| sp P12236 ADT3_HUMAN           | 2267.1798 |
| sp Q53H96 P5CR3_HUMAN          | 2793.4596 |
| sp Q8NC51 PAIRB_HUMAN          | 1111.5662 |
| sp P04040 CATA_HUMAN           | 1844.9461 |
| sp P02786 TFR1_HUMAN           | 1460.7048 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3246.5901 |
| sp P15151 PVR_HUMAN            | 2900.5066 |
| sp Q16719 KYNU_HUMAN           | 1913.9847 |
| sp Q15262 PTPRK_HUMAN          | 2990.412  |
| sp P49327 FAS_HUMAN            | 1775.9669 |
| sp Q00839 HNRPU_HUMAN          | 1492.7232 |
| sp Q9UHD8 SEPT9_HUMAN          | 1791.9115 |
| sp P35052 GPC1_HUMAN           | 1636.7879 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp Q8WU90 ZC3HF_HUMAN          | 1805.8809 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp Q9NW64 RBM22_HUMAN          | 1275.5302 |
| sp Q06830 PRDX1_HUMAN          | 3779.8254 |
| sp P46776 RL27A_HUMAN          | 2832.3389 |
| sp P82930 RT34_HUMAN           | 2726.3453 |
| sp O15144 ARPC2_HUMAN          | 4464.1835 |
| sp Q9UKY7 CDV3_HUMAN           | 3324.5899 |
| sp Q9H6R4 NOL6_HUMAN           | 1966.9724 |
| sp Q15459 SF3A1_HUMAN          | 3064.374  |
| sp Q9NXE4 NSMA3_HUMAN          | 1809.9084 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp O00232 PSD12_HUMAN          | 2096.1001 |
| sp P42704 LPPRC_HUMAN          | 2707.3911 |
| sp P37802 TAGL2_HUMAN          | 2611.284  |
| sp P30622 CLIP1_HUMAN          | 1555.8035 |
| sp Q16740 CLPP_HUMAN           | 1952.9262 |
| sp P49368 TCPG_HUMAN           | 1562.7511 |
| sp P06753 TPM3_HUMAN,sp P0949  | 1639.8305 |
| sp P32004 L1CAM_HUMAN          | 2060.9538 |
| sp Q02543 RL18A_HUMAN          | 2252.0419 |
| sp Q92769 HDAC2_HUMAN,sp Q135  | 2500.1369 |
| sp P00558 PGK1_HUMAN           | 1942.0299 |
| sp P50454 SERPH_HUMAN          | 3109.459  |
| sp Q96C57 CSTOS_HUMAN          | 1973.0357 |
| sp Q9NTI5 PDS5B_HUMAN          | 1497.6808 |
| sp O14745 NHRF1_HUMAN          | 1702.7587 |
| sp P62753 RS6_HUMAN            | 2407.1002 |
| sp Q07020 RL18_HUMAN           | 2754.3898 |

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| sp Q9UDY4 DNJB4_HUMAN          | 1850.8435 |
| sp P07195 LDHB_HUMAN           | 1500.7096 |
| sp O75369 FLNB_HUMAN           | 2088.9939 |
| sp P62917 RL8_HUMAN            | 3591.7371 |
| sp P16401 H15_HUMAN,sp P10412  | 1182.5881 |
| sp Q92804 RBP56_HUMAN          | 2157.0167 |
| sp Q8NI27 THOC2_HUMAN          | 1429.6891 |
| sp Q16891 MIC60_HUMAN          | 1747.8278 |
| sp O43390 HNRPR_HUMAN,sp O605  | 1574.6961 |
| sp P10586 PTPRF_HUMAN          | 3846.8238 |
| sp Q9H4I3 TRABD_HUMAN          | 2344.1919 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P24752 THIL_HUMAN           | 1642.7079 |
| sp P12956 XRCC6_HUMAN          | 1547.7112 |
| sp O95400 CD2B2_HUMAN          | 4597.1629 |
| sp P26038 MOES_HUMAN           | 2154.0189 |
| sp Q9NVP1 DDX18_HUMAN          | 3317.5155 |
| sp P20042 IF2B_HUMAN           | 1655.7501 |
| sp P61604 CH10_HUMAN           | 1671.8356 |
| sp O14880 MGST3_HUMAN          | 1962.9    |
| sp Q5VYK3 ECM29_HUMAN          | 2114.0037 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P31040 SDHA_HUMAN           | 1943.8982 |
| sp P18124 RL7_HUMAN            | 1736.8199 |
| sp P49756 RBM25_HUMAN          | 1209.6969 |
| sp P62318 SMD3_HUMAN           | 1940.0151 |
| sp Q99459 CDC5L_HUMAN          | 2460.138  |
| sp Q9Y287 ITM2B_HUMAN          | 1786.8308 |
| sp Q7KZF4 SND1_HUMAN           | 2943.4614 |
| sp Q15149 PLEC_HUMAN           | 1270.6558 |
| sp Q16891 MIC60_HUMAN          | 1931.0112 |
| sp P06756 ITAV_HUMAN           | 2105.9874 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp Q8IWS0 PHF6_HUMAN           | 2501.1969 |
| sp Q13177 PAK2_HUMAN           | 1555.7882 |
| sp P02786 TFR1_HUMAN           | 2193.0412 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp P50238 CRIP1_HUMAN          | 1724.7399 |
| sp P05787 K2C8_HUMAN           | 5378.4256 |
| sp Q16836 HCDH_HUMAN           | 1922.8945 |
| sp P04406 G3P_HUMAN            | 3548.7457 |
| sp P07900 HS90A_HUMAN,sp Q145i | 1204.6816 |
| sp Q8TDQ7 GNPI2_HUMAN,sp P469  | 2199.0558 |
| sp Q8NBS9 TXND5_HUMAN          | 1913.9636 |
| sp Q9NTJ3 SMC4_HUMAN           | 2343.207  |
| sp Q6YHK3 CD109_HUMAN          | 1381.7606 |
| sp O60884 DNJA2_HUMAN          | 1667.7977 |

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| sp Q16576 RBBP7_HUMAN | 3490.4644 |
| sp Q13162 PRDX4_HUMAN | 3266.6095 |
| sp P36578 RL4_HUMAN   | 1763.953  |
| sp Q9Y6M7 S4A7_HUMAN  | 1884.937  |
| sp P61160 ARP2_HUMAN  | 2638.2373 |
| sp Q96AG4 LRC59_HUMAN | 3026.6805 |
| sp P14866 HNRPL_HUMAN | 1444.6583 |
| sp P55884 EIF3B_HUMAN | 1996.9465 |
| sp P14618 KPYM_HUMAN  | 1879.8873 |
| sp P48651 PTSS1_HUMAN | 2807.1406 |
| sp Q14126 DSG2_HUMAN  | 2755.2838 |
| sp P25789 PSA4_HUMAN  | 2338.0569 |
| sp P23246 SFPQ_HUMAN  | 1845.9109 |
| sp Q92945 FUBP2_HUMAN | 2381.1975 |
| sp Q8N684 CPSF7_HUMAN | 2364.0288 |
| sp P51665 PSMD7_HUMAN | 1972.049  |
| sp P12814 ACTN1_HUMAN | 2266.1257 |
| sp Q96SU4 OSBL9_HUMAN | 2141.1442 |
| sp Q10471 GALT2_HUMAN | 2045.9595 |
| sp Q14566 MCM6_HUMAN  | 1863.7702 |
| sp Q15149 PLEC_HUMAN  | 1977.9684 |
| sp P38606 VATA_HUMAN  | 2450.303  |
| sp P50990 TCPQ_HUMAN  | 2096.0174 |
| sp P11413 G6PD_HUMAN  | 2262.0746 |
| sp Q01082 SPTB2_HUMAN | 1557.7311 |
| sp P31327 CPSM_HUMAN  | 3066.5047 |
| sp P02786 TFR1_HUMAN  | 2875.3235 |
| sp P18669 PGAM1_HUMAN | 2332.0033 |
| sp P15924 DESP_HUMAN  | 1900.0418 |
| sp Q96DI7 SNR40_HUMAN | 1915.8887 |
| sp P12236 ADT3_HUMAN  | 2267.1798 |
| sp P13639 EF2_HUMAN   | 1470.7355 |
| sp P62937 PPIA_HUMAN  | 2679.2453 |
| sp P10809 CH60_HUMAN  | 2243.191  |
| sp P07814 SYEP_HUMAN  | 2172.1004 |
| sp P10586 PTPRF_HUMAN | 3515.6377 |
| sp Q9NRN7 ADPPT_HUMAN | 1657.7923 |
| sp Q13586 STIM1_HUMAN | 1881.0207 |
| sp P62937 PPIA_HUMAN  | 1543.6903 |
| sp Q5JVF3 PCID2_HUMAN | 2165.9795 |
| sp Q9NXF1 TEX10_HUMAN | 1877.0775 |
| sp Q01105 SET_HUMAN   | 2296.1699 |
| sp P61604 CH10_HUMAN  | 1911.9902 |
| sp P78371 TCPB_HUMAN  | 1341.5884 |
| sp P32119 PRDX2_HUMAN | 1168.5764 |
| sp P20618 PSB1_HUMAN  | 1543.7882 |
| sp P62701 RS4X_HUMAN  | 2185.1644 |

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| sp P47897 SYQ_HUMAN            | 1775.8002 |
| sp P07900 HS90A_HUMAN,sp Q58F6 | 1126.5805 |
| sp P04406 G3P_HUMAN            | 3532.7508 |
| sp Q9Y490 TLN1_HUMAN           | 2162.0968 |
| sp Q9NTJ5 SAC1_HUMAN           | 1993.9779 |
| sp P62701 RS4X_HUMAN           | 1363.6884 |
| sp Q9BSJ8 ESYT1_HUMAN          | 1399.7572 |
| sp P16401 H15_HUMAN            | 1346.7558 |
| sp Q13045 FLII_HUMAN           | 2217.1147 |
| sp P05787 K2C8_HUMAN           | 1733.8584 |
| sp Q8TF68 ZN384_HUMAN          | 1826.7968 |
| sp O43399 TPD54_HUMAN          | 1824.9581 |
| sp P82921 RT21_HUMAN           | 1849.9244 |
| sp P51153 RAB13_HUMAN          | 1867.9428 |
| sp P08758 ANXA5_HUMAN          | 2359.1941 |
| sp P15529 MCP_HUMAN            | 1824.8716 |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp Q10713 MPPA_HUMAN           | 3018.3699 |
| sp Q06830 PRDX1_HUMAN          | 2179.0433 |
| sp Q9NR30 DDX21_HUMAN          | 3002.4873 |
| sp Q12959 DLG1_HUMAN,sp Q1570  | 1678.8097 |
| sp Q63HN8 RN213_HUMAN          | 2979.4574 |
| sp P62424 RL7A_HUMAN           | 1404.6781 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3669.6623 |
| sp P10606 COX5B_HUMAN          | 3229.4597 |
| sp P27635 RL10_HUMAN           | 1372.583  |
| sp P47914 RL29_HUMAN           | 2245.1339 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P21926 CD9_HUMAN            | 1310.6466 |
| sp P38646 GRP75_HUMAN          | 1842.8934 |
| sp P63279 UBC9_HUMAN           | 1638.8042 |
| sp Q9NW82 WDR70_HUMAN          | 2269.159  |
| sp P13639 EF2_HUMAN            | 4568.1992 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P55769 NH2L1_HUMAN          | 1523.762  |
| sp Q8WUM4 PDC6l_HUMAN          | 2098.0636 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1483.7493 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P11142 HSP7C_HUMAN          | 3725.7697 |
| sp Q92616 GCN1_HUMAN           | 1564.7344 |
| sp P12236 ADT3_HUMAN           | 2267.1798 |
| sp Q15149 PLEC_HUMAN           | 3189.5982 |
| sp Q96EE3 SEH1_HUMAN           | 2657.099  |
| sp P46776 RL27A_HUMAN          | 2832.3389 |
| sp Q7KZF4 SND1_HUMAN           | 1443.751  |
| sp O95816 BAG2_HUMAN           | 1732.8129 |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |



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| sp P50395 GDIB_HUMAN           | 3555.7562 |
| sp Q14566 MCM6_HUMAN           | 1082.5145 |
| sp Q8WUM0 NU133_HUMAN          | 1641.8587 |
| sp Q04637 IF4G1_HUMAN,sp O4343 | 1414.6729 |
| sp P62841 RS15_HUMAN           | 3364.669  |
| sp O75534 CSDE1_HUMAN          | 1818.8683 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1393.6336 |
| sp Q9NTK5 OLA1_HUMAN           | 2884.4899 |
| sp P50991 TCPD_HUMAN           | 1911.94   |
| sp P11387 TOP1_HUMAN           | 1894.7614 |
| sp Q14847 LASP1_HUMAN          | 1950.857  |
| sp P07814 SYEP_HUMAN           | 2943.4192 |
| sp P55209 NP1L1_HUMAN          | 1836.941  |
| sp P14866 HNRPL_HUMAN          | 2562.1485 |
| sp P49411 EFTU_HUMAN           | 1814.9713 |
| sp Q12788 TBL3_HUMAN           | 2478.2478 |
| sp Q9Y3E5 PTH2_HUMAN           | 2260.0041 |
| sp O43852 CALU_HUMAN           | 1748.8291 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P27797 CALR_HUMAN           | 2282.9927 |
| sp Q9UQ80 PA2G4_HUMAN          | 2716.2877 |
| sp Q15717 ELAV1_HUMAN          | 1931.984  |
| sp P14735 IDE_HUMAN            | 2982.4896 |
| sp Q93009 UBP7_HUMAN           | 2254.0729 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3669.6623 |
| sp Q9BVP2 GNL3_HUMAN           | 2035.0375 |
| sp Q6P2Q9 PRP8_HUMAN           | 1725.7859 |
| sp Q15365 PCBP1_HUMAN          | 3809.9002 |
| sp Q9Y4W2 LAS1L_HUMAN          | 2574.3152 |
| sp P39023 RL3_HUMAN            | 1491.7973 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3701.9047 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1709.8195 |
| sp P27816 MAP4_HUMAN           | 1675.8166 |
| sp Q9UHB6 LIMA1_HUMAN          | 2005.972  |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P62829 RL23_HUMAN           | 1443.7973 |
| sp P49915 GUAA_HUMAN           | 2992.4858 |
| sp Q9Y266 NUDC_HUMAN           | 2219.1083 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp O60506 HNRPQ_HUMAN          | 3653.7849 |
| sp P42892 ECE1_HUMAN           | 3104.4952 |
| sp Q13283 G3BP1_HUMAN          | 1931.8618 |
| sp Q15149 PLEC_HUMAN           | 1908.929  |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |

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| sp P21333 FLNA_HUMAN                        | 3996.9997 |
| sp P54577 SYYC_HUMAN                        | 2146.9695 |
| sp P08195 4F2_HUMAN                         | 2051.9854 |
| sp Q9Y314 NOSIP_HUMAN                       | 1805.8544 |
| sp P12277 KCRB_HUMAN                        | 3783.8124 |
| sp P78347 GTF2I_HUMAN                       | 2092.0452 |
| sp P68032 ACTC_HUMAN,sp P68133 ACTC_HUMAN   | 3653.6674 |
| sp Q9UHI6 DDX20_HUMAN                       | 1377.6459 |
| sp P16435 NCPR_HUMAN                        | 3264.5285 |
| sp P21399 ACOC_HUMAN                        | 3105.5407 |
| sp Q02878 RL6_HUMAN                         | 1595.8671 |
| sp P62913 RL11_HUMAN                        | 1195.5404 |
| sp P46060 RAGP1_HUMAN                       | 2609.2149 |
| sp P05787 K2C8_HUMAN                        | 2593.1854 |
| sp P35579 MYH9_HUMAN                        | 2471.2366 |
| sp Q12931 TRAP1_HUMAN                       | 1493.809  |
| sp P53999 TCP4_HUMAN                        | 1447.8035 |
| sp P30050 RL12_HUMAN                        | 2600.2388 |
| sp O43776 SYNC_HUMAN                        | 1960.8738 |
| sp P37802 TAGL2_HUMAN                       | 2852.3473 |
| sp P08729 K2C7_HUMAN                        | 1981.913  |
| sp P20908 CO5A1_HUMAN                       | 2559.2064 |
| sp P16403 H12_HUMAN                         | 1210.6558 |
| sp Q5TFE4 NT5D1_HUMAN                       | 2292.0851 |
| sp Q16531 DDB1_HUMAN                        | 2390.2417 |
| sp P12270 TPR_HUMAN                         | 1219.6561 |
| sp P13639 EF2_HUMAN                         | 1598.8304 |
| sp P50991 TCPD_HUMAN                        | 1927.9349 |
| sp Q15149 PLEC_HUMAN                        | 2456.2799 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI1 EF1A1_HUMAN | 3891.7913 |
| sp P18621 RL17_HUMAN                        | 1550.7511 |
| sp Q9Y3F4 STRAP_HUMAN                       | 2953.2613 |
| sp O15031 PLXB2_HUMAN                       | 1918.9281 |
| sp P19075 TSN8_HUMAN                        | 2967.439  |
| sp P53621 COPA_HUMAN                        | 3677.9055 |
| sp O75533 SF3B1_HUMAN                       | 2097.9563 |
| sp P26038 MOES_HUMAN                        | 1619.8267 |
| sp P08670 VIME_HUMAN                        | 1499.6926 |
| sp Q9Y285 SYFA_HUMAN                        | 2454.1672 |
| sp P50895 BCAM_HUMAN                        | 1612.7634 |
| sp O00571 DDX3X_HUMAN                       | 3105.5043 |
| sp Q9ULW0 TPX2_HUMAN                        | 1372.7099 |
| sp P51153 RAB13_HUMAN                       | 1867.9428 |
| sp P13010 XRCC5_HUMAN                       | 2090.0433 |
| sp P12956 XRCC6_HUMAN                       | 1491.8449 |
| sp P12277 KCRB_HUMAN                        | 3799.8073 |
| sp Q8IY67 RAVR1_HUMAN                       | 1547.8308 |

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| sp Q10567 AP1B1_HUMAN          | 1285.6779 |
| sp P11021 BIP_HUMAN            | 1503.7432 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P37837 TALDO_HUMAN          | 2783.4051 |
| sp P62937 PPIA_HUMAN           | 1453.6725 |
| sp P50914 RL14_HUMAN           | 1565.7375 |
| sp Q04637 IF4G1_HUMAN          | 1784.8945 |
| sp Q8N8Z6 DCBD1_HUMAN          | 2377.0319 |
| sp P42695 CNDD3_HUMAN          | 1681.894  |
| sp Q99733 NP1L4_HUMAN          | 2467.206  |
| sp O14602 IF1AY_HUMAN,sp P4781 | 1638.789  |
| sp O14602 IF1AY_HUMAN,sp P4781 | 1638.789  |
| sp Q9Y5Y5 PEX16_HUMAN          | 2830.2179 |
| sp Q9UBU9 NXF1_HUMAN           | 1906.9499 |
| sp P43121 MUC18_HUMAN          | 3153.6558 |
| sp Q9BTE1 DCTN5_HUMAN          | 1267.6925 |
| sp O43707 ACTN4_HUMAN          | 2314.1917 |
| sp P04075 ALDOA_HUMAN          | 1753.8635 |
| sp Q1KMD3 HNRL2_HUMAN          | 2337.1066 |
| sp Q15149 PLEC_HUMAN           | 1965.0068 |
| sp Q8NEY8 PPHLN_HUMAN          | 1687.7339 |
| sp Q29983 MICA_HUMAN           | 1380.6707 |
| sp P11717 MPRI_HUMAN           | 2870.1813 |
| sp Q9Y314 NOSIP_HUMAN          | 2031.8745 |
| sp P07814 SYEP_HUMAN           | 2343.0808 |
| sp P62277 RS13_HUMAN           | 1924.9101 |
| sp Q9Y520 PRC2C_HUMAN          | 1547.8056 |
| sp P23528 COF1_HUMAN           | 1986.8378 |
| sp O60701 UGDH_HUMAN           | 4092.0804 |
| sp Q8NI27 THOC2_HUMAN          | 1429.6891 |
| sp P29401 TKT_HUMAN            | 2845.4709 |
| sp P09960 LKHA4_HUMAN          | 1864.936  |
| sp O75882 ATRN_HUMAN           | 1490.7042 |
| sp P53680 AP2S1_HUMAN          | 1559.7005 |
| sp P11021 BIP_HUMAN            | 1512.7168 |
| sp P50395 GDIB_HUMAN           | 2469.1336 |
| sp Q03701 CEBPZ_HUMAN          | 1715.8519 |
| sp P25815 S100P_HUMAN          | 1871.9339 |
| sp Q9Y3A4 RRP7A_HUMAN,sp Q9N5  | 1537.7195 |
| sp O96008 TOM40_HUMAN          | 2624.1966 |
| sp Q9GZT3 SLIRP_HUMAN          | 2495.2517 |
| sp Q9H4L4 SENP3_HUMAN          | 1915.8893 |
| sp Q01813 PFKAP_HUMAN          | 1189.5728 |
| sp O60841 IF2P_HUMAN           | 1811.9054 |
| sp Q9Y5K8 VATD_HUMAN           | 3414.6004 |
| sp O75369 FLNB_HUMAN           | 1434.7355 |
| sp P13987 CD59_HUMAN           | 3083.3654 |

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| sp P16402 H13_HUMAN,sp Q02539  | 1774.8122 |
| sp P25685 DNJB1_HUMAN          | 1837.8119 |
| sp P35579 MYH9_HUMAN           | 1455.7569 |
| sp P47914 RL29_HUMAN           | 1729.8747 |
| sp P12270 TPR_HUMAN            | 3232.6577 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 1877.8207 |
| sp O75533 SF3B1_HUMAN          | 3566.7392 |
| sp P16615 AT2A2_HUMAN          | 2136.9964 |
| sp P62807 H2B1C_HUMAN,sp P588: | 1801.9138 |
| sp Q6N2I2 CAVN1_HUMAN          | 1615.7631 |
| sp P40227 TCPZ_HUMAN           | 1989.9466 |
| sp P62277 RS13_HUMAN           | 1924.9101 |
| sp P49257 LMAN1_HUMAN          | 3283.5891 |
| sp Q8TDN6 BRX1_HUMAN           | 2526.2611 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1959.0313 |
| sp P05023 AT1A1_HUMAN          | 2327.1798 |
| sp Q08211 DHX9_HUMAN           | 3659.8617 |
| sp Q9NZ01 TECR_HUMAN           | 2690.3803 |
| sp Q08J23 NSUN2_HUMAN          | 2472.0805 |
| sp P49327 FAS_HUMAN            | 2437.2523 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1709.8195 |
| sp P07954 FUMH_HUMAN           | 2725.3455 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp Q9NX58 LYAR_HUMAN           | 2055.965  |
| sp P08133 ANXA6_HUMAN          | 2295.1053 |
| sp Q9P2B2 FPRP_HUMAN           | 2471.0666 |
| sp Q9Y224 RTRAF_HUMAN          | 2822.2606 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1446.7355 |
| sp Q00839 HNRPU_HUMAN          | 1492.7232 |
| sp P16402 H13_HUMAN,sp P16401  | 1140.639  |
| sp P08670 VIME_HUMAN           | 1768.8778 |
| sp Q15185 TEBP_HUMAN           | 1930.9214 |
| sp Q13310 PABP4_HUMAN          | 1601.7256 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 2902.3596 |
| sp P36871 PGM1_HUMAN           | 3171.3914 |
| sp P60709 ACTB_HUMAN,sp P6803: | 1806.871  |
| sp Q6NYC8 PPR18_HUMAN          | 1684.8573 |
| sp P30622 CLIP1_HUMAN,sp Q9UDT | 1817.8908 |
| sp P35269 T2FA_HUMAN           | 1810.8785 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp O60313 OPA1_HUMAN           | 2338.123  |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2386.1839 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2404.2387 |
| sp P15311 EZRI_HUMAN           | 1323.6241 |
| sp P62826 RAN_HUMAN            | 3176.5244 |
| sp P09874 PARP1_HUMAN          | 1758.7849 |
| sp Q9HCU4 CELR2_HUMAN          | 2731.262  |

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| sp P62937 PPIA_HUMAN           | 1453.6725 |
| sp Q9P273 TEN3_HUMAN           | 2455.1656 |
| sp P31327 CPSM_HUMAN           | 1575.7682 |
| sp O14617 AP3D1_HUMAN          | 1714.8825 |
| sp Q13421 MSLN_HUMAN           | 2723.4745 |
| sp P30101 PDIA3_HUMAN          | 1364.6936 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp O60361 NDK8_HUMAN,sp P2239  | 2269.1532 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp Q9NR30 DDX21_HUMAN          | 2038.9861 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 3320.5296 |
| sp Q13263 TIF1B_HUMAN          | 1413.7405 |
| sp O15143 ARC1B_HUMAN          | 2601.2751 |
| sp Q02878 RL6_HUMAN            | 1556.7835 |
| sp Q6FI13 H2A2A_HUMAN,sp P2067 | 2538.4785 |
| sp Q92499 DDX1_HUMAN           | 2750.2494 |
| sp P08238 HS90B_HUMAN          | 4100.8896 |
| sp Q96QK1 VPS35_HUMAN          | 2291.2121 |
| sp P61247 RS3A_HUMAN           | 2386.1263 |
| sp Q8IUR0 TPPC5_HUMAN          | 1818.9087 |
| sp P14866 HNRPL_HUMAN          | 1444.6583 |
| sp Q9P0J0 NDUAD_HUMAN          | 2068.949  |
| sp P38117 ETFB_HUMAN           | 2941.3586 |
| sp Q96S52 PIGS_HUMAN           | 3663.8317 |
| sp P17096 HMGA1_HUMAN          | 1588.7845 |
| sp Q15126 PMVK_HUMAN           | 2411.1506 |
| sp Q14CX7 NAA25_HUMAN          | 2415.1019 |
| sp Q6P158 DHX57_HUMAN          | 2104.8655 |
| sp Q8NCW5 NNRE_HUMAN           | 2097.0677 |
| sp Q8TCS8 PNPT1_HUMAN          | 3053.495  |
| sp P52888 THOP1_HUMAN          | 1501.7606 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P15880 RS2_HUMAN            | 1745.8883 |
| sp O94925 GLSK_HUMAN           | 2800.2942 |
| sp Q6YHK3 CD109_HUMAN          | 1457.6939 |
| sp P42704 LPPRC_HUMAN          | 2743.3857 |
| sp Q9Y2Z4 SYYM_HUMAN           | 1489.7889 |
| sp P02786 TFR1_HUMAN           | 1410.7718 |
| sp P48509 CD151_HUMAN          | 1987.8946 |
| sp Q8TEM1 PO210_HUMAN          | 2069.0793 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P49916 DNLI3_HUMAN          | 2214.9423 |
| sp P78527 PRKDC_HUMAN          | 1798.856  |
| sp P13639 EF2_HUMAN            | 1558.8355 |
| sp P62333 PRS10_HUMAN          | 1629.8111 |
| sp O00429 DNM1L_HUMAN          | 1672.9876 |

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| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp Q13740 CD166_HUMAN          | 1821.8574 |
| sp P31040 SDHA_HUMAN           | 1153.5265 |
| sp P39023 RL3_HUMAN            | 1387.6983 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp P62244 RS15A_HUMAN          | 1339.6554 |
| sp P13667 PDIA4_HUMAN          | 1526.7365 |
| sp Q12906 ILF3_HUMAN           | 4604.0402 |
| sp Q14126 DSG2_HUMAN           | 1125.5567 |
| sp P17301 ITA2_HUMAN           | 3283.6877 |
| sp Q14789 GOGB1_HUMAN          | 1979.98   |
| sp Q9UG63 ABCF2_HUMAN          | 1765.8675 |
| sp Q96A26 F162A_HUMAN          | 1544.7623 |
| sp P78527 PRKDC_HUMAN          | 2565.192  |
| sp P13639 EF2_HUMAN            | 1334.599  |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp Q99832 TCPH_HUMAN           | 1476.7613 |
| sp P06733 ENOA_HUMAN           | 1320.6198 |
| sp P04844 RPN2_HUMAN           | 3791.9298 |
| sp P15880 RS2_HUMAN            | 2037.9731 |
| sp P00966 ASSY_HUMAN           | 2347.1518 |
| sp P60900 PSA6_HUMAN           | 1990.8692 |
| sp P49368 TCPG_HUMAN           | 2820.4505 |
| sp P48960 CD97_HUMAN           | 2918.4372 |
| sp Q96A65 EXOC4_HUMAN          | 2038.9232 |
| sp P62280 RS11_HUMAN           | 1144.6128 |
| sp P31327 CPSM_HUMAN           | 2626.3014 |
| sp P35606 COPB2_HUMAN          | 1499.7409 |
| sp P30040 ERP29_HUMAN          | 2334.0508 |
| sp P42766 RL35_HUMAN           | 1851.969  |
| sp O43395 PRPF3_HUMAN          | 2023.0011 |
| sp O75794 CD123_HUMAN          | 1701.7821 |
| sp P62701 RS4X_HUMAN           | 2335.2689 |
| sp P52907 CAZA1_HUMAN          | 2668.2922 |
| sp Q14677 EPN4_HUMAN           | 2567.1677 |
| sp P02786 TFR1_HUMAN           | 1160.5714 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q9UHQ9 NB5R1_HUMAN          | 2725.434  |
| sp P23528 COF1_HUMAN,sp P60981 | 1550.765  |
| sp Q9H7N4 SFR19_HUMAN          | 2117.0865 |
| sp Q14152 EIF3A_HUMAN          | 1632.7784 |
| sp P31327 CPSM_HUMAN           | 2886.5015 |
| sp P60842 IF4A1_HUMAN          | 1785.8567 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp Q9P289 STK26_HUMAN          | 2309.2307 |
| sp P41252 SYIC_HUMAN           | 1685.8453 |
| sp P21333 FLNA_HUMAN           | 1619.8155 |

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| sp P62424 RL7A_HUMAN           | 1269.6605 |
| sp O00299 CLIC1_HUMAN          | 3205.6152 |
| sp P22694 KAPCB_HUMAN,sp P1761 | 1857.8897 |
| sp P26373 RL13_HUMAN           | 1169.6445 |
| sp Q9H0D6 XRN2_HUMAN           | 2088.0316 |
| sp Q00610 CLH1_HUMAN           | 3472.6131 |
| sp P16402 H13_HUMAN,sp P10412  | 1191.6612 |
| sp P58107 EPIPL_HUMAN          | 1953.0207 |
| sp P20810 ICAL_HUMAN           | 1818.8748 |
| sp P62701 RS4X_HUMAN,sp Q8TD47 | 1491.718  |
| sp Q15233 NONO_HUMAN           | 1427.7045 |
| sp Q8NE71 ABCF1_HUMAN          | 1362.7256 |
| sp P21796 VDAC1_HUMAN          | 1640.8086 |
| sp P42704 LPPRC_HUMAN          | 2794.4218 |
| sp P56378 ATP68_HUMAN          | 1352.6473 |
| sp Q13505 MTX1_HUMAN           | 2284.16   |
| sp Q13813 SPTN1_HUMAN          | 1424.7048 |
| sp Q92804 RBP56_HUMAN          | 2157.0167 |
| sp Q13428 TCOF_HUMAN           | 3729.7733 |
| sp P43121 MUC18_HUMAN          | 1451.6463 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3191.425  |
| sp O75955 FLOT1_HUMAN          | 1844.9745 |
| sp P29692 EF1D_HUMAN,sp P24534 | 1249.7394 |
| sp P35579 MYH9_HUMAN           | 3356.5579 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp O43143 DHX15_HUMAN          | 3728.6837 |
| sp P10646 TFPI1_HUMAN          | 2607.0716 |
| sp P46013 KI67_HUMAN           | 1545.8225 |
| sp Q9UBM7 DHCR7_HUMAN          | 1423.6844 |
| sp Q15149 PLEC_HUMAN           | 1566.7103 |
| sp P62906 RL10A_HUMAN          | 1589.8599 |
| sp Q03167 TGBR3_HUMAN          | 3354.6885 |
| sp P16401 H15_HUMAN            | 1093.5768 |
| sp P36578 RL4_HUMAN            | 3027.6294 |
| sp P62269 RS18_HUMAN           | 1181.5425 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P21333 FLNA_HUMAN           | 1472.726  |
| sp P31948 STIP1_HUMAN          | 1764.8642 |
| sp Q15181 IPYR_HUMAN           | 4771.9915 |
| sp P51692 STA5B_HUMAN          | 2117.0178 |
| sp P78527 PRKDC_HUMAN          | 1092.5564 |
| sp P51805 PLXA3_HUMAN,sp Q9UIV | 1772.8482 |
| sp P49327 FAS_HUMAN            | 3434.6671 |
| sp Q01082 SPTB2_HUMAN          | 2437.1121 |
| sp P38919 IF4A3_HUMAN          | 4038.9238 |
| sp P40926 MDHM_HUMAN           | 2054.9983 |

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| sp P06744 G6PI_HUMAN                        | 1641.8362 |
| sp O43592 XPOT_HUMAN                        | 1896.9503 |
| sp P32969 RL9_HUMAN                         | 2257.0984 |
| sp Q92945 FUBP2_HUMAN                       | 2575.2121 |
| sp P51991 ROA3_HUMAN                        | 2095.011  |
| sp Q9UHI6 DDX20_HUMAN                       | 1975.917  |
| sp P13861 KAP2_HUMAN,sp P31323 KAP2_HUMAN   | 1888.9319 |
| sp Q9HB07 MYG1_HUMAN                        | 1908.8788 |
| sp Q4KMQ2 ANO6_HUMAN                        | 2481.0545 |
| sp Q14527 HLTF_HUMAN                        | 2600.2448 |
| sp P12268 IMDH2_HUMAN                       | 2893.2786 |
| sp P14384 CBPM_HUMAN                        | 1169.5288 |
| sp P63244 RACK1_HUMAN                       | 3222.5768 |
| sp O75369 FLNB_HUMAN                        | 1434.7355 |
| sp P18621 RL17_HUMAN                        | 2341.126  |
| sp Q12904 AIMP1_HUMAN                       | 1882.9831 |
| sp Q08345 DDR1_HUMAN                        | 1354.6266 |
| sp P11142 HSP7C_HUMAN                       | 3257.5022 |
| sp Q99735 MGST2_HUMAN                       | 1795.8206 |
| sp Q86Y07 VRK2_HUMAN                        | 2433.258  |
| sp P62333 PRS10_HUMAN                       | 1405.6838 |
| sp P15924 DESP_HUMAN                        | 1336.6371 |
| sp P18615 NELFE_HUMAN                       | 2078.9592 |
| sp P40429 RL13A_HUMAN                       | 1547.9035 |
| sp P62937 PPIA_HUMAN                        | 2679.2453 |
| sp P36578 RL4_HUMAN                         | 1640.8998 |
| sp P35659 DEK_HUMAN                         | 2136.1328 |
| sp P21333 FLNA_HUMAN                        | 1640.7651 |
| sp Q13148 TADBP_HUMAN                       | 3333.6782 |
| sp P60709 ACTB_HUMAN,sp P68032 ACTB_HUMAN   | 2375.277  |
| sp Q14204 DYHC1_HUMAN                       | 2970.4909 |
| sp P25789 PSA4_HUMAN                        | 1551.6801 |
| sp P35579 MYH9_HUMAN                        | 1350.5913 |
| sp E9PAV3 NACAM_HUMAN,sp Q13286 NACAM_HUMAN | 1961.051  |
| sp O95340 PAPS2_HUMAN                       | 3085.4855 |
| sp P52272 HNRPM_HUMAN                       | 1418.6466 |
| sp P08237 PFKAM_HUMAN                       | 1848.904  |
| sp P27824 CALX_HUMAN                        | 2458.1329 |
| sp Q96KR1 ZFR_HUMAN                         | 2367.2468 |
| sp P31327 CPSM_HUMAN                        | 4635.2856 |
| sp Q93009 UBP7_HUMAN                        | 2278.0511 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3 H3C_HUMAN     | 1182.6357 |
| sp P46013 KI67_HUMAN                        | 3362.634  |
| sp Q15418 KS6A1_HUMAN                       | 2226.0957 |
| sp A6NMY6 AXA2L_HUMAN,sp P07311 AXA2L_HUMAN | 1286.6177 |
| sp P05783 K1C18_HUMAN                       | 2389.1974 |
| sp P09382 LEG1_HUMAN                        | 1678.7627 |



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| sp P36578 RL4_HUMAN            | 951.5389  |
| sp Q9UHV9 PFD2_HUMAN           | 2807.3899 |
| sp P27824 CALX_HUMAN           | 2409.1576 |
| sp P19338 NUCL_HUMAN           | 2005.8945 |
| sp P49327 FAS_HUMAN            | 1497.7398 |
| sp Q8NEY8 PPHLN_HUMAN          | 1441.6262 |
| sp Q14157 UBP2L_HUMAN          | 3311.5416 |
| sp P38646 GRP75_HUMAN          | 1096.5553 |
| sp Q92973 TNPO1_HUMAN          | 1591.7163 |
| sp P30084 ECHM_HUMAN           | 2859.3814 |
| sp Q7L2H7 EIF3M_HUMAN          | 1345.6739 |
| sp O75475 PSIP1_HUMAN          | 1783.7861 |
| sp P49207 RL34_HUMAN           | 1450.6688 |
| sp P28074 PSB5_HUMAN           | 1604.8046 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp Q96T37 RBM15_HUMAN          | 3003.3246 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp Q15149 PLEC_HUMAN           | 3067.623  |
| sp Q7KZF4 SND1_HUMAN           | 1070.6012 |
| sp O94979 SC31A_HUMAN          | 2456.266  |
| sp P21926 CD9_HUMAN            | 4149.985  |
| sp P30048 PRDX3_HUMAN          | 2669.4177 |
| sp O15533 TPSN_HUMAN           | 2564.2482 |
| sp P30101 PDIA3_HUMAN          | 1364.6936 |
| sp Q13630 FCL_HUMAN            | 2730.4316 |
| sp P62917 RL8_HUMAN            | 1210.6346 |
| sp O43847 NRDC_HUMAN           | 2217.1681 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp P02786 TFR1_HUMAN           | 2891.3184 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp Q15758 AAAT_HUMAN           | 2810.4127 |
| sp P07814 SYEP_HUMAN           | 1231.5768 |
| sp P27797 CALR_HUMAN           | 1343.6874 |
| sp Q9H307 PININ_HUMAN          | 1524.7725 |
| sp Q9UNS2 CSN3_HUMAN           | 3087.4938 |
| sp O95573 ACSL3_HUMAN          | 2227.1624 |
| sp P31327 CPSM_HUMAN           | 2267.1362 |
| sp P02786 TFR1_HUMAN           | 2173.13   |
| sp Q99848 EBP2_HUMAN           | 1259.6874 |
| sp P04792 HSPB1_HUMAN          | 1664.7642 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3923.7811 |
| sp P13797 PLST_HUMAN           | 1940.9632 |
| sp P30153 2AAA_HUMAN,sp P30154 | 2463.2646 |
| sp P62269 RS18_HUMAN           | 1181.5425 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 3738.8417 |
| sp Q8WWY3 PRP31_HUMAN          | 3711.8421 |

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| sp Q16891 MIC60_HUMAN          | 4555.1912 |
| sp P61011 SRP54_HUMAN          | 1638.844  |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 1546.6974 |
| sp P33316 DUT_HUMAN            | 2429.1499 |
| sp Q15942 ZYX_HUMAN            | 2390.1727 |
| sp P04040 CATA_HUMAN           | 2287.0433 |
| sp Q9UI30 TR112_HUMAN          | 2286.0991 |
| sp P61088 UBE2N_HUMAN,sp Q5JXI | 1688.7868 |
| sp P46013 KI67_HUMAN           | 2090.0103 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P62995 TRA2B_HUMAN          | 2597.2286 |
| sp P13073 COX41_HUMAN          | 1278.6568 |
| sp Q03252 LMNB2_HUMAN          | 2046.9746 |
| sp P08195 4F2_HUMAN            | 1499.8096 |
| sp P58107 EPIPL_HUMAN          | 2464.158  |
| sp P63244 RACK1_HUMAN          | 3180.5146 |
| sp Q9Y3E5 PTH2_HUMAN           | 3079.619  |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 2352.1671 |
| sp P04080 CYTB_HUMAN           | 2654.2976 |
| sp O00541 PESC_HUMAN           | 1708.8937 |
| sp P05141 ADT2_HUMAN,sp P12236 | 1655.8308 |
| sp P06733 ENOA_HUMAN           | 2385.1812 |
| sp P02786 TFR1_HUMAN           | 1437.7252 |
| sp Q07020 RL18_HUMAN           | 1969.9997 |
| sp P11586 C1TC_HUMAN           | 1576.8097 |
| sp Q16576 RBBP7_HUMAN          | 3438.5674 |
| sp P05783 K1C18_HUMAN          | 3547.5977 |
| sp P78527 PRKDC_HUMAN          | 2240.2205 |
| sp P11021 BIP_HUMAN            | 1969.9453 |
| sp Q14204 DYHC1_HUMAN          | 1671.8542 |
| sp Q9UHD1 CHRD1_HUMAN          | 2044.0629 |
| sp Q92973 TNPO1_HUMAN          | 1591.7163 |
| sp P50238 CRIP1_HUMAN          | 3313.4016 |
| sp Q8WU90 ZC3HF_HUMAN          | 1805.8809 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp O75694 NU155_HUMAN          | 2220.1175 |
| sp P46940 IQGA1_HUMAN          | 2774.2745 |
| sp Q06830 PRDX1_HUMAN          | 2103.0783 |
| sp Q15262 PTPRK_HUMAN          | 2990.412  |
| sp P26639 SYTC_HUMAN           | 1645.7372 |
| sp P54709 AT1B3_HUMAN          | 1374.7507 |
| sp O15226 NKRF_HUMAN           | 1930.8697 |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp Q8WYA6 CTBL1_HUMAN          | 1810.8486 |
| sp Q9UKV3 ACINU_HUMAN          | 2126.0491 |
| sp P53618 COPB_HUMAN           | 2286.1896 |
| sp P52789 HXK2_HUMAN           | 2763.3789 |

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| sp Q00610 CLH1_HUMAN           | 2278.1991 |
| sp O43390 HNRPR_HUMAN,sp O605  | 1628.7327 |
| sp Q92841 DDX17_HUMAN          | 1694.8839 |
| sp P51991 ROA3_HUMAN           | 1972.8875 |
| sp Q9Y3I0 RTCB_HUMAN           | 2166.0449 |
| sp Q15181 IPYR_HUMAN           | 2265.0702 |
| sp P15924 DESP_HUMAN           | 1725.8533 |
| sp P22102 PUR2_HUMAN           | 3754.8705 |
| sp O14917 PCD17_HUMAN          | 1654.7587 |
| sp P31327 CPSM_HUMAN           | 1217.6193 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1260.5523 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2559.1323 |
| sp P84243 H33_HUMAN            | 1517.7587 |
| sp O75083 WDR1_HUMAN           | 1162.5731 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp P49411 EFTU_HUMAN           | 1814.9713 |
| sp P05198 IF2A_HUMAN           | 1468.6511 |
| sp Q9NZ45 CISD1_HUMAN          | 1160.5251 |
| sp P07814 SYEP_HUMAN           | 2172.1004 |
| sp Q969S3 ZN622_HUMAN          | 2546.2581 |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp P39748 FEN1_HUMAN           | 2202.0858 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp P78527 PRKDC_HUMAN          | 1648.8355 |
| sp P04004 VTNC_HUMAN           | 2369.0634 |
| sp Q02241 KIF23_HUMAN          | 1284.635  |
| sp P12956 XRCC6_HUMAN          | 1491.8449 |
| sp P12956 XRCC6_HUMAN          | 1491.8449 |
| sp Q99729 ROAA_HUMAN           | 1588.7192 |
| sp P07737 PROF1_HUMAN          | 2075.1085 |
| sp Q14978 NOLC1_HUMAN          | 1984.0378 |
| sp P83881 RL36A_HUMAN          | 1418.679  |
| sp P40429 RL13A_HUMAN          | 2369.1539 |
| sp P31948 STIP1_HUMAN          | 1896.8755 |
| sp P53618 COPB_HUMAN           | 3338.6531 |
| sp P05783 K1C18_HUMAN          | 1440.7209 |
| sp P53396 ACLY_HUMAN           | 2781.2518 |
| sp P02786 TFR1_HUMAN           | 1663.7326 |
| sp P46940 IQGA1_HUMAN          | 1550.794  |
| sp Q96DI7 SNR40_HUMAN          | 1932.8788 |
| sp Q12769 NU160_HUMAN          | 2769.3717 |
| sp Q8WW12 PCNP_HUMAN           | 1786.7871 |
| sp Q00610 CLH1_HUMAN           | 1547.8712 |
| sp O60353 FZD6_HUMAN           | 1371.6419 |
| sp O94979 SC31A_HUMAN          | 1498.8031 |

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| sp Q6YHK3 CD109_HUMAN          | 2448.1656 |
| sp P15924 DESP_HUMAN           | 1336.6371 |
| sp O60341 KDM1A_HUMAN          | 1513.7678 |
| sp Q9P2E9 RRBP1_HUMAN          | 1354.6477 |
| sp P00747 PLMN_HUMAN           | 1700.7035 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp Q9Y2H6 FND3A_HUMAN          | 1882.9247 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P07900 HS90A_HUMAN,sp P0825 | 1215.6248 |
| sp O60506 HNRPQ_HUMAN          | 2238.964  |
| sp P58107 EPIPL_HUMAN          | 2164.0073 |
| sp P12956 XRCC6_HUMAN          | 2003.98   |
| sp P62318 SMD3_HUMAN           | 1940.0151 |
| sp Q9UBU9 NXF1_HUMAN           | 1906.9499 |
| sp P35244 RFA3_HUMAN           | 2332.1344 |
| sp Q15276 RABE1_HUMAN          | 2083.9348 |
| sp Q86TC9 MYPN_HUMAN           | 1707.7522 |
| sp Q16695 H31T_HUMAN,sp Q71DI  | 1501.7637 |
| sp Q9GZS1 RPA49_HUMAN          | 1727.9206 |
| sp Q8WUM4 PDC6I_HUMAN          | 2242.1706 |
| sp P04843 RPN1_HUMAN           | 1960.0266 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp Q86UK7 ZN598_HUMAN          | 1653.706  |
| sp O60506 HNRPQ_HUMAN          | 2395.1907 |
| sp Q9BQG0 MBB1A_HUMAN          | 1668.8359 |
| sp P83881 RL36A_HUMAN,sp Q969C | 1461.7001 |
| sp P16104 H2AX_HUMAN,sp Q96QV  | 2595.5    |
| sp Q6UVK1 CSPG4_HUMAN          | 1310.6579 |
| sp Q86V81 THOC4_HUMAN          | 1171.5907 |
| sp P12814 ACTN1_HUMAN          | 3464.7464 |
| sp P30084 ECHM_HUMAN           | 1747.8682 |
| sp P62851 RS25_HUMAN           | 1579.8821 |
| sp P53597 SUCA_HUMAN           | 2574.3442 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp Q13433 S39A6_HUMAN          | 1884.8575 |
| sp P52272 HNRPM_HUMAN          | 1466.7729 |
| sp Q00839 HNRPU_HUMAN          | 1958.9949 |
| sp P04406 G3P_HUMAN            | 1420.7562 |
| sp Q00610 CLH1_HUMAN           | 2040.9905 |
| sp P26006 ITA3_HUMAN           | 1718.8628 |
| sp P50895 BCAM_HUMAN           | 1612.7634 |
| sp P17812 PYRG1_HUMAN          | 3578.706  |
| sp Q15149 PLEC_HUMAN           | 1633.806  |
| sp P43121 MUC18_HUMAN          | 1451.6463 |
| sp Q9H9A6 LRC40_HUMAN          | 1861.917  |

