

TABLE #3: A2058 CELLS; GLUC/TRYPsin DIGEST; AKT SUBSTRATE MOTIF (CST# 23C8D2)

		Normalized Fold Change			Gene Name	Protein Name	Site	Description	Accession	kD	Upstream Kinase	Downstream Target
Index	Index in Detail	Cpd 1 : DMSO	Cpd 2 : DMSO	Cpd 1+2 : DMSO								
1	Adaptor/scaffold											
3	2	1.1	1.5	1.4	ABI1; ABI1	Abi-1; Abi-1 iso3	322; 296	abl-interactor 1 isoform b	Q81ZP0; Q81ZP0-3	55; 49		
5	7	1.3	1.3	2.2	AHNAK	AHNAK	\$5782	AHNAK nucleoprotein isoform 1	Q09666	629		
8	10	1.6	-3.2	-2.8	CRK	Crk	125	v-crk sarcoma virus CT10 oncogene homolog isoform b	P46108	34		
10	13	-1.1	1.7	2.8	DLGAP4; DLGAP4	SAPAP4; SAPAP4 iso2	\$970; \$973	disks large-associated protein 4 isoform c	Q9Y2H0; Q9Y2H0-2	108; 108		
11	14	-2.1	1.6	1.6	ENAH; ENAH	Mena; Mena iso2	\$125; \$125	enabled homolog isoform a	Q8N8S7; Q8N8S7-2	67; 64		
12	15	1.9	1.2	1.4	GAB2	Gab2	\$391	GRB2-associated binding protein 2 isoform b	Q9UQC2	74		
13	17	1.7	-1.6	-1.8	IRS2	IRS-2	\$306	insulin receptor substrate 2	Q9Y4H2	137		
14	18	-1.1	1.2	IRS2	IRS2	IRS-2	402	insulin receptor substrate 2	Q9Y4H2	137		
17	21	-1.2	-9.7	-4.8	MACF1; MACF1	MACF1; MACF1 iso2	4897; 4911; 4395; 4409	microfilament and actin filament cross-linker protein isoform a	Q96PK2; Q9UPN3	670; 620		
18	23	-1.0	2.1	1.8	MICAL1	MICAL1	817	microtubule associated monooxygenase, calponin and LIM domain containing 1	Q8TDZ2	118		
19	24	1.8	4.0	3.5	MICAL1	MICAL1	818	microtubule associated monooxygenase, calponin and LIM domain containing 1	Q8TDZ2	118		
20	26	1.3	1.3	-1.3	RANBP3	RANBP3	\$124	RAN binding protein 3 isoform RANBP3-a	Q9H6Z4	60		
22	30	1.4	-1.1	-1.6	RANBP3	RANBP3	\$126	RAN binding protein 3 isoform RANBP3-a	Q9H6Z4	60	Akt1, RSK2, p90RSK	Ran
23	33	3.5	-1.3	-4.2	RICTOR	Rictor	1135	rapamycin-insensitive companion of mTOR	Q6R327	192		
24	Adhesion or extracellular matrix protein											
26	36	1.4	-1.0	1.8	DSP	desmoplakin	\$165	desmoplakin isoform II	P15924	332		
27	39	-3.5	1.0	-2.9	DSP	desmoplakin	\$165; \$166	desmoplakin isoform II	P15924	332		
28	41	1.5	-1.0	1.1	DSP	desmoplakin	\$166	desmoplakin isoform II	P15924	332		
29	42	1.9	2.3	1.7	MLLT4; MLLT4	afadin; afadin iso3	1109; 1109	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 isoform 2	P55196; P55196-3	206; 198		
30	43	1.3	-1.1	1.5	TJAP1	TJAP1	\$545	tight junction protein 4 (peripheral)	Q5JTD0	62		
31	Apoptosis											
32	51	2.9	-8.8	-15.7	AKT1S1	Akt1S1	\$246	AKT1 substrate 1 (proline-rich)	Q96B36	27	Akt1	14-3-3 eta
34	55	-3.1	-4.4	-6.1	BAD	Bad	74	BCL2-associated agonist of cell death	Q92934	18		
35	60	-2.7	-3.9	-6.8	BAD	Bad	\$75	BCL2-associated agonist of cell death	Q92934	18	Akt1, JNK1, MSK1, PAK5, PKACA, PKC1, PPP2CA, Pim1, Pim2, Pim3, RSK2, Raf1, p90RSK	14-3-3 beta, Bcl-2, Bcl-xL, JNK1
37	65	1.5	-1.7	-1.9	BAD	Bad	\$99	BCL2-associated agonist of cell death	Q92934	18	Akt1, PKACA, PKC1, PPP2CA, Pim1, Pim2, Pim3, p70S6K	14-3-3 beta, 14-3-3 zeta, Bcl-2, Bcl-xL, JNK1, PKN2