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| sp Q9Y305 ACOT9_HUMAN          | 2433.1886 |
| sp P50990 TCPQ_HUMAN           | 2510.2839 |
| sp Q9H0D6 XRN2_HUMAN           | 3268.6379 |
| sp Q6NZI2 CAVN1_HUMAN          | 1610.79   |
| sp P36578 RL4_HUMAN            | 1435.7671 |
| sp Q9NPH3 IL1AP_HUMAN          | 1925.0047 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1668.8141 |
| sp P04075 ALDOA_HUMAN          | 3537.6107 |
| sp P36578 RL4_HUMAN            | 1333.6125 |
| sp O60716 CTND1_HUMAN          | 2024.9738 |
| sp P23396 RS3_HUMAN            | 1748.8807 |
| sp Q96HS1 PGAM5_HUMAN          | 1866.8133 |
| sp Q9GZL7 WDR12_HUMAN          | 2409.225  |
| sp P15924 DESP_HUMAN           | 1453.7777 |
| sp Q92930 RAB8B_HUMAN,sp P610  | 1881.9585 |
| sp Q13740 CD166_HUMAN          | 3540.5991 |
| sp O75534 CSDE1_HUMAN          | 2526.1948 |
| sp P16401 H15_HUMAN            | 1251.6823 |
| sp Q08945 SSRP1_HUMAN          | 1758.9206 |
| sp Q9UIG0 BAZ1B_HUMAN          | 3184.6597 |
| sp O43390 HNRPR_HUMAN,sp O605  | 1628.7327 |
| sp P38646 GRP75_HUMAN          | 2550.2788 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1688.7862 |
| sp P62750 RL23A_HUMAN          | 1410.7143 |
| sp P11021 BIP_HUMAN            | 2161.0539 |
| sp O75874 IDHC_HUMAN           | 1633.9192 |
| sp P15170 ERF3A_HUMAN          | 3206.5012 |
| sp P08758 ANXA5_HUMAN          | 2359.1941 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q9NZ01 TECR_HUMAN           | 2690.3803 |
| sp P11142 HSP7C_HUMAN          | 3257.5022 |
| sp P49915 GUAA_HUMAN           | 2206.1746 |
| sp Q00341 VIGLN_HUMAN          | 1733.8584 |
| sp Q9Y3F4 STRAP_HUMAN          | 2622.2813 |
| sp Q13162 PRDX4_HUMAN          | 2840.3803 |
| sp Q96A72 MGN2_HUMAN,sp P613   | 2236.0225 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp Q15818 NPTX1_HUMAN          | 1691.8842 |
| sp P05783 K1C18_HUMAN          | 2389.1974 |
| sp Q9Y3U8 RL36_HUMAN           | 1526.7187 |
| sp P53701 CCHL_HUMAN           | 2060.9916 |
| sp P05787 K2C8_HUMAN           | 2500.1315 |
| sp P27824 CALX_HUMAN           | 3584.622  |
| sp P49207 RL34_HUMAN           | 1450.6688 |
| sp Q16891 MIC60_HUMAN          | 2537.1558 |
| sp Q92804 RBP56_HUMAN          | 2203.0831 |
| sp Q8IWS0 PHF6_HUMAN           | 2561.0841 |

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| sp P37837 TALDO_HUMAN          | 1936.0153 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1947.856  |
| sp P54886 P5CS_HUMAN           | 2027.984  |
| sp P55072 TERA_HUMAN           | 1911.0135 |
| sp P00338 LDHA_HUMAN           | 2270.1067 |
| sp Q09028 RBBP4_HUMAN,sp Q165  | 1517.7402 |
| sp P51116 FXR2_HUMAN           | 2082.0898 |
| sp P05787 K2C8_HUMAN           | 1537.7736 |
| sp Q6NXT1 ANR54_HUMAN          | 1190.6295 |
| sp Q16531 DDB1_HUMAN           | 1800.908  |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp Q7Z7K6 CENPV_HUMAN          | 2170.0695 |
| sp P18084 ITB5_HUMAN           | 2638.2446 |
| sp P10321 HLAC_HUMAN           | 2502.0823 |
| sp P62937 PPIA_HUMAN           | 4138.9041 |
| sp P08670 VIME_HUMAN,sp P17661 | 1783.8224 |
| sp P23246 SFPQ_HUMAN           | 1441.7201 |
| sp P31327 CPSM_HUMAN           | 1833.8601 |
| sp P40429 RL13A_HUMAN          | 1547.9035 |
| sp Q01518 CAP1_HUMAN           | 3306.6747 |
| sp P23921 RIR1_HUMAN           | 2024.0327 |
| sp P49327 FAS_HUMAN            | 2788.3014 |
| sp Q9Y570 PPME1_HUMAN          | 2012.9803 |
| sp Q15149 PLEC_HUMAN           | 1724.8078 |
| sp Q99829 CPNE1_HUMAN          | 1913.8836 |
| sp Q9Y262 EIF3L_HUMAN          | 3139.5291 |
| sp P27635 RL10_HUMAN           | 1372.583  |
| sp O75821 EIF3G_HUMAN          | 2123.0072 |
| sp Q8IYD1 ERF3B_HUMAN          | 2890.513  |
| sp Q9Y3B4 SF3B6_HUMAN          | 2228.0347 |
| sp P13639 EF2_HUMAN            | 1699.7916 |
| sp P61353 RL27_HUMAN           | 2978.4734 |
| sp P62913 RL11_HUMAN           | 1195.5404 |
| sp Q9BVL2 NUP58_HUMAN          | 2486.1503 |
| sp Q96SB3 NEB2_HUMAN           | 2277.0814 |
| sp Q16740 CLPP_HUMAN           | 1952.9262 |
| sp Q70CQ2 UBP34_HUMAN          | 3141.4351 |
| sp P62241 RS8_HUMAN            | 1838.9275 |
| sp P35579 MYH9_HUMAN           | 2448.1881 |
| sp Q00839 HNRPU_HUMAN          | 1469.6431 |
| sp P42704 LPPRC_HUMAN          | 1704.793  |
| sp P62753 RS6_HUMAN            | 1782.8835 |
| sp P84243 H33_HUMAN            | 1517.7587 |
| sp O43707 ACTN4_HUMAN          | 1904.9367 |
| sp Q8IXT5 RB12B_HUMAN          | 1860.7883 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2391.0934 |
| sp Q14320 FA50A_HUMAN          | 2363.1969 |

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| sp O75955 FLOT1_HUMAN           | 1844.9745 |
| sp P0DMV8 HS71A_HUMAN,sp PODI   | 1876.8744 |
| sp P42704 LPPRC_HUMAN           | 3230.6459 |
| sp Q9NVR2 INT10_HUMAN           | 2277.1794 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 1622.8668 |
| sp O75369 FLNB_HUMAN            | 4083.7857 |
| sp P23246 SFPQ_HUMAN            | 1768.7509 |
| sp P16401 H15_HUMAN,rev_sp P16  | 1205.6768 |
| sp P09429 HMGB1_HUMAN           | 1916.8905 |
| sp P43243 MATR3_HUMAN           | 1908.8788 |
| sp P35637 FUS_HUMAN             | 2464.9938 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI  | 998.5033  |
| sp P12956 XRCC6_HUMAN           | 1895.9265 |
| sp P49327 FAS_HUMAN             | 1938.0431 |
| sp Q9HCE1 MOV10_HUMAN           | 1421.7191 |
| sp P62805 H4_HUMAN              | 2018.1273 |
| sp Q01082 SPTB2_HUMAN           | 2266.1117 |
| sp P46778 RL21_HUMAN            | 1583.7766 |
| sp P54851 EMP2_HUMAN            | 1291.6197 |
| sp Q9Y237 PIN4_HUMAN            | 1746.8399 |
| sp P62888 RL30_HUMAN            | 2693.1929 |
| sp P08195 4F2_HUMAN             | 2276.278  |
| sp Q14847 LASP1_HUMAN           | 2204.9862 |
| sp Q687X5 STEA4_HUMAN           | 3854.9843 |
| sp P67936 TPM4_HUMAN            | 1938.8919 |
| sp P62937 PPIA_HUMAN            | 2679.2453 |
| sp P35613 BASI_HUMAN            | 3646.6232 |
| sp Q06265 EXOS9_HUMAN           | 1792.8964 |
| sp P46013 KI67_HUMAN            | 2425.1245 |
| sp P05026 AT1B1_HUMAN           | 2807.3766 |
| sp P62937 PPIA_HUMAN            | 2679.2453 |
| sp Q9HC38 GLOD4_HUMAN           | 2020.9967 |
| sp O95456 PSMG1_HUMAN           | 2418.1339 |
| sp Q6P2Q9 PRP8_HUMAN            | 2429.2379 |
| sp P08708 RS17_HUMAN            | 1570.7814 |
| sp P07237 PDIA1_HUMAN           | 3133.5972 |
| sp O75367 H2AY_HUMAN            | 1528.7886 |
| sp P35637 FUS_HUMAN             | 3382.3422 |
| sp P23528 COF1_HUMAN            | 2356.1369 |
| sp P26641 EF1G_HUMAN            | 1571.8559 |
| sp P19338 NUCL_HUMAN            | 1433.6059 |
| sp P62277 RS13_HUMAN            | 2105.0681 |
| sp Q9H7B2 RPF2_HUMAN            | 1792.8016 |
| sp Q14258 TRI25_HUMAN           | 1661.8988 |
| sp P29401 TKT_HUMAN             | 2845.4709 |
| sp P36776 LONM_HUMAN            | 1899.8785 |
| sp P21266 GSTM3_HUMAN           | 2446.242  |

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| sp Q9UPN3 MACF1_HUMAN          | 1547.7845 |
| sp Q13162 PRDX4_HUMAN          | 2599.2013 |
| sp Q01974 ROR2_HUMAN           | 2416.0325 |
| sp Q6IAA8 LTOR1_HUMAN          | 3605.873  |
| sp Q96DI7 SNR40_HUMAN          | 1915.8887 |
| sp Q02543 RL18A_HUMAN          | 1950.9721 |
| sp P49327 FAS_HUMAN            | 1344.6132 |
| sp P36578 RL4_HUMAN            | 965.5546  |
| sp Q06830 PRDX1_HUMAN          | 3779.8254 |
| sp Q06323 PSME1_HUMAN          | 2827.3375 |
| sp Q09666 AHNK_HUMAN           | 2515.1689 |
| sp O96013 PAK4_HUMAN           | 1318.6881 |
| sp P84098 RL19_HUMAN           | 1119.5673 |
| sp P61978 HNRPK_HUMAN          | 1249.6667 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P08670 VIME_HUMAN           | 1784.8727 |
| sp P05787 K2C8_HUMAN           | 2500.1315 |
| sp P18124 RL7_HUMAN            | 1516.7198 |
| sp Q13310 PABP4_HUMAN          | 2267.0416 |
| sp Q92499 DDX1_HUMAN           | 2981.3097 |
| sp P27105 STOM_HUMAN           | 2854.4688 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3653.6674 |
| sp Q9NRG9 AAAS_HUMAN           | 1867.9428 |
| sp P11142 HSP7C_HUMAN          | 2228.0195 |
| sp Q15942 ZYX_HUMAN            | 2390.1727 |
| sp P02786 TFR1_HUMAN           | 1235.651  |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P36578 RL4_HUMAN            | 2332.127  |
| sp O60506 HNRPO_HUMAN          | 1749.7999 |
| sp P06748 NPM_HUMAN            | 1436.726  |
| sp P62280 RS11_HUMAN           | 1398.682  |
| sp P29692 EF1D_HUMAN           | 1395.6055 |
| sp E9PAV3 NACAM_HUMAN,sp Q13   | 1745.924  |
| sp P62841 RS15_HUMAN           | 2057.0252 |
| sp P78527 PRKDC_HUMAN          | 1391.6834 |
| sp P62277 RS13_HUMAN           | 2105.0681 |
| sp Q96A49 SYAP1_HUMAN          | 3548.7271 |
| sp P38646 GRP75_HUMAN          | 1208.5972 |
| sp P55786 PSA_HUMAN            | 3262.6582 |
| sp P02786 TFR1_HUMAN           | 1310.6619 |
| sp Q15365 PCBP1_HUMAN,sp P577: | 1677.876  |
| sp Q9UBX3 DIC_HUMAN            | 2465.0991 |
| sp Q14847 LASP1_HUMAN          | 1950.857  |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1928.9091 |
| sp P49327 FAS_HUMAN            | 1797.9369 |
| sp P62805 H4_HUMAN             | 1634.8226 |



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| sp Q12931 TRAP1_HUMAN          | 1493.809  |
| sp P17844 DDX5_HUMAN           | 1744.9108 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp P29401 TKT_HUMAN            | 1609.8352 |
| sp Q15046 SYK_HUMAN            | 3577.7729 |
| sp P49642 PRI1_HUMAN           | 1408.6735 |
| sp P23396 RS3_HUMAN            | 1285.703  |
| sp P06748 NPM_HUMAN            | 2240.0418 |
| sp P23284 PPIB_HUMAN           | 2113.0004 |
| sp P62280 RS11_HUMAN           | 1144.6128 |
| sp P40227 TCPZ_HUMAN           | 1477.7525 |
| sp P16070 CD44_HUMAN           | 1238.5568 |
| sp P25685 DNJB1_HUMAN          | 1837.8119 |
| sp P24928 RPB1_HUMAN           | 2760.3566 |
| sp P08237 PFKAM_HUMAN          | 1507.6258 |
| sp P04406 G3P_HUMAN            | 1526.6745 |
| sp P40925 MDHC_HUMAN           | 1373.6827 |
| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp Q86U42 PABP2_HUMAN,sp A6N1  | 1697.8083 |
| sp P07237 PDIA1_HUMAN          | 3200.5183 |
| sp P02786 TFR1_HUMAN           | 2321.9569 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P09429 HMGB1_HUMAN          | 2434.0747 |
| sp P62753 RS6_HUMAN            | 1782.8835 |
| sp Q86X76 NIT1_HUMAN           | 2374.174  |
| sp Q9UL33 TPC2L_HUMAN          | 2624.106  |
| sp Q9P013 CWC15_HUMAN          | 1639.7802 |
| sp P35613 BASI_HUMAN           | 3646.6232 |
| sp Q14157 UBP2L_HUMAN          | 3311.5416 |
| sp P62277 RS13_HUMAN           | 1924.9101 |
| sp P11142 HSP7C_HUMAN          | 2940.4353 |
| sp O75390 CISY_HUMAN           | 2110.0557 |
| sp P25787 PSA2_HUMAN           | 3682.877  |
| sp P62753 RS6_HUMAN            | 1782.8835 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp Q969P0 IGSF8_HUMAN          | 4042.785  |
| sp P14625 ENPL_HUMAN           | 2203.0626 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q08J23 NSUN2_HUMAN          | 1541.766  |
| sp Q92878 RAD50_HUMAN          | 1717.8887 |
| sp O15371 EIF3D_HUMAN          | 1392.7038 |
| sp Q9Y224 RTRAF_HUMAN          | 1830.8213 |
| sp Q9P2B2 FPRP_HUMAN           | 4646.2559 |
| sp P27816 MAP4_HUMAN           | 1516.7634 |
| sp Q00169 PIPNA_HUMAN          | 2450.1754 |
| sp Q96DG6 CMBL_HUMAN           | 2245.991  |

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| sp Q15629 TRAM1_HUMAN          | 1074.4804 |
| sp P51114 FXR1_HUMAN           | 2731.3527 |
| sp Q13813 SPTN1_HUMAN          | 1668.9199 |
| sp P17812 PYRG1_HUMAN          | 3258.4784 |
| sp P23526 SAHH_HUMAN           | 3501.745  |
| sp P30419 NMT1_HUMAN           | 2388.1426 |
| sp P13639 EF2_HUMAN            | 3131.6114 |
| sp P78527 PRKDC_HUMAN          | 1692.8107 |
| sp Q14103 HNRPD_HUMAN          | 2116.0147 |
| sp P48668 K2C6C_HUMAN,sp P0426 | 1504.6794 |
| sp P14618 KPYM_HUMAN           | 1879.8873 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P62633 CNBP_HUMAN           | 2335.0144 |
| sp P35658 NU214_HUMAN          | 1468.7827 |
| sp P55265 DSRAD_HUMAN          | 2276.0419 |
| sp Q09666 AHNK_HUMAN           | 2580.1955 |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp O43847 NRDC_HUMAN           | 1919.8836 |
| sp P52272 HNRPM_HUMAN          | 1217.5863 |
| sp P55786 PSA_HUMAN            | 3262.6582 |
| sp P02786 TFR1_HUMAN           | 2282.0347 |
| sp Q93008 USP9X_HUMAN          | 1603.7631 |
| sp Q92688 AN32B_HUMAN          | 2791.4215 |
| sp Q92878 RAD50_HUMAN          | 1778.9237 |
| sp Q6NZI2 CAVN1_HUMAN          | 1615.7631 |
| sp P21333 FLNA_HUMAN           | 2328.1314 |
| sp Q13813 SPTN1_HUMAN          | 3060.4499 |
| sp Q58FF6 H90B4_HUMAN,sp P0796 | 2211.0695 |
| sp O75489 NDUS3_HUMAN          | 2525.2438 |
| sp P62841 RS15_HUMAN           | 2057.0252 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp Q15833 STXB2_HUMAN          | 2924.474  |
| sp P61927 RL37_HUMAN           | 1488.6667 |
| sp Q00341 VIGLN_HUMAN          | 1373.6939 |
| sp P62241 RS8_HUMAN            | 2097.9895 |
| sp O43390 HNRPR_HUMAN,sp O605  | 1574.6961 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3246.5901 |
| sp P38646 GRP75_HUMAN          | 3205.4952 |
| sp P02786 TFR1_HUMAN           | 2331.2032 |
| sp P51148 RAB5C_HUMAN          | 1873.9282 |
| sp Q9UJS0 CMC2_HUMAN           | 3072.5292 |
| sp Q9UHD1 CHRD1_HUMAN          | 2044.0629 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1360.7715 |
| sp Q7KZF4 SND1_HUMAN           | 2943.4614 |
| sp P36871 PGM1_HUMAN           | 3171.3914 |
| sp P53621 COPA_HUMAN           | 1796.952  |

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| sp P48147 PPCE_HUMAN           | 2177.9074 |
| sp P62937 PPIA_HUMAN           | 1109.5869 |
| sp Q09666 AHNK_HUMAN           | 1345.67   |
| sp O00170 AIP_HUMAN            | 1690.9406 |
| sp P06748 NPM_HUMAN            | 1308.631  |
| sp Q00341 VIGLN_HUMAN          | 1179.6037 |
| sp P05787 K2C8_HUMAN           | 1733.8584 |
| sp P78527 PRKDC_HUMAN          | 2173.1671 |
| sp Q5SRE5 NU188_HUMAN          | 2205.0835 |
| sp P25789 PSA4_HUMAN           | 1551.6801 |
| sp P62805 H4_HUMAN             | 1614.7638 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1283.7125 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2938.4535 |
| sp Q01518 CAP1_HUMAN           | 1716.8254 |
| sp O15144 ARPC2_HUMAN          | 1957.9422 |
| sp Q9Y624 JAM1_HUMAN           | 1677.7271 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2938.4535 |
| sp P41252 SYIC_HUMAN           | 2305.2206 |
| sp P16401 H15_HUMAN            | 1108.6241 |
| sp P21333 FLNA_HUMAN           | 1989.9506 |
| sp P04083 ANXA1_HUMAN          | 1409.6721 |
| sp Q00839 HNRPU_HUMAN          | 1453.6482 |
| sp P38646 GRP75_HUMAN          | 2618.2204 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1446.7355 |
| sp Q9BTE7 DCNL5_HUMAN          | 2013.0452 |
| sp Q14697 GANAB_HUMAN          | 2473.354  |
| sp Q92499 DDX1_HUMAN           | 1896.7995 |
| sp P13667 PDIA4_HUMAN          | 1823.957  |
| sp P50395 GDIB_HUMAN           | 3172.7271 |
| sp Q9P035 HACD3_HUMAN          | 3198.5946 |
| sp O14787 TNPO2_HUMAN,sp Q929  | 1481.809  |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp Q6YHK3 CD109_HUMAN          | 2606.2864 |
| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp O60506 HNRPQ_HUMAN          | 2698.3167 |
| sp P11021 BIP_HUMAN            | 2116.0589 |
| sp Q9BXK1 KLF16_HUMAN          | 1487.7117 |
| sp P31327 CPSM_HUMAN           | 2777.3793 |
| sp P62249 RS16_HUMAN           | 1438.6987 |
| sp P08559 ODPA_HUMAN           | 4156.9066 |
| sp Q5JRX3 PREP_HUMAN           | 2124.0487 |
| sp O75369 FLNB_HUMAN           | 1918.9425 |
| sp Q09666 AHNK_HUMAN           | 1404.6496 |
| sp P62910 RL32_HUMAN           | 2282.1439 |

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| sp P16401 H15_HUMAN            | 1065.5819 |
| sp P46013 KI67_HUMAN           | 1815.9003 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3923.7811 |
| sp P31327 CPSM_HUMAN           | 2518.238  |
| sp P53621 COPA_HUMAN           | 1796.952  |
| sp P08758 ANXA5_HUMAN          | 1995.9214 |
| sp Q15366 PCBP2_HUMAN          | 2625.3187 |
| sp Q7KZ85 SPT6H_HUMAN          | 3954.8258 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp Q9H0S4 DDX47_HUMAN          | 1398.7619 |
| sp P27797 CALR_HUMAN           | 1343.6874 |
| sp P0DN76 U2AF5_HUMAN,sp Q010  | 1859.8447 |
| sp P37802 TAGL2_HUMAN          | 2852.3473 |
| sp P13639 EF2_HUMAN            | 3340.6212 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp P35579 MYH9_HUMAN           | 1350.5913 |
| sp P07437 TBB5_HUMAN           | 2364.2035 |
| sp P18621 RL17_HUMAN           | 1097.5254 |
| sp Q15149 PLEC_HUMAN           | 2841.3504 |
| sp Q99832 TCPH_HUMAN           | 2288.1689 |
| sp Q71UI9 H2AV_HUMAN,sp POCOS! | 2666.3552 |
| sp O00567 NOP56_HUMAN          | 2060.0579 |
| sp Q9Y6N7 ROBO1_HUMAN          | 1193.5677 |
| sp Q15149 PLEC_HUMAN           | 1637.8625 |
| sp P30043 BLVRB_HUMAN          | 2353.1777 |
| sp O75694 NU155_HUMAN          | 3282.4202 |
| sp Q00610 CLH1_HUMAN           | 3620.8396 |
| sp P13639 EF2_HUMAN            | 1453.7599 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp P14618 KPYM_HUMAN           | 2072.9945 |
| sp Q13162 PRDX4_HUMAN          | 2599.2013 |
| sp P12956 XRCC6_HUMAN          | 2484.2689 |
| sp P63244 RACK1_HUMAN          | 2444.1682 |
| sp P62249 RS16_HUMAN           | 1664.8635 |
| sp P14625 ENPL_HUMAN           | 1855.8411 |
| sp P05787 K2C8_HUMAN           | 1404.6191 |
| sp P04406 G3P_HUMAN            | 2309.1652 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P55060 XPO2_HUMAN           | 2866.544  |
| sp P10809 CH60_HUMAN           | 3776.8203 |
| sp P61247 RS3A_HUMAN           | 3209.6067 |
| sp P62913 RL11_HUMAN           | 2747.2827 |
| sp P16402 H13_HUMAN,sp P10412  | 1169.6292 |
| sp P55072 TERA_HUMAN           | 1825.8305 |
| sp Q08J23 NSUN2_HUMAN          | 1541.766  |
| sp Q8IWS0 PHF6_HUMAN           | 2108.9487 |
| sp P30101 PDIA3_HUMAN          | 1291.5582 |

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| sp Q86Y56 DAAF5_HUMAN          | 2604.3006 |
| sp P49902 5NTC_HUMAN           | 1713.7999 |
| sp P62280 RS11_HUMAN           | 2538.2748 |
| sp P32004 L1CAM_HUMAN          | 3975.9544 |
| sp P49327 FAS_HUMAN            | 1439.7872 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P11234 RALB_HUMAN           | 2265.055  |
| sp P53990 IST1_HUMAN           | 1545.7861 |
| sp O14949 QCR8_HUMAN           | 1907.9894 |
| sp P26641 EF1G_HUMAN           | 1248.6139 |
| sp Q86UK7 ZN598_HUMAN          | 1653.706  |
| sp Q16531 DDB1_HUMAN           | 2375.2195 |
| sp P04406 G3P_HUMAN            | 3145.4736 |
| sp Q9NR30 DDX21_HUMAN          | 3228.5186 |
| sp P28288 ABCD3_HUMAN          | 1426.6841 |
| sp Q9NZI8 IF2B1_HUMAN          | 2295.2474 |
| sp Q71U36 TBA1A_HUMAN,sp PODF  | 1592.7181 |
| sp Q8NC51 PAIRB_HUMAN          | 1948.9603 |
| sp P62913 RL11_HUMAN           | 1678.8209 |
| sp Q9BQG0 MBB1A_HUMAN          | 1412.73   |
| sp Q8NC51 PAIRB_HUMAN          | 1111.5662 |
| sp P21333 FLNA_HUMAN           | 2222.1331 |
| sp P34897 GLYM_HUMAN           | 2188.1164 |
| sp P36578 RL4_HUMAN            | 2332.127  |
| sp P07437 TBB5_HUMAN           | 2222.1042 |
| sp P31327 CPSM_HUMAN           | 1817.8652 |
| sp P08195 4F2_HUMAN            | 1576.7257 |
| sp P53675 CLH2_HUMAN           | 2690.4279 |
| sp P17844 DDX5_HUMAN           | 1466.7405 |
| sp P26583 HMGB2_HUMAN          | 1748.8581 |
| sp Q03405 UPAR_HUMAN           | 3305.4531 |
| sp O15031 PLXB2_HUMAN          | 2462.1384 |
| sp Q10471 GALT2_HUMAN          | 1495.7453 |
| sp P21333 FLNA_HUMAN           | 1531.7743 |
| sp P08195 4F2_HUMAN            | 2374.1594 |
| sp P35637 FUS_HUMAN            | 3398.3371 |
| sp P05787 K2C8_HUMAN           | 1537.7736 |
| sp P55884 EIF3B_HUMAN          | 1887.8904 |
| sp P30622 CLIP1_HUMAN          | 1583.758  |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp P08238 HS90B_HUMAN,sp Q58F  | 1560.7573 |
| sp P21926 CD9_HUMAN            | 1375.6871 |
| sp Q13838 DX39B_HUMAN          | 2386.2169 |
| sp P46777 RL5_HUMAN            | 1554.7613 |
| sp P62861 RS30_HUMAN           | 1431.7398 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P49915 GUAA_HUMAN           | 3236.6176 |

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| sp P60174 TPIS_HUMAN           | 2517.2533 |
| sp P06733 ENOA_HUMAN           | 2372.0995 |
| sp P62937 PPIA_HUMAN           | 4122.9092 |
| sp P51858 HDGF_HUMAN           | 2144.0062 |
| sp Q5VT66 MARC1_HUMAN          | 2695.3898 |
| sp P22626 ROA2_HUMAN           | 2756.2211 |
| sp O76094 SRP72_HUMAN          | 1429.7314 |
| sp Q9Y2Q3 GSTK1_HUMAN          | 2281.1049 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P13639 EF2_HUMAN            | 3345.6227 |
| sp P38646 GRP75_HUMAN          | 2550.2788 |
| sp P07195 LDHB_HUMAN           | 1706.7999 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3701.9047 |
| sp P13639 EF2_HUMAN            | 1167.6387 |
| sp P06748 NPM_HUMAN            | 1541.7396 |
| sp P11142 HSP7C_HUMAN          | 3085.4062 |
| sp Q8TEQ6 GEMI5_HUMAN          | 2695.3857 |
| sp P53396 ACLY_HUMAN           | 1482.7467 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1531.7155 |
| sp Q16576 RBBP7_HUMAN          | 4262.8433 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1283.7125 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18i  | 1419.6895 |
| sp Q07955 SRSF1_HUMAN          | 2013.9684 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P09651 ROA1_HUMAN,sp Q32P5  | 1761.8646 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp Q8WXX5 DNJC9_HUMAN          | 1887.934  |
| sp P10606 COX5B_HUMAN          | 3229.4597 |
| sp P62249 RS16_HUMAN           | 1410.6925 |
| sp Q15365 PCBP1_HUMAN          | 2040.9972 |
| sp P00558 PGK1_HUMAN           | 2830.4541 |
| sp Q14320 FA50A_HUMAN          | 2363.1969 |
| sp Q13813 SPTN1_HUMAN          | 2242.127  |
| sp P16401 H15_HUMAN            | 1065.5819 |
| sp Q9BW27 NUP85_HUMAN          | 3237.4732 |
| sp O75369 FLNB_HUMAN           | 1770.8213 |
| sp P55209 NP1L1_HUMAN          | 1836.941  |
| sp O75369 FLNB_HUMAN           | 2097.0127 |
| sp P13929 ENOB_HUMAN,sp P0910. | 1930.9822 |
| sp P52292 IMA1_HUMAN           | 1600.8613 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp Q15149 PLEC_HUMAN           | 1724.8078 |
| sp P05787 K2C8_HUMAN           | 1420.614  |
| sp P11021 BIP_HUMAN            | 1512.7168 |
| sp P26599 PTBP1_HUMAN          | 3236.7618 |

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| sp P38646 GRP75_HUMAN          | 3072.4651 |
| sp P04183 KITH_HUMAN           | 2091.1616 |
| sp Q12931 TRAP1_HUMAN          | 1319.7449 |
| sp P52597 HNRPF_HUMAN          | 1542.8042 |
| sp O60784 TOM1_HUMAN           | 2622.2458 |
| sp P07737 PROF1_HUMAN          | 2282.1001 |
| sp P83731 RL24_HUMAN           | 1389.798  |
| sp Q03167 TGBR3_HUMAN          | 2568.3489 |
| sp P40227 TCPZ_HUMAN           | 1959.8487 |
| sp P62081 RS7_HUMAN            | 1855.8813 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3262.585  |
| sp Q96CB9 NSUN4_HUMAN          | 1920.9945 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 2208.9851 |
| sp P13639 EF2_HUMAN            | 3115.6165 |
| sp Q15149 PLEC_HUMAN           | 1503.8045 |
| sp P13639 EF2_HUMAN            | 4552.2043 |
| sp P10586 PTPRF_HUMAN          | 1555.8107 |
| sp P19075 TSN8_HUMAN           | 2967.439  |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp Q15181 IPYR_HUMAN           | 4771.9915 |
| sp P78527 PRKDC_HUMAN          | 4070.9862 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3208.5288 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3535.7154 |
| sp P05783 K1C18_HUMAN          | 1700.8105 |
| sp P02786 TFR1_HUMAN           | 1235.651  |
| sp Q9UNF0 PACN2_HUMAN          | 1902.9112 |
| sp O60361 NDK8_HUMAN,sp P2239  | 2603.2512 |
| sp P42766 RL35_HUMAN           | 1325.698  |
| sp P62987 RL40_HUMAN           | 1520.7154 |
| sp Q14160 SCRIB_HUMAN          | 2214.0441 |
| sp Q10471 GALT2_HUMAN          | 3705.6828 |
| sp P60842 IF4A1_HUMAN          | 1363.7136 |
| sp P49257 LMAN1_HUMAN          | 3267.5942 |
| sp P31939 PUR9_HUMAN           | 1495.7783 |
| sp P12814 ACTN1_HUMAN          | 2082.0534 |
| sp Q13263 TIF1B_HUMAN          | 2005.9489 |
| sp P32969 RL9_HUMAN            | 1335.6459 |
| sp Q16891 MIC60_HUMAN          | 1931.0112 |
| sp P20042 IF2B_HUMAN           | 1825.7764 |
| sp Q9UI26 IPO11_HUMAN          | 2556.2934 |
| sp P19338 NUCL_HUMAN           | 1597.8352 |
| sp O00159 MYO1C_HUMAN          | 1932.9469 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1475.682  |
| sp P09874 PARP1_HUMAN          | 1659.7252 |
| sp P05787 K2C8_HUMAN           | 1537.7736 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1550.6485 |
| sp Q9H0S4 DDX47_HUMAN          | 1133.6081 |

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| sp P19338 NUCL_HUMAN           | 3389.678  |
| sp O75643 U520_HUMAN           | 3130.4805 |
| sp P09234 RU1C_HUMAN           | 2606.1959 |
| sp Q9Y4D7 PLXD1_HUMAN          | 2149.0593 |
| sp Q99623 PHB2_HUMAN           | 2241.0835 |
| sp E9PAV3 NACAM_HUMAN,sp Q13   | 1745.924  |
| sp Q14157 UBP2L_HUMAN          | 3311.5416 |
| sp P46940 IQGA1_HUMAN          | 1178.5873 |
| sp P26599 PTBP1_HUMAN          | 3963.0054 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp Q96CS3 FAF2_HUMAN           | 2609.1744 |
| sp P26373 RL13_HUMAN           | 2623.3163 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp Q13162 PRDX4_HUMAN,sp Q068  | 1555.8246 |
| sp P08708 RS17_HUMAN           | 1397.6324 |
| sp Q9Y624 JAM1_HUMAN           | 2796.5749 |
| sp P53396 ACLY_HUMAN           | 1778.9778 |
| sp O95758 PTBP3_HUMAN          | 3204.588  |
| sp Q6YHK3 CD109_HUMAN          | 1457.6939 |
| sp P16402 H13_HUMAN,sp P10412  | 1191.6612 |
| sp P15121 ALDR_HUMAN           | 2135.1449 |
| sp O75821 EIF3G_HUMAN          | 1469.6358 |
| sp P52272 HNRPM_HUMAN          | 1630.8389 |
| sp P22307 NLTP_HUMAN           | 1980.9793 |
| sp P42704 LPPRC_HUMAN          | 3585.7344 |
| sp O15371 EIF3D_HUMAN          | 1187.5207 |
| sp Q9Y6M1 IF2B2_HUMAN,sp Q9NZ  | 2039.0146 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1483.7493 |
| sp P10599 THIO_HUMAN           | 1361.6099 |
| sp Q9BUF5 TBB6_HUMAN           | 3173.5914 |
| sp P62753 RS6_HUMAN            | 1751.8413 |
| sp P21333 FLNA_HUMAN           | 1390.7092 |
| sp Q13492 PICAL_HUMAN          | 3077.4441 |
| sp P23396 RS3_HUMAN            | 1285.703  |
| sp Q8NCA5 FA98A_HUMAN,sp Q52L  | 2508.1856 |
| sp P16435 NCPR_HUMAN           | 1585.6984 |
| sp P31040 SDHA_HUMAN           | 1943.8982 |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp P14618 KPYM_HUMAN           | 2843.267  |
| sp P50454 SERPH_HUMAN          | 1379.6041 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P31930 QCR1_HUMAN           | 4623.289  |
| sp Q9NQC3 RTN4_HUMAN           | 3467.7184 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2362.2896 |
| sp Q6YHK3 CD109_HUMAN          | 2760.3858 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1506.7143 |



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| sp P08729 K2C7_HUMAN           | 1981.913  |
| sp Q9H0D6 XRN2_HUMAN           | 2728.2803 |
| sp P40925 MDHC_HUMAN           | 1373.6827 |
| sp A2RRP1 NBAS_HUMAN           | 1450.7456 |
| sp P30085 KCY_HUMAN            | 1765.9437 |
| sp P13987 CD59_HUMAN           | 1972.8659 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2603.265  |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp P21291 CSRP1_HUMAN          | 1287.5455 |
| sp P42285 MTREX_HUMAN          | 2885.3    |
| sp P31949 S10AB_HUMAN          | 3752.7338 |
| sp O00534 VMA5A_HUMAN          | 1984.1357 |
| sp P17342 ANPRC_HUMAN          | 1325.6768 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P55769 NH2L1_HUMAN          | 1523.762  |
| sp Q06210 GFPT1_HUMAN          | 2004.9905 |
| sp P15121 ALDR_HUMAN           | 2414.1213 |
| sp Q92841 DDX17_HUMAN          | 1694.8839 |
| sp P23588 IF4B_HUMAN           | 3539.7056 |
| sp O95678 K2C75_HUMAN,sp P4866 | 1593.7675 |
| sp P29401 TKT_HUMAN,sp P51854  | 1055.5247 |
| sp P04406 G3P_HUMAN            | 3301.5747 |
| sp O15031 PLXB2_HUMAN          | 2695.2865 |
| sp Q00610 CLH1_HUMAN,sp P53675 | 1647.8178 |
| sp Q16695 H31T_HUMAN,sp Q71DI3 | 1531.7155 |
| sp P15531 NDKA_HUMAN,sp P22391 | 1540.7886 |
| sp O43707 ACTN4_HUMAN          | 2700.2701 |
| sp P12270 TPR_HUMAN            | 1391.7296 |
| sp P35658 NU214_HUMAN          | 1468.7827 |
| sp P49588 SYAC_HUMAN           | 2657.3081 |
| sp P61769 B2MG_HUMAN           | 3483.6041 |
| sp Q09666 AHNK_HUMAN           | 1669.9039 |
| sp Q14498 RBM39_HUMAN          | 2018.0797 |
| sp P07900 HS90A_HUMAN,sp Q58F6 | 1126.5805 |
| sp Q9Y277 VDAC3_HUMAN          | 2025.0167 |
| sp P11940 PABP1_HUMAN          | 1608.7672 |
| sp P05787 K2C8_HUMAN           | 1325.6463 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp Q00839 HNRPU_HUMAN          | 3854.6312 |
| sp O95340 PAPS2_HUMAN          | 1726.8097 |
| sp P60660 MYL6_HUMAN           | 3851.8353 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P26599 PTBP1_HUMAN          | 2308.2202 |
| sp P62917 RL8_HUMAN            | 1139.6186 |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp Q00610 CLH1_HUMAN           | 1509.7464 |
| sp O43707 ACTN4_HUMAN          | 2242.0807 |

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| sp Q9P2B2 FPRP_HUMAN           | 2659.1609 |
| sp P61604 CH10_HUMAN           | 1725.825  |
| sp P51397 DAP1_HUMAN           | 1942.9385 |
| sp P31943 HNRH1_HUMAN          | 3946.9451 |
| sp P36578 RL4_HUMAN            | 1333.6125 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp O75534 CSDE1_HUMAN          | 1900.8816 |
| sp P10809 CH60_HUMAN           | 1232.6037 |
| sp Q12904 AIMP1_HUMAN          | 1882.9831 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3208.5288 |
| sp Q24JP5 T132A_HUMAN          | 2518.2063 |
| sp P42704 LPPRC_HUMAN          | 2794.4218 |
| sp Q09666 AHNK_HUMAN           | 1595.7984 |
| sp P26599 PTBP1_HUMAN,sp O957: | 1560.8035 |
| sp P50895 BCAM_HUMAN           | 1612.7634 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P22234 PUR6_HUMAN           | 1374.6204 |
| sp Q07065 CKAP4_HUMAN          | 2213.1063 |
| sp Q07065 CKAP4_HUMAN          | 2325.0721 |
| sp P10586 PTPRF_HUMAN          | 1762.8349 |
| sp P52597 HNRPF_HUMAN          | 1374.6568 |
| sp Q13162 PRDX4_HUMAN,sp Q068  | 1555.8246 |
| sp Q99729 ROAA_HUMAN           | 1824.8934 |
| sp Q00839 HNRPU_HUMAN          | 1572.7784 |
| sp P18077 RL35A_HUMAN          | 1359.6895 |
| sp P19338 NUCL_HUMAN           | 1433.6059 |
| sp P09382 LEG1_HUMAN           | 2541.2071 |
| sp P43121 MUC18_HUMAN          | 3439.6566 |
| sp P09874 PARP1_HUMAN          | 2024.0215 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1620.7831 |
| sp Q92900 RENT1_HUMAN          | 4831.3615 |
| sp Q9UBQ0 VPS29_HUMAN          | 2361.2185 |
| sp P07910 HNRPC_HUMAN,sp P0DN  | 1667.8043 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1521.7576 |
| sp P38919 IF4A3_HUMAN          | 1784.9057 |
| sp Q9BQG0 MBB1A_HUMAN          | 1969.9745 |
| sp P50914 RL14_HUMAN           | 1235.6146 |
| sp O14880 MGST3_HUMAN          | 1962.9    |
| sp P21333 FLNA_HUMAN           | 1656.7025 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3923.7811 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp Q6PJQ5 FOXR2_HUMAN          | 1724.8225 |
| sp P49748 ACADV_HUMAN          | 1520.726  |
| sp P08195 4F2_HUMAN            | 1361.7078 |
| sp Q15424 SAFB1_HUMAN,sp Q141: | 1309.699  |

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| sp P10809 CH60_HUMAN           | 2522.2873 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp P27824 CALX_HUMAN           | 2738.3639 |
| sp P22626 ROA2_HUMAN,sp P0965: | 2075.9912 |
| sp Q92616 GCN1_HUMAN           | 2178.0416 |
| sp P62263 RS14_HUMAN           | 1479.7318 |
| sp O75844 FACE1_HUMAN          | 2662.3504 |
| sp Q86UP2 KTN1_HUMAN           | 2943.328  |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P14625 ENPL_HUMAN           | 1549.7884 |
| sp O15371 EIF3D_HUMAN          | 2678.3044 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 3535.7154 |
| sp P02786 TFR1_HUMAN           | 1160.5714 |
| sp Q15003 CND2_HUMAN           | 1987.0448 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp Q92973 TNPO1_HUMAN          | 1591.7163 |
| sp O75369 FLNB_HUMAN           | 2072.999  |
| sp P62917 RL8_HUMAN            | 1139.6186 |
| sp P26599 PTBP1_HUMAN          | 3236.7618 |
| sp P02786 TFR1_HUMAN           | 1460.7048 |
| sp O75400 PR40A_HUMAN          | 1789.7941 |
| sp P15529 MCP_HUMAN            | 2248.0623 |
| sp P52948 NUP98_HUMAN          | 1479.7318 |
| sp P12270 TPR_HUMAN            | 1219.6561 |
| sp P49327 FAS_HUMAN            | 2300.2628 |
| sp P02786 TFR1_HUMAN           | 1410.7718 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp O60749 SNX2_HUMAN           | 2495.277  |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3262.585  |
| sp P10586 PTPRF_HUMAN          | 3126.6237 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P48668 K2C6C_HUMAN,sp P0426 | 1504.6794 |
| sp Q86UE4 LYRIC_HUMAN          | 2155.0294 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1261.6051 |
| sp P26368 U2AF2_HUMAN          | 1362.6528 |
| sp Q9BT22 ALG1_HUMAN           | 2960.5066 |
| sp O75054 IGSF3_HUMAN          | 2837.1399 |
| sp Q16762 THTR_HUMAN           | 1669.8675 |
| sp Q02742 GCNT1_HUMAN          | 4011.034  |
| sp P43243 MATR3_HUMAN          | 2448.2788 |
| sp P55060 XPO2_HUMAN           | 1155.5673 |
| sp Q63HN8 RN213_HUMAN          | 1704.8254 |
| sp P60228 EIF3E_HUMAN          | 1808.8192 |
| sp P07900 HS90A_HUMAN,sp P0823 | 1845.8996 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp Q96I24 FUBP3_HUMAN          | 3457.7478 |

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| sp P61158 ARP3_HUMAN           | 3192.5292 |
| sp P04406 G3P_HUMAN            | 1261.6163 |
| sp Q15149 PLEC_HUMAN           | 1442.7075 |
| sp Q00610 CLH1_HUMAN           | 1547.8712 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1097.5465 |
| sp P11142 HSP7C_HUMAN          | 1394.7042 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1620.7831 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp P27816 MAP4_HUMAN           | 1675.8166 |
| sp P26358 DNMT1_HUMAN          | 2863.5636 |
| sp P05783 K1C18_HUMAN          | 2517.2924 |
| sp P12270 TPR_HUMAN            | 1461.71   |
| sp P08195 4F2_HUMAN            | 3456.7525 |
| sp Q7Z7K6 CENPV_HUMAN          | 2170.0695 |
| sp P53396 ACLY_HUMAN           | 1406.6976 |
| sp P49327 FAS_HUMAN            | 2625.2071 |
| sp P62937 PPIA_HUMAN           | 1575.7821 |
| sp P31939 PUR9_HUMAN           | 1778.9792 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp P23246 SFPQ_HUMAN           | 1441.7201 |
| sp P54709 AT1B3_HUMAN          | 1374.7507 |
| sp Q99798 ACON_HUMAN           | 3189.5942 |
| sp P43243 MATR3_HUMAN          | 1463.762  |
| sp P62424 RL7A_HUMAN           | 3018.4968 |
| sp P35579 MYH9_HUMAN           | 1469.7548 |
| sp Q15006 EMC2_HUMAN           | 2360.1471 |
| sp P07900 HS90A_HUMAN,sp Q58F: | 1126.5805 |
| sp Q15287 RNPS1_HUMAN          | 1877.887  |
| sp P37837 TALDO_HUMAN          | 1443.7358 |
| sp Q92841 DDX17_HUMAN          | 2014.9591 |
| sp P06744 G6PI_HUMAN           | 2493.3016 |
| sp P49257 LMAN1_HUMAN          | 1459.7783 |
| sp P62826 RAN_HUMAN            | 1153.588  |
| sp Q9BQ39 DDX50_HUMAN          | 2919.4614 |
| sp P13639 EF2_HUMAN            | 3340.6212 |
| sp Q99873 ANM1_HUMAN           | 2389.177  |
| sp O75947 ATP5H_HUMAN          | 2920.3511 |
| sp P21926 CD9_HUMAN            | 4149.985  |
| sp P48735 IDHP_HUMAN           | 2593.2673 |
| sp Q9UIW2 PLXA1_HUMAN          | 3886.7163 |
| sp P26599 PTBP1_HUMAN          | 2308.2202 |
| sp P51114 FXR1_HUMAN           | 2731.3527 |
| sp P34897 GLYM_HUMAN           | 2188.1164 |
| sp Q15233 NONO_HUMAN           | 2009.0139 |
| sp P27824 CALX_HUMAN           | 2425.1525 |
| sp P25705 ATPA_HUMAN           | 1316.7452 |
| sp Q9UHD8 SEPT9_HUMAN          | 1853.9384 |

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| sp P78527 PRKDC_HUMAN          | 1100.5866 |
| sp Q9Y624 JAM1_HUMAN           | 1862.9778 |
| sp P31948 STIP1_HUMAN          | 1278.5477 |
| sp Q96CW1 AP2M1_HUMAN          | 2695.3581 |
| sp Q9NZ45 CISD1_HUMAN          | 1505.766  |
| sp Q9UKV3 ACINU_HUMAN          | 1961.9555 |
| sp P43243 MATR3_HUMAN          | 2448.2788 |
| sp P09651 ROA1_HUMAN           | 1824.8067 |
| sp P07954 FUMH_HUMAN           | 3304.585  |
| sp P46063 RECQ1_HUMAN          | 1697.8698 |
| sp P04843 RPN1_HUMAN           | 1798.9505 |
| sp P61313 RL15_HUMAN           | 1529.7124 |
| sp Q9Y570 PPME1_HUMAN          | 3673.7657 |
| sp P56192 SYMC_HUMAN           | 2903.3146 |
| sp P35052 GPC1_HUMAN           | 3238.4435 |
| sp Q14318 FKBP8_HUMAN          | 2323.1267 |
| sp P38646 GRP75_HUMAN          | 2618.2204 |
| sp Q14203 DCTN1_HUMAN          | 1711.8417 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4134.8921 |
| sp Q15149 PLEC_HUMAN           | 2284.0244 |
| sp P61158 ARP3_HUMAN           | 1926.8636 |
| sp O43819 SCO2_HUMAN           | 2213.1077 |
| sp P13639 EF2_HUMAN            | 1558.8355 |
| sp Q9Y624 JAM1_HUMAN           | 2569.4116 |
| sp P26640 SYVC_HUMAN           | 1069.5193 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp P21964 COMT_HUMAN           | 2349.0987 |
| sp P43686 PRS6B_HUMAN          | 2761.3963 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp Q8WW12 PCNP_HUMAN           | 1710.9516 |
| sp P05787 K2C8_HUMAN           | 1404.6191 |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp P10809 CH60_HUMAN           | 2538.2822 |
| sp P22087 FBRL_HUMAN           | 2068.1317 |
| sp P36871 PGM1_HUMAN           | 1285.5476 |
| sp P21926 CD9_HUMAN            | 1375.6871 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp Q9BQ04 RBM4B_HUMAN,sp Q9B   | 2269.124  |
| sp P26006 ITA3_HUMAN           | 2301.9994 |
| sp P12956 XRCC6_HUMAN          | 2386.2429 |
| sp P27635 RL10_HUMAN           | 1067.5036 |
| sp Q9BUQ8 DDX23_HUMAN          | 1961.8611 |
| sp P35052 GPC1_HUMAN           | 2798.3511 |
| sp Q9BY67 CADM1_HUMAN          | 1329.6313 |

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| sp P62826 RAN_HUMAN            | 1666.8203 |
| sp P30086 PEBP1_HUMAN          | 2767.3049 |
| sp P19338 NUCL_HUMAN           | 1594.8566 |
| sp Q00796 DHSO_HUMAN           | 1575.8005 |
| sp P58107 EPIPL_HUMAN          | 2265.2304 |
| sp P84077 ARF1_HUMAN,sp P61204 | 2583.287  |
| sp P61619 S61A1_HUMAN          | 2651.4033 |
| sp P29317 EPHA2_HUMAN          | 3601.7116 |
| sp P14866 HNRPL_HUMAN          | 1387.7096 |
| sp Q99497 PARK7_HUMAN          | 3310.7384 |
| sp P36578 RL4_HUMAN            | 1763.953  |
| sp Q9BQG0 MBB1A_HUMAN          | 1418.8133 |
| sp P63313 TYB10_HUMAN          | 1882.9272 |
| sp P06730 IF4E_HUMAN           | 2305.1954 |
| sp Q09666 AHNK_HUMAN           | 1324.6486 |
| sp P05787 K2C8_HUMAN           | 1733.8584 |
| sp Q15233 NONO_HUMAN           | 2009.0139 |
| sp P15924 DESP_HUMAN           | 1828.9723 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 2387.1203 |
| sp Q08945 SSRP1_HUMAN          | 1509.6888 |
| sp Q14152 EIF3A_HUMAN          | 2454.208  |
| sp P23396 RS3_HUMAN            | 2196.0375 |
| sp O95373 IPO7_HUMAN           | 2118.0932 |
| sp P21926 CD9_HUMAN            | 4149.985  |
| sp P08238 HS90B_HUMAN          | 1577.7582 |
| sp Q9Y2X3 NOP58_HUMAN          | 2195.1011 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |
| sp P36542 ATPG_HUMAN           | 1420.731  |
| sp Q10471 GALT2_HUMAN          | 3705.6828 |
| sp P21964 COMT_HUMAN           | 2659.3428 |
| sp Q99797 MIPEP_HUMAN          | 2192.0902 |
| sp P24941 CDK2_HUMAN           | 1608.7784 |
| sp P18621 RL17_HUMAN           | 1512.7647 |
| sp P26640 SYVC_HUMAN           | 2518.2088 |
| sp P30084 ECHM_HUMAN           | 1847.9854 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P62249 RS16_HUMAN           | 2072.0102 |
| sp P16401 H15_HUMAN            | 1251.6823 |
| sp O15226 NKRF_HUMAN           | 1930.8697 |
| sp P07737 PROF1_HUMAN          | 2111.0899 |
| sp P62277 RS13_HUMAN           | 2018.0361 |
| sp Q15149 PLEC_HUMAN           | 2670.2636 |
| sp Q6YHK3 CD109_HUMAN          | 1457.6939 |
| sp Q15942 ZYG_HUMAN            | 2390.1727 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 2386.1839 |
| sp P07900 HS90A_HUMAN,sp Q145! | 1204.6816 |
| sp P07814 SYEP_HUMAN           | 2298.1743 |

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| sp P63218 GBG5_HUMAN           | 4150.0178 |
| sp Q02750 MP2K1_HUMAN,sp P365  | 1498.8508 |
| sp P00558 PGK1_HUMAN           | 2978.4114 |
| sp P06899 H2B1J_HUMAN,sp P5705 | 1973.9694 |
| sp P08195 4F2_HUMAN            | 1356.7765 |
| sp Q8NBS9 TXND5_HUMAN          | 2777.2254 |
| sp O75369 FLNB_HUMAN           | 2072.999  |
| sp Q9P2B2 FPRP_HUMAN           | 2471.0666 |
| sp P31327 CPSM_HUMAN           | 1908.904  |
| sp Q6UVK1 CSPG4_HUMAN          | 2485.2853 |
| sp Q9Y262 EIF3L_HUMAN          | 1837.8959 |
| sp Q96AX2 RAB37_HUMAN,sp Q152  | 1739.8479 |
| sp Q8N766 EMC1_HUMAN           | 1838.9639 |
| sp P53597 SUCA_HUMAN           | 2574.3442 |
| sp P05787 K2C8_HUMAN           | 1325.6463 |
| sp Q00839 HNRPU_HUMAN          | 1769.8771 |
| sp P26583 HMGB2_HUMAN          | 1788.7955 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp O00410 IPO5_HUMAN           | 2660.3165 |
| sp P60660 MYL6_HUMAN           | 2887.3772 |
| sp P49411 EFTU_HUMAN           | 1958.9408 |
| sp Q13155 AIMP2_HUMAN          | 2982.5815 |
| sp Q99873 ANM1_HUMAN           | 1964.9401 |
| sp Q07065 CKAP4_HUMAN          | 1943.9589 |
| sp P08195 4F2_HUMAN            | 2518.1864 |
| sp P78527 PRKDC_HUMAN          | 1706.8082 |
| sp P49327 FAS_HUMAN            | 2697.2969 |
| sp P30153 2AAA_HUMAN           | 2961.4576 |
| sp P04406 G3P_HUMAN            | 1526.6745 |
| sp Q15149 PLEC_HUMAN           | 1467.6049 |
| sp P17301 ITA2_HUMAN           | 3283.6877 |
| sp P29401 TKT_HUMAN            | 1145.5717 |
| sp Q8N4V1 MMGT1_HUMAN          | 3017.469  |
| sp Q9NP81 SYSM_HUMAN           | 1350.6932 |
| sp Q4KMQ2 ANO6_HUMAN           | 2481.0545 |
| sp Q96AG4 LRC59_HUMAN          | 3026.6805 |
| sp P00367 DHE3_HUMAN           | 2394.1968 |
| sp P13010 XRCC5_HUMAN          | 2090.0433 |
| sp O43707 ACTN4_HUMAN          | 1261.6415 |
| sp P62829 RL23_HUMAN           | 1214.6772 |
| sp P16402 H13_HUMAN,sp P16401  | 1140.639  |
| sp P29401 TKT_HUMAN            | 1776.9159 |
| sp Q13162 PRDX4_HUMAN,sp Q068  | 1555.8246 |
| sp Q00341 VIGLN_HUMAN          | 1733.8584 |
| sp P16401 H15_HUMAN            | 1065.5819 |
| sp Q92499 DDX1_HUMAN           | 2012.0037 |
| sp P06748 NPM_HUMAN            | 3125.4863 |

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| sp O95678 K2C75_HUMAN,sp P4866 | 1593.7675 |
| sp P47756 CAPZB_HUMAN          | 2251.0943 |
| sp P07814 SYEP_HUMAN           | 2298.1743 |
| sp P12956 XRCC6_HUMAN          | 1897.9058 |
| sp P49411 EFTU_HUMAN           | 1958.9408 |
| sp P31948 STIP1_HUMAN          | 1278.5477 |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp P06899 H2B1J_HUMAN,sp P5705 | 1164.5663 |
| sp P11717 MPRI_HUMAN           | 2870.1813 |
| sp P08238 HS90B_HUMAN,sp Q58F1 | 1588.6208 |
| sp Q96SI9 STRBP_HUMAN,sp Q1290 | 1162.6346 |
| sp Q9BY67 CADM1_HUMAN          | 1329.6313 |
| sp Q8NCW5 NNRE_HUMAN           | 2097.0677 |
| sp P30101 PDIA3_HUMAN          | 3262.4983 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1455.6419 |
| sp P21333 FLNA_HUMAN           | 1531.7743 |
| sp P43121 MUC18_HUMAN          | 3001.5035 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3923.7811 |
| sp P23229 ITA6_HUMAN           | 2148.9535 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp Q06830 PRDX1_HUMAN          | 1340.6248 |
| sp P36776 LONM_HUMAN           | 3371.6409 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P35579 MYH9_HUMAN,sp P3574  | 2025.0201 |
| sp P02786 TFR1_HUMAN           | 1160.5714 |
| sp P49748 ACADV_HUMAN          | 3887.9105 |
| sp P31949 S10AB_HUMAN          | 1922.9448 |
| sp Q03001 DYST_HUMAN           | 3252.5786 |
| sp Q92973 TNPO1_HUMAN          | 1591.7163 |
| sp P62081 RS7_HUMAN            | 1161.6394 |
| sp Q8N0Y7 PGAM4_HUMAN,sp P15:  | 1826.8799 |
| sp P26447 S10A4_HUMAN          | 1639.8781 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P52272 HNRPM_HUMAN          | 4424.2124 |
| sp P02786 TFR1_HUMAN           | 2282.0347 |
| sp P15311 EZRI_HUMAN,sp P26038 | 1739.8883 |
| sp P56192 SYMC_HUMAN           | 2887.3197 |
| sp P08648 ITA5_HUMAN           | 2765.3184 |
| sp Q00610 CLH1_HUMAN           | 2278.1991 |
| sp P06733 ENOA_HUMAN           | 1377.6888 |
| sp Q00839 HNRPU_HUMAN          | 1398.7242 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp Q9UHI6 DDX20_HUMAN          | 1955.9629 |
| sp P32322 P5CR1_HUMAN          | 2723.4065 |
| sp O43390 HNRPR_HUMAN,sp O605  | 1628.7327 |
| sp P32119 PRDX2_HUMAN          | 2128.0841 |
| sp P50991 TCPD_HUMAN           | 1469.7548 |



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| sp Q92499 DDX1_HUMAN           | 1743.7709 |
| sp P07237 PDIA1_HUMAN          | 1655.7315 |
| sp P14618 KPYM_HUMAN           | 3213.6194 |
| sp Q9H0A0 NAT10_HUMAN          | 3646.758  |
| sp P62136 PP1A_HUMAN,sp P6214C | 1991.9014 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp Q8TEQ6 GEMI5_HUMAN          | 1969.913  |
| sp O95678 K2C75_HUMAN,sp P486C | 1593.7675 |
| sp Q92804 RBP56_HUMAN          | 2157.0167 |
| sp P78527 PRKDC_HUMAN          | 1841.9081 |
| sp Q9H8Y5 ANKZ1_HUMAN          | 2146.0695 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2412.0791 |
| sp Q13724 MOGS_HUMAN           | 1190.6044 |
| sp Q9ULW0 TPX2_HUMAN           | 2486.3057 |
| sp O43395 PRPF3_HUMAN          | 2023.0011 |
| sp P16402 H13_HUMAN,sp Q02539  | 1431.6882 |
| sp P06733 ENOA_HUMAN           | 1377.6888 |
| sp Q00839 HNRPU_HUMAN          | 1096.5587 |
| sp O76021 RL1D1_HUMAN          | 1377.6525 |
| sp P60709 ACTB_HUMAN,sp P6803Z | 1614.8175 |
| sp P26599 PTBP1_HUMAN          | 1185.6758 |
| sp Q14498 RBM39_HUMAN          | 2018.0797 |
| sp Q9UQ80 PA2G4_HUMAN          | 2123.0283 |
| sp P21266 GSTM3_HUMAN          | 2971.4273 |
| sp P49748 ACADV_HUMAN          | 3194.3856 |
| sp Q8IYB3 SRRM1_HUMAN          | 1791.9883 |
| sp P23246 SFPQ_HUMAN           | 1755.8176 |
| sp Q14103 HNRPD_HUMAN          | 1953.9684 |
| sp P30043 BLVRB_HUMAN          | 2353.1777 |
| sp P32119 PRDX2_HUMAN          | 1168.5764 |
| sp Q8NC51 PAIRB_HUMAN          | 1371.667  |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1704.7811 |
| sp P50395 GDIB_HUMAN           | 2036.9844 |
| sp P09429 HMGB1_HUMAN          | 2434.0747 |
| sp Q00610 CLH1_HUMAN           | 1509.7464 |
| sp P08670 VIME_HUMAN           | 1504.6794 |
| sp O14979 HNRDL_HUMAN          | 1615.7301 |
| sp P49327 FAS_HUMAN            | 1781.942  |
| sp P25705 ATPA_HUMAN           | 2905.5086 |
| sp Q9UBW8 CSN7A_HUMAN          | 1461.8191 |
| sp Q58FF6 H90B4_HUMAN,sp P079C | 2211.0695 |
| sp P38646 GRP75_HUMAN          | 1208.5972 |
| sp P35232 PHB_HUMAN            | 3319.67   |
| sp O43707 ACTN4_HUMAN          | 2841.3868 |
| sp Q1KMD3 HNRL2_HUMAN          | 1465.6182 |
| sp P27797 CALR_HUMAN           | 3863.7326 |
| sp P41252 SYIC_HUMAN           | 1176.5815 |

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| sp P39023 RL3_HUMAN            | 1552.7845 |
| sp P99999 CYC_HUMAN            | 1994.9334 |
| sp Q9NR30 DDX21_HUMAN          | 2260.1059 |
| sp P05787 K2C8_HUMAN           | 1277.5888 |
| sp Q9BY89 K1671_HUMAN          | 2146.0079 |
| sp Q6PL18 ATAD2_HUMAN          | 1425.7504 |
| sp O43809 CPSF5_HUMAN          | 1607.7072 |
| sp P63244 RACK1_HUMAN          | 3180.5146 |
| sp P36578 RL4_HUMAN            | 1333.6125 |
| sp Q9ULF5 S39AA_HUMAN          | 2182.0616 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q92598 HS105_HUMAN          | 2893.28   |
| sp P62424 RL7A_HUMAN           | 1793.906  |
| sp P11142 HSP7C_HUMAN          | 3152.5302 |
| sp P13639 EF2_HUMAN            | 1453.7599 |
| sp P08621 RU17_HUMAN           | 1229.5863 |
| sp P35613 BASI_HUMAN           | 4232.8732 |
| sp P31948 STIP1_HUMAN          | 1278.5477 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1239.5594 |
| sp Q9P2B2 FPRP_HUMAN           | 1793.92   |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 2295.9646 |
| sp P52272 HNRPM_HUMAN          | 1418.6466 |
| sp P09960 LKHA4_HUMAN          | 3658.7023 |
| sp P50395 GDIB_HUMAN           | 1598.7399 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1370.7082 |
| sp P52907 CAZA1_HUMAN          | 2668.2922 |
| sp Q92499 DDX1_HUMAN           | 3072.5305 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3217.5925 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp P35658 NU214_HUMAN          | 2602.3252 |
| sp P78527 PRKDC_HUMAN          | 1073.5393 |
| sp P62805 H4_HUMAN             | 2018.1273 |
| sp Q9UGR2 Z3H7B_HUMAN          | 1857.8969 |
| sp P62244 RS15A_HUMAN          | 1339.6554 |
| sp Q7L2H7 EIF3M_HUMAN          | 1345.6739 |
| sp P46777 RL5_HUMAN            | 2570.2839 |
| sp Q14008 CKAP5_HUMAN          | 1523.8018 |
| sp Q96AE4 FUBP1_HUMAN          | 1664.7642 |
| sp P23526 SAHH_HUMAN           | 1373.6939 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp Q8N3U4 STAG2_HUMAN          | 3087.4066 |
| sp Q9H8H3 MET7A_HUMAN          | 3366.6078 |
| sp P62269 RS18_HUMAN           | 1512.83   |
| sp Q08211 DHX9_HUMAN           | 1382.6103 |
| sp O43823 AKAP8_HUMAN          | 1611.7174 |
| sp P21333 FLNA_HUMAN           | 2328.1314 |
| sp Q14126 DSG2_HUMAN           | 1916.9592 |

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| sp Q9Y2T3 GUAD_HUMAN           | 1932.8862 |
| sp Q9BZZ5 API5_HUMAN           | 1103.5863 |
| sp P17342 ANPRC_HUMAN          | 1325.6768 |
| sp O14975 S27A2_HUMAN          | 1971.8421 |
| sp P02786 TFR1_HUMAN           | 1582.897  |
| sp P15880 RS2_HUMAN            | 1745.8883 |
| sp P25705 ATPA_HUMAN           | 2172.0851 |
| sp Q15149 PLEC_HUMAN           | 3689.8366 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp Q13263 TIF1B_HUMAN          | 1306.6517 |
| sp O00170 AIP_HUMAN            | 1975.9536 |
| sp Q8IVF2 AHNK2_HUMAN          | 1578.7864 |
| sp P15121 ALDR_HUMAN           | 2135.1449 |
| sp O60664 PLIN3_HUMAN          | 3760.8254 |
| sp P12814 ACTN1_HUMAN          | 2082.0534 |
| sp P84098 RL19_HUMAN           | 1630.7813 |
| sp Q6UVK1 CSPG4_HUMAN          | 3653.7288 |
| sp P61158 ARP3_HUMAN           | 3999.0412 |
| sp Q09666 AHNK_HUMAN           | 1324.6486 |
| sp Q99714 HCD2_HUMAN           | 3899.9842 |
| sp O75832 PSD10_HUMAN          | 1801.9437 |
| sp Q9UHB6 LIMA1_HUMAN          | 2005.972  |
| sp P62851 RS25_HUMAN           | 1849.9098 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp Q96JP5 ZFP91_HUMAN          | 1562.759  |
| sp P51148 RAB5C_HUMAN          | 1873.9282 |
| sp P06733 ENOA_HUMAN           | 1068.5451 |
| sp P22695 QCR2_HUMAN           | 1459.7056 |
| sp P20929 NEBU_HUMAN           | 3294.633  |
| sp P31943 HNRH1_HUMAN          | 3946.9451 |
| sp P14923 PLAK_HUMAN           | 3414.7024 |
| sp P08670 VIME_HUMAN,sp P08725 | 1256.5885 |
| sp Q9UHN6 CEIP2_HUMAN          | 2580.1993 |
| sp P00558 PGK1_HUMAN           | 1122.6285 |
| sp P78347 GTF2I_HUMAN          | 2411.1865 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp O00410 IPO5_HUMAN           | 2660.3165 |
| sp P08670 VIME_HUMAN           | 2804.2923 |
| sp P13639 EF2_HUMAN            | 1437.765  |
| sp P25490 TYY1_HUMAN,sp O15391 | 2556.1162 |
| sp Q9BWF3 RBM4_HUMAN           | 2034.9793 |
| sp Q14978 NOLC1_HUMAN          | 1318.663  |
| sp Q14103 HNRPD_HUMAN          | 1241.6041 |
| sp Q99436 PSB7_HUMAN           | 1786.9254 |
| sp P62491 RB11A_HUMAN,sp Q1591 | 2627.3231 |
| sp Q8N556 AFAP1_HUMAN          | 1688.9097 |
| sp P62937 PPIA_HUMAN           | 2294.1219 |

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| sp P21333 FLNA_HUMAN           | 1989.9506 |
| sp Q8TEM1 PO210_HUMAN          | 3591.7628 |
| sp Q15125 EBP_HUMAN            | 1817.8908 |
| sp O15427 MOT4_HUMAN           | 1600.7845 |
| sp P16435 NCPR_HUMAN           | 3155.6365 |
| sp Q02543 RL18A_HUMAN          | 1935.8971 |
| sp Q6WCQ1 MPRIP_HUMAN          | 2583.2387 |
| sp P17174 AATC_HUMAN           | 2195.1144 |
| sp P51114 FXR1_HUMAN           | 2731.3527 |
| sp P51991 ROA3_HUMAN           | 1795.7948 |
| sp Q92598 HS105_HUMAN          | 1628.7947 |
| sp O00410 IPO5_HUMAN           | 2524.2016 |
| sp O00592 PODXL_HUMAN          | 1370.6718 |
| sp P22102 PUR2_HUMAN           | 2698.3133 |
| sp P56945 BCAR1_HUMAN          | 2580.2973 |
| sp P26447 S10A4_HUMAN          | 2292.0441 |
| sp P84098 RL19_HUMAN           | 1119.5673 |
| sp P28288 ABCD3_HUMAN          | 1426.6841 |
| sp Q7KZF4 SND1_HUMAN           | 2108.0401 |
| sp P04406 G3P_HUMAN            | 1526.6745 |
| sp Q9NVE7 PANK4_HUMAN          | 1887.9322 |
| sp P51610 HCFC1_HUMAN          | 2748.2928 |
| sp Q15041 AR6P1_HUMAN          | 1918.881  |
| sp Q9H819 DJC18_HUMAN,sp Q8TB  | 1264.6452 |
| sp P20700 LMNB1_HUMAN          | 2089.0215 |
| sp P02786 TFR1_HUMAN           | 2407.0928 |
| sp Q10589 BST2_HUMAN           | 3034.4731 |
| sp Q14498 RBM39_HUMAN          | 2018.0797 |
| sp P49736 MCM2_HUMAN           | 1858.8347 |
| sp Q92901 RL3L_HUMAN,sp P39023 | 1249.5588 |
| sp P05556 ITB1_HUMAN           | 1578.7566 |
| sp P62805 H4_HUMAN             | 1678.8236 |
| sp Q8WUA4 TF3C2_HUMAN          | 2761.317  |
| sp P05787 K2C8_HUMAN           | 1404.6191 |
| sp P53701 CCHL_HUMAN           | 2250.0263 |
| sp Q15149 PLEC_HUMAN           | 2948.3101 |
| sp Q15651 HMGN3_HUMAN          | 1808.9785 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp Q9NTJ5 SAC1_HUMAN           | 2294.1067 |
| sp Q9ULV4 COR1C_HUMAN          | 2032.0629 |
| sp P60866 RS20_HUMAN           | 1717.7366 |
| sp P26599 PTBP1_HUMAN          | 1185.6758 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1783.748  |
| sp P62987 RL40_HUMAN           | 1520.7154 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp Q00839 HNRPU_HUMAN          | 2694.3613 |
| sp P00966 ASSY_HUMAN           | 3091.4808 |

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| sp O14880 MGST3_HUMAN          | 1355.5234 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp P62913 RL11_HUMAN           | 2747.2827 |
| sp Q7KZ85 SPT6H_HUMAN          | 2500.1295 |
| sp Q8TDN6 BRX1_HUMAN           | 2757.3187 |
| sp P15328 FOLR1_HUMAN          | 2358.0811 |
| sp P46940 IQGA1_HUMAN          | 3070.4495 |
| sp O60506 HNRPQ_HUMAN          | 2698.3167 |
| sp P30101 PDIA3_HUMAN          | 1665.8039 |
| sp P61970 NTF2_HUMAN           | 5072.4181 |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp P07900 HS90A_HUMAN,sp Q145i | 1204.6816 |
| sp P63104 1433Z_HUMAN,sp P3194 | 1448.6718 |
| sp O94776 MTA2_HUMAN           | 1915.964  |
| sp Q00796 DH5O_HUMAN           | 1778.8509 |
| sp P04406 G3P_HUMAN            | 2750.2891 |
| sp A0AVT1 UBA6_HUMAN           | 2018.0684 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp Q9BTV4 TMM43_HUMAN          | 2135.0899 |
| sp P50570 DYN2_HUMAN           | 1695.858  |
| sp P00491 PNPH_HUMAN           | 2366.1194 |
| sp P0DPI2 GAL3A_HUMAN,sp A0A0E | 2938.3621 |
| sp P78527 PRKDC_HUMAN          | 1219.5945 |
| sp P15311 EZRI_HUMAN,sp P35241 | 1502.7518 |
| sp O60353 FZD6_HUMAN           | 1371.6419 |
| sp Q15629 TRAM1_HUMAN          | 1074.4804 |
| sp Q15149 PLEC_HUMAN           | 1424.7048 |
| sp P28288 ABCD3_HUMAN          | 1426.6841 |
| sp P49207 RL34_HUMAN           | 1450.6688 |
| sp P35244 RFA3_HUMAN           | 2332.1344 |
| sp P62851 RS25_HUMAN           | 1769.9312 |
| sp P08174 DAF_HUMAN            | 3845.8359 |
| sp O75436 VP26A_HUMAN          | 1689.9124 |
| sp Q07955 SRSF1_HUMAN          | 2013.9684 |
| sp P30050 RL12_HUMAN           | 1699.8053 |
| sp Q9H4M9 EHD1_HUMAN           | 2469.2904 |
| sp Q02790 FKBP4_HUMAN          | 2235.0848 |
| sp Q9UKM9 RALY_HUMAN           | 2368.0542 |
| sp P61247 RS3A_HUMAN           | 2758.2691 |
| sp Q7Z2W4 ZCCHV_HUMAN          | 2513.1742 |
| sp P61604 CH10_HUMAN           | 1231.6237 |
| sp P30085 KCY_HUMAN            | 2145.0742 |
| sp P10586 PTPRF_HUMAN          | 1573.726  |
| sp P83916 CBX1_HUMAN           | 1611.7125 |
| sp P20908 CO5A1_HUMAN          | 1091.5975 |
| sp P07195 LDHB_HUMAN           | 1706.7999 |
| sp P07900 HS90A_HUMAN,sp P0823 | 1215.6248 |

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| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp P12814 ACTN1_HUMAN          | 2013.9214 |
| sp P04083 ANXA1_HUMAN          | 2101.0579 |
| sp P49207 RL34_HUMAN           | 1450.6688 |
| sp P16403 H12_HUMAN            | 1210.6558 |
| sp P16403 H12_HUMAN            | 1065.6182 |
| sp Q6YHK3 CD109_HUMAN          | 2760.3858 |
| sp O75475 PSIP1_HUMAN          | 1705.8385 |
| sp Q92616 GCN1_HUMAN           | 2860.4706 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P54851 EMP2_HUMAN           | 1291.6197 |
| sp P22392 NDKB_HUMAN           | 2092.0041 |
| sp Q5BKZ1 ZN326_HUMAN          | 2106.9577 |
| sp P19623 SPEE_HUMAN           | 1681.8022 |
| sp P02786 TFR1_HUMAN           | 2337.9518 |
| sp P62249 RS16_HUMAN           | 1575.8872 |
| sp P51532 SMCA4_HUMAN          | 1860.9218 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp P04406 G3P_HUMAN            | 3129.4787 |
| sp P60866 RS20_HUMAN           | 1717.7366 |
| sp P62829 RL23_HUMAN           | 2167.1129 |
| sp P78527 PRKDC_HUMAN          | 1092.5564 |
| sp O75369 FLNB_HUMAN           | 1725.8322 |
| sp Q12788 TBL3_HUMAN           | 2478.2478 |
| sp P62136 PP1A_HUMAN,sp P36873 | 1762.8461 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp P07910 HNRPC_HUMAN          | 2248.1522 |
| sp P26358 DNMT1_HUMAN          | 2051.0575 |
| sp P51991 ROA3_HUMAN           | 2203.9667 |
| sp Q9NXE4 NSMA3_HUMAN          | 1809.9084 |
| sp Q9NVI1 FANCI_HUMAN          | 1181.6445 |
| sp P68366 TBA4A_HUMAN          | 3730.7396 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P46781 RS9_HUMAN            | 1680.8319 |
| sp P19338 NUCL_HUMAN           | 1433.6059 |
| sp P62701 RS4X_HUMAN           | 2802.2694 |
| sp Q96CN7 ISOC1_HUMAN          | 2644.396  |
| sp P55060 XPO2_HUMAN           | 2085.0426 |
| sp P27797 CALR_HUMAN           | 1400.7088 |
| sp P55072 TERA_HUMAN           | 1193.6768 |
| sp P08758 ANXA5_HUMAN          | 1321.6262 |
| sp P52597 HNRPF_HUMAN          | 3018.4294 |
| sp P11142 HSP7C_HUMAN          | 3085.4062 |
| sp P31040 SDHA_HUMAN           | 2991.4297 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P60709 ACTB_HUMAN,sp P63261 | 4185.825  |

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| sp Q15149 PLEC_HUMAN           | 1248.6826 |
| sp Q00839 HNRPU_HUMAN          | 2367.1707 |
| sp P52272 HNRPM_HUMAN          | 1217.5863 |
| sp P38919 IF4A3_HUMAN          | 2346.1856 |
| sp P29401 TKT_HUMAN            | 1517.7072 |
| sp P08758 ANXA5_HUMAN          | 1995.9214 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P25685 DNJB1_HUMAN          | 1837.8119 |
| sp Q96N67 DOCK7_HUMAN          | 3131.5088 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P78527 PRKDC_HUMAN          | 2698.3272 |
| sp P49792 RBP2_HUMAN           | 1855.7982 |
| sp Q99714 HCD2_HUMAN           | 3899.9842 |
| sp Q15149 PLEC_HUMAN           | 1496.7219 |
| sp P06748 NPM_HUMAN            | 3851.9503 |
| sp Q7L1Q6 BZW1_HUMAN           | 1551.7205 |
| sp Q13085 ACACA_HUMAN          | 3443.7541 |
| sp Q9Y2R4 DDX52_HUMAN          | 2041.9891 |
| sp Q15233 NONO_HUMAN           | 1427.7045 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp P40429 RL13A_HUMAN          | 1684.8348 |
| sp P52272 HNRPM_HUMAN          | 1802.8336 |
| sp P14384 CBPM_HUMAN           | 1169.5288 |
| sp Q93052 LPP_HUMAN            | 2296.9734 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp P06733 ENOA_HUMAN           | 5096.5641 |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp Q15149 PLEC_HUMAN           | 1424.7048 |
| sp P12956 XRCC6_HUMAN          | 1132.5764 |
| sp P22626 ROA2_HUMAN           | 2473.1802 |
| sp O75369 FLNB_HUMAN           | 2258.0968 |
| sp P26599 PTBP1_HUMAN          | 1057.5808 |
| sp P23526 SAHH_HUMAN           | 2937.3062 |
| sp O15042 SR140_HUMAN          | 1859.9054 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp P55795 HNRH2_HUMAN,sp P319  | 1338.6456 |
| sp Q13616 CUL1_HUMAN           | 2529.2248 |
| sp Q9Y3R4 NEUR2_HUMAN          | 2658.2885 |
| sp Q14683 SMC1A_HUMAN          | 2291.1104 |
| sp Q13523 PRP4B_HUMAN          | 1303.6884 |
| sp Q9Y224 RTRAF_HUMAN          | 3271.6725 |
| sp P23526 SAHH_HUMAN           | 3501.745  |
| sp P49411 EFTU_HUMAN           | 1873.9058 |
| sp Q15102 PA1B3_HUMAN          | 3771.7913 |
| sp Q9Y6A9 SPCS1_HUMAN          | 2168.0022 |
| sp P39023 RL3_HUMAN            | 1619.8923 |
| sp Q14204 DYHC1_HUMAN          | 2480.1608 |

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| sp Q92616 GCN1_HUMAN          | 2798.4194 |
| sp Q9Y3F4 STRAP_HUMAN         | 2675.2715 |
| sp P14735 IDE_HUMAN           | 2998.4845 |
| sp Q03167 TGBR3_HUMAN         | 3354.6885 |
| sp O95347 SMC2_HUMAN          | 1763.7903 |
| sp Q13151 ROA0_HUMAN          | 1561.7485 |
| sp P29401 TKT_HUMAN           | 1550.8093 |
| sp P08729 K2C7_HUMAN          | 2869.2977 |
| sp P62937 PIIA_HUMAN          | 3816.7512 |
| sp Q9BZK7 TBL1R_HUMAN         | 3206.488  |
| sp P26368 U2AF2_HUMAN         | 2851.3698 |
| sp Q8WW12 PCNP_HUMAN          | 1710.9516 |
| sp Q9Y3I0 RTCB_HUMAN          | 2712.417  |
| sp Q15181 IPYR_HUMAN          | 3739.7981 |
| sp P00558 PGK1_HUMAN          | 2617.2912 |
| sp P30041 PRDX6_HUMAN         | 2081.0238 |
| sp A6NHR9 SMHD1_HUMAN         | 2015.0728 |
| sp Q15758 AAAT_HUMAN          | 2810.4127 |
| sp P62826 RAN_HUMAN           | 1980.937  |
| sp Q9NZ01 TECR_HUMAN          | 2437.2199 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 2358.2795 |
| sp P21333 FLNA_HUMAN          | 2434.3009 |
| sp O15031 PLXB2_HUMAN         | 2680.3167 |
| sp P08621 RU17_HUMAN          | 1555.6362 |
| sp P31949 S10AB_HUMAN         | 1922.9448 |
| sp O43175 SERA_HUMAN          | 2239.1485 |
| sp P09874 PARP1_HUMAN         | 1586.7114 |
| sp P12270 TPR_HUMAN           | 1461.71   |
| sp Q13263 TIF1B_HUMAN         | 2005.9489 |
| sp P35579 MYH9_HUMAN,sp P3558 | 1441.7413 |
| sp Q7Z794 K2C1B_HUMAN,sp O956 | 1278.6245 |
| sp P42704 LPPRC_HUMAN         | 2794.4218 |
| sp P17174 AATC_HUMAN          | 3207.62   |
| sp P27635 RL10_HUMAN          | 1797.872  |
| sp P78406 RAE1L_HUMAN         | 2013.9756 |
| sp O60488 ACSL4_HUMAN         | 2327.0818 |
| sp P34897 GLYM_HUMAN          | 2773.3415 |
| sp P50991 TCPD_HUMAN          | 1058.5504 |
| sp Q12849 GRSF1_HUMAN         | 2652.37   |
| sp P22314 UBA1_HUMAN          | 2876.3882 |
| sp P23246 SFPQ_HUMAN          | 1441.7201 |
| sp P58107 EPIPL_HUMAN         | 5251.6911 |
| sp Q15758 AAAT_HUMAN          | 2810.4127 |
| sp Q14126 DSG2_HUMAN          | 4651.2693 |
| sp P00558 PGK1_HUMAN          | 2378.2482 |
| sp Q14573 ITPR3_HUMAN         | 2336.2046 |
| sp P62805 H4_HUMAN            | 1806.9186 |



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| sp P11021 BIP_HUMAN            | 2212.0913 |
| sp P17301 ITA2_HUMAN           | 1326.584  |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp Q8IY81 SPB1_HUMAN           | 1437.7324 |
| sp P27797 CALR_HUMAN           | 1343.6874 |
| sp Q9H6R0 DHX33_HUMAN          | 3446.7367 |
| sp P06733 ENOA_HUMAN           | 1730.8475 |
| sp P58107 EPIPL_HUMAN          | 1032.524  |
| sp Q9Y653 AGRG1_HUMAN          | 2550.3038 |
| sp O43776 SYNC_HUMAN           | 1323.6724 |
| sp P60174 TPIS_HUMAN           | 3911.9615 |
| sp P27816 MAP4_HUMAN           | 2169.0776 |
| sp P11498 PYC_HUMAN            | 1682.7801 |
| sp P15531 NDKA_HUMAN,sp P2239: | 1540.7886 |
| sp Q15149 PLEC_HUMAN           | 1961.8942 |
| sp P53985 MOT1_HUMAN           | 1663.7802 |
| sp P05787 K2C8_HUMAN           | 1325.6463 |
| sp Q96A33 CCD47_HUMAN          | 1808.9057 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1704.7811 |
| sp Q15436 SC23A_HUMAN          | 2310.0011 |
| sp P08237 PFKAM_HUMAN          | 1507.6258 |
| sp P62805 H4_HUMAN             | 1582.8719 |
| sp P05026 AT1B1_HUMAN          | 2807.3766 |
| sp P42704 LPPRC_HUMAN          | 2078.0069 |
| sp Q15149 PLEC_HUMAN           | 3689.8366 |
| sp P62316 SMD2_HUMAN           | 2440.0861 |
| sp P50895 BCAM_HUMAN           | 1612.7634 |
| sp Q14152 EIF3A_HUMAN          | 1632.7784 |
| sp Q14697 GANAB_HUMAN          | 2473.354  |
| sp Q8WUM4 PDC6I_HUMAN          | 2506.2227 |
| sp O95801 TTC4_HUMAN           | 1914.0323 |
| sp P17301 ITA2_HUMAN           | 1522.7668 |
| sp P52272 HNRPM_HUMAN          | 1418.6466 |
| sp Q969X6 UTP4_HUMAN           | 1973.986  |
| sp Q9Y2R0 COA3_HUMAN           | 1664.7828 |
| sp Q06830 PRDX1_HUMAN          | 2602.2122 |
| sp Q16881 TRXR1_HUMAN          | 1239.6711 |
| sp P12814 ACTN1_HUMAN          | 1234.6306 |
| sp P00338 LDHA_HUMAN           | 1442.7042 |
| sp O75400 PR40A_HUMAN          | 1789.7941 |
| sp P22314 UBA1_HUMAN           | 1873.9727 |
| sp Q06830 PRDX1_HUMAN          | 3077.4488 |
| sp P30085 KCY_HUMAN            | 2145.0742 |
| sp Q03252 LMNB2_HUMAN,sp P207  | 1267.6408 |
| sp P51970 NDUA8_HUMAN          | 2672.2792 |
| sp Q9NV96 CC50A_HUMAN          | 1487.7369 |
| sp Q8NE01 CNNM3_HUMAN          | 2844.4002 |

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| sp P25205 MCM3_HUMAN            | 1332.715  |
| sp Q7Z460 CLAP1_HUMAN           | 2825.3468 |
| sp P62807 H2B1C_HUMAN,sp P5887  | 1461.6664 |
| sp P32004 L1CAM_HUMAN           | 1347.6783 |
| sp P62807 H2B1C_HUMAN,sp P5887  | 1461.6664 |
| sp P60900 PSA6_HUMAN            | 1990.8692 |
| sp Q07812 BAX_HUMAN             | 2800.3702 |
| sp P78527 PRKDC_HUMAN           | 3586.6488 |
| sp P14866 HNRPL_HUMAN           | 2562.1485 |
| sp P14625 ENPL_HUMAN            | 1839.8315 |
| sp Q09666 AHNK_HUMAN            | 1338.6642 |
| sp P84098 RL19_HUMAN            | 1373.6108 |
| sp P06733 ENOA_HUMAN            | 1223.6762 |
| sp O75937 DNJC8_HUMAN           | 3830.9003 |
| sp Q8WVY7 UBCP1_HUMAN           | 2059.9276 |
| sp P27816 MAP4_HUMAN            | 1695.8428 |
| sp P63241 IF5A1_HUMAN,sp Q6IS14 | 2357.0304 |
| sp P23284 PIIB_HUMAN            | 1501.8181 |
| sp Q09666 AHNK_HUMAN            | 2593.2271 |
| sp P18621 RL17_HUMAN            | 1097.5254 |
| sp P58107 EPIPL_HUMAN           | 1032.524  |
| sp P12236 ADT3_HUMAN            | 1959.0425 |
| sp P30419 NMT1_HUMAN            | 2425.2529 |
| sp O95816 BAG2_HUMAN            | 3598.6344 |
| sp Q14204 DYHC1_HUMAN           | 1661.9352 |
| sp P41250 GARS_HUMAN            | 1869.9472 |
| sp Q9UHD8 SEPT9_HUMAN           | 2487.1489 |
| sp P63173 RL38_HUMAN            | 1188.5775 |
| sp P31327 CPSM_HUMAN            | 2646.3905 |
| sp P49773 HINT1_HUMAN           | 1641.7886 |
| sp P62633 CNBP_HUMAN            | 2335.0144 |
| sp Q14847 LASP1_HUMAN           | 3063.3855 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF   | 2611.2303 |
| sp P39023 RL3_HUMAN             | 2007.8884 |
| sp P39023 RL3_HUMAN             | 1424.6896 |
| sp P60709 ACTB_HUMAN,sp P68032  | 1232.6765 |
| sp P08754 GNAI3_HUMAN           | 1315.6408 |
| sp P05787 K2C8_HUMAN            | 1537.7736 |
| sp P09234 RU1C_HUMAN            | 1647.7529 |
| sp P02786 TFR1_HUMAN            | 1160.5714 |
| sp Q96HS1 PGAM5_HUMAN           | 3233.4578 |
| sp P52948 NUP98_HUMAN           | 1566.8366 |
| sp P26038 MOES_HUMAN            | 1332.6714 |
| sp Q15043 S39AE_HUMAN           | 2892.4618 |
| sp Q9UIG0 BAZ1B_HUMAN           | 1255.6085 |
| sp Q15046 SYK_HUMAN             | 1535.762  |
| sp P84077 ARF1_HUMAN,sp P61204  | 2603.265  |

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| sp P55010 IF5_HUMAN            | 3197.5128 |
| sp P10586 PTPRF_HUMAN          | 2733.2408 |
| sp Q9UHI6 DDX20_HUMAN          | 1975.917  |
| sp P08729 K2C7_HUMAN           | 1825.9462 |
| sp P14625 ENPL_HUMAN           | 2738.3163 |
| sp P55011 S12A2_HUMAN          | 1267.6237 |
| sp Q6YHK3 CD109_HUMAN          | 1528.7344 |
| sp P78527 PRKDC_HUMAN          | 1203.5197 |
| sp Q00610 CLH1_HUMAN           | 4030.9557 |
| sp Q13310 PABP4_HUMAN,sp P119  | 2560.1792 |
| sp Q15149 PLEC_HUMAN           | 1724.8078 |
| sp Q7Z2W4 ZCCHV_HUMAN          | 3907.974  |
| sp Q96C36 P5CR2_HUMAN          | 3164.6176 |
| sp P08240 SRPRA_HUMAN          | 2002.0147 |
| sp P50895 BCAM_HUMAN           | 1612.7634 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P62081 RS7_HUMAN            | 1161.6394 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp O43242 PSMD3_HUMAN          | 1379.6834 |
| sp Q562R1 ACTBL_HUMAN          | 2620.0992 |
| sp Q8WWM7 ATX2L_HUMAN          | 2751.3715 |
| sp P49773 HINT1_HUMAN          | 1641.7886 |
| sp P00387 NB5R3_HUMAN          | 1350.6204 |
| sp P07737 PROF1_HUMAN          | 1490.6282 |
| sp Q9BQG0 MBB1A_HUMAN          | 2367.0695 |
| sp Q00796 DH5O_HUMAN           | 2336.1682 |
| sp Q14152 EIF3A_HUMAN          | 1461.7464 |
| sp P52272 HNRPM_HUMAN          | 1466.7729 |
| sp P62937 PPIA_HUMAN           | 1109.5869 |
| sp Q15149 PLEC_HUMAN           | 3067.623  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2711.4092 |
| sp P63173 RL38_HUMAN           | 1681.8451 |
| sp Q00839 HNRPU_HUMAN          | 2383.1114 |
| sp P09429 HMGB1_HUMAN          | 1788.7955 |
| sp Q8IVF2 AHNK2_HUMAN          | 2843.4164 |
| sp P06733 ENOA_HUMAN           | 1068.5451 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp O00170 AIP_HUMAN            | 1975.9536 |
| sp P04406 G3P_HUMAN            | 3363.5354 |
| sp O75083 WDR1_HUMAN           | 1657.7948 |
| sp P53396 ACLY_HUMAN           | 2153.0463 |
| sp O14818 PSA7_HUMAN,sp Q8TAA  | 2445.1349 |
| sp P50395 GDIB_HUMAN           | 2036.9844 |
| sp P14625 ENPL_HUMAN           | 2738.3163 |
| sp Q06210 GFPT1_HUMAN          | 2004.9905 |
| sp Q9BQG0 MBB1A_HUMAN          | 1226.5932 |
| sp P09234 RU1C_HUMAN           | 1647.7529 |

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| sp P14735 IDE_HUMAN            | 2998.4845 |
| sp P40227 TCPZ_HUMAN           | 2344.1951 |
| sp P52943 CRIP2_HUMAN          | 1920.9265 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp P33992 MCM5_HUMAN           | 1571.7324 |
| sp Q7L576 CYFP1_HUMAN          | 3465.6589 |
| sp Q01650 LAT1_HUMAN           | 2457.2726 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp Q00610 CLH1_HUMAN           | 1649.9505 |
| sp P62269 RS18_HUMAN           | 1255.6408 |
| sp Q9UPN3 MACF1_HUMAN          | 2646.3118 |
| sp Q9UNS2 CSN3_HUMAN           | 3087.4938 |
| sp P49411 EFTU_HUMAN           | 1958.9408 |
| sp Q9UHB6 LIMA1_HUMAN          | 1790.845  |
| sp P20839 IMDH1_HUMAN          | 2824.3966 |
| sp Q99497 PARK7_HUMAN          | 2014.7785 |
| sp P07237 PDIA1_HUMAN          | 2215.0546 |
| sp P31040 SDHA_HUMAN           | 1153.5265 |
| sp Q9Y3E5 PTH2_HUMAN           | 1843.8523 |
| sp P05187 PPB1_HUMAN,sp P10696 | 1456.731  |
| sp P11388 TOP2A_HUMAN          | 1320.6058 |
| sp P05204 HMG2_HUMAN           | 1780.9723 |
| sp Q9H0S4 DDX47_HUMAN          | 1133.6081 |
| sp P07437 TBB5_HUMAN           | 2380.1984 |
| sp P29401 TKT_HUMAN            | 1857.9295 |
| sp P07737 PROF1_HUMAN          | 2203.2035 |
| sp P23284 PPIB_HUMAN           | 1838.8509 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1708.7944 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P09429 HMGB1_HUMAN          | 2434.0747 |
| sp P20700 LMNB1_HUMAN          | 2218.0365 |
| sp P07900 HS90A_HUMAN,sp P0823 | 2769.447  |
| sp Q9GZT3 SLIRP_HUMAN          | 2495.2517 |
| sp P05141 ADT2_HUMAN           | 1353.6525 |
| sp Q02878 RL6_HUMAN            | 2546.4836 |
| sp Q7Z794 K2C1B_HUMAN,sp O956  | 1278.6245 |
| sp P19338 NUCL_HUMAN           | 1095.5924 |
| sp P26599 PTBP1_HUMAN,sp O957  | 1560.8035 |
| sp P06748 NPM_HUMAN            | 1168.536  |
| sp Q92841 DDX17_HUMAN          | 1694.8839 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1490.7075 |
| sp P50990 TCPQ_HUMAN           | 1482.7501 |
| sp Q6P2Q9 PRP8_HUMAN           | 2455.2934 |
| sp Q9H0S4 DDX47_HUMAN          | 1398.7619 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P26599 PTBP1_HUMAN          | 1057.5808 |
| sp Q15233 NONO_HUMAN           | 1387.6732 |