41	70	1.1	1.7	1.9	NDRG2	NDRG2	\$330; \$332	N-myc downstream-regulated gene 2 isoform b	Q9UN36	41	PKCT, SGK	
42	71	1.3	1.8	2.1	NDRG2	NDRG2	\$330; \$334	N-myc downstream-regulated gene 2 isoform b	Q9UN36	41	SGK	
43	74	-1.8	-1.4	-1.2	NDRG2	NDRG2	\$332	N-myc downstream-regulated gene 2 isoform b	Q9UN36	41	PKCT, SGK	
45	Cell cycle regulation											
46	79	1.5	-1.0	1.5	CEP170	KAB1	1019	centrosomal protein 170kDa isoform beta	Q5SW79	175		
47	85	1.2	2.7	1.5	CEP170	KAB1	1019; 1023	centrosomal protein 170kDa isoform beta	Q5SW79	175		
49	91	1.9	5.2	3.0	CEP170	KAB1	1019; 1023; 1042	centrosomal protein 170kDa isoform beta	Q5SW79	175		
51	94	-1.3	2.0	1.2	CEP170	KAB1	1019; 1029	centrosomal protein 170kDa isoform beta	Q5SW79	175		
54	99	1.5	1.3	2.5	CEP170	KAB1	1019; 1042	centrosomal protein 170kDa isoform beta	Q5SW79	175		
55	100	-1.7	1.0	-1.2	CEP170	KAB1	\$1160	centrosomal protein 170kDa isoform beta	Q5SW79	175		
56	101	-1.1	2.7	-1.0	CEP170	KAB1	\$1160; \$1165	centrosomal protein 170kDa isoform beta	Q5SW79	175		
57	102	1.3	1.9	2.7	CEP170	KAB1	644	centrosomal protein 170kDa isoform beta	Q5SW79	175		
58	103	-2.0	1.4	2.2	CLASP1; CLASP1	CLASP1; CLASP1 iso3	\$646; \$646	CLIP-associating protein 1	Q7Z460; Q7Z460-3	169; 165		
59	106	1.1	2.6	1.3	DNAJC2	ZRF1	\$47	DnaJ (Hsp40) homolog, subfamily C, member 2 isoform 2	Q99543	72		
60	109	1.1	-11.6	-18.8	DNAJC2	ZRF1	\$47; \$49	DnaJ (Hsp40) homolog, subfamily C, member 2 isoform 2	Q99543	72		
61	112	-1.2	1.2	-1.7	TNKS1BP1	TNKS1BP1	\$1666	tankyrase 1-binding protein 1	Q9C0C2	182		
62	114	-3.1	-3.0	-5.3	ZZEF1	ZZEF1	1462	zinc finger, ZZ type with EF hand domain 1	O43149	331		
64	117	1.4	-1.2	-1.7	ZZEF1	ZZEF1	\$1464	zinc finger, ZZ type with EF hand domain 1	O43149	331		
65	Cell development/differentiation											
69	122	-1.0	1.6	-1.4	NDRG3	NDRG3	333	N-myc downstream-regulated gene 3 isoform b	Q9UGV2	41		
70	Chaperone											
71	125	-3.3	-1.2	-14.7	SGTA	SGTA	\$305	small glutamine-rich tetraatricopeptide	O43765	34		
73	Chromatin, DNA-binding, DNA repair or DNA replication protein											
74	182	-2.5	1.2	-3.5	CIC	capicua	356	capicua homolog	Q96RK0	164		
75	185	-1.8	1.7	-2.4	CIC	capicua	358	capicua homolog	Q96RK0	164		
76	186	1.0	1.0	-1.1	MLH1	MLH1	\$477	MutL protein homolog 1	P40692	85		
77	189	-5.5	-2.0	-10.0	TOPBP1	TOPBP1	\$1159	topoisomerase (DNA) II binding protein 1	Q92547	171		
78	Cytoskeletal protein											
79	190	-1.9	1.2	1.7	DBN1	DBN1	319	drebrin 1 isoform a	Q16643	71		
81	192	1.6	-1.3	-1.7	DMD; DMD	dystrophin; dystrophin iso13	3684; 955	dystrophin Dp427c isoform	P11532; NP_004005	427; 110		
82	193	2.3	2.1	1.5	FLNC	FLNC	\$2233	gamma filamin isoform b	Q14315	291		
86	200	-1.5	-1.7	-1.6	KIF13B	KIF13B	1793	kinesin family member 13B	Q9NQ78	203		
87	202	-1.2	-1.4	-1.4	KIF1B	KIF1B	\$1487	kinesin family member 1B isoform b	O60333	204		