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| sp Q96DG6 CMBL_HUMAN          | 2330.108  |
| sp P62244 RS15A_HUMAN         | 1323.7147 |
| sp Q15233 NONO_HUMAN          | 1427.7045 |
| sp Q13283 G3BP1_HUMAN         | 2690.2864 |
| sp Q14204 DYHC1_HUMAN         | 2404.1335 |
| sp P32970 CD70_HUMAN          | 1792.8744 |
| sp Q9UHB6 LIMA1_HUMAN         | 2005.972  |
| sp Q14738 2A5D_HUMAN,sp Q1336 | 2704.3571 |
| sp P10606 COX5B_HUMAN         | 3229.4597 |
| sp Q13586 STIM1_HUMAN         | 1488.7936 |
| sp P16435 NCPR_HUMAN          | 1594.8104 |
| sp P42892 ECE1_HUMAN          | 3104.4952 |
| sp P08670 VIME_HUMAN          | 1369.7453 |
| sp P49327 FAS_HUMAN           | 3741.6021 |
| sp P43121 MUC18_HUMAN         | 3439.6566 |
| sp P16403 H12_HUMAN           | 1261.7394 |
| sp P13987 CD59_HUMAN          | 3083.3654 |
| sp Q8IWS0 PHF6_HUMAN          | 1166.6084 |
| sp P62841 RS15_HUMAN          | 3364.669  |
| sp Q9Y3D3 RT16_HUMAN          | 1361.651  |
| sp P62333 PRS10_HUMAN         | 1405.6838 |
| sp P15531 NDKA_HUMAN          | 2262.0514 |
| sp Q9Y678 COPG1_HUMAN         | 2421.2288 |
| sp P15924 DESP_HUMAN          | 1313.698  |
| sp Q24JP5 T132A_HUMAN         | 2518.2063 |
| sp P55060 XPO2_HUMAN          | 2369.2227 |
| sp P53396 ACLY_HUMAN          | 2361.3056 |
| sp P62847 RS24_HUMAN          | 1560.797  |
| sp P42766 RL35_HUMAN          | 1752.8894 |
| sp P52272 HNRPM_HUMAN         | 1566.7023 |
| sp Q9HDC9 APMAP_HUMAN         | 1993.0997 |
| sp P31948 STIP1_HUMAN         | 1278.5477 |
| sp P53621 COPA_HUMAN          | 1791.8574 |
| sp P24534 EF1B_HUMAN          | 1563.6994 |
| sp P30101 PDIA3_HUMAN         | 3156.4312 |
| sp P52943 CRIP2_HUMAN         | 1277.6364 |
| sp P58107 EPIPL_HUMAN         | 1519.7995 |
| sp Q02543 RL18A_HUMAN         | 2252.0419 |
| sp Q00610 CLH1_HUMAN          | 1462.7205 |
| sp O75396 SC22B_HUMAN         | 1948.9279 |
| sp Q6UVK1 CSPG4_HUMAN         | 1547.7654 |
| sp Q9BTE3 MCMBP_HUMAN         | 2300.1471 |
| sp P23588 IF4B_HUMAN          | 2701.2791 |
| sp P25788 PSA3_HUMAN          | 1831.9316 |
| sp P19338 NUCL_HUMAN          | 2107.0209 |
| sp Q07666 KHDR1_HUMAN         | 1928.9996 |
| sp Q00610 CLH1_HUMAN          | 1547.8712 |

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| sp P10586 PTPRF_HUMAN          | 2733.2408 |
| sp P46940 IQGA1_HUMAN          | 2498.2111 |
| sp P14854 CX6B1_HUMAN          | 2183.9252 |
| sp P02786 TFR1_HUMAN           | 2891.3184 |
| sp P62805 H4_HUMAN             | 1650.8175 |
| sp Q92598 HS105_HUMAN          | 2893.28   |
| sp P04183 KITH_HUMAN           | 2014.9055 |
| sp Q14126 DSG2_HUMAN           | 1125.5567 |
| sp Q15233 NONO_HUMAN           | 1427.7045 |
| sp Q70J99 UN13D_HUMAN          | 2231.195  |
| sp Q9P2E9 RRBP1_HUMAN          | 4015.915  |
| sp P36871 PGM1_HUMAN           | 2032.0153 |
| sp Q8IY81 SPB1_HUMAN           | 1385.7303 |
| sp P60900 PSA6_HUMAN           | 1990.8692 |
| sp P02786 TFR1_HUMAN           | 2331.2032 |
| sp P46013 KI67_HUMAN           | 2860.3814 |
| sp P62826 RAN_HUMAN            | 1153.588  |
| sp P45880 VDAC2_HUMAN          | 1475.766  |
| sp P09874 PARP1_HUMAN          | 1758.7849 |
| sp P60866 RS20_HUMAN           | 1717.7366 |
| sp P15531 NDKA_HUMAN,sp P2239: | 1540.7886 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |
| sp Q8N752 KC1AL_HUMAN,sp P487: | 2528.1318 |
| sp P68104 EF1A1_HUMAN,sp Q5VTf | 3345.6875 |
| sp O75369 FLNB_HUMAN           | 2891.3032 |
| sp P62424 RL7A_HUMAN           | 2163.1437 |
| sp P51398 RT29_HUMAN           | 1520.8239 |
| sp A6ZKI3 RTL8C_HUMAN          | 2069.2361 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1475.682  |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp Q13162 PRDX4_HUMAN          | 3792.8094 |
| sp P54819 KAD2_HUMAN           | 1103.5724 |
| sp P07814 SYEP_HUMAN           | 2343.0808 |
| sp P46776 RL27A_HUMAN          | 2832.3389 |
| sp P27694 RFA1_HUMAN           | 2114.9869 |
| sp P35052 GPC1_HUMAN           | 1636.7879 |
| sp P10809 CH60_HUMAN           | 1925.0292 |
| sp Q9NZ01 TECR_HUMAN           | 2690.3803 |
| sp Q6UVK1 CSPG4_HUMAN          | 1360.6987 |
| sp O76094 SRP72_HUMAN          | 1796.8615 |
| sp P07814 SYEP_HUMAN           | 2298.1743 |
| sp Q08J23 NSUN2_HUMAN          | 2488.0754 |
| sp Q8WWI5 CTL1_HUMAN           | 1640.8014 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1069.5842 |
| sp P08758 ANXA5_HUMAN          | 2359.1941 |
| sp P05787 K2C8_HUMAN           | 1420.614  |
| sp P60709 ACTB_HUMAN,sp P68032 | 1598.8226 |

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| sp O15371 EIF3D_HUMAN          | 1706.7536 |
| sp Q9UBQ5 EIF3K_HUMAN          | 2182.063  |
| sp Q9BW27 NUP85_HUMAN          | 3759.7297 |
| sp Q9UMR2 DD19B_HUMAN,sp Q9N   | 2195.0463 |
| sp P06899 H2B1J_HUMAN,sp P5705 | 1164.5663 |
| sp P46940 IQGA1_HUMAN          | 1924.9465 |
| sp P05783 K1C18_HUMAN          | 1917.8897 |
| sp P46940 IQGA1_HUMAN          | 1346.7194 |
| sp Q07955 SRSF1_HUMAN          | 2404.1481 |
| sp P45880 VDAC2_HUMAN          | 2077.0368 |
| sp Q9NPJ6 MED4_HUMAN           | 2541.3187 |
| sp P30419 NMT1_HUMAN           | 2553.3479 |
| sp P00558 PGK1_HUMAN           | 1554.8042 |
| sp P53680 AP2S1_HUMAN          | 1559.7005 |
| sp Q01813 PFKAP_HUMAN          | 1943.9663 |
| sp Q9Y6N7 ROBO1_HUMAN          | 2398.123  |
| sp Q9UHB6 LIMA1_HUMAN          | 3045.3813 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp P13639 EF2_HUMAN            | 2217.0107 |
| sp P23246 SFPQ_HUMAN           | 1431.6743 |
| sp Q71RC2 LARP4_HUMAN          | 2949.527  |
| sp O75116 ROCK2_HUMAN          | 1666.8063 |
| sp P61927 RL37_HUMAN           | 1124.5978 |
| sp Q14204 DYHC1_HUMAN          | 2188.0987 |
| sp P16435 NCPR_HUMAN           | 1585.6984 |
| sp P78527 PRKDC_HUMAN          | 1654.7814 |
| sp P61604 CH10_HUMAN           | 1911.9902 |
| sp Q13421 MSLN_HUMAN           | 1743.8792 |
| sp P40261 NNMT_HUMAN           | 1208.6554 |
| sp P18124 RL7_HUMAN            | 2506.1872 |
| sp P68366 TBA4A_HUMAN          | 2753.2028 |
| sp P31689 DNJA1_HUMAN          | 2048.9803 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 1090.5183 |
| sp Q16531 DDB1_HUMAN           | 1800.908  |
| sp O43390 HNRPR_HUMAN          | 2439.1693 |
| sp P13639 EF2_HUMAN            | 1470.7355 |
| sp P34897 GLYM_HUMAN           | 1516.7522 |
| sp P62873 GBB1_HUMAN,sp Q9HAV  | 3924.7216 |
| sp P30101 PDIA3_HUMAN          | 2711.2749 |
| sp P62917 RL8_HUMAN            | 1023.5713 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp Q7KZF4 SND1_HUMAN           | 1070.6012 |
| sp Q00610 CLH1_HUMAN           | 2040.9905 |
| sp O75533 SF3B1_HUMAN          | 2288.1648 |
| sp Q9Y277 VDAC3_HUMAN          | 3966.8449 |
| sp P11387 TOP1_HUMAN           | 1670.8668 |
| sp P55039 DRG2_HUMAN           | 1475.6576 |

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| sp Q15046 SYK_HUMAN            | 1535.762  |
| sp P12277 KCRB_HUMAN           | 3783.8124 |
| sp P50991 TCPD_HUMAN           | 1498.8395 |
| sp P08670 VIME_HUMAN           | 1369.7453 |
| sp P25685 DNJB1_HUMAN          | 1629.8111 |
| sp P78527 PRKDC_HUMAN          | 2387.2229 |
| sp Q02880 TOP2B_HUMAN,sp P113  | 1768.809  |
| sp Q92616 GCN1_HUMAN           | 1999.986  |
| sp P28482 MK01_HUMAN           | 1522.778  |
| sp Q9NRZ9 HELLS_HUMAN          | 1768.8996 |
| sp P05787 K2C8_HUMAN           | 1404.6191 |
| sp Q92499 DDX1_HUMAN           | 2965.3148 |
| sp P05787 K2C8_HUMAN           | 2436.2496 |
| sp Q13332 PTPRS_HUMAN          | 1852.8744 |
| sp Q9BTE1 DCTN5_HUMAN          | 1267.6925 |
| sp P21926 CD9_HUMAN            | 4149.985  |
| sp P00558 PGK1_HUMAN           | 1927.8548 |
| sp P0DMV8 HS71A_HUMAN,sp PODI  | 2018.0433 |
| sp P18621 RL17_HUMAN           | 1512.7647 |
| sp P45880 VDAC2_HUMAN          | 1752.8206 |
| sp O14979 HNRDL_HUMAN          | 2089.9626 |
| sp O00148 DX39A_HUMAN,sp Q138  | 2108.9902 |
| sp Q08945 SSRP1_HUMAN          | 2064.0375 |
| sp Q12931 TRAP1_HUMAN          | 2214.9966 |
| sp P22626 ROA2_HUMAN           | 2756.2211 |
| sp P50213 IDH3A_HUMAN          | 2182.1569 |
| sp P41252 SYIC_HUMAN           | 2075.0364 |
| sp Q92499 DDX1_HUMAN           | 2750.2494 |
| sp P22087 FBRL_HUMAN           | 2283.2587 |
| sp P68363 TBA1B_HUMAN,sp P6836 | 3586.7443 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp Q8N8S7 ENAH_HUMAN           | 2073.9657 |
| sp O95816 BAG2_HUMAN           | 1732.8129 |
| sp P19338 NUCL_HUMAN           | 1351.666  |
| sp O43707 ACTN4_HUMAN          | 2370.1757 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp P62913 RL11_HUMAN           | 1522.7198 |
| sp O14874 BCKD_HUMAN           | 1334.6215 |
| sp P17174 AATC_HUMAN           | 2195.1144 |
| sp P07910 HNRPC_HUMAN          | 2264.1471 |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P46777 RL5_HUMAN            | 962.4934  |
| sp Q15084 PDIA6_HUMAN          | 2252.1113 |
| sp P63244 RACK1_HUMAN          | 1600.8283 |
| sp P07237 PDIA1_HUMAN          | 1905.8996 |
| sp Q5JVF3 PCID2_HUMAN          | 1819.9217 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |



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| sp P27824 CALX_HUMAN           | 1158.5782 |
| sp Q9BWE0 REPI1_HUMAN          | 1781.8485 |
| sp Q5VYK3 ECM29_HUMAN          | 1442.7657 |
| sp P35579 MYH9_HUMAN           | 3031.4258 |
| sp P00491 PNPH_HUMAN           | 2366.1194 |
| sp P78527 PRKDC_HUMAN          | 1076.5866 |
| sp P78527 PRKDC_HUMAN          | 1203.5197 |
| sp Q9NQR4 NIT2_HUMAN           | 2283.1423 |
| sp P19338 NUCL_HUMAN           | 1351.666  |
| sp P61158 ARP3_HUMAN           | 2135.0834 |
| sp P98175 RBM10_HUMAN          | 2051.9436 |
| sp Q9P2B2 FPRP_HUMAN           | 1927.8523 |
| sp P30622 CLIP1_HUMAN          | 1555.8035 |
| sp P61247 RS3A_HUMAN           | 1243.6449 |
| sp P61247 RS3A_HUMAN           | 3209.6067 |
| sp Q04637 IF4G1_HUMAN,sp O4343 | 1661.8665 |
| sp P31040 SDHA_HUMAN           | 1959.8931 |
| sp P62424 RL7A_HUMAN           | 1568.7583 |
| sp Q14137 BOP1_HUMAN           | 1971.9374 |
| sp P26640 SYVC_HUMAN           | 2297.1063 |
| sp Q8IY81 SPB1_HUMAN           | 1217.5717 |
| sp Q14697 GANAB_HUMAN          | 1860.072  |
| sp P11021 BIP_HUMAN            | 3318.6694 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp P08133 ANXA6_HUMAN          | 2311.1002 |
| sp P10809 CH60_HUMAN           | 1349.7919 |
| sp P09874 PARP1_HUMAN          | 1659.7252 |
| sp P07737 PROF1_HUMAN          | 1414.7378 |
| sp P27824 CALX_HUMAN           | 2409.1576 |
| sp P53396 ACLY_HUMAN           | 2638.3789 |
| sp P58107 EPIPL_HUMAN          | 2530.2591 |
| sp P14635 CCNB1_HUMAN          | 1814.9639 |
| sp P07737 PROF1_HUMAN          | 1430.7327 |
| sp O60353 FZD6_HUMAN           | 1371.6419 |
| sp Q13263 TIF1B_HUMAN          | 1783.9325 |
| sp Q16531 DDB1_HUMAN           | 1541.7263 |
| sp P62987 RL40_HUMAN,sp P62979 | 1477.7487 |
| sp P38646 GRP75_HUMAN          | 1096.5553 |
| sp P49327 FAS_HUMAN            | 2697.2969 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1261.6051 |
| sp Q00839 HNRPU_HUMAN          | 2920.3807 |
| sp P06213 INSR_HUMAN           | 1288.6663 |
| sp P55072 TERA_HUMAN           | 1825.8305 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1439.766  |
| sp Q8WWQ0 PHIP_HUMAN           | 2595.2493 |
| sp P22307 NLTP_HUMAN           | 1980.9793 |
| sp P40926 MDHM_HUMAN           | 3005.4627 |

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| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp P43243 MATR3_HUMAN          | 1201.588  |
| sp P14384 CBPM_HUMAN           | 1169.5288 |
| sp Q15149 PLEC_HUMAN           | 1134.5782 |
| sp P61020 RAB5B_HUMAN,sp P2033 | 1958.0183 |
| sp Q92552 RT27_HUMAN           | 2071.9163 |
| sp P12004 PCNA_HUMAN           | 1815.8866 |
| sp P18621 RL17_HUMAN           | 2341.126  |
| sp Q01813 PFKAP_HUMAN          | 1943.9663 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P26599 PTBP1_HUMAN          | 3142.5724 |
| sp P05783 K1C18_HUMAN          | 2517.2924 |
| sp P16402 H13_HUMAN,sp P16401  | 1490.7365 |
| sp Q9BQ04 RBM4B_HUMAN,sp Q9B   | 1718.8588 |
| sp P60842 IF4A1_HUMAN          | 1207.6125 |
| sp P56945 BCAR1_HUMAN          | 2580.2973 |
| sp Q9Y5L4 TIM13_HUMAN          | 1913.8789 |
| sp P49257 LMAN1_HUMAN          | 1459.7783 |
| sp P52597 HNRPF_HUMAN          | 1374.6568 |
| sp Q96DU9 PABP5_HUMAN,sp P119  | 1600.8097 |
| sp P25786 PSA1_HUMAN           | 1836.9945 |
| sp P25685 DNJB1_HUMAN          | 1629.8111 |
| sp P53621 COPA_HUMAN           | 1485.6922 |
| sp P49411 EFTU_HUMAN           | 1958.9408 |
| sp P11021 BIP_HUMAN            | 2161.0539 |
| sp P32969 RL9_HUMAN            | 1335.6459 |
| sp O14975 S27A2_HUMAN          | 1854.9112 |
| sp P29401 TKT_HUMAN            | 1245.5302 |
| sp P54136 SYRC_HUMAN           | 1506.7355 |
| sp P36578 RL4_HUMAN            | 1333.6125 |
| sp P63279 UBC9_HUMAN           | 1415.6721 |
| sp P06730 IF4E_HUMAN           | 2261.0812 |
| sp Q96AX2 RAB37_HUMAN,sp Q152  | 1739.8479 |
| sp O95782 AP2A1_HUMAN          | 2694.3224 |
| sp Q09666 AHNK_HUMAN           | 1418.6111 |
| sp P78527 PRKDC_HUMAN          | 2859.4225 |
| sp O00303 EIF3F_HUMAN          | 2598.1658 |
| sp P04844 RPN2_HUMAN           | 1293.6313 |
| sp Q96ST2 IWS1_HUMAN           | 1445.7013 |
| sp P62829 RL23_HUMAN           | 1342.7721 |
| sp Q00610 CLH1_HUMAN,sp P53675 | 1663.8127 |
| sp P10809 CH60_HUMAN           | 1349.7919 |
| sp Q09666 AHNK_HUMAN           | 1629.7895 |
| sp Q14114 LRP8_HUMAN           | 2618.2401 |
| sp P09496 CLCA_HUMAN           | 1600.8825 |
| sp Q14152 EIF3A_HUMAN          | 1887.9189 |
| sp O75367 H2AY_HUMAN           | 1397.7303 |

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| sp Q15149 PLEC_HUMAN           | 1566.7103 |
| sp P41221 WNT5A_HUMAN          | 1414.6477 |
| sp P62269 RS18_HUMAN           | 1181.5425 |
| sp P17931 LEG3_HUMAN           | 1884.8788 |
| sp P00558 PGK1_HUMAN           | 2244.0229 |
| sp P62841 RS15_HUMAN           | 3364.669  |
| sp P63244 RACK1_HUMAN          | 3249.4495 |
| sp P56182 RRP1_HUMAN           | 1867.9105 |
| sp P47897 SYQ_HUMAN            | 3085.5655 |
| sp P50991 TCPD_HUMAN           | 2135.1263 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1051.5298 |
| sp P13797 PLST_HUMAN           | 2517.119  |
| sp P41252 SYIC_HUMAN           | 2701.2483 |
| sp P55854 SUMO3_HUMAN,sp P619  | 1671.8468 |
| sp P58107 EPIPL_HUMAN          | 2164.0073 |
| sp Q13813 SPTN1_HUMAN          | 1435.6692 |
| sp P26599 PTBP1_HUMAN          | 1997.9847 |
| sp P11142 HSP7C_HUMAN          | 3411.6657 |
| sp P05187 PPB1_HUMAN,sp P10696 | 1456.731  |
| sp Q8NHW5 RLA0L_HUMAN,sp P053  | 1865.9523 |
| sp O60313 OPA1_HUMAN           | 2351.1757 |
| sp Q15293 RCN1_HUMAN           | 1688.8006 |
| sp P60842 IF4A1_HUMAN          | 2370.2002 |
| sp P29401 TKT_HUMAN            | 1857.9295 |
| sp P39023 RL3_HUMAN            | 1268.7088 |
| sp P62995 TRA2B_HUMAN          | 2145.9531 |
| sp O75369 FLNB_HUMAN           | 2130.013  |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1069.5768 |
| sp P15531 NDKA_HUMAN,sp P2239  | 1180.6452 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2563.0955 |
| sp P49454 CENPF_HUMAN          | 3039.3707 |
| sp P38646 GRP75_HUMAN          | 1842.8934 |
| sp Q676U5 A16L1_HUMAN          | 1631.8267 |
| sp Q99460 PSMD1_HUMAN          | 2112.064  |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P42677 RS27_HUMAN           | 1773.8533 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P41252 SYIC_HUMAN           | 1176.5815 |
| sp Q9UHB6 LIMA1_HUMAN          | 2410.0727 |
| sp P02545 LMNA_HUMAN           | 1334.6103 |
| sp Q13619 CUL4A_HUMAN          | 2411.2043 |
| sp P62263 RS14_HUMAN           | 1578.8076 |
| sp P0DMV8 HS71A_HUMAN,sp P0DI  | 2501.1706 |
| sp P04439 HLAA_HUMAN,sp P01893 | 4241.9261 |
| sp P29401 TKT_HUMAN            | 2421.1383 |
| sp Q9ULF5 S39AA_HUMAN          | 1757.906  |
| sp Q15942 ZYG_HUMAN            | 2390.1727 |

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| sp Q16881 TRXR1_HUMAN          | 1723.9356 |
| sp P05787 K2C8_HUMAN           | 1554.7791 |
| sp P50990 TCPQ_HUMAN           | 1482.7501 |
| sp P27635 RL10_HUMAN           | 1067.5036 |
| sp P04075 ALDOA_HUMAN          | 1684.8268 |
| sp A8MWD9 RUXGL_HUMAN,sp P62   | 1115.5611 |
| sp P50454 SERPH_HUMAN          | 2739.4079 |
| sp P30519 HMOX2_HUMAN          | 2379.1106 |
| sp Q9Y3U8 RL36_HUMAN           | 1526.7187 |
| sp Q14204 DYHC1_HUMAN          | 3487.7756 |
| sp P36578 RL4_HUMAN            | 2499.225  |
| sp P54819 KAD2_HUMAN           | 1103.5724 |
| sp P31327 CPSM_HUMAN           | 3339.6697 |
| sp Q5JVS0 HABP4_HUMAN          | 2934.506  |
| sp P18206 VINC_HUMAN           | 2724.3389 |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp P38606 VATA_HUMAN           | 2620.3133 |
| sp P19338 NUCL_HUMAN           | 1351.666  |
| sp P08559 ODPA_HUMAN           | 4156.9066 |
| sp P62829 RL23_HUMAN           | 1342.7721 |
| sp P62263 RS14_HUMAN           | 1479.7318 |
| sp P05783 K1C18_HUMAN          | 2501.2975 |
| sp P02786 TFR1_HUMAN           | 1582.897  |
| sp P00491 PNPH_HUMAN           | 2382.1143 |
| sp Q13724 MOGS_HUMAN           | 2802.4188 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 1560.7573 |
| sp Q15233 NONO_HUMAN           | 1427.7045 |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P35579 MYH9_HUMAN           | 1200.606  |
| sp Q13813 SPTN1_HUMAN          | 2138.9981 |
| sp P78344 IF4G2_HUMAN          | 2244.2116 |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp P63092 GNAS2_HUMAN,sp Q5JW  | 2042.0221 |
| sp P55209 NP1L1_HUMAN          | 1836.941  |
| sp O60888 CUTA_HUMAN           | 2500.2672 |
| sp P31689 DNJA1_HUMAN          | 3742.8115 |
| sp P07900 HS90A_HUMAN          | 1353.7252 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P62424 RL7A_HUMAN           | 1547.8308 |
| sp O75367 H2AY_HUMAN           | 1724.9097 |
| sp P14735 IDE_HUMAN            | 2039.9953 |
| sp P53396 ACLY_HUMAN           | 1840.8784 |
| sp P78347 GTF2I_HUMAN          | 3239.5564 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 2886.4876 |
| sp P29692 EF1D_HUMAN           | 1532.7583 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp O95295 SNAPN_HUMAN          | 1421.6899 |

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| sp Q99460 PSMD1_HUMAN          | 2112.064  |
| sp P78527 PRKDC_HUMAN          | 1540.6464 |
| sp P30085 KCY_HUMAN            | 1765.9437 |
| sp Q71U36 TBA1A_HUMAN,sp P0DP  | 4684.2618 |
| sp Q14839 CHD4_HUMAN           | 1967.9986 |
| sp P00338 LDHA_HUMAN           | 1841.0087 |
| sp O76021 RL1D1_HUMAN          | 1566.746  |
| sp Q8WW12 PCNP_HUMAN           | 1480.7198 |
| sp Q9Y6X3 SCC4_HUMAN           | 2293.1136 |
| sp P05362 ICAM1_HUMAN          | 1721.8584 |
| sp P51991 ROA3_HUMAN           | 1795.7948 |
| sp P78527 PRKDC_HUMAN          | 1847.9087 |
| sp Q7KZF4 SND1_HUMAN           | 2943.4614 |
| sp O15347 HMGB3_HUMAN          | 1695.8679 |
| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1550.6485 |
| sp Q9NX40 OCAD1_HUMAN          | 2685.2341 |
| sp P63244 RACK1_HUMAN          | 1441.7024 |
| sp P42704 LPPRC_HUMAN          | 2743.4069 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1384.6735 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P32322 P5CR1_HUMAN          | 2723.4065 |
| sp O00422 SAP18_HUMAN          | 2048.0367 |
| sp P13667 PDIA4_HUMAN          | 1901.9312 |
| sp Q9Y262 EIF3L_HUMAN          | 1837.8959 |
| sp Q5VTR2 BRE1A_HUMAN          | 2088.8894 |
| sp P06748 NPM_HUMAN            | 1069.5768 |
| sp Q8NC51 PAIRB_HUMAN          | 1024.5342 |
| sp Q14978 NOLC1_HUMAN          | 2141.0793 |
| sp P20810 ICAL_HUMAN           | 1818.8748 |
| sp P58107 EPIPL_HUMAN          | 1829.8584 |
| sp P02786 TFR1_HUMAN           | 2173.13   |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 2106.0005 |
| sp P60842 IF4A1_HUMAN          | 2062.8361 |
| sp P99999 CYC_HUMAN            | 1629.8012 |
| sp Q96C36 P5CR2_HUMAN          | 3164.6176 |
| sp Q14166 TTL12_HUMAN          | 3020.4048 |
| sp Q92616 GCN1_HUMAN           | 2243.162  |
| sp Q6PKG0 LARP1_HUMAN          | 2244.0885 |
| sp P06576 ATPB_HUMAN           | 3860.8244 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp Q07020 RL18_HUMAN           | 1969.9997 |
| sp Q7Z2W4 ZCCHV_HUMAN          | 2160.0575 |
| sp P42166 LAP2A_HUMAN          | 1637.7645 |
| sp Q9Y6E2 BZW2_HUMAN           | 1359.6895 |
| sp P31947 1433S_HUMAN          | 1813.9323 |
| sp Q9Y3U8 RL36_HUMAN           | 1214.6217 |

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| sp P17987 TCPA_HUMAN           | 2817.2114 |
| sp Q13162 PRDX4_HUMAN          | 3266.6095 |
| sp O75691 UTP20_HUMAN          | 2283.0981 |
| sp P23588 IF4B_HUMAN           | 3116.4655 |
| sp P15924 DESP_HUMAN           | 1336.6371 |
| sp P40429 RL13A_HUMAN          | 1684.8348 |
| sp P08238 HS90B_HUMAN,sp Q58F1 | 1560.7573 |
| sp Q96ST3 SIN3A_HUMAN          | 1745.8009 |
| sp P15531 NDKA_HUMAN,sp P2239  | 1540.7886 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp O60506 HNRPO_HUMAN          | 2435.1856 |
| sp Q13769 THOC5_HUMAN          | 3365.6754 |
| sp Q13496 MTM1_HUMAN           | 3256.6497 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P14618 KPYM_HUMAN           | 1402.6663 |
| sp P49327 FAS_HUMAN            | 1938.9608 |
| sp Q7KYR7 BT2A1_HUMAN,sp Q8W1  | 1738.8315 |
| sp P49327 FAS_HUMAN            | 1296.7038 |
| sp P99999 CYC_HUMAN            | 1230.6496 |
| sp P49588 SYAC_HUMAN           | 2242.1052 |
| sp P27824 CALX_HUMAN           | 1544.6842 |
| sp O76094 SRP72_HUMAN          | 2416.3577 |
| sp Q9Y6X3 SCC4_HUMAN           | 2111.9847 |
| sp Q9Y2R5 RT17_HUMAN           | 2644.2955 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |
| sp P11387 TOP1_HUMAN           | 1425.7041 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P02545 LMNA_HUMAN           | 1334.6103 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp P38405 GNAL_HUMAN,sp P6309  | 2220.0058 |
| sp Q9ULF5 S39AA_HUMAN          | 2203.1525 |
| sp Q9UKV3 ACINU_HUMAN          | 1961.9555 |
| sp P10809 CH60_HUMAN           | 1382.7479 |
| sp P08670 VIME_HUMAN           | 1729.8774 |
| sp P15531 NDKA_HUMAN,sp P2239  | 1540.7886 |
| sp P00558 PGK1_HUMAN           | 2958.5491 |
| sp P37802 TAGL2_HUMAN          | 2852.3473 |
| sp Q00839 HNRPU_HUMAN          | 1242.5914 |
| sp P62750 RL23A_HUMAN          | 1410.7143 |
| sp P30041 PRDX6_HUMAN          | 2809.3878 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1687.8345 |
| sp P07737 PROF1_HUMAN          | 1804.8843 |
| sp P23246 SFPQ_HUMAN           | 1845.9109 |
| sp P62277 RS13_HUMAN           | 1924.9101 |
| sp P11142 HSP7C_HUMAN          | 3257.5022 |
| sp P15880 RS2_HUMAN            | 2169.0048 |
| sp Q14847 LASP1_HUMAN          | 1542.6925 |

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| sp P02545 LMNA_HUMAN           | 1334.6103 |
| sp Q05639 EF1A2_HUMAN,sp P681C | 1806.8346 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp Q9Y230 RUVB2_HUMAN          | 2271.1495 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 4262.987  |
| sp P99999 CYC_HUMAN            | 2332.0933 |
| sp P05204 HMGN2_HUMAN          | 1780.9723 |
| sp Q9Y2W2 WBP11_HUMAN          | 1494.7175 |
| sp P32969 RL9_HUMAN            | 1494.7242 |
| sp P02786 TFR1_HUMAN           | 1235.651  |
| sp Q15019 SEPT2_HUMAN          | 2750.334  |
| sp P62937 PPIA_HUMAN           | 4800.2476 |
| sp P30041 PRDX6_HUMAN          | 2845.2753 |
| sp P61586 RHOA_HUMAN           | 1623.7563 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1069.5768 |
| sp P48643 TCPE_HUMAN           | 2340.0185 |
| sp Q9UKV8 AGO2_HUMAN           | 2126.0505 |
| sp P50395 GDIB_HUMAN           | 1598.7399 |
| sp Q14980 NUMA1_HUMAN          | 1708.809  |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1531.7155 |
| sp P15880 RS2_HUMAN            | 1745.8883 |
| sp P62701 RS4X_HUMAN           | 1363.6884 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp P07900 HS90A_HUMAN          | 3363.5679 |
| sp Q05D32 CTSL2_HUMAN          | 2626.4119 |
| sp P30626 SORCN_HUMAN          | 2275.0791 |
| sp P52948 NUP98_HUMAN          | 3133.4557 |
| sp P30740 ILEU_HUMAN           | 2349.0907 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2748.4083 |
| sp Q9BY89 K1671_HUMAN          | 2146.0079 |
| sp P50395 GDIB_HUMAN           | 2036.9844 |
| sp O75431 MTX2_HUMAN           | 2801.5116 |
| sp P05787 K2C8_HUMAN           | 2500.1315 |
| sp P62701 RS4X_HUMAN,sp P22090 | 2736.2641 |
| sp P27348 1433T_HUMAN          | 2889.4318 |
| sp Q86UK7 ZN598_HUMAN          | 1653.706  |
| sp P50990 TCPQ_HUMAN           | 2096.0174 |
| sp P46060 RAGP1_HUMAN          | 2609.2149 |
| sp O75390 CISY_HUMAN           | 1677.8574 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1384.6735 |
| sp P14618 KPYM_HUMAN           | 1879.8873 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1580.8232 |
| sp Q9NZT2 OGFR_HUMAN           | 1438.5895 |
| sp Q92841 DDX17_HUMAN          | 3701.8876 |
| sp P62304 RUXE_HUMAN           | 1881.0182 |
| sp Q86UP2 KTN1_HUMAN           | 2730.333  |
| sp Q9NZJ0 DTL_HUMAN            | 1644.7566 |

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| sp Q09666 AHNK_HUMAN           | 1365.6097 |
| sp P05161 ISG15_HUMAN          | 1920.9806 |
| sp P22102 PUR2_HUMAN           | 2036.0215 |
| sp Q05519 SRS11_HUMAN          | 1704.8723 |
| sp P10586 PTPRF_HUMAN          | 2448.1995 |
| sp Q12959 DLG1_HUMAN           | 3496.6971 |
| sp P26038 MOES_HUMAN           | 2027.9834 |
| sp P19105 ML12A_HUMAN,sp O149  | 1584.7209 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1900.0094 |
| sp Q86UP2 KTN1_HUMAN           | 2224.0859 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1446.7355 |
| sp P16401 H15_HUMAN            | 1093.5768 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1614.8175 |
| sp P08729 K2C7_HUMAN           | 1637.8009 |
| sp Q08AF3 SLFN5_HUMAN          | 2783.3047 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2768.3367 |
| sp Q12965 MYO1E_HUMAN          | 2803.2912 |
| sp P21333 FLNA_HUMAN           | 1766.7748 |
| sp Q92769 HDAC2_HUMAN,sp Q135  | 2165.947  |
| sp Q7KZF4 SND1_HUMAN           | 1074.5458 |
| sp P36871 PGM1_HUMAN           | 3222.5833 |
| sp P51610 HCFC1_HUMAN          | 3764.7814 |
| sp P07237 PDIA1_HUMAN          | 1324.6452 |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp P31040 SDHA_HUMAN           | 2991.4297 |
| sp P63104 1433Z_HUMAN,sp P3194 | 1448.6718 |
| sp A1L0T0 ILVBL_HUMAN          | 1661.9101 |
| sp P52565 GDIR1_HUMAN          | 2081.9728 |
| sp P04406 G3P_HUMAN            | 2478.3118 |
| sp P63244 RACK1_HUMAN          | 2444.1682 |
| sp Q03518 TAP1_HUMAN           | 3616.8526 |
| sp P13073 COX41_HUMAN          | 1278.6568 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1673.8189 |
| sp P06753 TPM3_HUMAN           | 1480.7773 |
| sp Q9HB90 RRAGC_HUMAN          | 1904.9381 |
| sp P10586 PTPRF_HUMAN          | 1778.8298 |
| sp P43121 MUC18_HUMAN          | 2400.1936 |
| sp P09651 ROA1_HUMAN           | 2263.0804 |
| sp Q9NQC3 RTN4_HUMAN           | 3467.7184 |
| sp P11940 PABP1_HUMAN          | 1548.7573 |
| sp P07237 PDIA1_HUMAN          | 2129.0681 |
| sp P61247 RS3A_HUMAN           | 1541.7223 |
| sp P12814 ACTN1_HUMAN          | 1234.6306 |
| sp P08754 GNAI3_HUMAN,sp P0947 | 1803.9043 |
| sp P27816 MAP4_HUMAN           | 1090.5043 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp P84090 ERH_HUMAN            | 1229.6656 |



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| sp Q8WXX5 DNJC9_HUMAN          | 1731.8329 |
| sp P50395 GDIB_HUMAN           | 1598.7399 |
| sp Q08J23 NSUN2_HUMAN          | 2488.0754 |
| sp P05787 K2C8_HUMAN           | 2436.2496 |
| sp Q15149 PLEC_HUMAN           | 1637.8625 |
| sp Q12931 TRAP1_HUMAN          | 1900.9319 |
| sp Q02878 RL6_HUMAN            | 1737.9149 |
| sp Q5VYK3 ECM29_HUMAN          | 3285.6154 |
| sp P36871 PGM1_HUMAN           | 1523.6892 |
| sp Q08945 SSRP1_HUMAN          | 1812.8934 |
| sp P20908 CO5A1_HUMAN          | 1091.5975 |
| sp P50238 CRIP1_HUMAN          | 1892.9203 |
| sp Q99729 ROAA_HUMAN           | 1716.8141 |
| sp P43243 MATR3_HUMAN          | 1908.8788 |
| sp P00338 LDHA_HUMAN           | 1841.0087 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P61247 RS3A_HUMAN           | 1541.7223 |
| sp P14618 KPYM_HUMAN           | 1428.6919 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp Q15691 MARE1_HUMAN          | 2274.1321 |
| sp P48509 CD151_HUMAN          | 2144.9653 |
| sp P62701 RS4X_HUMAN           | 1161.5666 |
| sp P06748 NPM_HUMAN            | 1168.536  |
| sp P06733 ENOA_HUMAN           | 1377.6888 |
| sp Q12792 TWF1_HUMAN           | 3048.5152 |
| sp O75083 WDR1_HUMAN           | 1162.5731 |
| sp Q9NX40 OCAD1_HUMAN          | 2685.2341 |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp P23526 SAHH_HUMAN           | 2937.3062 |
| sp P07237 PDIA1_HUMAN          | 2015.9741 |
| sp Q9HA77 SYCM_HUMAN           | 1490.7478 |
| sp Q15233 NONO_HUMAN           | 2010.0283 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1614.8175 |
| sp P06748 NPM_HUMAN            | 1069.5768 |
| sp P78406 RAE1L_HUMAN          | 2382.1644 |
| sp O43707 ACTN4_HUMAN          | 2371.0321 |
| sp Q92859 NEO1_HUMAN           | 2774.3915 |
| sp P04439 HLAA_HUMAN,sp P01885 | 2245.095  |
| sp Q6UVK1 CSPG4_HUMAN          | 1360.6987 |
| sp P62888 RL30_HUMAN           | 3637.6817 |
| sp P09622 DLDH_HUMAN           | 1809.9625 |
| sp P27635 RL10_HUMAN           | 1645.8424 |
| sp P00338 LDHA_HUMAN           | 2106.9858 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P00558 PGK1_HUMAN           | 1327.6408 |
| sp Q6P2E9 EDC4_HUMAN           | 2244.0481 |
| sp Q7L2H7 EIF3M_HUMAN          | 1345.6739 |

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| sp Q9H0S4 DDX47_HUMAN          | 1133.6081 |
| sp P61313 RL15_HUMAN           | 2276.145  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2375.277  |
| sp P05787 K2C8_HUMAN           | 5394.4205 |
| sp P35579 MYH9_HUMAN           | 3356.5579 |
| sp P27824 CALX_HUMAN           | 2722.369  |
| sp Q9UJU6 DBNL_HUMAN           | 1706.7285 |
| sp Q96CM8 ACSF2_HUMAN          | 2139.0015 |
| sp Q09666 AHNK_HUMAN           | 1411.6264 |
| sp P62280 RS11_HUMAN           | 1824.8036 |
| sp P35579 MYH9_HUMAN           | 1889.9523 |
| sp P05783 K1C18_HUMAN          | 1370.6678 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1475.682  |
| sp Q9Y624 JAM1_HUMAN           | 2419.1114 |
| sp O00429 DNM1L_HUMAN          | 3311.7476 |
| sp P30044 PRDX5_HUMAN          | 3310.6332 |
| sp P50416 CPT1A_HUMAN          | 1449.7001 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P11940 PABP1_HUMAN          | 1548.7573 |
| sp P78527 PRKDC_HUMAN          | 2240.2205 |
| sp Q9NZ01 TECR_HUMAN           | 1954.9326 |
| sp Q8NBU5 ATAD1_HUMAN          | 1547.7845 |
| sp P49959 MRE11_HUMAN          | 1652.8311 |
| sp P21333 FLNA_HUMAN           | 1820.8727 |
| sp Q13813 SPTN1_HUMAN          | 1424.7048 |
| sp Q14166 TTL12_HUMAN          | 2278.0014 |
| sp P48556 PSMD8_HUMAN          | 1379.7773 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2768.3367 |
| sp P08621 RU17_HUMAN           | 1571.6311 |
| sp Q9Y287 ITM2B_HUMAN          | 1786.8308 |
| sp P05783 K1C18_HUMAN          | 1488.746  |
| sp P25786 PSA1_HUMAN           | 1836.9945 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp Q9NTK5 OLA1_HUMAN           | 2884.4899 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1506.8406 |
| sp Q96EX1 SIM12_HUMAN          | 1696.8784 |
| sp P40429 RL13A_HUMAN,sp Q6NV  | 1378.7643 |
| sp P63104 1433Z_HUMAN,sp P3194 | 1448.6718 |
| sp O94826 TOM70_HUMAN          | 2318.1478 |
| sp Q13838 DX39B_HUMAN          | 1148.619  |
| sp P62805 H4_HUMAN             | 1614.7638 |
| sp P05787 K2C8_HUMAN           | 1828.9029 |
| sp Q13162 PRDX4_HUMAN          | 2503.2271 |
| sp P14618 KPYM_HUMAN           | 2843.267  |
| sp Q14444 CAPR1_HUMAN          | 2301.1376 |
| sp Q9BXP5 SRRT_HUMAN           | 1561.81   |
| sp P13987 CD59_HUMAN           | 3083.3654 |

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| sp P13639 EF2_HUMAN            | 2339.103  |
| sp P33991 MCM4_HUMAN           | 1917.9472 |
| sp P62937 PPIA_HUMAN           | 2027.9364 |
| sp P49321 NASP_HUMAN           | 3257.7118 |
| sp Q08945 SSRP1_HUMAN          | 1430.6864 |
| sp Q99832 TCPH_HUMAN           | 1471.7783 |
| sp Q14061 COX17_HUMAN          | 1912.8845 |
| sp O75691 UTP20_HUMAN          | 2496.3087 |
| sp Q15149 PLEC_HUMAN           | 1442.7075 |
| sp P62987 RL40_HUMAN,sp P62979 | 1461.7538 |
| sp P62826 RAN_HUMAN            | 1153.588  |
| sp Q07065 CKAP4_HUMAN          | 1850.9989 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp Q8WUA4 TF3C2_HUMAN          | 2761.317  |
| sp P50993 AT1A2_HUMAN,sp P1363 | 1961.0292 |
| sp O43175 SERA_HUMAN           | 1758.7917 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P05783 K1C18_HUMAN          | 1370.6678 |
| sp P39748 FEN1_HUMAN           | 2045.9847 |
| sp P54709 AT1B3_HUMAN          | 1857.8341 |
| sp P26447 S10A4_HUMAN          | 1242.6245 |
| sp Q14134 TRI29_HUMAN          | 2525.3278 |
| sp Q09666 AHNK_HUMAN           | 2336.1471 |
| sp P07737 PROF1_HUMAN          | 1347.6783 |
| sp Q15233 NONO_HUMAN           | 1135.5298 |
| sp Q08J23 NSUN2_HUMAN          | 2104.1065 |
| sp P48739 PIPNB_HUMAN          | 2996.4305 |
| sp P52597 HNRPF_HUMAN          | 2433.2064 |
| sp O15371 EIF3D_HUMAN          | 2678.3044 |
| sp P51659 DHB4_HUMAN           | 1667.8308 |
| sp P19105 ML12A_HUMAN,sp O149  | 1584.7209 |
| sp P17931 LEG3_HUMAN           | 1884.8788 |
| sp Q15149 PLEC_HUMAN           | 3237.7285 |
| sp P54709 AT1B3_HUMAN          | 1857.8341 |
| sp P17480 UBF1_HUMAN           | 1754.8264 |
| sp Q10589 BST2_HUMAN           | 2906.3781 |
| sp Q15276 RABE1_HUMAN          | 2083.9348 |
| sp Q9Y2Q3 GSTK1_HUMAN          | 1730.9025 |
| sp Q96AC1 FERM2_HUMAN          | 1737.8726 |
| sp Q8IWS0 PHF6_HUMAN           | 2829.1584 |
| sp P07814 SYEP_HUMAN           | 1437.6565 |
| sp P00558 PGK1_HUMAN           | 3475.7367 |
| sp P42765 THIM_HUMAN           | 3029.5242 |
| sp P49327 FAS_HUMAN            | 2633.2003 |
| sp Q8WUD1 RAB2B_HUMAN,sp P61   | 1576.7555 |
| sp P09874 PARP1_HUMAN          | 1758.7849 |
| sp Q00839 HNRPU_HUMAN          | 1292.6361 |

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| sp Q13283 G3BP1_HUMAN          | 3919.9567 |
| sp P23396 RS3_HUMAN            | 1285.703  |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1062.473  |
| sp P62249 RS16_HUMAN           | 1575.8872 |
| sp Q15149 PLEC_HUMAN           | 1305.7405 |
| sp P06733 ENOA_HUMAN           | 3336.5979 |
| sp O14617 AP3D1_HUMAN          | 2315.0926 |
| sp P08670 VIME_HUMAN,sp P08725 | 1256.5885 |
| sp P50914 RL14_HUMAN           | 1208.7129 |
| sp P62753 RS6_HUMAN            | 1137.6142 |
| sp P49411 EFTU_HUMAN           | 4760.1516 |
| sp P26641 EF1G_HUMAN           | 1319.651  |
| sp P43487 RANG_HUMAN           | 2935.3599 |
| sp Q9BUJ2 HNRL1_HUMAN          | 1707.8216 |
| sp Q9UBK8 MTRR_HUMAN           | 2418.2642 |
| sp P61927 RL37_HUMAN           | 1225.551  |
| sp P42167 LAP2B_HUMAN          | 1262.7095 |
| sp Q15459 SF3A1_HUMAN          | 1516.7522 |
| sp P78527 PRKDC_HUMAN          | 1219.5945 |
| sp P62937 PPIA_HUMAN           | 1109.5869 |
| sp Q01813 PFKAP_HUMAN          | 1943.9663 |
| sp P00441 SODC_HUMAN           | 1348.6008 |
| sp P11387 TOP1_HUMAN           | 2723.2795 |
| sp P00491 PNPH_HUMAN           | 2382.1143 |
| sp P62081 RS7_HUMAN            | 1852.9167 |
| sp Q14204 DYHC1_HUMAN          | 3187.703  |
| sp Q9BY67 CADM1_HUMAN          | 1329.6313 |
| sp P10586 PTPRF_HUMAN          | 3655.7439 |
| sp P30101 PDIA3_HUMAN          | 1291.5582 |
| sp Q15149 PLEC_HUMAN           | 2857.3453 |
| sp P23528 COF1_HUMAN           | 1505.7072 |
| sp P62805 H4_HUMAN             | 1614.7638 |
| sp P39748 FEN1_HUMAN           | 1306.6517 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp Q13242 SRSF9_HUMAN          | 2418.1638 |
| sp Q9Y490 TLN1_HUMAN           | 1838.9163 |
| sp Q9Y2L1 RRP44_HUMAN          | 2508.1227 |
| sp O00159 MYO1C_HUMAN          | 1459.662  |
| sp P05362 ICAM1_HUMAN          | 1349.6939 |
| sp P08670 VIME_HUMAN           | 2253.1893 |
| sp Q16777 H2A2C_HUMAN          | 1124.5462 |
| sp P10586 PTPRF_HUMAN          | 2457.2176 |
| sp P07195 LDHB_HUMAN           | 1500.7096 |
| sp P60174 TPIS_HUMAN           | 3443.7031 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P11021 BIP_HUMAN            | 1708.7767 |
| sp P36578 RL4_HUMAN            | 951.5389  |

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| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1490.7075 |
| sp P08670 VIME_HUMAN,sp P17661 | 1783.8224 |
| sp P23921 RIR1_HUMAN           | 2504.2911 |
| sp P24311 COX7B_HUMAN          | 1111.5298 |
| sp P31948 STIP1_HUMAN          | 3708.7478 |
| sp P62917 RL8_HUMAN            | 1210.6346 |
| sp O95782 AP2A1_HUMAN          | 1779.8792 |
| sp P27797 CALR_HUMAN           | 1467.6882 |
| sp P06733 ENOA_HUMAN           | 2939.4036 |
| sp Q96SI9 STRBP_HUMAN,sp Q1290 | 1525.7923 |
| sp P17987 TCPA_HUMAN           | 4072.9787 |
| sp P31948 STIP1_HUMAN          | 1278.5477 |
| sp P58107 EPIPL_HUMAN          | 4270.1732 |
| sp Q14118 DAG1_HUMAN           | 1861.9574 |
| sp Q08J23 NSUN2_HUMAN          | 2472.0805 |
| sp P32004 L1CAM_HUMAN          | 2017.8986 |
| sp P62937 PPIA_HUMAN           | 2294.1219 |
| sp P10586 PTPRF_HUMAN          | 1778.8298 |
| sp P33176 KINH_HUMAN           | 1249.6303 |
| sp P26640 SYVC_HUMAN           | 1069.5193 |
| sp P08195 4F2_HUMAN            | 2276.278  |
| sp P62917 RL8_HUMAN            | 1210.6346 |
| sp Q5VWI1 TCRGL_HUMAN,sp O147  | 1814.8475 |
| sp P11142 HSP7C_HUMAN          | 1603.7453 |
| sp P26599 PTBP1_HUMAN          | 1057.5808 |
| sp O60884 DNJA2_HUMAN          | 3761.8425 |
| sp Q15149 PLEC_HUMAN           | 1061.5618 |
| sp Q15149 PLEC_HUMAN           | 1233.6506 |
| sp Q9Y624 JAM1_HUMAN           | 2041.9051 |
| sp Q15942 ZYX_HUMAN            | 4290.0002 |
| sp Q8NEY8 PPHLN_HUMAN          | 1441.6262 |
| sp P17812 PYRG1_HUMAN          | 3578.706  |
| sp Q9P2J5 SYLC_HUMAN           | 2438.2264 |
| sp P04083 ANXA1_HUMAN          | 2530.1244 |
| sp Q15149 PLEC_HUMAN           | 1239.6459 |
| sp P04083 ANXA1_HUMAN          | 1409.6721 |
| sp P08397 HEM3_HUMAN           | 2016.9694 |
| sp Q9GZZ1 NAA50_HUMAN          | 2136.0707 |
| sp Q8WTV0 SCRB1_HUMAN          | 2085.9717 |
| sp P55327 TPD52_HUMAN          | 2552.3221 |
| sp P10412 H14_HUMAN            | 1307.7197 |
| sp P31327 CPSM_HUMAN           | 3066.5047 |
| sp P62280 RS11_HUMAN           | 2538.2748 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1783.748  |
| sp P68366 TBA4A_HUMAN          | 2753.2028 |
| sp P21291 CSRP1_HUMAN          | 1287.5455 |

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| sp P15311 EZRI_HUMAN,sp P26038 | 1739.8883 |
| sp P48729 KC1A_HUMAN           | 1714.8566 |
| sp P62987 RL40_HUMAN,sp P62979 | 1461.7538 |
| sp Q9NV06 DCA13_HUMAN          | 2134.9953 |
| sp P20839 IMDH1_HUMAN          | 2824.3966 |
| sp Q9Y639 NPTN_HUMAN           | 3480.4775 |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp Q13112 CAF1B_HUMAN          | 1496.726  |
| sp P20700 LMNB1_HUMAN          | 1195.6449 |
| sp P10412 H14_HUMAN            | 1022.5397 |
| sp P10412 H14_HUMAN            | 1134.6397 |
| sp P34897 GLYM_HUMAN           | 2188.1164 |
| sp P41252 SYIC_HUMAN           | 1176.5815 |
| sp Q13547 HDAC1_HUMAN          | 1654.8137 |
| sp P42766 RL35_HUMAN           | 1549.7736 |
| sp P62805 H4_HUMAN             | 2018.1273 |
| sp P28482 MK01_HUMAN           | 1522.778  |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp Q08211 DHX9_HUMAN           | 1382.6103 |
| sp Q14118 DAG1_HUMAN           | 3790.7744 |
| sp Q8N257 H2B3B_HUMAN,sp P068  | 1475.682  |
| sp P35232 PHB_HUMAN            | 3236.6412 |
| sp O00629 IMA3_HUMAN           | 3998.9684 |
| sp P40926 MDHM_HUMAN           | 1797.8897 |
| sp Q15149 PLEC_HUMAN           | 1566.7103 |
| sp P23284 PPIB_HUMAN           | 1492.643  |
| sp P05556 ITB1_HUMAN           | 1789.892  |
| sp Q13085 ACACA_HUMAN          | 3257.5373 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1440.746  |
| sp Q96HS1 PGAM5_HUMAN          | 1531.7089 |
| sp Q49A26 GLYR1_HUMAN          | 1688.8562 |
| sp P11940 PABP1_HUMAN          | 2015.9986 |
| sp P51531 SMCA2_HUMAN,sp P515  | 1629.7246 |
| sp P21333 FLNA_HUMAN           | 1213.6343 |
| sp Q9Y4D7 PLXD1_HUMAN          | 2653.321  |
| sp O75369 FLNB_HUMAN           | 2797.4399 |
| sp Q9Y617 SERC_HUMAN           | 1830.9437 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1062.473  |
| sp P07237 PDIA1_HUMAN          | 1620.8035 |
| sp P04792 HSPB1_HUMAN          | 1839.8487 |
| sp Q01813 PFKAP_HUMAN          | 1189.5728 |
| sp P45880 VDAC2_HUMAN          | 1874.9374 |
| sp O43395 PRPF3_HUMAN          | 1765.8483 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P07195 LDHB_HUMAN           | 1103.5724 |
| sp Q9NXA8 SIR5_HUMAN           | 2347.1345 |
| sp Q8TC12 RDH11_HUMAN          | 2511.2605 |

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| sp Q6YHK3 CD109_HUMAN          | 1457.6939 |
| sp P40429 RL13A_HUMAN          | 1547.9035 |
| sp P16401 H15_HUMAN            | 1093.5768 |
| sp Q12965 MYO1E_HUMAN          | 1261.6415 |
| sp O15143 ARC1B_HUMAN          | 1403.6834 |
| sp P63244 RACK1_HUMAN          | 1441.7024 |
| sp Q8NCA5 FA98A_HUMAN,sp Q52L  | 2508.1856 |
| sp Q96TA1 NIBA2_HUMAN          | 2679.2969 |
| sp Q14690 RRP5_HUMAN           | 2326.2031 |
| sp P29401 TKT_HUMAN            | 2174.0644 |
| sp Q99798 ACON_HUMAN           | 1712.8807 |
| sp P12270 TPR_HUMAN            | 1589.8413 |
| sp P0DPI2 GAL3A_HUMAN,sp A0A0E | 1179.5706 |
| sp P62424 RL7A_HUMAN           | 1568.7583 |
| sp Q9H4M9 EHD1_HUMAN           | 2469.2904 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P30101 PDIA3_HUMAN          | 1711.7842 |
| sp Q86VP6 CAND1_HUMAN          | 3221.5955 |
| sp P08621 RU17_HUMAN           | 1555.6362 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1446.7355 |
| sp P62917 RL8_HUMAN            | 1306.7245 |
| sp P35221 CTNA1_HUMAN          | 3194.607  |
| sp O43592 XPOT_HUMAN           | 2857.4149 |
| sp Q99757 THIOM_HUMAN          | 3161.5063 |
| sp O14617 AP3D1_HUMAN          | 1733.9134 |
| sp P18124 RL7_HUMAN            | 1516.7198 |
| sp P23284 PPIB_HUMAN           | 1501.8181 |
| sp Q9Y2A7 NCKP1_HUMAN          | 2364.2074 |
| sp Q9BS26 ERP44_HUMAN          | 4712.144  |
| sp P17301 ITA2_HUMAN           | 1326.584  |
| sp Q14157 UBP2L_HUMAN          | 3311.5416 |
| sp Q14432 PDE3A_HUMAN          | 2320.2175 |
| sp P84098 RL19_HUMAN           | 1119.5673 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1598.8226 |
| sp Q00610 CLH1_HUMAN           | 1462.7205 |
| sp P08758 ANXA5_HUMAN          | 2231.0991 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 2352.1671 |
| sp O75475 PSIP1_HUMAN          | 1348.6987 |
| sp P26640 SYVC_HUMAN           | 4593.1502 |
| sp Q9Y2Q3 GSTK1_HUMAN          | 2281.1049 |
| sp Q6WCQ1 MPRIP_HUMAN          | 2583.2387 |
| sp P04406 G3P_HUMAN            | 1420.7562 |
| sp Q9UKD2 MRT4_HUMAN           | 2098.9556 |
| sp Q09666 AHNK_HUMAN           | 1750.8811 |
| sp Q09666 AHNK_HUMAN           | 1356.6206 |
| sp P43243 MATR3_HUMAN          | 2526.1083 |
| sp Q9BRP8 PYM1_HUMAN           | 3700.8625 |

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| sp P13639 EF2_HUMAN            | 1699.7916 |
| sp P82933 RT09_HUMAN           | 1807.9145 |
| sp Q9Y3F4 STRAP_HUMAN          | 2616.2418 |
| sp Q13740 CD166_HUMAN          | 3540.5991 |
| sp P16401 H15_HUMAN,sp P10412  | 1182.5881 |
| sp P23396 RS3_HUMAN            | 1220.6077 |
| sp Q08752 PPID_HUMAN           | 1775.9683 |
| sp Q8N684 CPSF7_HUMAN          | 1979.0034 |
| sp P02786 TFR1_HUMAN           | 2407.0928 |
| sp Q9P258 RCC2_HUMAN           | 1264.5796 |
| sp P46940 IQGA1_HUMAN          | 1218.6245 |
| sp O75369 FLNB_HUMAN           | 3464.718  |
| sp P53396 ACLY_HUMAN           | 2099.0746 |
| sp P06733 ENOA_HUMAN           | 1320.6198 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp O75534 CSDE1_HUMAN          | 1900.8816 |
| sp Q9NZ01 TECR_HUMAN           | 2180.0824 |
| sp Q92508 PIEZ1_HUMAN          | 2133.028  |
| sp P62277 RS13_HUMAN           | 2018.0361 |
| sp Q13619 CUL4A_HUMAN,sp Q136  | 1544.6929 |
| sp P26640 SYVC_HUMAN           | 3093.4648 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1467.7544 |
| sp Q15345 LRC41_HUMAN          | 1911.0102 |
| sp P55265 DSRAD_HUMAN          | 1596.8161 |
| sp Q96AG4 LRC59_HUMAN          | 2920.4164 |
| sp P55060 XPO2_HUMAN           | 1155.5673 |
| sp P62304 RUXE_HUMAN           | 3335.5214 |
| sp O60888 CUTA_HUMAN           | 2500.2672 |
| sp P42704 LPPRC_HUMAN          | 1704.793  |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1883.7884 |
| sp P09012 SNRPA_HUMAN          | 2134.0695 |
| sp P48960 CD97_HUMAN           | 2918.4372 |
| sp P83916 CBX1_HUMAN           | 1611.7125 |
| sp P52597 HNRPF_HUMAN          | 1542.8042 |
| sp P17301 ITA2_HUMAN           | 1502.8093 |
| sp P22234 PUR6_HUMAN           | 2297.1396 |
| sp Q5HYI8 RABL3_HUMAN          | 1504.6834 |
| sp O75083 WDR1_HUMAN           | 1918.9101 |
| sp A1L0T0 ILVBL_HUMAN          | 1661.9101 |
| sp P62701 RS4X_HUMAN           | 1363.6884 |
| sp O75694 NU155_HUMAN          | 3282.4202 |
| sp P62277 RS13_HUMAN           | 1924.9101 |
| sp P04406 G3P_HUMAN            | 2309.1652 |
| sp Q92598 HS105_HUMAN          | 2893.28   |
| sp P49207 RL34_HUMAN           | 1223.6438 |
| sp P61927 RL37_HUMAN           | 1124.5978 |
| sp P63241 IF5A1_HUMAN,sp Q9GZv | 1570.7926 |



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| sp P16401 H15_HUMAN,sp P10412  | 1233.7081 |
| sp Q92688 AN32B_HUMAN          | 1857.9949 |
| sp Q9H0A0 NAT10_HUMAN          | 2210.0103 |
| sp P06748 NPM_HUMAN            | 3165.6995 |
| sp P43121 MUC18_HUMAN          | 1451.6463 |
| sp Q15691 MARE1_HUMAN          | 1390.7205 |
| sp Q6GMV3 PTRD1_HUMAN          | 4165.0289 |
| sp P30043 BLVRB_HUMAN          | 1748.8668 |
| sp Q9NV96 CC50A_HUMAN          | 1487.7369 |
| sp P20700 LMNB1_HUMAN          | 2218.0365 |
| sp P18621 RL17_HUMAN           | 1097.5254 |
| sp Q9ULF5 S39AA_HUMAN          | 2425.1835 |
| sp O75380 NDUS6_HUMAN          | 2591.1776 |
| sp P32004 L1CAM_HUMAN          | 2033.8935 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1133.5102 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1822.8659 |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2579.0904 |
| sp P62701 RS4X_HUMAN           | 1363.6884 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3345.6875 |
| sp P12268 IMDH2_HUMAN          | 2282.1543 |
| sp Q14697 GANAB_HUMAN          | 2473.354  |
| sp Q7Z794 K2C1B_HUMAN,sp O956  | 1278.6245 |
| sp Q5VYK3 ECM29_HUMAN          | 3683.8182 |
| sp O15067 PUR4_HUMAN           | 1922.9064 |
| sp Q6UVK1 CSPG4_HUMAN          | 1360.6987 |
| sp Q96KR1 ZFR_HUMAN,sp Q96SI9  | 1239.5785 |
| sp Q01813 PFKAP_HUMAN          | 1189.5728 |
| sp P11142 HSP7C_HUMAN          | 1823.9377 |
| sp P06753 TPM3_HUMAN,sp P0949  | 1639.8305 |
| sp Q9H6Z4 RANB3_HUMAN          | 2461.3329 |
| sp P61020 RAB5B_HUMAN,sp P2032 | 1958.0183 |
| sp Q96P16 RPR1A_HUMAN,sp Q9NC  | 2900.4781 |
| sp Q96T37 RBM15_HUMAN          | 3003.3246 |
| sp Q16891 MIC60_HUMAN          | 3165.6128 |
| sp Q9H3P7 GCP60_HUMAN          | 3713.7494 |
| sp P55265 DSRAD_HUMAN          | 2236.08   |
| sp Q09666 AHNK_HUMAN           | 1418.6111 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 997.4941  |
| sp P32004 L1CAM_HUMAN          | 2270.1154 |
| sp P21796 VDAC1_HUMAN          | 1920.933  |
| sp P49411 EFTU_HUMAN           | 4760.1516 |
| sp O75533 SF3B1_HUMAN          | 3582.7341 |
| sp P84098 RL19_HUMAN           | 1373.6108 |
| sp Q8N556 AFAP1_HUMAN          | 1492.8137 |
| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp P39019 RS19_HUMAN           | 1606.741  |

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| sp P21291 CSRP1_HUMAN          | 1288.6048 |
| sp P27797 CALR_HUMAN           | 1343.6874 |
| sp O00571 DDX3X_HUMAN,sp O155  | 1233.57   |
| sp Q9NZB2 F120A_HUMAN          | 2559.3155 |
| sp P04075 ALDOA_HUMAN          | 3537.6107 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2491.2707 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1384.6735 |
| sp O43795 MYO1B_HUMAN          | 3178.5724 |
| sp P02786 TFR1_HUMAN           | 2596.3061 |
| sp Q14204 DYHC1_HUMAN          | 2404.1335 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp Q13813 SPTN1_HUMAN          | 1435.6692 |
| sp P53999 TCP4_HUMAN           | 1447.8035 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |
| sp P06748 NPM_HUMAN            | 1219.5146 |
| sp P26599 PTBP1_HUMAN          | 1057.5808 |
| sp P16401 H15_HUMAN            | 1065.5819 |
| sp P50991 TCPD_HUMAN           | 1498.8395 |
| sp P08195 4F2_HUMAN            | 2276.278  |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp P43121 MUC18_HUMAN          | 1470.7402 |
| sp P48556 PSMD8_HUMAN          | 4525.1714 |
| sp P62244 RS15A_HUMAN          | 1339.6554 |
| sp P55265 DSRAD_HUMAN          | 2852.3902 |
| sp P26639 SYTC_HUMAN           | 2784.3606 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1133.5102 |
| sp P26641 EF1G_HUMAN           | 1248.6139 |
| sp P49207 RL34_HUMAN           | 1739.8083 |
| sp P07195 LDHB_HUMAN           | 3484.7193 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp P38919 IF4A3_HUMAN          | 3850.9525 |
| sp Q9BQG0 MBB1A_HUMAN          | 1969.9745 |
| sp O00116 ADAS_HUMAN           | 2901.4405 |
| sp Q13200 PSMD2_HUMAN          | 2241.0637 |
| sp P62917 RL8_HUMAN            | 1253.6768 |
| sp P22102 PUR2_HUMAN           | 1210.6346 |
| sp Q8TDD1 DDX54_HUMAN          | 1336.6888 |
| sp O95758 PTBP3_HUMAN          | 3204.588  |
| sp Q09666 AHNK_HUMAN           | 1789.892  |
| sp P02786 TFR1_HUMAN           | 2282.0347 |
| sp P10809 CH60_HUMAN           | 1382.7479 |
| sp P22314 UBA1_HUMAN           | 3941.9786 |
| sp P00558 PGK1_HUMAN           | 3136.478  |
| sp P10586 PTPRF_HUMAN          | 2733.2408 |
| sp P00491 PNPH_HUMAN           | 2382.1143 |
| sp P06748 NPM_HUMAN            | 1557.7345 |
| sp P53621 COPA_HUMAN           | 1874.9738 |

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| sp Q15233 NONO_HUMAN           | 1908.8748 |
| sp P38919 IF4A3_HUMAN          | 1613.7362 |
| sp P27797 CALR_HUMAN           | 2044.9266 |
| sp P61981 1433G_HUMAN,sp P631C | 1699.8893 |
| sp P26599 PTBP1_HUMAN          | 1033.4829 |
| sp P38159 RBMX_HUMAN           | 1943.9589 |
| sp Q9H6Z4 RANB3_HUMAN          | 2510.2554 |
| sp P62917 RL8_HUMAN            | 1253.6768 |
| sp Q6YHK3 CD109_HUMAN          | 1133.5757 |
| sp Q9BQ39 DDX50_HUMAN,sp Q9N   | 1159.5873 |
| sp P62753 RS6_HUMAN            | 1922.9585 |
| sp Q6YHK3 CD109_HUMAN          | 1399.7347 |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp P10412 H14_HUMAN            | 1235.6874 |
| sp P35659 DEK_HUMAN            | 2113.1394 |
| sp P13987 CD59_HUMAN           | 1562.7188 |
| sp O43143 DHX15_HUMAN          | 2075.0146 |
| sp P46013 KI67_HUMAN           | 1130.5833 |
| sp Q13813 SPTN1_HUMAN          | 1634.8556 |
| sp P06733 ENOA_HUMAN           | 1224.6463 |
| sp Q00610 CLH1_HUMAN           | 2269.1743 |
| sp P62888 RL30_HUMAN           | 3637.6817 |
| sp P36871 PGM1_HUMAN           | 1285.5476 |
| sp P23246 SFPQ_HUMAN           | 1441.7201 |
| sp Q15041 AR6P1_HUMAN          | 1918.881  |
| sp O15042 SR140_HUMAN          | 1697.8599 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1928.9091 |
| sp P13010 XRCC5_HUMAN          | 1590.8617 |
| sp Q92598 HS105_HUMAN          | 1796.921  |
| sp Q15029 U5S1_HUMAN           | 1289.6728 |
| sp Q15149 PLEC_HUMAN           | 1552.7733 |
| sp Q9Y5B9 SP16H_HUMAN          | 1993.9455 |
| sp P30044 PRDX5_HUMAN          | 3438.7282 |
| sp P49368 TCPG_HUMAN           | 2820.4505 |
| sp O75131 CPNE3_HUMAN          | 2396.1932 |
| sp Q7KZF4 SND1_HUMAN           | 1070.6012 |
| sp P62258 1433E_HUMAN          | 2596.2068 |
| sp P49327 FAS_HUMAN            | 2697.2969 |
| sp Q5JRA6 TGO1_HUMAN           | 1221.5778 |
| sp P04406 G3P_HUMAN            | 2309.1652 |
| sp P04844 RPN2_HUMAN           | 2349.1237 |
| sp Q96JB5 CK5P3_HUMAN          | 2412.0441 |
| sp P17987 TCPA_HUMAN           | 1729.9251 |
| sp P52272 HNRPM_HUMAN          | 1312.6663 |
| sp P42704 LPPRC_HUMAN          | 1611.8178 |
| sp Q92616 GCN1_HUMAN           | 1705.9614 |
| sp P36542 ATPG_HUMAN           | 1796.8549 |

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| sp Q9Y5B9 SP16H_HUMAN          | 2535.2718 |
| sp Q9UKN8 TF3C4_HUMAN          | 2947.4464 |
| sp P30041 PRDX6_HUMAN          | 1628.8774 |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp Q9BWF3 RBM4_HUMAN           | 2053.9739 |
| sp P27816 MAP4_HUMAN           | 2013.9868 |
| sp Q01813 PFKAP_HUMAN          | 1189.5728 |
| sp O75534 CSDE1_HUMAN          | 2052.0025 |
| sp Q14126 DSG2_HUMAN           | 2755.2838 |
| sp P62424 RL7A_HUMAN           | 2337.0795 |
| sp Q00839 HNRPU_HUMAN          | 1572.7784 |
| sp P16403 H12_HUMAN            | 970.5084  |
| sp P00505 AATM_HUMAN           | 2509.0631 |
| sp Q8NE01 CNNM3_HUMAN          | 2844.4002 |
| sp Q15046 SYK_HUMAN            | 2107.0772 |
| sp P00558 PGK1_HUMAN           | 2724.1466 |
| sp P36578 RL4_HUMAN            | 1476.6885 |
| sp P30044 PRDX5_HUMAN          | 1917.9295 |
| sp P31689 DNJA1_HUMAN          | 1898.8435 |
| sp P16401 H15_HUMAN,rev_sp P16 | 1205.6768 |
| sp P07900 HS90A_HUMAN,sp P0823 | 1215.6248 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1360.7715 |
| sp P35579 MYH9_HUMAN           | 1200.606  |
| sp P84098 RL19_HUMAN           | 1119.5673 |
| sp P0CW18 PRS56_HUMAN          | 1415.7197 |
| sp P42704 LPPRC_HUMAN          | 2794.4218 |
| sp P10809 CH60_HUMAN           | 2538.2822 |
| sp P11142 HSP7C_HUMAN          | 2228.0195 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2539.1901 |
| sp P55265 DSRAD_HUMAN          | 2575.1505 |
| sp P07900 HS90A_HUMAN,sp Q58F6 | 1126.5805 |
| sp P02786 TFR1_HUMAN           | 4290.1307 |
| sp P14174 MIF_HUMAN            | 6700.2789 |
| sp P10412 H14_HUMAN            | 1307.7197 |
| sp Q9H0D6 XRN2_HUMAN           | 2088.0316 |
| sp P62829 RL23_HUMAN           | 1799.8797 |
| sp Q7Z2Z2 EFL1_HUMAN           | 1975.0455 |
| sp P61764 STXB1_HUMAN          | 2720.2541 |
| sp P31327 CPSM_HUMAN           | 1159.551  |
| sp Q00341 VIGLN_HUMAN          | 2012.0215 |
| sp P21796 VDAC1_HUMAN          | 1640.8086 |
| sp P31327 CPSM_HUMAN           | 2967.5553 |
| sp Q15233 NONO_HUMAN           | 1832.8442 |
| sp P49790 NU153_HUMAN          | 1764.8002 |
| sp P08195 4F2_HUMAN            | 1460.7399 |
| sp Q6ZMR3 LDH6A_HUMAN,sp P003  | 1114.5407 |
| sp P61604 CH10_HUMAN           | 1231.6237 |

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| sp P62269 RS18_HUMAN           | 1675.7995 |
| sp P53396 ACLY_HUMAN           | 2006.0572 |
| sp O95372 LYPA2_HUMAN          | 1301.6616 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp Q00325 MPCP_HUMAN           | 1669.8352 |
| sp P50895 BCAM_HUMAN           | 1837.7649 |
| sp P06576 ATPB_HUMAN           | 2300.0743 |
| sp P37108 SRP14_HUMAN          | 1392.7137 |
| sp P40939 ECHA_HUMAN           | 1823.9166 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1760.8325 |
| sp Q12906 ILF3_HUMAN           | 3022.4641 |
| sp P10809 CH60_HUMAN           | 1232.6037 |
| sp P02786 TFR1_HUMAN           | 1235.651  |
| sp Q9H7B2 RPF2_HUMAN           | 1792.8016 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P07737 PROF1_HUMAN          | 1919.9113 |
| sp P49327 FAS_HUMAN            | 2788.3014 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 998.5033  |
| sp P14625 ENPL_HUMAN           | 2058.9608 |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp P39656 OST48_HUMAN          | 1909.0309 |
| sp P54278 PMS2_HUMAN           | 2391.084  |
| sp Q9Y3F4 STRAP_HUMAN          | 2750.3763 |
| sp P21333 FLNA_HUMAN           | 2742.2926 |
| sp P55072 TERA_HUMAN           | 1726.9519 |
| sp P78527 PRKDC_HUMAN          | 1220.6513 |
| sp Q13332 PTPRS_HUMAN          | 2703.2354 |
| sp Q09666 AHNK_HUMAN           | 1376.5893 |
| sp P18621 RL17_HUMAN           | 2341.126  |
| sp Q8N0Y7 PGAM4_HUMAN,sp P18   | 2884.265  |
| sp P16403 H12_HUMAN            | 1409.7878 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp Q58FG0 HS905_HUMAN,sp P079  | 2103.0677 |
| sp Q969X6 UTP4_HUMAN           | 1697.8009 |
| sp P31948 STIP1_HUMAN          | 2562.1908 |
| sp Q01650 LAT1_HUMAN           | 2412.1227 |
| sp P62633 CNBP_HUMAN           | 2045.8142 |
| sp P20700 LMNB1_HUMAN          | 2431.1656 |
| sp Q8NCW5 NNRE_HUMAN           | 3568.8065 |
| sp Q63HN8 RN213_HUMAN          | 1837.0019 |
| sp Q14204 DYHC1_HUMAN          | 1776.8101 |
| sp Q9BT78 CSN4_HUMAN           | 2743.3956 |
| sp P21333 FLNA_HUMAN           | 3425.5293 |
| sp P14384 CBPM_HUMAN           | 3410.689  |
| sp P13010 XRCC5_HUMAN          | 1487.762  |
| sp Q13813 SPTN1_HUMAN          | 2054.9756 |
| sp P78527 PRKDC_HUMAN          | 1562.7577 |

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| sp Q9H6B4 CLMP_HUMAN           | 3809.8207 |
| sp O75694 NU155_HUMAN          | 2381.136  |
| sp P49792 RBP2_HUMAN           | 3199.4624 |
| sp O60264 SMCA5_HUMAN          | 1673.8162 |
| sp O95573 ACSL3_HUMAN          | 2148.0528 |
| sp P35613 BASI_HUMAN           | 2034.0786 |
| sp P23396 RS3_HUMAN            | 2166.0633 |
| sp Q8NC51 PAIRB_HUMAN          | 1111.5662 |
| sp P40937 RFC5_HUMAN           | 2392.1919 |
| sp Q96AG4 LRC59_HUMAN          | 1867.0455 |
| sp Q9Y617 SERC_HUMAN           | 2234.1834 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1501.7637 |
| sp Q8NFJ5 RAI3_HUMAN           | 4971.2788 |
| sp P50991 TCPD_HUMAN           | 3574.7899 |
| sp P27816 MAP4_HUMAN           | 1422.6739 |
| sp P16152 CBR1_HUMAN           | 1584.7454 |
| sp P04075 ALDOA_HUMAN          | 1496.7623 |
| sp Q7Z5L9 I2BP2_HUMAN,sp Q9H1E | 3031.3051 |
| sp P10809 CH60_HUMAN           | 1232.6037 |
| sp Q6RFH5 WDR74_HUMAN          | 3381.6452 |
| sp P08238 HS90B_HUMAN,sp Q58FI | 1369.7201 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P08238 HS90B_HUMAN,sp P1462 | 1740.853  |
| sp P07900 HS90A_HUMAN          | 2195.0205 |
| sp Q09666 AHNK_HUMAN           | 1595.7984 |
| sp Q99623 PHB2_HUMAN           | 1732.8342 |
| sp P09874 PARP1_HUMAN          | 2984.426  |
| sp P26599 PTBP1_HUMAN          | 3963.0054 |
| sp Q01813 PFKAP_HUMAN          | 1189.5728 |
| sp Q9BTX1 NDC1_HUMAN           | 2534.215  |
| sp P61978 HNRPK_HUMAN          | 1249.6667 |
| sp P02786 TFR1_HUMAN           | 1235.651  |
| sp O43707 ACTN4_HUMAN          | 3008.5091 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1133.5102 |
| sp Q9Y4D7 PLXD1_HUMAN          | 3654.5054 |
| sp P04406 G3P_HUMAN            | 3145.4736 |
| sp P78527 PRKDC_HUMAN          | 1654.7814 |
| sp Q14152 EIF3A_HUMAN          | 1350.6317 |
| sp P07195 LDHB_HUMAN           | 1103.5724 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1928.9091 |
| sp P23528 COF1_HUMAN           | 1633.8022 |
| sp O76021 RL1D1_HUMAN          | 1694.841  |
| sp Q9UNX4 WDR3_HUMAN           | 2519.3206 |
| sp P20290 BTF3_HUMAN           | 3410.6565 |
| sp O43175 SERA_HUMAN           | 3148.6802 |
| sp P52597 HNRPF_HUMAN          | 1698.9053 |
| sp Q08945 SSRP1_HUMAN          | 1509.6888 |

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| sp Q71UI9 H2AV_HUMAN,sp POCOS! | 2065.132  |
| sp P14618 KPYM_HUMAN           | 2603.2802 |
| sp Q14118 DAG1_HUMAN           | 3688.7104 |
| sp P05787 K2C8_HUMAN           | 1537.7736 |
| sp Q9UHD1 CHRD1_HUMAN          | 2094.0456 |
| sp Q9BPX3 CND3_HUMAN           | 2197.1604 |
| sp P19338 NUCL_HUMAN           | 2027.8749 |
| sp P18084 ITB5_HUMAN           | 2284.8718 |
| sp Q99623 PHB2_HUMAN           | 1716.8393 |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp O00592 PODXL_HUMAN          | 1446.7718 |
| sp P07814 SYEP_HUMAN           | 3496.6245 |
| sp P22392 NDKB_HUMAN           | 1906.9061 |
| sp P46940 IQGA1_HUMAN          | 1515.7821 |
| sp P62826 RAN_HUMAN            | 1284.5986 |
| sp Q9UKV3 ACINU_HUMAN          | 1961.9555 |
| sp P18621 RL17_HUMAN           | 1097.5254 |
| sp P49257 LMAN1_HUMAN          | 3283.5891 |
| sp P43243 MATR3_HUMAN          | 1463.762  |
| sp Q96DA6 TIM14_HUMAN          | 2121.0565 |
| sp P00558 PGK1_HUMAN           | 3136.478  |
| sp Q16832 DDR2_HUMAN           | 2241.0702 |
| sp Q9Y6K9 NEMO_HUMAN           | 2782.3715 |
| sp Q16762 THTR_HUMAN           | 1669.8675 |
| sp P58107 EPIPL_HUMAN          | 3674.8461 |
| sp P17844 DDX5_HUMAN           | 1774.856  |
| sp P50395 GDIB_HUMAN           | 2435.125  |
| sp Q15785 TOM34_HUMAN          | 2197.1453 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp O76094 SRP72_HUMAN          | 1796.8615 |
| sp Q15233 NONO_HUMAN           | 2010.0283 |
| sp Q92616 GCN1_HUMAN           | 1516.7232 |
| sp O95208 EPN2_HUMAN,sp Q8IYW  | 1335.5956 |
| sp P04083 ANXA1_HUMAN          | 1353.6888 |
| sp P35579 MYH9_HUMAN           | 1469.7548 |
| sp O75340 PDCD6_HUMAN          | 2539.1649 |
| sp P52907 CAZA1_HUMAN          | 1358.6619 |
| sp P30084 ECHM_HUMAN           | 1747.8682 |
| sp P54819 KAD2_HUMAN           | 1785.9373 |
| sp P08243 ASNS_HUMAN           | 1707.9196 |
| sp O60664 PLIN3_HUMAN          | 3276.6626 |
| sp Q13547 HDAC1_HUMAN          | 2397.1826 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1062.473  |
| sp Q12788 TBL3_HUMAN           | 2761.3058 |
| sp P49207 RL34_HUMAN           | 1612.8712 |
| sp Q15149 PLEC_HUMAN           | 1317.7041 |
| sp P19338 NUCL_HUMAN           | 1356.7289 |

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| sp P06733 ENOA_HUMAN           | 1268.5561 |
| sp P31947 1433S_HUMAN          | 1813.9323 |
| sp Q07020 RL18_HUMAN           | 1758.9013 |
| sp P55084 ECHB_HUMAN           | 2458.1839 |
| sp P02786 TFR1_HUMAN           | 2571.9941 |
| sp A6NHR9 SMHD1_HUMAN          | 2015.0728 |
| sp Q86YQ8 CPNE8_HUMAN          | 2319.1457 |
| sp P07910 HNRPC_HUMAN,sp P0DM  | 1667.8043 |
| sp P17858 PFKAL_HUMAN          | 2601.2446 |
| sp P50990 TCPQ_HUMAN           | 2402.1974 |
| sp P12270 TPR_HUMAN            | 1219.6561 |
| sp P49454 CENPF_HUMAN          | 3039.3707 |
| sp P08708 RS17_HUMAN           | 1380.6925 |
| sp P26641 EF1G_HUMAN           | 1571.8559 |
| sp O60361 NDK8_HUMAN,sp P2239  | 1680.7955 |
| sp Q9NZ32 ARP10_HUMAN          | 3340.753  |
| sp P07237 PDIA1_HUMAN          | 1482.7103 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 798.3872  |
| sp Q14232 EI2BA_HUMAN          | 1655.7977 |
| sp P13010 XRCC5_HUMAN          | 2695.2362 |
| sp O00410 IPO5_HUMAN           | 1638.7638 |
| sp P62851 RS25_HUMAN           | 1053.607  |
| sp P51610 HCFC1_HUMAN          | 1323.6095 |
| sp P60900 PSA6_HUMAN           | 2623.3282 |
| sp P22234 PUR6_HUMAN           | 1343.647  |
| sp P31930 QCR1_HUMAN           | 4623.289  |
| sp Q6P996 PDXD1_HUMAN          | 2558.2976 |
| sp P18583 SON_HUMAN            | 1923.0313 |
| sp P14618 KPYM_HUMAN           | 2753.3007 |
| sp P56211 ARP19_HUMAN          | 1867.8853 |
| sp Q01082 SPTB2_HUMAN          | 1802.8323 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 894.4447  |
| sp P35052 GPC1_HUMAN           | 1636.7879 |
| sp Q92841 DDX17_HUMAN          | 2514.2537 |
| sp O75369 FLNB_HUMAN           | 2368.1329 |
| sp P02786 TFR1_HUMAN           | 2378.1219 |
| sp Q14204 DYHC1_HUMAN          | 2092.0953 |
| sp Q92804 RBP56_HUMAN          | 2331.178  |
| sp Q9UNX3 RL26L_HUMAN,sp P612! | 2182.1495 |
| sp Q14847 LASP1_HUMAN          | 1542.6925 |
| sp P05187 PPB1_HUMAN           | 2663.2173 |
| sp P53597 SUCA_HUMAN           | 1426.7391 |
| sp P16435 NCPR_HUMAN           | 1804.9108 |
| sp P52272 HNRPM_HUMAN          | 2393.1032 |
| sp Q07666 KHDR1_HUMAN          | 2322.011  |
| sp Q93088 BHMT1_HUMAN          | 4263.0558 |
| sp P18621 RL17_HUMAN           | 1550.7511 |



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| sp P14384 CBPM_HUMAN           | 3394.6941 |
| sp Q9BSJ8 ESYT1_HUMAN          | 1632.8107 |
| sp P13797 PLST_HUMAN           | 1779.8527 |
| sp Q86VP6 CAND1_HUMAN          | 1581.7999 |
| sp Q9NTJ3 SMC4_HUMAN           | 2027.9912 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1062.473  |
| sp P54886 P5CS_HUMAN           | 2468.186  |
| sp P11021 BIP_HUMAN            | 2012.0215 |
| sp P98160 PGBM_HUMAN           | 2968.4501 |
| sp O75521 ECI2_HUMAN           | 2073.9612 |
| sp P08865 RSSA_HUMAN           | 2969.4018 |
| sp P62314 SMD1_HUMAN           | 2710.4357 |
| sp P30048 PRDX3_HUMAN          | 2078.0466 |
| sp P08195 4F2_HUMAN            | 3724.7704 |
| sp P05386 RLA1_HUMAN           | 4133.0488 |
| sp Q13155 AIMP2_HUMAN          | 1602.8141 |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp Q8IVT2 MISP_HUMAN           | 2062.9556 |
| sp Q96DG6 CMBL_HUMAN           | 3010.5903 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1455.6419 |
| sp P51553 IDH3G_HUMAN          | 2830.4146 |
| sp Q9UQE7 SMC3_HUMAN           | 2184.0223 |
| sp P42704 LPPRC_HUMAN          | 1760.8192 |
| sp P62987 RL40_HUMAN,sp P62979 | 1477.7487 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P21291 CSRP1_HUMAN          | 1278.6357 |
| sp P40939 ECHA_HUMAN           | 3881.9575 |
| sp P22695 QCR2_HUMAN           | 2659.2667 |
| sp P00491 PNPH_HUMAN           | 2382.1143 |
| sp Q09666 AHNK_HUMAN           | 1315.7136 |
| sp P09874 PARP1_HUMAN          | 2984.426  |
| sp P27816 MAP4_HUMAN           | 2185.1127 |
| sp P35637 FUS_HUMAN            | 2464.9938 |
| sp Q15149 PLEC_HUMAN           | 1714.8526 |
| sp P22626 ROA2_HUMAN           | 1662.8213 |
| sp Q92841 DDX17_HUMAN          | 2179.9051 |
| sp P27824 CALX_HUMAN           | 2738.3639 |
| sp P16401 H15_HUMAN,rev_sp P16 | 1205.6768 |
| sp Q9UHB6 LIMA1_HUMAN          | 1235.6146 |
| sp P82933 RT09_HUMAN           | 1739.7897 |
| sp P14625 ENPL_HUMAN           | 2738.3163 |
| sp Q9H0S4 DDX47_HUMAN          | 2181.0637 |
| sp P38919 IF4A3_HUMAN          | 2259.9525 |
| sp P10412 H14_HUMAN            | 1307.7197 |
| sp P21796 VDAC1_HUMAN          | 2299.206  |
| sp P60842 IF4A1_HUMAN          | 1207.6125 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |

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| sp Q96CP2 FWCH2_HUMAN          | 3234.6278 |
| sp O94776 MTA2_HUMAN           | 1967.0007 |
| sp P78527 PRKDC_HUMAN          | 1122.5054 |
| sp Q12905 ILF2_HUMAN           | 3289.5878 |
| sp P62750 RL23A_HUMAN          | 1147.5986 |
| sp Q14118 DAG1_HUMAN           | 3790.7744 |
| sp P14618 KPYM_HUMAN           | 1428.6919 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P78527 PRKDC_HUMAN          | 1405.7678 |
| sp Q9BVA1 TBB2B_HUMAN,sp Q138  | 2352.1671 |
| sp P40939 ECHA_HUMAN           | 2029.9601 |
| sp Q13151 ROA0_HUMAN           | 2380.1124 |
| sp Q9UMR2 DD19B_HUMAN,sp Q9N   | 2076.964  |
| sp P27824 CALX_HUMAN           | 1639.7842 |
| sp P05783 K1C18_HUMAN          | 3547.5977 |
| sp P13498 CY24A_HUMAN          | 2886.4737 |
| sp P37268 FDFT_HUMAN           | 3100.4349 |
| sp P05787 K2C8_HUMAN           | 2727.2698 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1547.6708 |
| sp P51991 ROA3_HUMAN           | 2078.9797 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp Q9Y266 NUDC_HUMAN           | 1835.7495 |
| sp P05556 ITB1_HUMAN           | 1789.892  |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P35998 PRS7_HUMAN           | 1318.6782 |
| sp P06733 ENOA_HUMAN           | 2385.1812 |
| sp P08670 VIME_HUMAN           | 1504.6794 |
| sp Q02878 RL6_HUMAN            | 1595.8671 |
| sp Q9GZT3 SLIRP_HUMAN          | 2762.3677 |
| sp Q5JTH9 RRP12_HUMAN          | 2257.1671 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp Q01813 PFKAP_HUMAN          | 2741.3297 |
| sp Q14980 NUMA1_HUMAN          | 1192.5837 |
| sp P18621 RL17_HUMAN           | 1686.8036 |
| sp Q08J23 NSUN2_HUMAN          | 1541.766  |
| sp P22314 UBA1_HUMAN           | 1873.9727 |
| sp P31942 HNRH3_HUMAN          | 1660.7845 |
| sp P22234 PUR6_HUMAN           | 2297.1396 |
| sp P62258 1433E_HUMAN          | 3191.5445 |
| sp P50395 GDIB_HUMAN           | 3762.9819 |
| sp P09429 HMGB1_HUMAN          | 1081.5404 |
| sp P16152 CBR1_HUMAN           | 2026.9385 |
| sp P62750 RL23A_HUMAN          | 1147.5986 |
| sp O95678 K2C75_HUMAN,sp P0872 | 1168.5724 |
| sp Q12874 SF3A3_HUMAN          | 2167.0296 |
| sp P16435 NCPR_HUMAN           | 1804.9108 |
| sp Q2NL82 TSR1_HUMAN           | 1726.8566 |

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| sp P60842 IF4A1_HUMAN          | 1697.7937 |
| sp P42704 LPPRC_HUMAN          | 2356.1654 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 2902.3596 |
| sp Q9UGU0 TCF20_HUMAN          | 2308.0621 |
| sp P07737 PROF1_HUMAN          | 1490.6282 |
| sp P21333 FLNA_HUMAN           | 2434.3009 |
| sp Q13283 G3BP1_HUMAN          | 2059.9568 |
| sp P06756 ITAV_HUMAN           | 2105.9874 |
| sp Q93052 LPP_HUMAN            | 2296.9734 |
| sp O75794 CD123_HUMAN          | 1701.7821 |
| sp Q04760 LGUL_HUMAN           | 2143.0157 |
| sp Q9UIG0 BAZ1B_HUMAN          | 1488.7242 |
| sp O95678 K2C75_HUMAN,sp P486t | 1848.937  |
| sp Q9Y6X3 SCC4_HUMAN           | 2592.286  |
| sp O43464 HTRA2_HUMAN          | 2829.4562 |
| sp Q8NFB3 NUP43_HUMAN          | 3695.7452 |
| sp Q8IVF2 AHNK2_HUMAN          | 3634.7746 |
| sp P62826 RAN_HUMAN            | 1284.5986 |
| sp Q13435 SF3B2_HUMAN          | 1589.9029 |
| sp Q15404 RSU1_HUMAN           | 2174.0968 |
| sp Q9H6R4 NOL6_HUMAN           | 1966.9724 |
| sp P52292 IMA1_HUMAN           | 1600.8613 |
| sp Q01518 CAP1_HUMAN           | 1104.5564 |
| sp P52272 HNRPM_HUMAN          | 1217.5863 |
| sp P04406 G3P_HUMAN            | 1963.0375 |
| sp P39023 RL3_HUMAN            | 1387.6983 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 2902.3596 |
| sp O43143 DHX15_HUMAN          | 3728.6837 |
| sp P11388 TOP2A_HUMAN          | 1320.6058 |
| sp Q00341 VIGLN_HUMAN          | 2012.0215 |
| sp P05787 K2C8_HUMAN           | 2484.1366 |
| sp Q9BSJ8 ESYT1_HUMAN          | 3271.6626 |
| sp Q8IWS0 PHF6_HUMAN           | 2717.1852 |
| sp P05787 K2C8_HUMAN           | 1537.7736 |
| sp P35659 DEK_HUMAN            | 1215.6288 |
| sp Q86U38 NOP9_HUMAN           | 2883.4225 |
| sp Q7L576 CYFP1_HUMAN          | 3465.6589 |
| sp P26641 EF1G_HUMAN           | 2526.124  |
| sp P26038 MOES_HUMAN           | 2148.0236 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1062.473  |
| sp P22626 ROA2_HUMAN           | 1534.7264 |
| sp O00303 EIF3F_HUMAN          | 2598.1658 |
| sp Q9UP95 S12A4_HUMAN          | 1730.8588 |
| sp Q14247 SRC8_HUMAN           | 1803.7812 |
| sp Q13098 CSN1_HUMAN           | 3416.6525 |
| sp P61158 ARP3_HUMAN           | 2135.0834 |
| sp Q03252 LMNB2_HUMAN          | 1439.7045 |

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| sp P25205 MCM3_HUMAN           | 1474.782  |
| sp P62263 RS14_HUMAN           | 1479.7318 |
| sp Q96AG4 LRC59_HUMAN          | 1864.8737 |
| sp P14625 ENPL_HUMAN           | 2738.3163 |
| sp P55795 HNRH2_HUMAN,sp P319  | 1338.6456 |
| sp P14618 KPYM_HUMAN           | 4426.1169 |
| sp Q06830 PRDX1_HUMAN          | 1321.6038 |
| sp Q86VP6 CAND1_HUMAN          | 2241.0987 |
| sp Q9UNF0 PACN2_HUMAN          | 1376.5779 |
| sp P43243 MATR3_HUMAN          | 2991.4978 |
| sp P53582 MAP11_HUMAN          | 3411.6803 |
| sp P62266 RS23_HUMAN           | 1152.4836 |
| sp P62807 H2B1C_HUMAN,sp P5887 | 1461.6664 |
| sp P49792 RBP2_HUMAN           | 1747.8199 |
| sp P46940 IQGA1_HUMAN          | 1805.9272 |
| sp P09651 ROA1_HUMAN           | 2263.0804 |
| sp Q15365 PCBP1_HUMAN          | 2126.0062 |
| sp Q00796 DHSO_HUMAN           | 1994.0037 |
| sp Q6UVK1 CSPG4_HUMAN          | 1360.6987 |
| sp Q96A72 MG2_HUMAN,sp P613    | 2037.0015 |
| sp Q9NRJ5 PAPOB_HUMAN,sp P510  | 3045.5811 |
| sp O00571 DDX3X_HUMAN          | 2543.0547 |
| sp P05362 ICAM1_HUMAN          | 1349.6939 |
| sp P61978 HNRPK_HUMAN          | 5458.5861 |
| sp Q96A26 F162A_HUMAN          | 1544.7623 |
| sp P05783 K1C18_HUMAN          | 1440.7209 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp P62633 CNBP_HUMAN           | 1535.7038 |
| sp P11172 UMPS_HUMAN           | 2353.1658 |
| sp P26599 PTBP1_HUMAN,sp Q9UK  | 987.5025  |
| sp Q09666 AHNK_HUMAN           | 2336.1471 |
| sp P04083 ANXA1_HUMAN          | 1874.9374 |
| sp P12814 ACTN1_HUMAN          | 1234.6306 |
| sp P36871 PGM1_HUMAN           | 1725.8396 |
| sp P39023 RL3_HUMAN            | 2007.8884 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1806.871  |
| sp Q16629 SRSF7_HUMAN          | 1915.9276 |
| sp Q96QK1 VPS35_HUMAN          | 1267.5694 |
| sp P05556 ITB1_HUMAN           | 1830.8346 |
| sp P07437 TBB5_HUMAN           | 2364.2035 |
| sp P67936 TPM4_HUMAN,sp P0795  | 1494.793  |
| sp P42766 RL35_HUMAN           | 1851.969  |
| sp Q8IXQ3 CIO40_HUMAN          | 1733.8526 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp Q92878 RAD50_HUMAN          | 1267.6044 |
| sp P21333 FLNA_HUMAN           | 1801.8846 |
| sp P00558 PGK1_HUMAN           | 2268.1031 |

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| sp P07237 PDIA1_HUMAN          | 2399.1315 |
| sp P62277 RS13_HUMAN           | 1908.9152 |
| sp P26038 MOES_HUMAN           | 2477.1598 |
| sp P52789 HXK2_HUMAN           | 2355.207  |
| sp Q86V81 THOC4_HUMAN          | 3339.634  |
| sp P35052 GPC1_HUMAN           | 2798.3511 |
| sp P05787 K2C8_HUMAN           | 1576.7151 |
| sp Q15149 PLEC_HUMAN           | 1305.7405 |
| sp P62750 RL23A_HUMAN          | 1147.5986 |
| sp Q6FI13 H2A2A_HUMAN,sp P2067 | 2538.4785 |
| sp Q9Y3T9 NOC2L_HUMAN          | 2298.1289 |
| sp P46781 RS9_HUMAN            | 1398.7368 |
| sp P62937 PPIA_HUMAN           | 1511.6252 |
| sp P52597 HNRPF_HUMAN          | 1374.6568 |
| sp P39023 RL3_HUMAN            | 1387.6983 |
| sp P52597 HNRPF_HUMAN          | 1542.8042 |
| sp P08729 K2C7_HUMAN           | 1581.7635 |
| sp P62829 RL23_HUMAN           | 2123.9946 |
| sp Q8NI36 WDR36_HUMAN          | 1262.6619 |
| sp P04406 G3P_HUMAN            | 3145.4736 |
| sp Q96SI9 STRBP_HUMAN,sp Q1290 | 1162.6346 |
| sp Q14152 EIF3A_HUMAN          | 1350.6317 |
| sp P49792 RBP2_HUMAN           | 1855.7982 |
| sp P14625 ENPL_HUMAN,sp Q58FF3 | 1480.7562 |
| sp Q92804 RBP56_HUMAN          | 2219.078  |
| sp P49748 ACADV_HUMAN          | 1520.726  |
| sp P05783 K1C18_HUMAN          | 1488.746  |
| sp Q9UQ35 SRRM2_HUMAN          | 2419.1696 |
| sp P16402 H13_HUMAN,sp P10412  | 1191.6612 |
| sp P50238 CRIP1_HUMAN          | 3313.4016 |
| sp P62263 RS14_HUMAN           | 1559.8671 |
| sp P62805 H4_HUMAN             | 1521.7787 |
| sp P16435 NCPR_HUMAN           | 3264.5285 |
| sp Q15392 DHC24_HUMAN          | 2282.9943 |
| sp P20700 LMNB1_HUMAN          | 1272.6714 |
| sp P35580 MYH10_HUMAN,sp P357  | 1435.7056 |
| sp Q9UIW2 PLXA1_HUMAN          | 3477.628  |
| sp P61604 CH10_HUMAN           | 1671.8356 |
| sp P55786 PSA_HUMAN            | 1080.6179 |
| sp Q14320 FA50A_HUMAN          | 2363.1969 |
| sp Q9Y230 RUVB2_HUMAN          | 2271.1495 |
| sp Q5VT66 MARC1_HUMAN          | 2695.3898 |
| sp P12268 IMDH2_HUMAN          | 2835.4014 |
| sp P11387 TOP1_HUMAN           | 1542.7718 |
| sp P11021 BIP_HUMAN            | 3302.6572 |
| sp O76094 SRP72_HUMAN          | 1993.9745 |
| sp Q9NTI5 PDS5B_HUMAN          | 2088.9752 |

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| sp P63104 1433Z_HUMAN          | 2151.0888 |
| sp Q9H0X4 F234A_HUMAN          | 1374.7044 |
| sp O75380 NDUS6_HUMAN          | 2591.1776 |
| sp Q14103 HNRPD_HUMAN          | 1643.7614 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp Q10713 MPPA_HUMAN           | 2384.1648 |
| sp Q00610 CLH1_HUMAN           | 2040.9905 |
| sp P46781 RS9_HUMAN            | 2086.0695 |
| sp Q02878 RL6_HUMAN            | 1556.7835 |
| sp O15371 EIF3D_HUMAN          | 1187.5207 |
| sp Q92616 GCN1_HUMAN           | 1705.9614 |
| sp Q15233 NONO_HUMAN           | 1135.5298 |
| sp Q9BY89 K1671_HUMAN          | 1948.9854 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 3730.7396 |
| sp Q09666 AHNK_HUMAN           | 1331.6254 |
| sp Q09666 AHNK_HUMAN           | 1013.5546 |
| sp O60488 ACSL4_HUMAN,sp O955: | 2425.2053 |
| sp P20618 PSB1_HUMAN           | 3832.8513 |
| sp P61604 CH10_HUMAN           | 2783.4058 |
| sp P05386 RLA1_HUMAN           | 4560.2919 |
| sp P16401 H15_HUMAN,sp P10412  | 1381.7201 |
| sp O15031 PLXB2_HUMAN          | 2446.1435 |
| sp P50991 TCPD_HUMAN           | 1854.9509 |
| sp O43707 ACTN4_HUMAN          | 1385.7303 |
| sp P05141 ADT2_HUMAN,sp P1223: | 1559.8671 |
| sp O60832 DKC1_HUMAN           | 2921.2992 |
| sp Q16543 CDC37_HUMAN          | 1688.6923 |
| sp O43707 ACTN4_HUMAN          | 2358.0836 |
| sp Q00839 HNRPU_HUMAN          | 1469.6431 |
| sp P60709 ACTB_HUMAN,sp P6803: | 1232.6765 |
| sp P39023 RL3_HUMAN            | 1552.7845 |
| sp P14618 KPYM_HUMAN           | 2587.2853 |
| sp Q08345 DDR1_HUMAN           | 1354.6266 |
| sp P11766 ADHX_HUMAN           | 1571.7402 |
| sp P62995 TRA2B_HUMAN          | 2597.2286 |
| sp P09874 PARP1_HUMAN          | 2371.1947 |
| sp Q15366 PCBP2_HUMAN          | 2026.9816 |
| sp P54886 P5CS_HUMAN           | 2027.984  |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1239.5594 |
| sp P42167 LAP2B_HUMAN          | 3771.7725 |
| sp Q9UNF0 PACN2_HUMAN          | 1376.5779 |
| sp Q13200 PSMD2_HUMAN          | 2342.1866 |
| sp Q9UIJ7 KAD3_HUMAN           | 2710.3755 |
| sp P37802 TAGL2_HUMAN          | 1305.6426 |
| sp P06733 ENOA_HUMAN           | 3336.5979 |
| sp P78310 CXAR_HUMAN           | 1584.8988 |
| sp P43121 MUC18_HUMAN          | 1451.6463 |

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| sp Q92900 RENT1_HUMAN          | 2187.1246 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp P05787 K2C8_HUMAN           | 1993.8575 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1576.7555 |
| sp O75390 CISY_HUMAN           | 2314.0715 |
| sp Q14997 PSME4_HUMAN          | 2693.3013 |
| sp Q9Y265 RUVB1_HUMAN          | 2115.0596 |
| sp P49327 FAS_HUMAN            | 1344.6132 |
| sp P31689 DNJA1_HUMAN          | 2048.9803 |
| sp P11021 BIP_HUMAN            | 1969.9453 |
| sp P68104 EF1A1_HUMAN,sp Q5VT! | 4262.987  |
| sp Q9NP66 HM20A_HUMAN          | 2446.1805 |
| sp P21333 FLNA_HUMAN           | 1471.8511 |
| sp P61088 UBE2N_HUMAN          | 1239.6571 |
| sp Q9UJG1 MSPD1_HUMAN          | 1577.6933 |
| sp P63173 RL38_HUMAN           | 2010.0197 |
| sp P50914 RL14_HUMAN           | 1042.5659 |
| sp Q13310 PABP4_HUMAN          | 1601.7256 |
| sp P39748 FEN1_HUMAN           | 1810.8625 |
| sp P52272 HNRPM_HUMAN          | 1418.6466 |
| sp Q5VWI1 TCRGL_HUMAN,sp O147  | 1814.8475 |
| sp P62081 RS7_HUMAN            | 3994.9834 |
| sp Q8NEY8 PPHLN_HUMAN          | 1687.7339 |
| sp Q8NHW5 RLA0L_HUMAN,sp P05:  | 3670.8189 |
| sp P61769 B2MG_HUMAN           | 1658.8992 |
| sp P36871 PGM1_HUMAN           | 3222.5833 |
| sp P62249 RS16_HUMAN           | 1575.8872 |
| sp P13010 XRCC5_HUMAN          | 1823.9029 |
| sp P26373 RL13_HUMAN           | 2088.9952 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 2902.3596 |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp Q15084 PDIA6_HUMAN          | 2777.3409 |
| sp Q13332 PTPRS_HUMAN          | 4732.1915 |
| sp P29401 TKT_HUMAN            | 2363.1315 |
| sp P39023 RL3_HUMAN            | 2443.206  |
| sp P30101 PDIA3_HUMAN          | 3043.4056 |
| sp P07900 HS90A_HUMAN,sp Q145! | 1811.9265 |
| sp P27824 CALX_HUMAN           | 2594.274  |
| sp P60709 ACTB_HUMAN,sp Q6S8J3 | 3003.3365 |
| sp P52597 HNRPF_HUMAN          | 1542.8042 |
| sp Q8WUM4 PDC6I_HUMAN          | 1513.7413 |
| sp P09651 ROA1_HUMAN           | 3133.4563 |
| sp O75367 H2AY_HUMAN           | 1528.7886 |
| sp P16403 H12_HUMAN            | 1095.5924 |
| sp P06748 NPM_HUMAN            | 1234.583  |
| sp P55265 DSRAD_HUMAN          | 1639.7631 |
| sp P98082 DAB2_HUMAN           | 2243.1335 |

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| sp P62280 RS11_HUMAN           | 1144.6128 |
| sp Q16658 FSCN1_HUMAN          | 1396.6987 |
| sp P78527 PRKDC_HUMAN          | 1100.5866 |
| sp P15328 FOLR1_HUMAN          | 1890.8717 |
| sp Q04637 IF4G1_HUMAN          | 2257.0287 |
| sp Q9Y3F4 STRAP_HUMAN          | 2622.2813 |
| sp Q16891 MIC60_HUMAN          | 4427.1591 |
| sp P30044 PRDX5_HUMAN          | 3173.5768 |
| sp Q7Z417 NUFP2_HUMAN          | 2231.0495 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1133.5102 |
| sp P35613 BASI_HUMAN           | 3662.6181 |
| sp Q13442 HAP28_HUMAN          | 1425.6558 |
| sp P07910 HNRPC_HUMAN,sp P0DN  | 1640.9138 |
| sp Q6NUK1 SCMC1_HUMAN          | 1571.7984 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P23528 COF1_HUMAN,sp Q9Y28: | 2273.1256 |
| sp Q16531 DDB1_HUMAN           | 2390.2417 |
| sp P08238 HS90B_HUMAN          | 3552.5481 |
| sp Q13332 PTPRS_HUMAN          | 4732.1915 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1062.473  |
| sp Q8IZP9 AGRG2_HUMAN          | 2027.8798 |
| sp Q10713 MPPA_HUMAN           | 3320.6525 |
| sp P11388 TOP2A_HUMAN          | 1320.6058 |
| sp P13639 EF2_HUMAN            | 1626.7638 |
| sp Q9Y2H6 FND3A_HUMAN          | 1882.9247 |
| sp P19338 NUCL_HUMAN           | 1253.6292 |
| sp P78371 TCPB_HUMAN           | 2079.996  |
| sp P49915 GUAA_HUMAN           | 2992.4858 |
| sp Q01167 FOXK2_HUMAN          | 4697.3368 |
| sp O15498 YKT6_HUMAN           | 1934.9877 |
| sp P41227 NAA10_HUMAN          | 1718.8839 |
| sp Q06830 PRDX1_HUMAN          | 2338.1052 |
| sp Q14697 GANAB_HUMAN          | 1860.072  |
| sp Q13740 CD166_HUMAN          | 1821.8574 |
| sp P04075 ALDOA_HUMAN          | 1684.8268 |
| sp O95298 NDUC2_HUMAN          | 1832.8734 |
| sp Q92621 NU205_HUMAN          | 1474.7555 |
| sp P54819 KAD2_HUMAN           | 1103.5724 |
| sp P07437 TBB5_HUMAN           | 2380.1984 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp O95831 AIFM1_HUMAN          | 3558.7671 |
| sp Q8N556 AFAP1_HUMAN          | 2529.3439 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |
| sp P52272 HNRPM_HUMAN          | 1418.6466 |
| sp P42766 RL35_HUMAN           | 1453.7929 |
| sp P26599 PTBP1_HUMAN          | 2340.0254 |
| sp Q99848 EBP2_HUMAN           | 1259.6874 |



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| sp P13639 EF2_HUMAN            | 1167.6387 |
| sp P52272 HNRPM_HUMAN          | 1217.5863 |
| sp P46063 RECQ1_HUMAN          | 1697.8698 |
| sp P18621 RL17_HUMAN           | 2341.126  |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp Q99729 ROAA_HUMAN           | 1651.7552 |
| sp P62899 RL31_HUMAN           | 1369.6626 |
| sp P41252 SYIC_HUMAN           | 1176.5815 |
| sp P39023 RL3_HUMAN            | 1552.7845 |
| sp Q9UHB6 LIMA1_HUMAN          | 1790.845  |
| sp P42704 LPPRC_HUMAN          | 2997.5634 |
| sp Q6UVK1 CSPG4_HUMAN          | 1531.7705 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P32119 PRDX2_HUMAN          | 1168.5764 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P50914 RL14_HUMAN           | 1042.5659 |
| sp Q6YHK3 CD109_HUMAN          | 2628.198  |
| sp P49327 FAS_HUMAN            | 2641.202  |
| sp P62258 1433E_HUMAN          | 3319.6395 |
| sp Q16881 TRXR1_HUMAN          | 1723.9356 |
| sp P09874 PARP1_HUMAN          | 2788.3344 |
| sp P30050 RL12_HUMAN           | 1205.6656 |
| sp Q96SI9 STRBP_HUMAN,sp Q1290 | 2085.9967 |
| sp P31040 SDHA_HUMAN           | 1386.6779 |
| sp P04040 CATA_HUMAN           | 2287.0433 |
| sp Q99797 MIPEP_HUMAN          | 1951.921  |
| sp P62805 H4_HUMAN             | 997.5193  |
| sp Q12906 ILF3_HUMAN           | 3022.4641 |
| sp Q08211 DHX9_HUMAN           | 1345.7606 |
| sp Q12906 ILF3_HUMAN           | 1827.8527 |
| sp Q9Y2S7 PDIP2_HUMAN          | 2194.127  |
| sp P27816 MAP4_HUMAN           | 1676.9349 |
| sp Q7Z3B1 NEGR1_HUMAN          | 2702.2976 |
| sp P62424 RL7A_HUMAN           | 1568.7583 |
| sp P49327 FAS_HUMAN            | 2319.1893 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp P07900 HS90A_HUMAN          | 1756.8479 |
| sp Q5JTV8 TOIP1_HUMAN          | 2010.0898 |
| sp P15529 MCP_HUMAN            | 2248.0623 |
| sp Q04637 IF4G1_HUMAN,sp O4343 | 1983.9468 |
| sp P46778 RL21_HUMAN           | 2192.159  |
| sp Q01082 SPTB2_HUMAN          | 1872.9078 |
| sp Q14974 IMB1_HUMAN           | 3678.7294 |
| sp Q00341 VIGLN_HUMAN          | 1179.6037 |
| sp P78527 PRKDC_HUMAN          | 2518.2665 |
| sp Q09028 RBBP4_HUMAN,sp Q165  | 1517.7402 |
| sp P32119 PRDX2_HUMAN          | 1168.5764 |

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| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1602.8366 |
| sp P35579 MYH9_HUMAN           | 1889.9523 |
| sp O75475 PSIP1_HUMAN          | 3664.8454 |
| sp P31948 STIP1_HUMAN          | 1817.8584 |
| sp Q14690 RRP5_HUMAN           | 1799.8802 |
| sp Q9NZN4 EHD2_HUMAN           | 3554.6988 |
| sp P29401 TKT_HUMAN            | 1145.5717 |
| sp Q9ULF5 S39AA_HUMAN          | 1757.906  |
| sp Q9UL03 INT6_HUMAN           | 2206.0655 |
| sp P16401 H15_HUMAN,sp P10412  | 1253.6252 |
| sp Q9BS26 ERP44_HUMAN          | 1614.8042 |
| sp Q9Y3F4 STRAP_HUMAN          | 2580.2344 |
| sp Q96SI9 STRBP_HUMAN,sp Q1290 | 1525.7923 |
| sp P35613 BASI_HUMAN           | 5055.2967 |
| sp P19338 NUCL_HUMAN           | 1704.941  |
| sp P52272 HNRPM_HUMAN          | 2092.0185 |
| sp P61201 CSN2_HUMAN           | 2649.2962 |
| sp Q02790 FKBP4_HUMAN          | 1841.9233 |
| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1636.778  |
| sp Q9UKG1 DP13A_HUMAN          | 2693.3297 |
| sp Q9NTJ3 SMC4_HUMAN           | 2027.9912 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1446.7355 |
| sp O00429 DNM1L_HUMAN          | 2127.1437 |
| sp P62805 H4_HUMAN             | 997.5193  |
| sp P08754 GNAI3_HUMAN,sp P0947 | 1803.9043 |
| sp Q9P0L0 VAPA_HUMAN           | 2773.288  |
| sp P0DP23 CALM1_HUMAN,sp P0DF  | 1950.8959 |
| sp P52565 GDIR1_HUMAN          | 1920.904  |
| sp P51003 PAPOA_HUMAN          | 1624.8461 |
| sp P61020 RAB5B_HUMAN,sp P203: | 1958.0183 |
| sp Q9BSH4 TACO1_HUMAN          | 2693.2715 |
| sp P17987 TCPA_HUMAN           | 1493.7297 |
| sp Q14847 LASP1_HUMAN          | 2006.7862 |
| sp P42167 LAP2B_HUMAN          | 2635.3282 |
| sp O60784 TOM1_HUMAN           | 2622.2458 |
| sp Q8IY81 SPB1_HUMAN           | 1240.5837 |
| sp P46782 RS5_HUMAN            | 2735.296  |
| sp Q9HB71 CYBP_HUMAN           | 2888.459  |
| sp Q14152 EIF3A_HUMAN          | 1632.7784 |
| sp P18084 ITB5_HUMAN           | 2614.3279 |
| sp P37802 TAGL2_HUMAN          | 1305.6426 |
| sp P28288 ABCD3_HUMAN          | 1426.6841 |
| sp Q92598 HS105_HUMAN          | 1628.7947 |
| sp P07900 HS90A_HUMAN,sp P082: | 2769.447  |
| sp P78527 PRKDC_HUMAN          | 2549.1971 |
| sp Q86UE4 LYRIC_HUMAN          | 2155.0294 |
| sp P08238 HS90B_HUMAN          | 1442.6718 |

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| sp P38646 GRP75_HUMAN          | 1208.5972 |
| sp P11021 BIP_HUMAN            | 3302.6572 |
| sp P00966 ASSY_HUMAN           | 2347.1518 |
| sp P35251 RFC1_HUMAN           | 1980.9905 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp P62841 RS15_HUMAN           | 2057.0252 |
| sp P50238 CRIP1_HUMAN          | 1724.7399 |
| sp P78527 PRKDC_HUMAN          | 1847.9087 |
| sp P46940 IQGA1_HUMAN          | 1178.5873 |
| sp Q9UL25 RAB21_HUMAN          | 2060.0215 |
| sp P05787 K2C8_HUMAN           | 1404.6191 |
| sp P46013 KI67_HUMAN           | 1545.8225 |
| sp Q8TDN6 BRX1_HUMAN           | 1591.759  |
| sp P45880 VDAC2_HUMAN          | 3573.8315 |
| sp P04075 ALDOA_HUMAN          | 1264.6048 |
| sp P62266 RS23_HUMAN           | 1891.9428 |
| sp Q9H361 PABP3_HUMAN,sp P119  | 1815.9771 |
| sp P39019 RS19_HUMAN           | 1653.8648 |
| sp O75083 WDR1_HUMAN           | 1707.8468 |
| sp Q96QK1 VPS35_HUMAN          | 2291.2121 |
| sp Q9BZK7 TBL1R_HUMAN          | 2163.096  |
| sp Q12931 TRAP1_HUMAN          | 1380.6422 |
| sp P50502 F10A1_HUMAN,sp Q8NFI | 1399.7381 |
| sp Q15149 PLEC_HUMAN           | 2644.3425 |
| sp P58743 S26A5_HUMAN          | 3317.741  |
| sp P14625 ENPL_HUMAN           | 2572.1654 |
| sp P53597 SUCA_HUMAN           | 1426.7391 |
| sp Q6P2Q9 PRP8_HUMAN           | 1381.7102 |
| sp P61927 RL37_HUMAN           | 1124.5978 |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P05386 RLA1_HUMAN           | 4560.2919 |
| sp P07195 LDHB_HUMAN           | 3484.7193 |
| sp P62136 PP1A_HUMAN,sp P6214C | 2737.2768 |
| sp Q8NCA5 FA98A_HUMAN          | 1494.8195 |
| sp Q9HB71 CYBP_HUMAN           | 2888.459  |
| sp P17301 ITA2_HUMAN           | 4437.1131 |
| sp P07099 HYEP_HUMAN           | 2991.3482 |
| sp Q99832 TCPH_HUMAN           | 2288.1689 |
| sp Q15366 PCBP2_HUMAN          | 2625.3187 |
| sp O75367 H2AY_HUMAN           | 1658.9243 |
| sp Q96QK1 VPS35_HUMAN          | 1267.5694 |
| sp Q8IWS0 PHF6_HUMAN           | 2108.9487 |
| sp O00592 PODXL_HUMAN          | 1370.6718 |
| sp Q9ULC4 MCTS1_HUMAN          | 3081.5337 |
| sp Q07666 KHDR1_HUMAN          | 1478.763  |
| sp P02786 TFR1_HUMAN           | 1160.5714 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |

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| sp P30101 PDIA3_HUMAN          | 3039.4859 |
| sp P69849 NOMO3_HUMAN,sp Q15   | 2964.4869 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 998.5033  |
| sp P61769 B2MG_HUMAN           | 3483.6041 |
| sp Q08211 DHX9_HUMAN           | 1540.7093 |
| sp P05783 K1C18_HUMAN          | 2517.2924 |
| sp P08754 GNAI3_HUMAN,sp P0947 | 1803.9043 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp Q15262 PTPRK_HUMAN          | 2990.412  |
| sp O14545 TRAD1_HUMAN          | 2364.1321 |
| sp O75530 EED_HUMAN            | 1873.9534 |
| sp Q8TCS8 PNPT1_HUMAN          | 3250.5393 |
| sp Q15293 RCN1_HUMAN           | 4014.8144 |
| sp P14618 KPYM_HUMAN           | 2753.3007 |
| sp P51397 DAP1_HUMAN           | 1556.7583 |
| sp P06703 S10A6_HUMAN          | 1338.6416 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp Q9UQ80 PA2G4_HUMAN          | 2716.2877 |
| sp P36578 RL4_HUMAN            | 951.5389  |
| sp Q9ULC4 MCTS1_HUMAN          | 3081.5337 |
| sp P25391 LAMA1_HUMAN          | 2615.2762 |
| sp Q8TC12 RDH11_HUMAN          | 2511.2605 |
| sp P46940 IQGA1_HUMAN          | 2498.2111 |
| sp P04083 ANXA1_HUMAN          | 1409.6721 |
| sp P26599 PTBP1_HUMAN          | 1057.5808 |
| sp P07108 ACBP_HUMAN           | 2153.9616 |
| sp P37837 TALDO_HUMAN          | 1715.9094 |
| sp P37837 TALDO_HUMAN          | 1635.7893 |
| sp P36578 RL4_HUMAN            | 1581.7886 |
| sp O94776 MTA2_HUMAN           | 1915.964  |
| sp P23246 SFPQ_HUMAN           | 1441.7201 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1133.5102 |
| sp P26599 PTBP1_HUMAN          | 3963.0054 |
| sp P49720 PSB3_HUMAN           | 2006.9983 |
| sp P14618 KPYM_HUMAN           | 3690.6665 |
| sp Q8IYB8 SUV3_HUMAN           | 2951.3971 |
| sp P31040 SDHA_HUMAN           | 2991.4297 |
| sp P23921 RIR1_HUMAN           | 2361.1311 |
| sp P05783 K1C18_HUMAN          | 2373.2025 |
| sp Q13619 CUL4A_HUMAN          | 1324.7027 |
| sp Q5SNT2 TM201_HUMAN          | 1408.7463 |
| sp Q03701 CEBPZ_HUMAN          | 1715.8519 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp P62280 RS11_HUMAN           | 1398.682  |
| sp P04406 G3P_HUMAN            | 2309.1652 |
| sp P50990 TCPO_HUMAN           | 2782.3596 |

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| sp P13010 XRCC5_HUMAN          | 1935.8963 |
| sp P22626 ROA2_HUMAN           | 2257.9772 |
| sp P62987 RL40_HUMAN           | 1520.7154 |
| sp P0DMV8 HS71A_HUMAN,sp PODI  | 2018.0433 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P50895 BCAM_HUMAN           | 1612.7634 |
| sp O75955 FLOT1_HUMAN          | 2078.9294 |
| sp P61769 B2MG_HUMAN           | 1714.805  |
| sp Q6UVK1 CSPG4_HUMAN          | 1360.6987 |
| sp P84098 RL19_HUMAN           | 2395.1404 |
| sp Q6UVK1 CSPG4_HUMAN          | 1479.7106 |
| sp Q9ULF5 S39AA_HUMAN          | 2203.1525 |
| sp P32004 L1CAM_HUMAN          | 2041.0116 |
| sp Q8NE01 CNNM3_HUMAN          | 2844.4002 |
| sp P51991 ROA3_HUMAN           | 1972.8875 |
| sp P53396 ACLY_HUMAN           | 1395.7246 |
| sp P51665 PSMD7_HUMAN          | 1731.8733 |
| sp P67870 CSK2B_HUMAN          | 3872.69   |
| sp P35579 MYH9_HUMAN           | 1408.6947 |
| sp Q15833 STXB2_HUMAN          | 2924.474  |
| sp P62140 PP1B_HUMAN           | 3239.5671 |
| sp P43121 MUC18_HUMAN          | 2602.3279 |
| sp P46783 RS10_HUMAN           | 1479.6783 |
| sp P19338 NUCL_HUMAN           | 1704.941  |
| sp P11142 HSP7C_HUMAN          | 2244.0144 |
| sp Q15393 SF3B3_HUMAN          | 1615.7049 |
| sp P20700 LMNB1_HUMAN          | 1272.6714 |
| sp P26599 PTBP1_HUMAN          | 1016.5403 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2555.185  |
| sp Q15233 NONO_HUMAN           | 1444.6987 |
| sp P49327 FAS_HUMAN            | 2624.3122 |
| sp P02786 TFR1_HUMAN           | 2997.472  |
| sp P06733 ENOA_HUMAN           | 1268.5561 |
| sp Q9ULV4 COR1C_HUMAN          | 2032.0629 |
| sp Q13162 PRDX4_HUMAN          | 2503.2271 |
| sp Q9P0L0 VAPA_HUMAN           | 2789.2829 |
| sp Q08945 SSRP1_HUMAN          | 2176.0629 |
| sp P05787 K2C8_HUMAN           | 1733.8584 |
| sp Q13283 G3BP1_HUMAN          | 2736.3144 |
| sp O60264 SMCA5_HUMAN,sp P283  | 2462.2131 |
| sp Q14764 MVP_HUMAN            | 2630.2435 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1133.5102 |
| sp P13639 EF2_HUMAN            | 1699.7916 |
| sp P17987 TCPA_HUMAN           | 2817.2114 |
| sp P46939 UTRO_HUMAN           | 2848.4832 |
| sp Q9H8Y5 ANKZ1_HUMAN          | 2146.0695 |
| sp Q00610 CLH1_HUMAN,sp P5367! | 1381.7606 |

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| sp P19338 NUCL_HUMAN           | 1591.857  |
| sp Q05519 SRS11_HUMAN          | 1704.8723 |
| sp Q96KR1 ZFR_HUMAN,sp Q96SI9  | 1239.5785 |
| sp P27635 RL10_HUMAN           | 1797.872  |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp P06733 ENOA_HUMAN           | 3336.5979 |
| sp Q96J84 KIRR1_HUMAN          | 1865.9094 |
| sp P00558 PGK1_HUMAN           | 1063.5008 |
| sp Q9HD20 AT131_HUMAN          | 1742.8951 |
| sp Q15233 NONO_HUMAN           | 1339.6408 |
| sp P05387 RLA2_HUMAN           | 2421.2064 |
| sp P49327 FAS_HUMAN            | 1674.7712 |
| sp P57105 SYJ2B_HUMAN          | 2704.382  |
| sp P05787 K2C8_HUMAN           | 2484.1366 |
| sp P15924 DESP_HUMAN           | 3314.6817 |
| sp P23588 IF4B_HUMAN           | 1396.6008 |
| sp Q96KR1 ZFR_HUMAN,sp Q96SI9  | 1239.5785 |
| sp P13639 EF2_HUMAN            | 1453.7599 |
| sp P06213 INSR_HUMAN           | 1096.5302 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp O00592 PODXL_HUMAN          | 1446.7718 |
| sp Q09666 AHNK_HUMAN           | 1013.5546 |
| sp P26038 MOES_HUMAN           | 1613.8049 |
| sp P10586 PTPRF_HUMAN          | 1954.9385 |
| sp Q03252 LMNB2_HUMAN,sp P025  | 1298.599  |
| sp P14618 KPYM_HUMAN           | 1402.6663 |
| sp Q14247 SRC8_HUMAN           | 1611.7311 |
| sp P78527 PRKDC_HUMAN          | 2203.1195 |
| sp Q92616 GCN1_HUMAN           | 1432.7059 |
| sp P50914 RL14_HUMAN           | 1042.5659 |
| sp P13639 EF2_HUMAN            | 1334.599  |
| sp P68032 ACTC_HUMAN,sp P63267 | 2798.3473 |
| sp O95163 ELP1_HUMAN           | 2897.4963 |
| sp P46783 RS10_HUMAN,sp Q9NQ3  | 1905.9441 |
| sp P00367 DHE3_HUMAN,sp P49448 | 2090.0983 |
| sp P06733 ENOA_HUMAN           | 4588.1275 |
| sp P62805 H4_HUMAN             | 1486.6688 |
| sp P62081 RS7_HUMAN            | 1584.8049 |
| sp O00303 EIF3F_HUMAN          | 3145.5415 |
| sp O75643 U520_HUMAN           | 2139.0273 |
| sp Q8IW45 NNRD_HUMAN           | 3291.6564 |
| sp Q01974 ROR2_HUMAN           | 2416.0325 |
| sp Q12800 TFCP2_HUMAN          | 4235.0885 |
| sp Q16531 DDB1_HUMAN           | 1633.9079 |
| sp P39019 RS19_HUMAN           | 1509.7715 |
| sp P32119 PRDX2_HUMAN          | 1483.8035 |
| sp Q9UBQ0 VPS29_HUMAN          | 2489.3134 |

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| sp P62277 RS13_HUMAN           | 1784.8832 |
| sp Q15149 PLEC_HUMAN           | 1581.7093 |
| sp Q15149 PLEC_HUMAN           | 1368.7038 |
| sp O00299 CLIC1_HUMAN          | 3333.7101 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp Q99798 ACON_HUMAN           | 2149.0328 |
| sp Q8WVC6 DCAKD_HUMAN          | 1823.8438 |
| sp P26006 ITA3_HUMAN           | 1718.8628 |
| sp Q14247 SRC8_HUMAN           | 1464.6634 |
| sp Q96P16 RPR1A_HUMAN,sp Q9NC  | 2900.4781 |
| sp P25205 MCM3_HUMAN           | 1332.715  |
| sp P21796 VDAC1_HUMAN          | 1724.7893 |
| sp P14618 KPYM_HUMAN           | 1373.6748 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1232.6765 |
| sp Q09666 AHNK_HUMAN           | 1365.6097 |
| sp P62750 RL23A_HUMAN          | 1271.6622 |
| sp P52597 HNRPF_HUMAN          | 1374.6568 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp Q13442 HAP28_HUMAN          | 1425.6558 |
| sp P61247 RS3A_HUMAN           | 1142.5972 |
| sp P43121 MUC18_HUMAN          | 3829.8833 |
| sp P36578 RL4_HUMAN            | 1349.6074 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1097.5465 |
| sp P23919 KTHY_HUMAN           | 1520.7406 |
| sp O15020 SPTN2_HUMAN          | 3052.5578 |
| sp Q96MU7 YTDC1_HUMAN          | 2280.14   |
| sp P14618 KPYM_HUMAN           | 1879.8873 |
| sp O75821 EIF3G_HUMAN          | 2123.0072 |
| sp P31930 QCR1_HUMAN           | 2813.3039 |
| sp P99999 CYC_HUMAN            | 2332.0933 |
| sp Q9NZ45 CISD1_HUMAN          | 2351.0198 |
| sp P62805 H4_HUMAN             | 1662.8287 |
| sp Q92499 DDX1_HUMAN           | 2204.9004 |
| sp P40227 TCPZ_HUMAN           | 1482.6951 |
| sp Q7L8L6 FAKD5_HUMAN          | 1978.9531 |
| sp Q13283 G3BP1_HUMAN          | 3055.3948 |
| sp P35637 FUS_HUMAN            | 1748.837  |
| sp Q06830 PRDX1_HUMAN          | 1340.6248 |
| sp P34932 HSP74_HUMAN          | 1846.9002 |
| sp P13987 CD59_HUMAN           | 3083.3654 |
| sp O00154 BACH_HUMAN           | 1286.6289 |
| sp P05787 K2C8_HUMAN           | 1277.5888 |
| sp P36578 RL4_HUMAN            | 1897.9356 |
| sp Q96SB4 SRPK1_HUMAN,sp Q9UP  | 2707.2449 |
| sp Q96E39 RMXL1_HUMAN,sp P381  | 1676.6438 |
| sp Q96QK1 VPS35_HUMAN          | 1243.5721 |
| sp Q9BY67 CADM1_HUMAN          | 1329.6313 |

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| sp P38646 GRP75_HUMAN          | 2550.2788 |
| sp Q6PKG0 LARP1_HUMAN          | 2228.0936 |
| sp P26447 S10A4_HUMAN          | 1242.6245 |
| sp P23588 IF4B_HUMAN           | 3118.5499 |
| sp P31327 CPSM_HUMAN           | 2147.1851 |
| sp P08670 VIME_HUMAN           | 1639.7914 |
| sp Q9HAV4 XPO5_HUMAN           | 1854.9298 |
| sp P05787 K2C8_HUMAN           | 1733.8584 |
| sp P33991 MCM4_HUMAN           | 2103.0637 |
| sp P26373 RL13_HUMAN           | 1169.6445 |
| sp P07437 TBB5_HUMAN           | 5102.3377 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 3262.585  |
| sp P18621 RL17_HUMAN           | 1566.746  |
| sp Q8NHW5 RLA0L_HUMAN,sp P05:  | 1565.7872 |
| sp O60832 DKC1_HUMAN           | 2011.9422 |
| sp Q10567 AP1B1_HUMAN,sp P630: | 3188.5877 |
| sp Q9Y262 EIF3L_HUMAN          | 1509.7212 |
| sp P15121 ALDR_HUMAN           | 4479.2057 |
| sp Q9HCJ3 RAVR2_HUMAN          | 3118.5419 |
| sp Q6UVK1 CSPG4_HUMAN          | 1310.6579 |
| sp P05198 IF2A_HUMAN           | 2432.1471 |
| sp Q9NRF8 PYRG2_HUMAN          | 2163.1113 |
| sp P62987 RL40_HUMAN,sp P62979 | 1477.7487 |
| sp O43747 AP1G1_HUMAN          | 2541.2859 |
| sp P18621 RL17_HUMAN           | 1566.746  |
| sp O60568 PLOD3_HUMAN          | 2937.5084 |
| sp P17812 PYRG1_HUMAN          | 2597.2762 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P53007 TXTP_HUMAN           | 1047.5349 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1180.5612 |
| sp P61421 VA0D1_HUMAN          | 1389.6816 |
| sp P52209 6PGD_HUMAN           | 1594.7627 |
| sp P42765 THIM_HUMAN           | 3545.7559 |
| sp P31327 CPSM_HUMAN           | 1159.551  |
| sp O94979 SC31A_HUMAN          | 1498.8031 |
| sp P14923 PLAK_HUMAN           | 2714.4796 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2748.4083 |
| sp Q9Y5B9 SP16H_HUMAN          | 1124.521  |
| sp Q5UIP0 RIF1_HUMAN           | 1497.7212 |
| sp P08729 K2C7_HUMAN           | 2466.1339 |
| sp Q2TAY7 SMU1_HUMAN           | 1514.6572 |
| sp P50238 CRIP1_HUMAN          | 3313.4016 |
| sp P08670 VIME_HUMAN           | 1784.8727 |
| sp P12814 ACTN1_HUMAN          | 2266.1257 |
| sp P00558 PGK1_HUMAN           | 2219.0634 |
| sp Q15366 PCBP2_HUMAN          | 2625.3187 |
| sp P30101 PDIA3_HUMAN          | 1711.7842 |



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| sp P18077 RL35A_HUMAN          | 1359.6895 |
| sp P13639 EF2_HUMAN            | 1699.7916 |
| sp P07237 PDIA1_HUMAN          | 1482.7103 |
| sp Q13813 SPTN1_HUMAN          | 1634.8556 |
| sp Q00839 HNRPU_HUMAN          | 1990.9457 |
| sp P02786 TFR1_HUMAN           | 2579.2391 |
| sp P12236 ADT3_HUMAN           | 2267.1798 |
| sp P49327 FAS_HUMAN            | 1786.8382 |
| sp P50914 RL14_HUMAN           | 1223.6146 |
| sp P04406 G3P_HUMAN            | 1411.6732 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P78527 PRKDC_HUMAN          | 1847.9087 |
| sp P43121 MUC18_HUMAN          | 1467.6412 |
| sp Q06830 PRDX1_HUMAN          | 2338.1052 |
| sp P68036 UB2L3_HUMAN          | 2475.2726 |
| sp Q01082 SPTB2_HUMAN          | 2807.3627 |
| sp P62987 RL40_HUMAN,sp P62979 | 1542.7678 |
| sp P21333 FLNA_HUMAN           | 3313.6005 |
| sp O75643 U520_HUMAN           | 1678.9142 |
| sp O14980 XPO1_HUMAN           | 1125.5607 |
| sp Q13332 PTPRS_HUMAN          | 1852.8744 |
| sp P02786 TFR1_HUMAN           | 2331.2032 |
| sp P61088 UBE2N_HUMAN          | 2265.1827 |
| sp P62847 RS24_HUMAN           | 1576.7919 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp P23588 IF4B_HUMAN           | 1268.5058 |
| sp Q04637 IF4G1_HUMAN,sp O4343 | 1661.8665 |
| sp Q92621 NU205_HUMAN          | 1420.7133 |
| sp Q13442 HAP28_HUMAN          | 1425.6558 |
| sp Q9UHD8 SEPT9_HUMAN          | 1579.7478 |
| sp Q14258 TRI25_HUMAN          | 2474.3421 |
| sp Q00839 HNRPU_HUMAN          | 1453.6482 |
| sp Q13509 TBB3_HUMAN           | 2108.9803 |
| sp P07237 PDIA1_HUMAN          | 1655.7315 |
| sp Q02790 FKBP4_HUMAN          | 2235.0848 |
| sp Q8NI27 THOC2_HUMAN          | 1171.5662 |
| sp Q9Y6N7 ROBO1_HUMAN          | 1176.5411 |
| sp P83916 CBX1_HUMAN           | 1611.7125 |
| sp P08670 VIME_HUMAN           | 1321.6303 |
| sp P49411 EFTU_HUMAN           | 1814.9713 |
| sp Q96KG9 SCYL1_HUMAN          | 2684.3493 |
| sp O75475 PSIP1_HUMAN,sp Q7Z4V | 1454.6401 |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 1062.473  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp Q9H0A0 NAT10_HUMAN          | 1931.9517 |
| sp P31040 SDHA_HUMAN           | 1959.8931 |
| sp Q9Y6N7 ROBO1_HUMAN          | 1335.6493 |

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| sp Q10589 BST2_HUMAN           | 3034.4731 |
| sp P35613 BASI_HUMAN           | 1195.6601 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P08670 VIME_HUMAN,sp P08725 | 1256.5885 |
| sp O43707 ACTN4_HUMAN          | 2664.3218 |
| sp Q9BZK7 TBL1R_HUMAN          | 1964.9592 |
| sp Q15477 SKIV2_HUMAN          | 2328.0632 |
| sp Q9NX47 MARH5_HUMAN          | 1766.8159 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1069.5842 |
| sp P08670 VIME_HUMAN           | 2623.3857 |
| sp Q01813 PFKAP_HUMAN          | 1823.9393 |
| sp Q9BQG0 MBB1A_HUMAN          | 3089.6146 |
| sp P42167 LAP2B_HUMAN          | 2079.0861 |
| sp P46778 RL21_HUMAN           | 1567.7817 |
| sp P56192 SYMC_HUMAN           | 1964.9129 |
| sp P50991 TCPD_HUMAN           | 1058.5504 |
| sp P36578 RL4_HUMAN            | 1581.7886 |
| sp P37802 TAGL2_HUMAN          | 2852.3473 |
| sp P29401 TKT_HUMAN            | 1858.9247 |
| sp O00299 CLIC1_HUMAN          | 1633.7948 |
| sp Q13332 PTPRS_HUMAN          | 4748.1864 |
| sp Q8IYA6 CKP2L_HUMAN          | 1868.9592 |
| sp P78347 GTF2I_HUMAN          | 2548.3286 |
| sp P23284 PPIB_HUMAN           | 1985.9946 |
| sp Q03001 DYST_HUMAN           | 1785.817  |
| sp Q9HCE1 MOV10_HUMAN          | 1995.0062 |
| sp P04406 G3P_HUMAN            | 1841.9346 |
| sp P21333 FLNA_HUMAN           | 1766.7748 |
| sp Q9UHD8 SEPT9_HUMAN          | 1960.9967 |
| sp P18124 RL7_HUMAN            | 2216.163  |
| sp P62937 PPIA_HUMAN           | 4138.9041 |
| sp Q9UNX3 RL26L_HUMAN,sp P6121 | 2182.1495 |
| sp P46926 GNPI1_HUMAN          | 2136.1289 |
| sp Q8IVT2 MISP_HUMAN           | 2362.1302 |
| sp P25685 DNJB1_HUMAN          | 1837.8119 |
| sp P09622 DLDH_HUMAN           | 1693.8788 |
| sp Q9P2J5 SYLC_HUMAN           | 2438.2264 |
| sp P09012 SNRPA_HUMAN          | 1566.8002 |
| sp P49327 FAS_HUMAN            | 2624.3122 |
| sp Q9UQE7 SMC3_HUMAN           | 2231.0416 |
| sp Q13045 FLII_HUMAN           | 4006.9218 |
| sp Q8N8S7 ENAH_HUMAN           | 3514.6237 |
| sp P18621 RL17_HUMAN           | 1512.7647 |
| sp P52888 THOP1_HUMAN          | 1501.7606 |
| sp Q14964 RB39A_HUMAN,sp Q9HC  | 1753.8635 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp Q13421 MSLN_HUMAN           | 4011.9717 |

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| sp P08195 4F2_HUMAN            | 2276.278  |
| sp P22626 ROA2_HUMAN           | 1534.7264 |
| sp P68032 ACTC_HUMAN,sp P63267 | 4520.0523 |
| sp P62701 RS4X_HUMAN,sp Q8TD47 | 1560.8035 |
| sp P38646 GRP75_HUMAN          | 1842.8934 |
| sp Q9NW82 WDR70_HUMAN          | 2269.159  |
| sp P49327 FAS_HUMAN            | 1356.6826 |
| sp Q9HD20 AT131_HUMAN          | 2404.2387 |
| sp P62277 RS13_HUMAN           | 1577.8777 |
| sp P14866 HNRPL_HUMAN          | 3282.5027 |
| sp P27824 CALX_HUMAN           | 2059.9527 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P62899 RL31_HUMAN           | 1369.6626 |
| sp P16401 H15_HUMAN,rev_sp P16 | 1205.6768 |
| sp P05387 RLA2_HUMAN           | 2549.3013 |
| sp P62424 RL7A_HUMAN           | 2007.0425 |
| sp P23396 RS3_HUMAN            | 1399.6766 |
| sp Q8IVT2 MISP_HUMAN           | 2062.9556 |
| sp Q96CS3 FAF2_HUMAN           | 2609.1744 |
| sp P06753 TPM3_HUMAN,sp P6793  | 1592.7431 |
| sp Q9BZE4 NOG1_HUMAN           | 1631.7328 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2928.4691 |
| sp Q6UVK1 CSPG4_HUMAN          | 3790.9139 |
| sp P14384 CBPM_HUMAN           | 3394.6941 |
| sp Q7Z2W4 ZCCHV_HUMAN          | 1532.6855 |
| sp Q1KMD3 HNRL2_HUMAN          | 2453.2584 |
| sp Q15149 PLEC_HUMAN           | 1961.8942 |
| sp P33176 KINH_HUMAN           | 1249.6303 |
| sp P53621 COPA_HUMAN           | 1841.9887 |
| sp P39019 RS19_HUMAN           | 1809.9659 |
| sp Q15181 IPYR_HUMAN           | 3368.6176 |
| sp Q12874 SF3A3_HUMAN          | 2167.0296 |
| sp Q9BUJ2 HNRL1_HUMAN          | 1835.9166 |
| sp Q9H361 PABP3_HUMAN,sp P119  | 1815.9771 |
| sp P07900 HS90A_HUMAN,sp Q58F6 | 1142.5754 |
| sp P42766 RL35_HUMAN           | 1453.7929 |
| sp O94906 PRP6_HUMAN           | 2077.0125 |
| sp P05141 ADT2_HUMAN,sp P12236 | 1655.8308 |
| sp Q8WUM4 PDC6I_HUMAN          | 1518.6375 |
| sp Q8IWS0 PHF6_HUMAN           | 1223.6299 |
| sp P26038 MOES_HUMAN           | 1304.6725 |
| sp P05556 ITB1_HUMAN           | 2215.1848 |
| sp P16435 NCPR_HUMAN           | 2804.3406 |
| sp P08174 DAF_HUMAN            | 2476.0992 |
| sp Q93009 UBP7_HUMAN           | 1751.8301 |
| sp Q05519 SRS11_HUMAN          | 1704.8723 |
| sp Q71DI3 H32_HUMAN            | 3881.824  |

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| sp P31327 CPSM_HUMAN           | 1188.6027 |
| sp P05787 K2C8_HUMAN           | 2593.1854 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3105.4172 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2719.1966 |
| sp Q09666 AHNK_HUMAN           | 2609.222  |
| sp P61978 HNRPK_HUMAN          | 1467.7318 |
| sp P35052 GPC1_HUMAN           | 2722.3676 |
| sp O75475 PSIP1_HUMAN          | 1280.5819 |
| sp Q92930 RAB8B_HUMAN,sp P610  | 1881.9585 |
| sp Q9NVJ2 ARL8B_HUMAN,sp Q96B  | 2748.481  |
| sp P39023 RL3_HUMAN            | 3308.6652 |
| sp P08758 ANXA5_HUMAN          | 1321.6262 |
| sp P05787 K2C8_HUMAN           | 1338.7507 |
| sp Q14247 SRC8_HUMAN           | 1464.6634 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2611.2303 |
| sp P63279 UBC9_HUMAN           | 1415.6721 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 3730.7396 |
| sp Q9NZ01 TECR_HUMAN           | 2180.0824 |
| sp Q13813 SPTN1_HUMAN          | 1627.7413 |
| sp P00441 SODC_HUMAN           | 1348.6008 |
| sp Q00796 DH5O_HUMAN           | 1994.0037 |
| sp P43003 EAA1_HUMAN           | 1911.9077 |
| sp P26373 RL13_HUMAN           | 1169.6445 |
| sp P51991 ROA3_HUMAN           | 1704.8683 |
| sp P26368 U2AF2_HUMAN          | 2665.3422 |
| sp Q13162 PRDX4_HUMAN          | 2503.2271 |
| sp Q92616 GCN1_HUMAN           | 3569.8326 |
| sp P04406 G3P_HUMAN            | 1228.62   |
| sp P62280 RS11_HUMAN           | 1144.6128 |
| sp Q96J84 KIRR1_HUMAN          | 1865.9094 |
| sp Q14103 HNRPD_HUMAN          | 1771.8563 |
| sp P05787 K2C8_HUMAN           | 1338.7507 |
| sp P35251 RFC1_HUMAN           | 3820.8083 |
| sp Q16695 H31T_HUMAN,sp Q71DI  | 1629.8587 |
| sp P51511 MMP15_HUMAN          | 2290.127  |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp A6NCN8 TEX52_HUMAN          | 2518.2452 |
| sp P04406 G3P_HUMAN            | 3604.7144 |
| sp P62280 RS11_HUMAN           | 1824.8036 |
| sp P06733 ENOA_HUMAN           | 3336.5979 |
| sp Q8TEQ6 GEMI5_HUMAN          | 1969.913  |
| sp P62826 RAN_HUMAN            | 1609.7637 |
| sp Q14118 DAG1_HUMAN           | 2055.9722 |
| sp P04818 TYSY_HUMAN           | 1934.9738 |
| sp P05141 ADT2_HUMAN,sp Q9H0C  | 2177.047  |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 2727.4041 |
| sp P18084 ITB5_HUMAN           | 1430.6711 |

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| sp P62937 PPIA_HUMAN          | 2679.2453 |
| sp Q96AE4 FUBP1_HUMAN         | 2479.1649 |
| sp Q99497 PARK7_HUMAN         | 2370.9845 |
| sp P14625 ENPL_HUMAN          | 2203.0626 |
| sp P10586 PTPRF_HUMAN         | 1778.8298 |
| sp Q96N21 AP4AT_HUMAN         | 2594.2799 |
| sp P39019 RS19_HUMAN          | 1809.9659 |
| sp Q7L2H7 EIF3M_HUMAN         | 1345.6739 |
| sp Q5SRE5 NU188_HUMAN         | 1858.9533 |
| sp P62269 RS18_HUMAN          | 1181.5425 |
| sp P35579 MYH9_HUMAN          | 1720.8308 |
| sp P21333 FLNA_HUMAN          | 5081.3335 |
| sp O14980 XPO1_HUMAN          | 2072.0864 |
| sp P55854 SUMO3_HUMAN,sp P619 | 1250.6329 |
| sp P25398 RS12_HUMAN          | 1385.6649 |
| sp P27635 RL10_HUMAN          | 1067.5036 |
| sp O75534 CSDE1_HUMAN         | 2052.0025 |
| sp P22314 UBA1_HUMAN          | 2150.0168 |
| sp P22392 NDKB_HUMAN          | 2092.0041 |
| sp O75608 LYPA1_HUMAN         | 3381.6295 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 1180.5612 |
| sp P62937 PPIA_HUMAN          | 1575.7821 |
| sp P38646 GRP75_HUMAN         | 3887.7176 |
| sp P61247 RS3A_HUMAN          | 1295.622  |
| sp Q13310 PABP4_HUMAN         | 1585.7307 |
| sp Q9Y6E2 BZW2_HUMAN          | 1561.7889 |
| sp P08581 MET_HUMAN           | 1672.8494 |
| sp P83731 RL24_HUMAN          | 2165.984  |
| sp P08729 K2C7_HUMAN          | 2869.2977 |
| sp Q99832 TCPH_HUMAN          | 2443.2959 |
| sp P42704 LPPRC_HUMAN         | 1704.793  |
| sp P40429 RL13A_HUMAN         | 2369.1539 |
| sp O00534 VMA5A_HUMAN         | 1984.1357 |
| sp P62304 RUXE_HUMAN          | 3335.5214 |
| sp P60900 PSA6_HUMAN          | 1990.8692 |
| sp Q02750 MP2K1_HUMAN         | 2806.4436 |
| sp Q8N257 H2B3B_HUMAN,sp P628 | 3105.4172 |
| sp P43246 MSH2_HUMAN          | 1970.9109 |
| sp Q9NZ45 CISD1_HUMAN         | 2351.0198 |
| sp P08240 SRPRA_HUMAN         | 4129.9426 |
| sp Q15459 SF3A1_HUMAN         | 1859.9265 |
| sp P07919 QCR6_HUMAN,sp A0A09 | 1791.8363 |
| sp Q6YHK3 CD109_HUMAN         | 1653.829  |
| sp Q8IWX8 CHERP_HUMAN         | 2889.4582 |
| sp P31943 HNRH1_HUMAN         | 3946.9451 |
| sp P04406 G3P_HUMAN           | 3129.4787 |
| sp O00299 CLIC1_HUMAN         | 2234.0491 |

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| sp P27797 CALR_HUMAN           | 1014.4407 |
| sp Q9P2J5 SYLC_HUMAN           | 1697.8546 |
| sp P35579 MYH9_HUMAN           | 2650.2704 |
| sp Q5UIP0 RIF1_HUMAN           | 1497.7212 |
| sp P04406 G3P_HUMAN            | 1351.6983 |
| sp O15357 SHIP2_HUMAN          | 1515.7569 |
| sp P13987 CD59_HUMAN           | 1972.8659 |
| sp P30086 PEBP1_HUMAN          | 2989.428  |
| sp P04843 RPN1_HUMAN           | 1576.7621 |
| sp O75937 DNJC8_HUMAN          | 3674.7992 |
| sp P78347 GTF2I_HUMAN          | 1994.9262 |
| sp P05386 RLA1_HUMAN           | 2551.3475 |
| sp P11172 UMPS_HUMAN           | 2353.1658 |
| sp O95573 ACSL3_HUMAN          | 3709.9178 |
| sp Q92945 FUBP2_HUMAN          | 2314.119  |
| sp P20700 LMNB1_HUMAN          | 2218.0365 |
| sp P23396 RS3_HUMAN            | 1297.6262 |
| sp O95347 SMC2_HUMAN           | 1759.8992 |
| sp Q8N752 KC1AL_HUMAN,sp P487: | 2528.1318 |
| sp O15143 ARC1B_HUMAN          | 1403.6834 |
| sp Q14160 SCRIB_HUMAN          | 3694.8744 |
| sp P20700 LMNB1_HUMAN          | 2852.4291 |
| sp P61981 1433G_HUMAN,sp P631C | 1124.5576 |
| sp Q00610 CLH1_HUMAN           | 1462.7205 |
| sp P17987 TCPA_HUMAN           | 1493.7297 |
| sp Q8NBU5 ATAD1_HUMAN          | 1547.7845 |
| sp P04406 G3P_HUMAN            | 1643.8407 |
| sp Q13616 CUL1_HUMAN           | 2212.131  |
| sp P12814 ACTN1_HUMAN          | 1234.6306 |
| sp P83731 RL24_HUMAN           | 1613.8083 |
| sp Q15262 PTPRK_HUMAN          | 2990.412  |
| sp P16070 CD44_HUMAN           | 1556.7372 |
| sp P31939 PUR9_HUMAN           | 2811.3095 |
| sp P62805 H4_HUMAN             | 2018.1273 |
| sp P08670 VIME_HUMAN,sp P08725 | 1256.5885 |
| sp Q9Y624 JAM1_HUMAN           | 1677.7271 |
| sp P62805 H4_HUMAN             | 997.5193  |
| sp P13639 EF2_HUMAN            | 1437.765  |
| sp O43395 PRPF3_HUMAN          | 1765.8483 |
| sp Q03405 UPAR_HUMAN           | 3305.4531 |
| sp Q6PJQ5 FOXR2_HUMAN          | 1708.8276 |
| sp P06744 G6PI_HUMAN           | 1121.5353 |
| sp P02786 TFR1_HUMAN           | 1235.651  |
| sp P53396 ACLY_HUMAN           | 3552.832  |
| sp P62847 RS24_HUMAN           | 2578.1322 |
| sp Q92466 DDB2_HUMAN           | 3474.7031 |
| sp P05787 K2C8_HUMAN           | 1733.8584 |

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| sp P16402 H13_HUMAN,sp P16401  | 1362.6416 |
| sp P30101 PDIA3_HUMAN          | 2899.424  |
| sp P05141 ADT2_HUMAN,sp P12235 | 1591.7783 |
| sp P50991 TCPD_HUMAN           | 1927.9349 |
| sp P26641 EF1G_HUMAN           | 2785.2548 |
| sp P11586 C1TC_HUMAN           | 2561.3013 |
| sp P62280 RS11_HUMAN           | 1144.6128 |
| sp P50895 BCAM_HUMAN           | 2579.2405 |
| sp P07900 HS90A_HUMAN,sp P0823 | 1343.7197 |
| sp O14980 XPO1_HUMAN           | 2450.1655 |
| sp Q9H4A3 WNK1_HUMAN           | 2463.1707 |
| sp O75369 FLNB_HUMAN           | 1358.683  |
| sp Q92499 DDX1_HUMAN           | 2040.0026 |
| sp P16403 H12_HUMAN            | 1261.7394 |
| sp P29992 GNA11_HUMAN          | 1670.7536 |
| sp Q8TCS8 PNPT1_HUMAN          | 2302.2607 |
| sp Q9P2N6 KANL3_HUMAN          | 4379.1546 |
| sp P15121 ALDR_HUMAN           | 1647.8832 |
| sp Q9Y4A5 TRRAP_HUMAN          | 3337.5997 |
| sp Q6YHK3 CD109_HUMAN          | 2904.4618 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 1069.5842 |
| sp O15131 IMA6_HUMAN,sp O6068  | 4228.1508 |
| sp P62899 RL31_HUMAN           | 1081.5556 |
| sp P46782 RS5_HUMAN            | 2183.078  |
| sp O00303 EIF3F_HUMAN          | 2582.1709 |
| sp O43175 SERA_HUMAN           | 3749.9087 |
| sp P02545 LMNA_HUMAN           | 1710.8537 |
| sp P20908 CO5A1_HUMAN          | 2760.2708 |
| sp P31948 STIP1_HUMAN          | 2790.3171 |
| sp O00541 PESC_HUMAN           | 1121.5102 |
| sp Q15005 SPCS2_HUMAN          | 2809.2905 |
| sp Q92973 TNPO1_HUMAN          | 2925.4623 |
| sp P62424 RL7A_HUMAN           | 1568.7583 |
| sp Q9BY67 CADM1_HUMAN          | 1329.6313 |
| sp P16401 H15_HUMAN,sp P10412  | 1182.5881 |
| sp O00148 DX39A_HUMAN,sp Q138  | 1439.766  |
| sp P43121 MUC18_HUMAN          | 1470.7402 |
| sp P54709 AT1B3_HUMAN          | 1532.6855 |
| sp P04075 ALDOA_HUMAN          | 1264.6048 |
| sp P49327 FAS_HUMAN            | 1797.9369 |
| sp P10809 CH60_HUMAN           | 1382.7479 |
| sp Q01955 CO4A3_HUMAN          | 2974.4897 |
| sp Q9Y316 MEMO1_HUMAN          | 3374.5448 |
| sp P04406 G3P_HUMAN            | 3548.7457 |
| sp P02786 TFR1_HUMAN           | 2596.3061 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1483.7493 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 1320.6561 |

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| sp P09661 RU2A_HUMAN          | 1562.8417 |
| sp Q9UG63 ABCF2_HUMAN         | 1239.5996 |
| sp O75351 VPS4B_HUMAN,sp Q9UN | 2006.0877 |
| sp Q92616 GCN1_HUMAN          | 2843.4957 |
| sp Q15149 PLEC_HUMAN          | 1134.5782 |
| sp P26447 S10A4_HUMAN         | 1284.6561 |
| sp P10599 THIO_HUMAN          | 1361.6099 |
| sp P05787 K2C8_HUMAN          | 1733.8584 |
| sp P13010 XRCC5_HUMAN         | 3640.6668 |
| sp P49792 RBP2_HUMAN          | 3497.7301 |
| sp P62753 RS6_HUMAN           | 1782.8835 |
| sp Q9NWT1 PK1IP_HUMAN         | 2222.0678 |
| sp Q96JB5 CK5P3_HUMAN         | 2412.0441 |
| sp P18124 RL7_HUMAN           | 1736.8199 |
| sp P35613 BASI_HUMAN          | 1195.6601 |
| sp Q9H0C8 ILKAP_HUMAN         | 1906.965  |
| sp P78527 PRKDC_HUMAN         | 3586.6488 |
| sp A6ZKI3 RTL8C_HUMAN         | 2069.2361 |
| sp O94826 TOM70_HUMAN         | 1808.9057 |
| sp O00148 DX39A_HUMAN         | 1976.9592 |
| sp P09429 HMGB1_HUMAN         | 2434.0747 |
| sp P52272 HNRPM_HUMAN         | 1758.9338 |
| sp P05787 K2C8_HUMAN          | 1733.8584 |
| sp P07099 HYEP_HUMAN          | 4250.0518 |
| sp P0CG40 SP9_HUMAN,sp P08047 | 1260.6099 |
| sp P31040 SDHA_HUMAN          | 1112.5251 |
| sp P62266 RS23_HUMAN          | 1152.4836 |
| sp Q02218 ODO1_HUMAN          | 2340.2253 |
| sp Q13442 HAP28_HUMAN         | 1425.6558 |
| sp Q8NHW5 RLA0L_HUMAN,sp P05: | 1865.9523 |
| sp Q02543 RL18A_HUMAN         | 1926.8669 |
| sp P55265 DSRAD_HUMAN         | 1218.6649 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3 | 1182.6357 |
| sp Q15067 ACOX1_HUMAN         | 1536.7209 |
| sp Q9Y2X3 NOP58_HUMAN         | 2335.1301 |
| sp Q06830 PRDX1_HUMAN         | 3779.8254 |
| sp P21333 FLNA_HUMAN          | 2783.2787 |
| sp Q03405 UPAR_HUMAN          | 2888.3644 |
| sp P04075 ALDOA_HUMAN         | 1773.8533 |
| sp P12277 KCRB_HUMAN          | 3783.8124 |
| sp P46777 RL5_HUMAN           | 1432.7198 |
| sp P02786 TFR1_HUMAN          | 1460.7048 |
| sp P52272 HNRPM_HUMAN         | 1735.828  |
| sp P28288 ABCD3_HUMAN         | 1426.6841 |
| sp P10586 PTPRF_HUMAN         | 4348.1135 |
| sp P11021 BIP_HUMAN           | 3302.6572 |
| sp Q14166 TTL12_HUMAN         | 1902.9799 |



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| sp Q99613 EIF3C_HUMAN,sp B5ME: | 1506.8406 |
| sp P07900 HS90A_HUMAN          | 2195.0205 |
| sp P16403 H12_HUMAN            | 1124.5826 |
| sp P33176 KINH_HUMAN           | 1565.7508 |
| sp P08238 HS90B_HUMAN,sp Q58F  | 1560.7573 |
| sp P09429 HMGB1_HUMAN          | 2434.0747 |
| sp P10809 CH60_HUMAN           | 1382.7479 |
| sp O60568 PLOD3_HUMAN          | 2351.0892 |
| sp Q9BZZ5 API5_HUMAN           | 2224.1739 |
| sp Q01813 PFKAP_HUMAN          | 1830.9363 |
| sp Q01813 PFKAP_HUMAN          | 1830.9363 |
| sp P16402 H13_HUMAN,sp P16401  | 1362.6416 |
| sp Q00839 HNRPU_HUMAN          | 1469.6431 |
| sp P52272 HNRPM_HUMAN          | 2248.1196 |
| sp P62826 RAN_HUMAN            | 2020.9279 |
| sp Q15149 PLEC_HUMAN           | 1270.6558 |
| sp Q14258 TRI25_HUMAN          | 1725.8362 |
| sp O75694 NU155_HUMAN          | 1412.6572 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1097.5254 |
| sp P26641 EF1G_HUMAN           | 1248.6139 |
| sp P08047 SP1_HUMAN,sp Q02446  | 1256.6149 |
| sp P23396 RS3_HUMAN            | 3010.3841 |
| sp P38919 IF4A3_HUMAN          | 1171.6237 |
| sp P58743 S26A5_HUMAN          | 3317.741  |
| sp P50990 TCPQ_HUMAN           | 2402.1974 |
| sp Q96J84 KIRR1_HUMAN          | 1865.9094 |
| sp P43243 MATR3_HUMAN          | 1463.762  |
| sp P27824 CALX_HUMAN           | 2738.3639 |
| sp P62829 RL23_HUMAN           | 1443.7973 |
| sp O75153 CLU_HUMAN            | 2279.1474 |
| sp P48643 TCPE_HUMAN           | 2968.5492 |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P15151 PVR_HUMAN            | 2703.162  |
| sp O43447 PPIH_HUMAN           | 1893.0182 |
| sp O75367 H2AY_HUMAN           | 1770.9152 |
| sp Q14839 CHD4_HUMAN           | 1295.7523 |
| sp P30153 2AAA_HUMAN           | 2815.3752 |
| sp P07108 ACBP_HUMAN           | 1456.6623 |
| sp O75083 WDR1_HUMAN           | 4211.7754 |
| sp P16435 NCPR_HUMAN           | 2804.3406 |
| sp Q8N8S7 ENAH_HUMAN           | 2073.9657 |
| sp Q9BRR6 ADPGK_HUMAN          | 2311.1307 |
| sp P31939 PUR9_HUMAN           | 2228.0889 |
| sp P02786 TFR1_HUMAN           | 2337.9518 |
| sp Q15149 PLEC_HUMAN           | 2421.2322 |
| sp Q13428 TCOF_HUMAN           | 1060.5302 |
| sp Q9Y262 EIF3L_HUMAN          | 1509.7212 |

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| sp P27824 CALX_HUMAN           | 2594.274  |
| sp P49327 FAS_HUMAN            | 2649.1952 |
| sp P60842 IF4A1_HUMAN          | 1785.8567 |
| sp Q14247 SRC8_HUMAN           | 1494.6562 |
| sp P07355 ANXA2_HUMAN          | 1232.5673 |
| sp P05386 RLA1_HUMAN           | 4560.2919 |
| sp Q9Y287 ITM2B_HUMAN          | 1786.8308 |
| sp P23246 SFPQ_HUMAN           | 1441.7201 |
| sp Q13283 G3BP1_HUMAN          | 1931.8618 |
| sp Q07020 RL18_HUMAN           | 1969.9997 |
| sp P08670 VIME_HUMAN           | 1499.6926 |
| sp P16403 H12_HUMAN            | 1065.6182 |
| sp P08237 PFKAM_HUMAN          | 2439.1707 |
| sp Q13283 G3BP1_HUMAN          | 2690.2864 |
| sp P16403 H12_HUMAN            | 1210.6558 |
| sp P42166 LAP2A_HUMAN          | 1637.7645 |
| sp P41091 IF2G_HUMAN,sp Q2VIR3 | 1649.8737 |
| sp P10412 H14_HUMAN            | 1037.5506 |
| sp P78347 GTF2I_HUMAN          | 1912.0458 |
| sp P24941 CDK2_HUMAN           | 1943.0364 |
| sp P32969 RL9_HUMAN            | 1335.6459 |
| sp P16435 NCPR_HUMAN           | 1467.747  |
| sp P01130 LDLR_HUMAN           | 4341.9738 |
| sp P00338 LDHA_HUMAN           | 1691.8002 |
| sp P48449 ERG7_HUMAN           | 2336.1947 |
| sp Q63HN8 RN213_HUMAN          | 2315.1368 |
| sp P51531 SMCA2_HUMAN,sp P515  | 2127.1034 |
| sp P53396 ACLY_HUMAN           | 1610.8417 |
| sp P53007 TXTP_HUMAN           | 1798.8275 |
| sp Q96HC4 PDLI5_HUMAN          | 1174.5731 |
| sp P07195 LDHB_HUMAN           | 1500.7096 |
| sp P78371 TCPB_HUMAN           | 1688.9097 |
| sp Q15149 PLEC_HUMAN           | 1368.7038 |
| sp Q8WXH0 SYNE2_HUMAN          | 2498.3454 |
| sp P35637 FUS_HUMAN            | 3398.3371 |
| sp P52943 CRIP2_HUMAN          | 1920.9265 |
| sp P06733 ENOA_HUMAN           | 3181.4193 |
| sp Q02241 KIF23_HUMAN          | 1284.635  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp Q969P0 IGSF8_HUMAN          | 1176.5597 |
| sp Q13813 SPTN1_HUMAN          | 1390.6477 |
| sp Q09028 RBBP4_HUMAN,sp Q165  | 1517.7402 |
| sp Q8IXI2 MIRO1_HUMAN          | 1504.6769 |
| sp P50502 F10A1_HUMAN,sp Q8IZP | 1838.005  |
| sp P26641 EF1G_HUMAN           | 2386.1845 |
| sp P55145 MANF_HUMAN           | 2120.1266 |
| sp P00966 ASSY_HUMAN           | 2474.2304 |

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| sp P31327 CPSM_HUMAN           | 3066.5047 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp O75934 SPF27_HUMAN          | 1533.7324 |
| sp Q8NEY8 PPHLN_HUMAN          | 1687.7339 |
| sp Q16666 IF16_HUMAN           | 1975.9098 |
| sp P37108 SRP14_HUMAN          | 2793.3781 |
| sp P21333 FLNA_HUMAN           | 3685.8873 |
| sp P35579 MYH9_HUMAN           | 3206.4107 |
| sp P52597 HNRPF_HUMAN          | 3018.4294 |
| sp P49327 FAS_HUMAN            | 1797.9369 |
| sp P62906 RL10A_HUMAN          | 1680.8247 |
| sp P34897 GLYM_HUMAN           | 2608.205  |
| sp O60832 DKC1_HUMAN           | 2011.9422 |
| sp P38159 RBMX_HUMAN           | 1406.683  |
| sp Q9UUK9 NUDT5_HUMAN          | 1693.8464 |
| sp P62266 RS23_HUMAN           | 1152.4836 |
| sp O76021 RL1D1_HUMAN          | 1377.6525 |
| sp Q99832 TCPH_HUMAN           | 2443.2959 |
| sp P29992 GNA11_HUMAN          | 1670.7536 |
| sp P62195 PRS8_HUMAN           | 1290.6932 |
| sp P60709 ACTB_HUMAN,sp P68032 | 1550.6485 |
| sp P21926 CD9_HUMAN            | 1310.6466 |
| sp P26038 MOES_HUMAN           | 1460.7664 |
| sp P04632 CPNS1_HUMAN          | 1766.79   |
| sp P11387 TOP1_HUMAN           | 1670.8668 |
| sp P46781 RS9_HUMAN            | 1595.8671 |
| sp P11586 C1TC_HUMAN           | 2195.9331 |
| sp Q15424 SAFB1_HUMAN,sp Q1411 | 1309.699  |
| sp Q9UNF1 MAGD2_HUMAN          | 3593.7989 |
| sp P45974 UBP5_HUMAN           | 1722.8325 |
| sp Q63HN8 RN213_HUMAN          | 1837.0019 |
| sp P00558 PGK1_HUMAN           | 1047.5059 |
| sp Q02543 RL18A_HUMAN          | 2252.0419 |
| sp Q13425 SNTB2_HUMAN          | 2153.1191 |
| sp Q9UPN3 MACF1_HUMAN          | 2646.3118 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 1783.748  |
| sp P05198 IF2A_HUMAN           | 1468.6511 |
| sp P05783 K1C18_HUMAN          | 1370.6678 |
| sp Q15149 PLEC_HUMAN           | 1640.8621 |
| sp Q92769 HDAC2_HUMAN          | 1640.7981 |
| sp O75376 NCOR1_HUMAN          | 1250.6255 |
| sp P21926 CD9_HUMAN            | 1375.6871 |
| sp P05387 RLA2_HUMAN           | 2549.3013 |
| sp Q9NYU2 UGGG1_HUMAN          | 3354.5582 |
| sp P78347 GTF2I_HUMAN          | 2208.0487 |
| sp Q9H2P0 ADNP_HUMAN           | 1485.6677 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1704.7811 |

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| sp P31327 CPSM_HUMAN           | 3842.7774 |
| sp Q15369 ELOC_HUMAN           | 2298.0701 |
| sp Q15366 PCBP2_HUMAN          | 2625.3187 |
| sp P62280 RS11_HUMAN           | 1824.8036 |
| sp P61247 RS3A_HUMAN           | 1921.9098 |
| sp P60709 ACTB_HUMAN,sp P63261 | 2748.4083 |
| sp P26885 FKBP2_HUMAN          | 1656.8359 |
| sp P62937 PPIA_HUMAN           | 4122.9092 |
| sp P22314 UBA1_HUMAN           | 2500.285  |
| sp Q9H583 HEAT1_HUMAN          | 2630.3989 |
| sp P11940 PABP1_HUMAN          | 1548.7573 |
| sp P08708 RS17_HUMAN           | 1380.6925 |
| sp Q9UNX3 RL26L_HUMAN,sp P612! | 1456.7232 |
| sp Q9ULV4 COR1C_HUMAN          | 1237.584  |
| sp P08238 HS90B_HUMAN          | 3236.4206 |
| sp P10586 PTPRF_HUMAN          | 3075.5917 |
| sp P46013 KI67_HUMAN           | 2425.1245 |
| sp Q08945 SSRP1_HUMAN          | 2064.0375 |
| sp Q13162 PRDX4_HUMAN          | 2304.095  |
| sp Q13263 TIF1B_HUMAN          | 2683.1721 |
| sp Q7KZF4 SND1_HUMAN           | 2250.1393 |
| sp P39748 FEN1_HUMAN           | 1180.5724 |
| sp O60701 UGDH_HUMAN           | 3102.3854 |
| sp P04406 G3P_HUMAN            | 2478.3118 |
| sp Q92499 DDX1_HUMAN           | 2965.3148 |
| sp O00567 NOP56_HUMAN          | 1474.8031 |
| sp P11387 TOP1_HUMAN           | 1425.7041 |
| sp P41252 SYIC_HUMAN           | 2305.2206 |
| sp Q71U36 TBA1A_HUMAN,sp P683  | 3730.7396 |
| sp Q14240 IF4A2_HUMAN,sp P6084 | 1581.7246 |
| sp P84098 RL19_HUMAN           | 1119.5673 |
| sp O95834 EMAL2_HUMAN          | 2777.2578 |
| sp P39023 RL3_HUMAN            | 2443.206  |
| sp Q9BWJ5 SF3B5_HUMAN          | 2924.3941 |
| sp P00558 PGK1_HUMAN           | 1554.8042 |
| sp P49327 FAS_HUMAN            | 2788.3014 |
| sp P10412 H14_HUMAN            | 1022.5397 |
| sp P62266 RS23_HUMAN           | 1401.7001 |
| sp Q09161 NCBP1_HUMAN          | 1672.6826 |
| sp O43707 ACTN4_HUMAN          | 2023.0011 |
| sp P08621 RU17_HUMAN           | 1555.6362 |
| sp P68104 EF1A1_HUMAN,sp Q5VTi | 4150.887  |
| sp P23246 SFPQ_HUMAN           | 1431.6743 |
| sp Q8WXG6 MADD_HUMAN           | 2227.0869 |
| sp O75396 SC22B_HUMAN          | 1948.9279 |
| sp P02545 LMNA_HUMAN           | 1281.6929 |
| sp P16403 H12_HUMAN            | 1409.7878 |

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| sp P05161 ISG15_HUMAN          | 1920.9806 |
| sp Q13813 SPTN1_HUMAN          | 2116.0589 |
| sp O95340 PAPS2_HUMAN          | 2422.1262 |
| sp P22694 KAPCB_HUMAN,sp P1761 | 1857.8897 |
| sp Q06830 PRDX1_HUMAN          | 1321.6038 |
| sp P05783 K1C18_HUMAN          | 3411.526  |
| sp P62937 PPIA_HUMAN           | 2679.2453 |
| sp O14980 XPO1_HUMAN           | 2641.354  |
| sp O75533 SF3B1_HUMAN          | 2179.0639 |
| sp Q5GLZ8 HERC4_HUMAN          | 2166.1321 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1928.9091 |
| sp P11021 BIP_HUMAN            | 1503.7432 |
| sp P50416 CPT1A_HUMAN          | 1679.7732 |
| sp Q6P2Q9 PRP8_HUMAN           | 3594.8255 |
| sp Q9Y2Q3 GSTK1_HUMAN          | 2739.3877 |
| sp P04908 H2A1B_HUMAN,sp Q930  | 1496.7107 |
| sp P58743 S26A5_HUMAN          | 3317.741  |
| sp P62314 SMD1_HUMAN           | 2710.4357 |
| sp P27824 CALX_HUMAN           | 2425.1525 |
| sp Q13813 SPTN1_HUMAN          | 1424.7048 |
| sp P50238 CRIP1_HUMAN          | 1892.9203 |
| sp P49327 FAS_HUMAN            | 3741.6021 |
| sp P07237 PDIA1_HUMAN          | 2206.043  |
| sp O95340 PAPS2_HUMAN          | 3085.4855 |
| sp P13995 MTDC_HUMAN           | 2883.4991 |
| sp P18621 RL17_HUMAN           | 1566.746  |
| sp P06748 NPM_HUMAN            | 2769.2267 |
| sp P52597 HNRPF_HUMAN          | 2751.318  |
| sp P62805 H4_HUMAN             | 1634.8226 |
| sp Q13620 CUL4B_HUMAN          | 1716.822  |
| sp Q92900 RENT1_HUMAN          | 4183.2178 |
| sp Q92901 RL3L_HUMAN,sp P39023 | 1249.5588 |
| sp P78527 PRKDC_HUMAN          | 1076.5866 |
| sp P62937 PPIA_HUMAN           | 4138.9041 |
| sp Q14247 SRC8_HUMAN           | 1687.7689 |
| sp O14787 TNPO2_HUMAN          | 1594.749  |
| sp Q01085 TIAR_HUMAN           | 3146.2845 |
| sp P25685 DNJB1_HUMAN          | 1837.8119 |
| sp P30101 PDIA3_HUMAN          | 3262.4983 |
| sp P06748 NPM_HUMAN            | 1556.7082 |
| sp P40939 ECHA_HUMAN           | 2304.1209 |
| sp O00303 EIF3F_HUMAN          | 4499.0785 |
| sp P02545 LMNA_HUMAN           | 2540.3221 |
| sp P46781 RS9_HUMAN            | 1115.536  |
| sp P51531 SMCA2_HUMAN,sp P515  | 1020.524  |
| sp P06576 ATPB_HUMAN           | 2759.2596 |
| sp P55769 NH2L1_HUMAN          | 2556.2676 |

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| sp P07814 SYEP_HUMAN           | 2758.2951 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 3907.7862 |
| sp P26599 PTBP1_HUMAN,sp Q9UK  | 987.5025  |
| sp Q15942 ZYX_HUMAN            | 1363.75   |
| sp O95678 K2C75_HUMAN,sp P486  | 1848.937  |
| sp Q9BYX7 ACTBM_HUMAN,sp POC   | 1820.8866 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp Q9Y446 PKP3_HUMAN           | 1891.9541 |
| sp P10809 CH60_HUMAN           | 1898.905  |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp Q9Y2V2 CHSP1_HUMAN          | 4270.9859 |
| sp P40926 MDHM_HUMAN           | 2695.4367 |
| sp P33176 KINH_HUMAN           | 1565.7508 |
| sp P62917 RL8_HUMAN            | 1253.6768 |
| sp P49792 RBP2_HUMAN           | 1877.8544 |
| sp Q5ZPR3 CD276_HUMAN          | 2904.3851 |
| sp P14174 MIF_HUMAN            | 1705.8345 |
| sp P58743 S26A5_HUMAN          | 3317.741  |
| sp Q96HS1 PGAM5_HUMAN          | 1515.714  |
| sp Q7KYR7 BT2A1_HUMAN,sp Q8W   | 1738.8315 |
| sp P49327 FAS_HUMAN            | 2649.1952 |
| sp Q9BZZ5 API5_HUMAN           | 2767.4221 |
| sp P60174 TPIS_HUMAN           | 2315.1474 |
| sp Q15233 NONO_HUMAN           | 1444.6987 |
| sp Q8IUE6 H2A2B_HUMAN          | 1207.5833 |
| sp P09661 RU2A_HUMAN           | 2890.4308 |
| sp P13984 T2FB_HUMAN           | 2634.235  |
| sp P30153 2AAA_HUMAN,sp P3015  | 1566.8617 |
| sp P62266 RS23_HUMAN           | 1152.4836 |
| sp Q8WZ42 TITIN_HUMAN          | 1677.7846 |
| sp Q08380 LG3BP_HUMAN          | 2445.1237 |
| sp P14625 ENPL_HUMAN           | 2572.1654 |
| sp Q12972 PP1R8_HUMAN          | 1611.8522 |
| sp Q8IZV5 RDH10_HUMAN          | 3594.7624 |
| sp P14866 HNRPL_HUMAN          | 3574.5078 |
| sp P33316 DUT_HUMAN            | 2144.0572 |
| sp P31948 STIP1_HUMAN          | 1817.8584 |
| sp P49411 EFTU_HUMAN           | 2325.1893 |
| sp Q9Y4D7 PLXD1_HUMAN          | 1519.7089 |
| sp Q8NI27 THOC2_HUMAN          | 2791.3276 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp Q01082 SPTB2_HUMAN          | 2266.1117 |
| sp P48735 IDHP_HUMAN           | 1633.8828 |
| sp Q02790 FKBP4_HUMAN          | 1350.682  |
| sp Q15629 TRAM1_HUMAN          | 1210.667  |
| sp P10586 PTPRF_HUMAN          | 3126.6237 |
| sp Q9NRF8 PYRG2_HUMAN          | 2163.1113 |

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| sp Q9H8Y5 ANKZ1_HUMAN          | 1685.8274 |
| sp O75396 SC22B_HUMAN          | 2598.3006 |
| sp P83731 RL24_HUMAN           | 1613.8083 |
| sp P14618 KPYM_HUMAN           | 1054.5659 |
| sp Q9UK59 DBR1_HUMAN           | 1565.766  |
| sp P61247 RS3A_HUMAN           | 1295.622  |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 1989.9643 |
| sp P14314 GLU2B_HUMAN          | 1240.634  |
| sp Q15233 NONO_HUMAN           | 1282.5691 |
| sp P07910 HNRPC_HUMAN          | 2406.1427 |
| sp P00491 PNPH_HUMAN           | 2382.1143 |
| sp P07355 ANXA2_HUMAN          | 1232.5673 |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1185.5778 |
| sp Q9UQ80 PA2G4_HUMAN          | 2700.2928 |
| sp P31327 CPSM_HUMAN           | 2529.1403 |
| sp P07900 HS90A_HUMAN,sp Q145i | 1204.6816 |
| sp P38159 RBMX_HUMAN           | 1406.683  |
| sp P13639 EF2_HUMAN            | 1453.7599 |
| sp Q14103 HNRPD_HUMAN          | 1679.7865 |
| sp P20929 NEBU_HUMAN           | 3294.633  |
| sp Q15067 ACOX1_HUMAN          | 1751.7825 |
| sp P13639 EF2_HUMAN            | 3131.6114 |
| sp Q07157 ZO1_HUMAN            | 2848.345  |
| sp Q9NX63 MIC19_HUMAN          | 1927.8436 |
| sp Q9Y624 JAM1_HUMAN           | 1677.7271 |
| sp P56589 PEX3_HUMAN           | 1865.8908 |
| sp P18621 RL17_HUMAN           | 1772.7689 |
| sp P05783 K1C18_HUMAN          | 1440.7209 |
| sp P63010 AP2B1_HUMAN          | 2589.4054 |
| sp Q9UHX1 PUF60_HUMAN          | 1351.6741 |
| sp P46777 RL5_HUMAN            | 1690.8275 |
| sp P49327 FAS_HUMAN            | 2319.1893 |
| sp Q15149 PLEC_HUMAN           | 1255.6044 |
| sp Q9Y3D6 FIS1_HUMAN           | 1434.6627 |
| sp Q9Y2X3 NOP58_HUMAN          | 2195.1011 |
| sp Q6PQ5 FOXR2_HUMAN           | 1708.8276 |
| sp P62277 RS13_HUMAN           | 1243.6561 |
| sp P06733 ENOA_HUMAN           | 1314.6932 |
| sp P42766 RL35_HUMAN           | 1851.969  |
| sp P10586 PTPRF_HUMAN          | 1555.8107 |
| sp O43670 ZN207_HUMAN          | 1274.6983 |
| sp Q53LP3 SWAHC_HUMAN          | 1750.9002 |
| sp P05026 AT1B1_HUMAN          | 2807.3766 |
| sp P15924 DESP_HUMAN           | 1507.7341 |
| sp P48643 TCPE_HUMAN           | 2036.0653 |
| sp P31040 SDHA_HUMAN           | 1282.6558 |
| sp Q9NR30 DDX21_HUMAN          | 3100.4237 |

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| sp Q00839 HNRPU_HUMAN          | 1292.6361 |
| sp P32969 RL9_HUMAN            | 1335.6459 |
| sp A6NMY6 AXA2L_HUMAN,sp P073  | 3050.5812 |
| sp P31327 CPSM_HUMAN           | 2092.0589 |
| sp P62873 GBB1_HUMAN,sp P62873 | 2336.2165 |
| sp O76021 RL1D1_HUMAN          | 1576.7773 |
| sp P31949 S10AB_HUMAN          | 4363.0777 |
| sp Q14690 RRP5_HUMAN           | 1305.6313 |
| sp P62826 RAN_HUMAN            | 1284.5986 |
| sp Q9GZS1 RPA49_HUMAN          | 1727.9206 |
| sp P62269 RS18_HUMAN           | 1181.5425 |
| sp P61158 ARP3_HUMAN           | 2135.0834 |
| sp Q13098 CSN1_HUMAN           | 3416.6525 |
| sp P61160 ARP2_HUMAN           | 2622.2424 |
| sp P46778 RL21_HUMAN           | 1567.7817 |
| sp Q08211 DHX9_HUMAN           | 995.4308  |
| sp P46781 RS9_HUMAN            | 1680.8319 |
| sp P61513 RL37A_HUMAN          | 2253.0194 |
| sp Q12906 ILF3_HUMAN           | 1866.9727 |
| sp Q9Y5L0 TNPO3_HUMAN          | 2737.4902 |
| sp Q09666 AHNK_HUMAN           | 1699.8781 |
| sp P10586 PTPRF_HUMAN          | 1908.9357 |
| sp P18621 RL17_HUMAN           | 1686.8036 |
| sp P13073 COX41_HUMAN          | 1278.6568 |
| sp Q00325 MPCP_HUMAN           | 1842.988  |
| sp P05787 K2C8_HUMAN           | 2436.2496 |
| sp P46013 KI67_HUMAN           | 3376.6497 |
| sp Q86UP2 KTN1_HUMAN           | 2008.0113 |
| sp Q6YHK3 CD109_HUMAN          | 1381.7606 |
| sp Q86VP6 CAND1_HUMAN          | 1610.794  |
| sp P07237 PDIA1_HUMAN          | 1620.8035 |
| sp P61313 RL15_HUMAN           | 1901.9384 |
| sp P04083 ANXA1_HUMAN          | 1409.6721 |
| sp O75475 PSIP1_HUMAN          | 1715.9319 |
| sp P00367 DHE3_HUMAN,sp P49448 | 2090.0983 |
| sp P09429 HMGB1_HUMAN          | 1081.5404 |
| sp Q71U36 TBA1A_HUMAN,sp P0DP  | 1239.5594 |
| sp Q01167 FOXK2_HUMAN          | 4697.3368 |
| sp P27824 CALX_HUMAN           | 2722.369  |
| sp Q15637 SF01_HUMAN           | 1896.8715 |
| sp Q14204 DYHC1_HUMAN          | 3086.5601 |
| sp O75533 SF3B1_HUMAN          | 3296.5698 |
| sp Q16629 SRSF7_HUMAN          | 1966.9272 |
| sp Q969P0 IGSF8_HUMAN          | 1337.6398 |
| sp Q9Y5B9 SP16H_HUMAN          | 1560.6838 |
| sp Q13435 SF3B2_HUMAN          | 1589.9029 |
| sp Q8NBS9 TXND5_HUMAN          | 2777.2254 |



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| sp P33240 CSTF2_HUMAN          | 1712.9461 |
| sp P68104 EF1A1_HUMAN,sp Q5VTI | 1651.9145 |
| sp Q9BRT2 UQCC2_HUMAN          | 2146.0041 |
| sp P62937 PIIA_HUMAN           | 1543.6903 |
| sp Q15392 DHC24_HUMAN          | 1082.5145 |
| sp P49327 FAS_HUMAN            | 3305.5841 |
| sp P31327 CPSM_HUMAN           | 1817.8652 |
| sp P43243 MATR3_HUMAN          | 1201.588  |
| sp P43121 MUC18_HUMAN          | 1451.6463 |
| sp P49327 FAS_HUMAN            | 1786.8382 |
| sp Q00169 PIPNA_HUMAN          | 2450.1754 |
| sp P53680 AP2S1_HUMAN          | 1559.7005 |
| sp Q9ULW0 TPX2_HUMAN           | 1372.7099 |
| sp Q13283 G3BP1_HUMAN          | 2059.9568 |
| sp P39748 FEN1_HUMAN           | 1180.5724 |
| sp Q9NZ01 TECR_HUMAN           | 2437.2199 |
| sp Q9HCU4 CELR2_HUMAN          | 3050.2633 |
| sp P14174 MIF_HUMAN            | 6700.2789 |
| sp Q14318 FKBP8_HUMAN          | 2112.0058 |
| sp Q6UVK1 CSPG4_HUMAN          | 3667.808  |
| sp P55769 NH2L1_HUMAN          | 2556.2676 |
| sp Q15437 SC23B_HUMAN          | 2676.3581 |
| sp P13639 EF2_HUMAN            | 1048.4686 |
| sp Q86Y07 VRK2_HUMAN           | 2433.258  |
| sp Q7Z2W4 ZCCHV_HUMAN          | 1532.6855 |
| sp P0DN76 U2AF5_HUMAN,sp Q010  | 2060.9084 |
| sp P00966 ASSY_HUMAN           | 4051.9448 |
| sp Q16695 H31T_HUMAN,sp Q6NXT  | 1446.7355 |
| sp Q08211 DHX9_HUMAN           | 2100.9501 |
| sp P53396 ACLY_HUMAN           | 2127.0273 |
| sp P40926 MDHM_HUMAN           | 1252.5837 |
| sp P62140 PP1B_HUMAN           | 1107.5673 |
| sp O95347 SMC2_HUMAN           | 1763.7903 |
| sp P22314 UBA1_HUMAN           | 3497.7579 |
| sp Q02543 RL18A_HUMAN          | 1935.8971 |
| sp P35579 MYH9_HUMAN           | 1720.8308 |
| sp Q99460 PSMD1_HUMAN          | 2112.064  |
| sp P35579 MYH9_HUMAN           | 1408.6947 |
| sp P51511 MMP15_HUMAN          | 4502.9297 |
| sp P07910 HNRPC_HUMAN,sp P0DN  | 1640.9138 |
| sp Q03405 UPAR_HUMAN           | 3305.4531 |
| sp P27797 CALR_HUMAN           | 1467.6882 |
| sp Q5GLZ8 HERC4_HUMAN          | 3414.7089 |
| sp P05556 ITB1_HUMAN           | 2916.5557 |
| sp Q96T88 UHRF1_HUMAN          | 2999.5393 |
| sp P13639 EF2_HUMAN            | 1699.7916 |
| sp Q9UBB4 ATX10_HUMAN          | 1453.662  |

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| sp Q8NI27 THOC2_HUMAN          | 1171.5662 |
| sp P62917 RL8_HUMAN            | 1023.5713 |
| sp Q92616 GCN1_HUMAN           | 2670.3245 |
| sp P13639 EF2_HUMAN            | 1966.9346 |
| sp P23193 TCEA1_HUMAN          | 2305.9943 |
| sp O14579 COPE_HUMAN           | 1543.7307 |
| sp P63173 RL38_HUMAN           | 1771.9356 |
| sp P02545 LMNA_HUMAN           | 1334.6103 |
| sp P31948 STIP1_HUMAN          | 2317.1624 |
| sp P14625 ENPL_HUMAN           | 2738.3163 |
| sp Q8WXF1 PSPC1_HUMAN          | 1485.7252 |
| sp P98082 DAB2_HUMAN           | 2243.1335 |
| sp P10412 H14_HUMAN            | 980.4927  |
| sp Q4ZHG4 FNDC1_HUMAN          | 2379.1376 |
| sp P43121 MUC18_HUMAN          | 2416.1885 |
| sp P22102 PUR2_HUMAN           | 1643.7726 |
| sp Q99757 THIOM_HUMAN          | 3161.5063 |
| sp P07954 FUMH_HUMAN           | 3304.585  |
| sp Q96L21 RL10L_HUMAN,sp P2763 | 1185.5778 |
| sp O43707 ACTN4_HUMAN,sp P356  | 1807.8741 |
| sp P63241 IF5A1_HUMAN,sp Q9GZV | 1688.7862 |
| sp Q13200 PSMD2_HUMAN          | 3708.9224 |
| sp O60825 F262_HUMAN           | 2353.13   |
| sp Q13813 SPTN1_HUMAN          | 3327.5949 |
| sp Q9Y3U8 RL36_HUMAN           | 1224.6463 |
| sp P49773 HINT1_HUMAN          | 1641.7886 |
| sp P18583 SON_HUMAN            | 2184.0447 |
| sp P08670 VIME_HUMAN           | 2693.2821 |
| sp P04844 RPN2_HUMAN           | 3133.5891 |
| sp Q01813 PFKAP_HUMAN          | 1581.8403 |
| sp P27824 CALX_HUMAN           | 2722.369  |
| sp P23588 IF4B_HUMAN           | 1511.6277 |
| sp Q8NI27 THOC2_HUMAN          | 2462.2118 |
| sp Q99797 MIPEP_HUMAN          | 1951.921  |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P62987 RL40_HUMAN,sp P62979 | 1461.7538 |
| sp P08238 HS90B_HUMAN,sp Q58Fi | 1560.7573 |
| sp P35606 COPB2_HUMAN          | 1499.7409 |
| sp P25705 ATPA_HUMAN           | 1316.7452 |
| sp P62987 RL40_HUMAN,sp P62979 | 2326.1805 |
| sp P29401 TKT_HUMAN            | 1857.9295 |
| sp P83731 RL24_HUMAN           | 2465.2697 |
| sp Q9BVJ6 UT14A_HUMAN          | 2199.096  |
| sp Q00610 CLH1_HUMAN           | 1251.6136 |
| sp P52948 NUP98_HUMAN          | 2276.1801 |
| sp P09382 LEG1_HUMAN           | 1678.7627 |
| sp Q09666 AHNK_HUMAN           | 2438.1866 |

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| sp Q15041 AR6P1_HUMAN          | 1699.7988 |
| sp Q8WXX5 DNJC9_HUMAN          | 1820.9309 |
| sp P27824 CALX_HUMAN           | 1456.7562 |
| sp P15531 NDKA_HUMAN           | 2626.2672 |
| sp P68032 ACTC_HUMAN,sp P63267 | 2782.3524 |
| sp P62424 RL7A_HUMAN           | 1461.6996 |
| sp P05362 ICAM1_HUMAN          | 1813.9686 |
| sp P23526 SAHH_HUMAN           | 3501.745  |
| sp Q9NV96 CC50A_HUMAN          | 1487.7369 |
| sp P17844 DDX5_HUMAN           | 1288.6663 |
| sp P08237 PFKAM_HUMAN          | 1507.6258 |
| sp Q9Y5B9 SP16H_HUMAN          | 1124.521  |
| sp Q9P0J1 PDP1_HUMAN           | 2722.3537 |
| sp Q09666 AHNK_HUMAN           | 2580.1955 |
| sp O00159 MYO1C_HUMAN          | 1459.662  |
| sp Q16832 DDR2_HUMAN           | 2344.0695 |
| sp P46781 RS9_HUMAN            | 1389.7214 |
| sp P78527 PRKDC_HUMAN          | 1032.5968 |
| sp P78527 PRKDC_HUMAN          | 2075.0939 |
| sp Q15149 PLEC_HUMAN           | 2367.1318 |
| sp P06733 ENOA_HUMAN           | 1467.7821 |
| sp Q6P2Q9 PRP8_HUMAN           | 1573.7307 |
| sp Q6DD88 ATLA3_HUMAN          | 2910.5379 |
| sp P49207 RL34_HUMAN           | 1606.7699 |
| sp P16403 H12_HUMAN            | 970.5084  |
| sp P40937 RFC5_HUMAN           | 3453.7165 |
| sp Q8NC51 PAIRB_HUMAN          | 1673.8988 |
| sp Q02878 RL6_HUMAN            | 1165.5298 |
| sp P62826 RAN_HUMAN            | 2167.0653 |
| sp P20618 PSB1_HUMAN           | 3832.8513 |
| sp Q9NZU7 CABP1_HUMAN          | 2059.0182 |
| sp P07195 LDHB_HUMAN           | 1855.0244 |
| sp P17844 DDX5_HUMAN,sp Q9284  | 1435.7419 |
| sp O15144 ARPC2_HUMAN          | 1675.8166 |
| sp Q9NZ01 TECR_HUMAN           | 2690.3803 |
| sp Q01105 SET_HUMAN,sp P0DMEO  | 1458.6811 |
| sp P32004 L1CAM_HUMAN          | 4586.2619 |
| sp Q9H3K6 BOLA2_HUMAN          | 3483.6881 |
| sp P29401 TKT_HUMAN            | 2845.4709 |
| sp P83881 RL36A_HUMAN,sp Q969C | 1226.5568 |
| sp P35251 RFC1_HUMAN           | 3820.8083 |
| sp P13639 EF2_HUMAN            | 1626.7638 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp Q00610 CLH1_HUMAN           | 1373.6286 |
| sp Q07666 KHDR1_HUMAN          | 1478.763  |
| sp P11717 MPRI_HUMAN           | 2731.4505 |
| sp P53396 ACLY_HUMAN           | 1778.9778 |

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| sp Q15149 PLEC_HUMAN           | 1503.8045 |
| sp P14625 ENPL_HUMAN           | 2572.1654 |
| sp P60866 RS20_HUMAN           | 1717.7366 |
| sp P14618 KPYM_HUMAN           | 1590.8002 |
| sp O00505 IMA4_HUMAN           | 4055.9899 |
| sp P62917 RL8_HUMAN            | 3591.7371 |
| sp Q15654 TRIP6_HUMAN          | 2346.9755 |
| sp O00232 PSD12_HUMAN          | 2079.1034 |
| sp O43707 ACTN4_HUMAN,sp P128  | 1324.6412 |
| sp P51153 RAB13_HUMAN          | 1739.8479 |
| sp P58107 EPIPL_HUMAN          | 3181.5754 |
| sp P58743 S26A5_HUMAN          | 3317.741  |
| sp P38646 GRP75_HUMAN          | 3072.4651 |
| sp Q8WWY3 PRP31_HUMAN          | 3711.8421 |
| sp Q9UNF1 MAGD2_HUMAN          | 3593.7989 |
| sp P08195 4F2_HUMAN            | 2193.0226 |
| sp P39019 RS19_HUMAN           | 1266.6568 |
| sp Q13619 CUL4A_HUMAN          | 3856.0445 |
| sp P60891 PRPS1_HUMAN          | 1650.8366 |
| sp Q12906 ILF3_HUMAN           | 3884.7543 |
| sp Q9HDC9 APMAP_HUMAN          | 1993.0997 |
| sp P10586 PTPRF_HUMAN          | 2432.1397 |
| sp Q99832 TCPH_HUMAN           | 1528.6657 |
| sp P78527 PRKDC_HUMAN          | 1116.5465 |
| sp P05455 LA_HUMAN             | 2318.1358 |
| sp P35573 GDE_HUMAN            | 2689.2265 |
| sp O75533 SF3B1_HUMAN          | 2288.1648 |
| sp P15328 FOLR1_HUMAN          | 2358.0811 |
| sp Q9BUQ8 DDX23_HUMAN          | 1961.8611 |
| sp O60313 OPA1_HUMAN           | 2338.123  |
| sp P21926 CD9_HUMAN            | 3460.6101 |
| sp O00151 PDLI1_HUMAN          | 2123.9259 |
| sp O60341 KDM1A_HUMAN          | 1513.7678 |
| sp P51991 ROA3_HUMAN           | 1795.7948 |
| sp P0CW18 PRS56_HUMAN          | 1415.7197 |
| sp Q14008 CKAP5_HUMAN          | 1523.8018 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1629.8587 |
| sp P60174 TPIS_HUMAN           | 3246.6197 |
| sp Q9UJG1 MSPD1_HUMAN          | 1577.6933 |
| sp P60903 S10AA_HUMAN          | 2743.3415 |
| sp O60244 MED14_HUMAN          | 2246.2423 |
| sp Q9Y624 JAM1_HUMAN           | 1677.7271 |
| sp P49959 MRE11_HUMAN          | 1652.8311 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P16070 CD44_HUMAN           | 1556.7372 |
| sp Q9NZN4 EHD2_HUMAN           | 3554.6988 |
| sp P04792 HSPB1_HUMAN          | 2209.0903 |

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| sp Q15149 PLEC_HUMAN           | 1581.7093 |
| sp Q9H4M9 EHD1_HUMAN           | 2469.2904 |
| sp Q8TDN6 BRX1_HUMAN           | 1591.759  |
| sp Q8IVF2 AHNK2_HUMAN          | 3243.6511 |
| sp P09012 SNRPA_HUMAN          | 1566.8002 |
| sp P46778 RL21_HUMAN           | 1567.7817 |
| sp P49419 AL7A1_HUMAN          | 3563.7395 |
| sp P78344 IF4G2_HUMAN          | 1662.8114 |
| sp P04406 G3P_HUMAN            | 1383.6419 |
| sp Q86SE5 RALYL_HUMAN,sp P0791 | 1443.6816 |
| sp P17025 ZN182_HUMAN          | 1258.6167 |
| sp Q86VP6 CAND1_HUMAN          | 1581.7999 |
| sp Q09666 AHNK_HUMAN           | 2612.1676 |
| sp P02786 TFR1_HUMAN           | 2337.9518 |
| sp P53618 COPB_HUMAN           | 1592.7583 |
| sp Q9BUQ8 DDX23_HUMAN          | 2102.8898 |
| sp P16402 H13_HUMAN,sp P16401  | 1490.7365 |
| sp P26641 EF1G_HUMAN           | 1738.8234 |
| sp P62937 PPIA_HUMAN           | 4800.2476 |
| sp P14316 IRF2_HUMAN           | 1693.8399 |
| sp O75390 CISY_HUMAN           | 2110.0557 |
| sp Q71U36 TBA1A_HUMAN,sp P0DF  | 2611.2303 |
| sp Q00610 CLH1_HUMAN           | 2917.4723 |
| sp P62081 RS7_HUMAN            | 1661.9756 |
| sp P13639 EF2_HUMAN            | 1910.9473 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 2358.2795 |
| sp P08621 RU17_HUMAN           | 1555.6362 |
| sp Q86UP2 KTN1_HUMAN           | 1852.8955 |
| sp Q99798 ACON_HUMAN           | 2965.5325 |
| sp Q04724 TLE1_HUMAN,sp Q04727 | 1401.6347 |
| sp Q13310 PABP4_HUMAN          | 2350.0754 |
| sp Q14204 DYHC1_HUMAN          | 3086.5601 |
| sp P60842 IF4A1_HUMAN          | 3573.6473 |
| sp P55265 DSRAD_HUMAN          | 1596.8161 |
| sp P22626 ROA2_HUMAN           | 2188.1025 |
| sp P00558 PGK1_HUMAN           | 2503.2152 |
| sp Q13155 AIMP2_HUMAN          | 2982.5815 |
| sp P49327 FAS_HUMAN            | 2641.202  |
| sp P62269 RS18_HUMAN           | 1181.5425 |
| sp Q12931 TRAP1_HUMAN          | 1900.9319 |
| sp P16403 H12_HUMAN            | 1210.6558 |
| sp Q14126 DSG2_HUMAN           | 3597.7767 |
| sp P31327 CPSM_HUMAN           | 3089.5267 |
| sp Q16695 H31T_HUMAN,sp Q71DI: | 1501.7637 |
| sp O76021 RL1D1_HUMAN          | 1962.0786 |
| sp Q13813 SPTN1_HUMAN          | 1435.6692 |
| sp P48556 PSMD8_HUMAN          | 3165.4965 |

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| sp P63104 1433Z_HUMAN          | 1828.9054 |
| sp P27824 CALX_HUMAN           | 2738.3639 |
| sp P62081 RS7_HUMAN            | 1161.6394 |
| sp P31689 DNJA1_HUMAN          | 2510.2401 |
| sp Q13740 CD166_HUMAN          | 2999.491  |
| sp O75436 VP26A_HUMAN          | 2778.3824 |
| sp P26373 RL13_HUMAN           | 2623.3163 |
| sp P23528 COF1_HUMAN           | 1986.8378 |
| sp P14174 MIF_HUMAN            | 6700.2789 |
| sp P22626 ROA2_HUMAN           | 2273.9721 |
| sp Q06265 EXOS9_HUMAN          | 1792.8964 |
| sp Q09666 AHNK_HUMAN           | 1390.605  |
| sp Q86VP6 CAND1_HUMAN          | 2241.0987 |
| sp P19338 NUCL_HUMAN           | 1356.7289 |
| sp Q9BVA1 TBB2B_HUMAN,sp P043  | 1483.7493 |
| sp Q14103 HNRPD_HUMAN          | 1953.9684 |
| sp Q99497 PARK7_HUMAN          | 1998.7836 |
| sp Q96HS1 PGAM5_HUMAN          | 1866.8133 |
| sp P07900 HS90A_HUMAN,sp P0823 | 1342.6001 |
| sp Q8TDD1 DDX54_HUMAN          | 1336.6888 |
| sp P68400 CSK21_HUMAN,sp Q8NE1 | 3437.6416 |
| sp P05141 ADT2_HUMAN           | 1610.8012 |
| sp P50213 IDH3A_HUMAN          | 2182.1569 |
| sp Q6UVK1 CSPG4_HUMAN          | 3667.808  |
| sp Q9UNX3 RL26L_HUMAN,sp P6121 | 1537.6871 |
| sp P08729 K2C7_HUMAN           | 2869.2977 |
| sp Q9Y320 TMX2_HUMAN           | 1895.8472 |
| sp Q15149 PLEC_HUMAN           | 1424.7048 |
| sp P25398 RS12_HUMAN           | 1641.7821 |
| sp P05783 K1C18_HUMAN          | 2389.1974 |
| sp O60869 EDF1_HUMAN           | 1664.7907 |
| sp P46778 RL21_HUMAN           | 1187.5935 |
| sp P30041 PRDX6_HUMAN          | 1358.6718 |
| sp Q15393 SF3B3_HUMAN          | 1615.7049 |
| sp Q09666 AHNK_HUMAN           | 1411.6264 |
| sp Q7L1Q6 BZW1_HUMAN           | 2215.062  |
| sp Q6FI13 H2A2A_HUMAN,sp P049C | 997.4941  |
| sp P35579 MYH9_HUMAN           | 1252.5935 |
| sp Q02543 RL18A_HUMAN          | 1046.5033 |
| sp Q9BTE3 MCMBP_HUMAN          | 2300.1471 |
| sp P78527 PRKDC_HUMAN          | 1768.8592 |
| sp Q09666 AHNK_HUMAN           | 1013.5546 |
| sp P36578 RL4_HUMAN            | 1333.6125 |
| sp Q9UHB6 LIMA1_HUMAN          | 2928.4022 |
| sp Q96HS1 PGAM5_HUMAN          | 1790.8985 |
| sp P62899 RL31_HUMAN           | 1081.5556 |
| sp P16403 H12_HUMAN            | 982.5084  |

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| sp P26641 EF1G_HUMAN           | 5229.5142 |
| sp O95831 AIFM1_HUMAN          | 2016.9429 |
| sp P68032 ACTC_HUMAN,sp P68133 | 3669.6623 |
| sp Q7Z6Z7 HUWE1_HUMAN          | 2932.3702 |
| sp P42167 LAP2B_HUMAN          | 2079.0861 |
| sp P58743 S26A5_HUMAN          | 3317.741  |
| sp P61011 SRP54_HUMAN          | 2153.0926 |
| sp P16070 CD44_HUMAN           | 1238.5568 |
| sp P39656 OST48_HUMAN          | 1909.0309 |
| sp Q92973 TNPO1_HUMAN          | 1607.7112 |
| sp Q92878 RAD50_HUMAN          | 1267.6044 |
| sp P05787 K2C8_HUMAN           | 1325.6463 |
| sp Q9P0L0 VAPA_HUMAN           | 2789.2829 |
| sp Q15233 NONO_HUMAN           | 1424.6684 |
| sp O00231 PSD11_HUMAN          | 1790.9778 |
| sp Q9NXW2 DJB12_HUMAN          | 2388.1862 |
| sp Q9UIG0 BAZ1B_HUMAN          | 1416.6972 |
| sp P78527 PRKDC_HUMAN          | 2204.1493 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3429.6697 |
| sp Q6NXT2 H3C_HUMAN,sp Q71DI3  | 1182.6357 |
| sp P21796 VDAC1_HUMAN          | 2142.0342 |
| sp P14618 KPYM_HUMAN           | 1402.6663 |
| sp P35659 DEK_HUMAN            | 1215.6288 |
| sp P84090 ERH_HUMAN            | 1229.6656 |
| sp P05783 K1C18_HUMAN          | 1370.6678 |
| sp P60709 ACTB_HUMAN,sp P68032 | 2391.2719 |
| sp P09496 CLCA_HUMAN           | 1600.8825 |
| sp P42766 RL35_HUMAN           | 1752.8894 |
| sp Q9H361 PABP3_HUMAN,sp P119  | 1738.9618 |
| sp Q13492 PICAL_HUMAN          | 3128.5514 |
| sp P34932 HSP74_HUMAN          | 1515.7053 |
| sp P62249 RS16_HUMAN           | 1410.6925 |
| sp P31040 SDHA_HUMAN           | 1282.6558 |
| sp Q9P021 CRIPT_HUMAN          | 2289.9531 |
| sp Q9Y3R4 NEUR2_HUMAN          | 2658.2885 |
| sp Q8N257 H2B3B_HUMAN,sp P628  | 3445.6646 |
| sp P62917 RL8_HUMAN            | 1253.6768 |
| sp Q9P258 RCC2_HUMAN           | 3442.6205 |
| sp Q14258 TRI25_HUMAN          | 2020.9854 |
| sp O75131 CPNE3_HUMAN          | 2137.0956 |
| sp P07437 TBB5_HUMAN           | 2902.3299 |
| sp P06576 ATPB_HUMAN           | 2769.42   |
| sp P06748 NPM_HUMAN            | 1234.583  |
| sp P63167 DYL1_HUMAN           | 1610.794  |
| sp Q8NC51 PAIRB_HUMAN          | 1172.5826 |
| sp Q8IUD2 RB6I2_HUMAN          | 2477.236  |
| sp O76021 RL1D1_HUMAN          | 1576.7773 |

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| sp P14174 MIF_HUMAN            | 6700.2789 |
| sp Q9Y3T9 NOC2L_HUMAN          | 1795.8927 |
| sp P27105 STOM_HUMAN           | 2854.4688 |
| sp Q9NZL9 MAT2B_HUMAN          | 1854.857  |
| sp P06899 H2B1J_HUMAN,sp P5705 | 1973.9694 |
| sp P22314 UBA1_HUMAN           | 2876.3882 |
| sp Q15436 SC23A_HUMAN          | 1524.6481 |
| sp P08174 DAF_HUMAN            | 1923.9612 |
| sp Q13433 S39A6_HUMAN          | 1884.8575 |
| sp Q9UQE7 SMC3_HUMAN           | 2377.1689 |
| sp Q12907 LMAN2_HUMAN          | 2026.9207 |
| sp Q9BXP5 SRRT_HUMAN           | 1429.615  |
| sp Q86V81 THOC4_HUMAN          | 1155.5309 |
| sp P16403 H12_HUMAN            | 1261.7394 |
| sp P25398 RS12_HUMAN           | 1641.7821 |
| sp O00429 DNM1L_HUMAN          | 1672.9876 |
| sp O15427 MOT4_HUMAN           | 1651.773  |
| sp P35613 BASI_HUMAN           | 1195.6601 |
| sp P06748 NPM_HUMAN            | 1406.7082 |
| sp Q15262 PTPRK_HUMAN          | 1575.7794 |
| sp O60488 ACSL4_HUMAN          | 1383.6419 |
| sp P52272 HNRPM_HUMAN          | 2103.0677 |
| sp Q8NBU5 ATAD1_HUMAN          | 1547.7845 |
| sp O00571 DDX3X_HUMAN,sp O155  | 1233.57   |
| sp O75533 SF3B1_HUMAN          | 2097.9563 |
| sp P46779 RL28_HUMAN           | 1320.6132 |
| sp P02545 LMNA_HUMAN           | 1580.8046 |
| sp P38606 VATA_HUMAN           | 1901.9312 |
| sp P21333 FLNA_HUMAN           | 1852.9068 |
| sp P31327 CPSM_HUMAN           | 3159.4998 |
| sp P02786 TFR1_HUMAN           | 2173.13   |
| sp P26038 MOES_HUMAN           | 2477.1598 |
| sp P62805 H4_HUMAN             | 1806.9186 |
| sp P31949 S10AB_HUMAN          | 2416.1257 |
| sp Q9BY44 EIF2A_HUMAN          | 2307.2474 |
| sp Q08117 TLE5_HUMAN           | 2157.0742 |
| sp P62280 RS11_HUMAN           | 1635.8832 |
| sp P02545 LMNA_HUMAN           | 1842.8344 |
| sp P18621 RL17_HUMAN           | 1097.5254 |
| sp P62937 PPIA_HUMAN           | 1543.6903 |
| sp P15924 DESP_HUMAN           | 1333.6878 |
| sp O43707 ACTN4_HUMAN,sp P128  | 1324.6412 |
| sp P14384 CBPM_HUMAN           | 3221.462  |
| sp Q03405 UPAR_HUMAN           | 3305.4531 |
| sp Q2NL82 TSR1_HUMAN           | 1668.8875 |
| sp O00592 PODXL_HUMAN          | 1370.6718 |
| sp Q02218 ODO1_HUMAN           | 2340.2253 |



|                       |           |
|-----------------------|-----------|
| sp P49588 SYAC_HUMAN  | 1384.6371 |
| sp P10586 PTPRF_HUMAN | 4179.0735 |
| sp P23396 RS3_HUMAN   | 3010.3841 |
| sp P61313 RL15_HUMAN  | 1901.9384 |
| sp O14979 HNRDL_HUMAN | 1615.7301 |
| sp P31948 STIP1_HUMAN | 1328.6725 |



| pepA             | kposA | pepA_id    | accessionA | uniprotA | modposA | startPosA | pdbsA  |
|------------------|-------|------------|------------|----------|---------|-----------|--------|
| TIAPALVSKK       | 8     | TIAPALVSK  | P06733     | ENOA_HUM | 80      | 71        | 2PSN   |
| DILEKK           | 4     | DILEKK_4_I | P07900     | HS90A_HU | 581     | 576       | 3Q6M   |
| DILEKK           | 4     | DILEKK_4_I | P07900     | HS90A_HU | 581     | 576       | 3Q6M   |
| DILEKK           | 4     | DILEKK_4_I | P07900     | HS90A_HU | 581     | 576       | 3Q6M   |
| ELISNSSDALDKIR   | 11    | ELISNSSDA  | P07900     | HS90A_HU | 58      | 46        | P07900 |
| FYEQFSKNIK       | 6     | FYEQFSKNI  | P07900     | HS90A_HU | 443     | 436       | 3Q6M   |
| FYEQFSKNIK       | 6     | FYEQFSKNI  | P07900     | HS90A_HU | 443     | 436       | 3Q6M   |
| IKELVK           | 1     | IKELVK_1_I | P07900     | HS90A_HU | 204     | 202       | P07900 |
| IMKAQALR         | 2     | IMKAQALR   | P07900     | HS90A_HU | 615     | 612       | 3Q6M   |
| IM[147.04]KAQALR | 2     | IM[147.04] | P07900     | HS90A_HU | 615     | 612       | 3Q6M   |
| IM[147.04]KAQALR | 2     | IM[147.04] | P07900     | HS90A_HU | 615     | 612       | 3Q6M   |
| KNNIK            | 0     | KNNIK_0_F  | P07900     | HS90A_HU | 358     | 357       | P07900 |
| TKPIWTR          | 1     | TKPIWTR_1  | P07900     | HS90A_HU | 294     | 292       | P07900 |
| APFDLFENKK       | 8     | APFDLFENK  | P08238     | HS90B_HU | 347     | 338       | P08238 |
| DILEKK           | 4     | DILEKK_4_I | P07900     | HS90A_HU | 581     | 576       | 3Q6M   |
| EILDKK           | 4     | EILDKK_4_I | P08238     | HS90B_HU | 573     | 568       | P08238 |
| FYEAFSKNLK       | 6     | FYEAFSKNL  | P08238     | HS90B_HU | 435     | 428       | 3PRY   |
| FYEAFSKNLK       | 6     | FYEAFSKNL  | P08238     | HS90B_HU | 435     | 428       | 3PRY   |
| FYEQFSKNIK       | 6     | FYEQFSKNI  | P07900     | HS90A_HU | 443     | 436       | 3Q6M   |
| FYEQFSKNIK       | 6     | FYEQFSKNI  | P07900     | HS90A_HU | 443     | 436       | 3Q6M   |
| FYEQFSKNIK       | 6     | FYEQFSKNI  | P07900     | HS90A_HU | 443     | 436       | 3Q6M   |
| APFDLFENKK       | 8     | APFDLFENK  | P08238     | HS90B_HU | 347     | 338       | P08238 |
| APFDLFENKK       | 8     | APFDLFENK  | P08238     | HS90B_HU | 347     | 338       | P08238 |
| EILDKK           | 4     | EILDKK_4_I | P08238     | HS90B_HU | 573     | 568       | P08238 |
| ELISNASDALDKIR   | 11    | ELISNASDA  | P08238     | HS90B_HU | 53      | 41        | P08238 |
| ETQKSIYYITGESK   | 3     | ETQKSIYYIT | P08238     | HS90B_HU | 481     | 477       | 3PRY   |
| FYEAFSKNLK       | 6     | FYEAFSKNL  | P08238     | HS90B_HU | 435     | 428       | 3PRY   |
| FYEAFSKNLK       | 6     | FYEAFSKNL  | P08238     | HS90B_HU | 435     | 428       | 3PRY   |
| FYEAFSKNLK       | 6     | FYEAFSKNL  | P08238     | HS90B_HU | 435     | 428       | 3PRY   |
| FYEAFSKNLK       | 6     | FYEAFSKNL  | P08238     | HS90B_HU | 435     | 428       | P08238 |
| FYEAFSKNLK       | 6     | FYEAFSKNL  | P08238     | HS90B_HU | 435     | 428       | P08238 |
| FYEAFSKNLK       | 6     | FYEAFSKNL  | P08238     | HS90B_HU | 435     | 428       | 3PRY   |
| GTKVILHLK        | 2     | GTKVILHLK  | P08238     | HS90B_HU | 180     | 177       | P08238 |
| GTKVILHLK        | 2     | GTKVILHLK  | P08238     | HS90B_HU | 180     | 177       | P08238 |
| GTKVILHLK        | 2     | GTKVILHLK  | P08238     | HS90B_HU | 180     | 177       | P08238 |
| IMKAQALR         | 2     | IMKAQALR   | P08238     | HS90B_HU | 607     | 604       | P08238 |
| IMKAQALR         | 2     | IMKAQALR   | P08238     | HS90B_HU | 607     | 604       | P08238 |
| IMKAQALR         | 2     | IMKAQALR   | P08238     | HS90B_HU | 607     | 604       | P08238 |
| IM[147.04]KAQALR | 2     | IM[147.04] | P08238     | HS90B_HU | 607     | 604       | P08238 |
| IM[147.04]KAQALR | 2     | IM[147.04] | P08238     | HS90B_HU | 607     | 604       | P08238 |
| IM[147.04]KAQALR | 2     | IM[147.04] | P08238     | HS90B_HU | 607     | 604       | P08238 |
| KM[147.04]EESKAK | 5     | KM[147.04] | P08238     | HS90B_HU | 557     | 551       | P08238 |
| KNIVK            | 0     | KNIVK_0_F  | P08238     | HS90B_HU | 406     | 405       | 3PRY   |
| KNNIK            | 0     | KNNIK_0_F  | P08238     | HS90B_HU | 350     | 349       | 3PRY   |
| KVEKVTISNR       | 3     | KVEKVTISN  | P08238     | HS90B_HU | 577     | 573       | P08238 |
| LDSGKELK         | 4     | LDSGKELK_  | P08238     | HS90B_HU | 69      | 64        | P08238 |

|                   |                     |           |     |               |
|-------------------|---------------------|-----------|-----|---------------|
| LDSGKELK          | 4 LDSGKELK_ P08238  | HS90B_HU  | 69  | 64 P08238     |
| MEESKAK           | 4 MEESKAK_ P08238   | HS90B_HU  | 557 | 552 P08238    |
| MEESKAK           | 4 MEESKAK_ P08238   | HS90B_HU  | 557 | 552 P08238    |
| M[147.04]KETQK    | 1 M[147.04] P08238  | HS90B_HU  | 477 | 475 3PRY      |
| NNIKLYVR          | 3 NNIKLYVR_ P08238  | HS90B_HU  | 354 | 350 P08238    |
| NNIKLYVR          | 3 NNIKLYVR_ P08238  | HS90B_HU  | 354 | 350 3PRY      |
| QKAEADKNDK        | 1 QKAEADKN P08238   | HS90B_HU  | 641 | 639 P08238_PC |
| RAPFDLFENKK       | 9 RAPFDLFEN P08238  | HS90B_HU  | 347 | 337 P08238    |
| TKPIWTR           | 1 TKPIWTR_1 P08238  | HS90B_HU  | 286 | 284 P08238    |
| TKPIWTR           | 1 TKPIWTR_1 P08238  | HS90B_HU  | 286 | 284 P08238    |
| VEKVTISNR         | 2 VEKVTISNR P08238  | HS90B_HU  | 577 | 574 P08238    |
| YESLTDPSKLD SGK   | 8 YESLTDPSK P08238  | HS90B_HU  | 64  | 55 P08238     |
| FYEAFSKNLK        | 6 FYEAFSKNL P08238  | HS90B_HU  | 435 | 428 3PRY      |
| FYEAFSKNLK        | 6 FYEAFSKNL P08238  | HS90B_HU  | 435 | 428 3PRY      |
| HDSPEDVKR         | 7 HDSPEDVK P31948   | STIP1_HUN | 486 | 478 P31948    |
| KAAALEAMK         | 0 KAAALEAM P31948   | STIP1_HUN | 434 | 433 P31948    |
| KAAALEAM[147.04]K | 0 KAAALEAM P31948   | STIP1_HUN | 434 | 433 P31948    |
| ELISNASDALDKIR    | 11 ELISNASDA P08238 | HS90B_HU  | 53  | 41 P08238     |

| pdbA_type | pepB                         | kposB | pepB_id       | accessionB | uniprotB    |
|-----------|------------------------------|-------|---------------|------------|-------------|
| Structure | FYEAFSKNLK                   | 6     | FYEAFSKNL     | P08238     | HS90B_HUMAN |
| Structure | DNSTMGYMAAKK                 | 10    | DNSTMGYM      | P07900     | HS90A_HUMAN |
| Structure | DNSTM[147.04]GYM[147.04]AAKK | 10    | DNSTM[147.04] | P07900     | HS90A_HUMAN |
| Structure | VEKVVVSNR                    | 2     | VEKVVVSNR     | P07900     | HS90A_HUMAN |
| Phyre     | ADLINNLGTIAKSGTK             | 11    | ADLINNLGT     | P07900     | HS90A_HUMAN |
| Structure | CLELFTELAEDKENYKK            | 11    | CLELFTELA     | P07900     | HS90A_HUMAN |
| Structure | FYEQFSKNIK                   | 6     | FYEQFSKNI     | P07900     | HS90A_HUMAN |
| Phyre     | TKPIWTR                      | 1     | TKPIWTR_1     | P07900     | HS90A_HUMAN |
| Structure | FYEQFSKNIK                   | 6     | FYEQFSKNI     | P07900     | HS90A_HUMAN |
| Structure | FYEQFSKNIK                   | 6     | FYEQFSKNI     | P07900     | HS90A_HUMAN |
| Structure | VEKVVVSNR                    | 2     | VEKVVVSNR     | P07900     | HS90A_HUMAN |
| Phyre     | FYEQFSKNIK                   | 6     | FYEQFSKNI     | P07900     | HS90A_HUMAN |
| Phyre     | LDSGKELHINLIPNK              | 4     | LDSGKELHI     | P07900     | HS90A_HUMAN |
| Phyre     | FYEQFSKNIK                   | 6     | FYEQFSKNI     | P07900     | HS90A_HUMAN |
| Structure | FYEAFSKNLK                   | 6     | FYEAFSKNL     | P08238     | HS90B_HUMAN |
| Phyre     | FYEQFSKNIK                   | 6     | FYEQFSKNI     | P07900     | HS90A_HUMAN |
| Structure | FYEQFSKNIK                   | 6     | FYEQFSKNI     | P07900     | HS90A_HUMAN |
| Structure | KHLEINPDHSIIETLR             | 0     | KHLEINPDF     | P07900     | HS90A_HUMAN |
| Structure | KHLEINPDHPIVETLR             | 0     | KHLEINPDF     | P08238     | HS90B_HUMAN |
| Structure | RAPFDLFENKK                  | 9     | RAPFDLFEN     | P08238     | HS90B_HUMAN |
| Structure | LILEQMOKDPQALSEHLK           | 7     | LILEQMOKI     | P31948     | STIP1_HUMAN |
| Phyre     | ELISNASDALDKIR               | 11    | ELISNASDA     | P08238     | HS90B_HUMAN |
| Phyre     | FYEAFSKNLK                   | 6     | FYEAFSKNL     | P08238     | HS90B_HUMAN |
| Phyre     | VEKVTISNR                    | 2     | VEKVTISNR     | P08238     | HS90B_HUMAN |
| Phyre     | ADLINNLGTIAKSGTK             | 11    | ADLINNLGT     | P08238     | HS90B_HUMAN |
| Structure | SLVSVTKEGLELPEDEEEKK         | 6     | SLVSVTKEG     | P08238     | HS90B_HUMAN |
| Structure | CLELFSELAEDKENYKK            | 11    | CLELFSELA     | P08238     | HS90B_HUMAN |
| Structure | FYEAFSKNLK                   | 6     | FYEAFSKNL     | P08238     | HS90B_HUMAN |
| Structure | GFEVVYMTPEIDYCVQQKKEFDGK     | 19    | GFEVVYMT      | P08238     | HS90B_HUMAN |
| Phyre     | KHLEINPDHPIVETLR             | 0     | KHLEINPDF     | P08238     | HS90B_HUMAN |
| Phyre     | RAPFDLFENKK                  | 9     | RAPFDLFEN     | P08238     | HS90B_HUMAN |
| Structure | SIYYITGESKEQVANSFAVER        | 9     | SIYYITGESK    | P08238     | HS90B_HUMAN |
| Phyre     | EKYIDQEELNK                  | 1     | EKYIDQEEL     | P08238     | HS90B_HUMAN |
| Phyre     | IKEKYIDQEELNK                | 3     | IKEKYIDQEI    | P08238     | HS90B_HUMAN |
| Phyre     | YESLTDPSKLDGKELK             | 13    | YESLTDPSK     | P08238     | HS90B_HUMAN |
| Phyre     | DNSTMGYMMAKK                 | 10    | DNSTMGYM      | P08238     | HS90B_HUMAN |
| Phyre     | FYEAFSKNLK                   | 6     | FYEAFSKNL     | P08238     | HS90B_HUMAN |
| Phyre     | KHLEINPDHPIVETLR             | 0     | KHLEINPDF     | P08238     | HS90B_HUMAN |
| Phyre     | FYEAFSKNLK                   | 6     | FYEAFSKNL     | P08238     | HS90B_HUMAN |
| Phyre     | KHLEINPDHPIVETLR             | 0     | KHLEINPDF     | P08238     | HS90B_HUMAN |
| Phyre     | VEKVTISNR                    | 2     | VEKVTISNR     | P08238     | HS90B_HUMAN |
| Phyre     | VEKVTISNR                    | 2     | VEKVTISNR     | P08238     | HS90B_HUMAN |
| Structure | ILKVIR                       | 2     | ILKVIR_2_F    | P08238     | HS90B_HUMAN |
| Structure | FYEAFSKNLK                   | 6     | FYEAFSKNL     | P08238     | HS90B_HUMAN |
| Phyre     | ETQKSIYYITGESK               | 3     | ETQKSIYYIT    | P08238     | HS90B_HUMAN |
| Phyre     | GTKVILHLK                    | 2     | GTKVILHLK     | P08238     | HS90B_HUMAN |

|           |                        |                     |             |
|-----------|------------------------|---------------------|-------------|
| Phyre     | TKPIWTR                | 1 TKPIWTR_1P08238   | HS90B_HUMAN |
| Phyre     | FENLCKIMK              | 5 FENLCKIMK P08238  | HS90B_HUMAN |
| Phyre     | KVEKVTISNR             | 3 KVEKVTISN P08238  | HS90B_HUMAN |
| Structure | SIYYITGESKEQVANSASFVER | 9 SIYYITGESK P08238 | HS90B_HUMAN |
| Phyre     | APFDLFENKK             | 8 APFDLFENK P08238  | HS90B_HUMAN |
| Structure | YIDQEELNKTPIWTR        | 8 YIDQEELNK P08238  | HS90B_HUMAN |
| Docking   | QKAEADKNDK             | 1 QKAEADKN P08238   | HS90B_HUMAN |
| Phyre     | KFYEAFSKNLK            | 7 KFYEAFSKN P08238  | HS90B_HUMAN |
| Phyre     | EKYIDQEELNK            | 1 EKYIDQEEL P08238  | HS90B_HUMAN |
| Phyre     | YESLTDPSKLD SGKELK     | 13 YESLTDPSK P08238 | HS90B_HUMAN |
| Phyre     | FENLCKIMK              | 5 FENLCKIMK P08238  | HS90B_HUMAN |
| Phyre     | ELKIDIIPNPQER          | 2 ELKIDIIPNP P08238 | HS90B_HUMAN |
| Structure | DYTKAMD VYQK           | 3 DYTKAMD\ P31948   | STIP1_HUMAN |
| Structure | LILEQMQKDPQAL SEHLK    | 7 LILEQMQKI P31948  | STIP1_HUMAN |
| Phyre     | FYEAFSKNLK             | 6 FYEAFSKNL P08238  | HS90B_HUMAN |
| Phyre     | FYEAFSKNLK             | 6 FYEAFSKNL P08238  | HS90B_HUMAN |
| Phyre     | FYEAFSKNLK             | 6 FYEAFSKNL P08238  | HS90B_HUMAN |
| Phyre     | KTSDFNTFLAQEGCTK       | 0 KTSDFNTFL Q9UHD1  | CHRD1_HUMAN |

| modposB | startPosB | pdbB   | pdbB_type | distance | NetworkDi: | NumberIDs | Confidence | NumProtAl |
|---------|-----------|--------|-----------|----------|------------|-----------|------------|-----------|
| 435     | 428       | 3PRY   | Structure | ####     | 1          | 1,0       | 0.98       | 1         |
| 631     | 620       | 3Q6M   | Structure | 11.34    | Intra      | 1,0       | 1          | 12        |
| 631     | 620       | 3Q6M   | Structure | 11.34    | Intra      | 0,1       | 1          | 12        |
| 585     | 582       | 3Q6M   | Structure | 9.76     | Intra      | 2,0       | 1          | 12        |
| 112     | 100       | P07900 | Phyre     | 16.82    | Intra      | 2,3       | 1          | 12        |
| 431     | 419       | 3Q6M   | Structure | 18.47    | Intra      | 1,0       | 1          | 12        |
| 443     | 436       | 3Q6M   | Structure | 36.47    | 1          | 2,2       | 1          | 12        |
| 294     | 292       | P07900 | Phyre     | 16.9     | Intra      | 1,0       | 1          | 12        |
| 443     | 436       | 3Q6M   | Structure | 20.38    | Intra      | 2,1       | 1          | 12        |
| 443     | 436       | 3Q6M   | Structure | 20.38    | Intra      | 9,3       | 1          | 12        |
| 585     | 582       | 3Q6M   | Structure | 23.75    | Intra      | 0,1       | 1          | 12        |
| 443     | 436       | P07900 | Phyre     | 17.81    | Intra      | 1,0       | 1          | 12        |
| 74      | 69        | P07900 | Phyre     | 20.93    | Intra      | 2,0       | 1          | 12        |
| 443     | 436       | 3Q6M   | Structure | ####     | 1          | 1,1       | 1          | 7         |
| 435     | 428       | 3PRY   | Structure | ####     | 1          | 1,0       | 1          | 7         |
| 443     | 436       | 3Q6M   | Structure | ####     | 1          | 1,0       | 1          | 7         |
| 443     | 436       | 3Q6M   | Structure | ####     | 1          | 10,4      | 1          | 7         |
| 632     | 631       | 3Q6M   | Structure | ####     | 1          | 1,0       | 1          | 7         |
| 624     | 623       | P08238 | Phyre     | ####     | 1          | 3,1       | 1          | 7         |
| 347     | 337       | P08238 | Phyre     | ####     | 1          | 2,0       | 1          | 7         |
| 513     | 505       | P31948 | Phyre     | ####     | 1          | 2,0       | 1          | 1         |
| 53      | 41        | P08238 | Phyre     | 44.73    | Intra      | 1,0       | 1          | 37        |
| 435     | 428       | P08238 | Phyre     | 17.89    | Intra      | 7,2       | 1          | 37        |
| 577     | 574       | P08238 | Phyre     | 9.76     | Intra      | 1,0       | 1          | 37        |
| 107     | 95        | P08238 | Phyre     | 16.82    | Intra      | 3,5       | 1          | 37        |
| 538     | 531       | 3PRY   | Structure | 17.03    | Intra      | 1,0       | 1          | 37        |
| 423     | 411       | 3PRY   | Structure | 18.47    | Intra      | 4,1       | 1          | 37        |
| 435     | 428       | 3PRY   | Structure | 28.74    | 1          | 3,2       | 1          | 37        |
| 526     | 506       | 3PRY   | Structure | 18.6     | Intra      | 0,1       | 1          | 37        |
| 624     | 623       | P08238 | Phyre     | 29.1     | Intra      | 2,2       | 1          | 37        |
| 347     | 337       | P08238 | Phyre     | 17.89    | Intra      | 7,3       | 1          | 37        |
| 491     | 481       | 3PRY   | Structure | 17.17    | Intra      | 0,1       | 1          | 37        |
| 275     | 273       | P08238 | Phyre     | 23.03    | Intra      | 3,1       | 1          | 37        |
| 275     | 271       | P08238 | Phyre     | 23.03    | Intra      | 2,0       | 1          | 37        |
| 69      | 55        | P08238 | Phyre     | 17.13    | Intra      | 1,0       | 1          | 37        |
| 623     | 612       | P08238 | Phyre     | 14.32    | Intra      | 1,0       | 1          | 37        |
| 435     | 428       | P08238 | Phyre     | 20.38    | Intra      | 5,2       | 1          | 37        |
| 624     | 623       | P08238 | Phyre     | 16.24    | Intra      | 3,0       | 1          | 37        |
| 435     | 428       | P08238 | Phyre     | 20.38    | Intra      | 11,1      | 1          | 37        |
| 624     | 623       | P08238 | Phyre     | 16.24    | Intra      | 2,0       | 1          | 37        |
| 577     | 574       | P08238 | Phyre     | 23.75    | Intra      | 0,1       | 1          | 37        |
| 577     | 574       | P08238 | Phyre     | 13.74    | Intra      | 1,0       | 1          | 37        |
| 402     | 399       | 3PRY   | Structure | 6.47     | Intra      | 0,1       | 1          | 37        |
| 435     | 428       | 3PRY   | Structure | 17.81    | Intra      | 5,0       | 1          | 37        |
| 481     | 477       | P08238 | Phyre     | 27.72    | Intra      | 1,0       | 1          | 37        |
| 180     | 177       | P08238 | Phyre     | 17.13    | Intra      | 2,0       | 1          | 37        |

|     |     |           |           |       |       |       |      |    |
|-----|-----|-----------|-----------|-------|-------|-------|------|----|
| 286 | 284 | P08238    | Phyre     | 20.93 | Intra | 1,2   | 1    | 37 |
| 565 | 559 | P08238    | Phyre     | 10.95 | Intra | 1,0   | 1    | 37 |
| 577 | 573 | P08238    | Phyre     | 13.74 | Intra | 1,0   | 1    | 37 |
| 491 | 481 | 3PRY      | Structure | 23.83 | Intra | 0,1   | 1    | 37 |
| 347 | 338 | P08238    | Phyre     | 18.61 | Intra | 2,0   | 1    | 37 |
| 284 | 275 | 3PRY      | Structure | 18.43 | Intra | 1,0   | 1    | 37 |
| 641 | 639 | P08238_PC | Docking   | 11.88 |       | 1 3,0 | 1    | 37 |
| 435 | 427 | P08238    | Phyre     | 17.89 | Intra | 1,0   | 1    | 37 |
| 275 | 273 | P08238    | Phyre     | 28.45 | Intra | 2,1   | 1    | 37 |
| 69  | 55  | P08238    | Phyre     | 20.93 | Intra | 6,2   | 1    | 37 |
| 565 | 559 | P08238    | Phyre     | 9.07  | Intra | 1,0   | 1    | 37 |
| 72  | 69  | P08238    | Phyre     | 16.02 | Intra | 1,1   | 1    | 37 |
| 446 | 442 | P31948    | Phyre     | ####  |       | 1 1,0 | 0.98 | 5  |
| 513 | 505 | P31948    | Phyre     | ####  |       | 1 1,0 | 0.99 | 5  |
| 435 | 428 | 3PRY      | Structure | ####  |       | 1 2,0 | 1    | 5  |
| 435 | 428 | 3PRY      | Structure | ####  |       | 1 0,1 | 0.93 | 5  |
| 435 | 428 | 3PRY      | Structure | ####  |       | 1 0,1 | 0.98 | 5  |
| 198 | 197 | ####      | ####      |       |       | 1 3,0 | 1    | 1  |

| MS2ScanN | MS2PrecCharge |
|----------|---------------|
| 20132    | 4             |
| 16347    | 4             |
| 7638     | 4             |
| 15969    | 4             |
| 25405    | 4             |
| 28420    | 5             |
| 20835    | 4             |
| 17296    | 4             |
| 18898    | 4             |
| 17788    | 4             |
| 8337     | 4             |
| 14327    | 4             |
| 21507    | 5             |
| 24480    | 4             |
| 20680    | 4             |
| 17187    | 4             |
| 21718    | 4             |
| 21741    | 5             |
| 19723    | 4             |
| 20909    | 4             |
| 20971    | 5             |
| 27418    | 4             |
| 25699    | 5             |
| 15209    | 4             |
| 26475    | 4             |
| 22376    | 4             |
| 28678    | 5             |
| 22936    | 4             |
| 11343    | 4             |
| 20589    | 6             |
| 22947    | 5             |
| 12693    | 4             |
| 17983    | 4             |
| 16162    | 5             |
| 18294    | 5             |
| 17549    | 4             |
| 20016    | 4             |
| 18346    | 5             |
| 18798    | 4             |
| 16511    | 6             |
| 5577     | 4             |
| 9014     | 4             |
| 9042     | 4             |
| 16789    | 4             |
| 16851    | 5             |
| 15145    | 4             |



|       |   |
|-------|---|
| 16270 | 4 |
| 17178 | 4 |
| 10058 | 4 |
| 10361 | 4 |
| 24754 | 4 |
| 20669 | 5 |
| 4092  | 4 |
| 21233 | 5 |
| 17967 | 4 |
| 18961 | 4 |
| 19222 | 4 |
| 24535 | 4 |
| 19949 | 4 |
| 23009 | 5 |
| 14661 | 4 |
| 7667  | 4 |
| 10536 | 4 |
| 25119 | 4 |