88	205	-1.7	1.1	1.6	KIF23; KIF23	KIF23; KIF23 iso2	\$911; \$807	kinesin family member 23 isoform 2	Q02241; Q02241-2	110; 98	AurB, PLK1; AurB, PLK1	
89	211	2.3	2.1	1.6	KIF23; KIF23	KIF23; KIF23 iso2	\$911; \$912; \$807; \$808	kinesin family member 23 isoform 2	Q02241; Q02241-2	110; 98	AurB, PLK1; AurB, PLK1	
90	213	1.9	1.9	1.5	KIF23; KIF23	KIF23; KIF23 iso2	\$911; \$913; \$807; \$809	kinesin family member 23 isoform 2	Q02241; Q02241-2	110; 98	AurB, PLK1; AurB, PLK1	
91	217	-1.8	-1.2	1.1	KIF23; KIF23	KIF23; KIF23 iso2	\$912; \$808	kinesin family member 23 isoform 2	Q02241; Q02241-2	110; 98	PLK1; PLK1	
93	228	1.3	1.2	2.2	LMNA; LMNA	lamin A/C; lamin A/C iso2	10; 10	lamin A/C isoform 2	P02545; P02545-2	74; 65		
96	232	-1.7	-1.1	1.4	LMNA; LMNA	lamin A/C; lamin A/C iso2	\$301; \$301	lamin A/C isoform 2	P02545; P02545-2	74; 65	Akt1; Akt1	
98	240	-1.5	-6.1	-2.5	LMNA; LMNA	lamin A/C; lamin A/C iso2	\$403; \$403	lamin A/C isoform 2	P02545; P02545-2	74; 65		
103	253	1.4	-3.5	-2.3	LMNA; LMNA	lamin A/C; lamin A/C iso2	\$403; \$406; \$403; \$406	lamin A/C isoform 2	P02545; P02545-2	74; 65		
109	287	1.3	-3.7	-2.5	LMNA; LMNA	lamin A/C; lamin A/C iso2	\$404; \$404	lamin A/C isoform 2	P02545; P02545-2	74; 65	Akt1; Akt1	
113	351	-2.1	-6.2	-4.1	LMNA; LMNA	lamin A/C; lamin A/C iso2	\$404; \$407; 414; \$404; \$407; 414	lamin A/C isoform 2	P02545; P02545-2	74; 65	Akt1; Akt1	
122	377	-3.6	-1.8	2.0	NES; NES	nestin; nestin iso2	\$346; \$345	nestin	P48681; CA446780	177; 177		
123	380	-2.0	-1.0	2.8	NES; NES	nestin; nestin iso2	\$346; \$352; \$345; \$351	nestin	P48681; CA446780	177; 177		
125	382	1.3	2.2	1.2	PALLD	palladin	\$1101	palladin	Q8WX93	151		
127	385	1.1	2.3	2.3	PLEC1	plectin 1 iso11	\$20	plectin 1 isoform 1	Q15149-4	516		
128	386	1.6	2.1	1.9	PLEC1	plectin 1 iso11	\$21	plectin 1 isoform 1	Q15149-4	516		
129	387	-4.0	-2.8	-2.9	PLEC1; PLEC1; PLEC1; PLEC1	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	2886; 2776; 2735; 2753; 2749	plectin 1 isoform 1	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516		
131	389	1.4	-1.5	-1.3	PLEC1; PLEC1; PLEC1; PLEC1	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	\$4382; \$4389; \$4272; \$4279; \$4231; \$4238; \$4249; \$4256; \$4245; \$4252	plectin 1 isoform 1	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516		
132	390	1.6	-1.3	1.1	PLEC1; PLEC1; PLEC1; PLEC1	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	\$4382; \$4391; \$4272; \$4281; \$4231; \$4240; \$4249; \$4258; \$4245; \$4254	plectin 1 isoform 1	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516		

Peptide	Charge	Calc. m/z	Count in Details	Average RT	Intensity								Average Raw Intensity				Normalized Fold Change		
					DMSO (CS6112)	DMSO (CS6113)	Cpd 1 (CS6114)	Cpd 1 (CS6115)	Cpd 2 (CS6116)	Cpd 2 (CS6117)	Cpd 1+2 (CS6118)	Cpd 1+2 (CS6119)	DMSO	Cpd 1	Cpd 2	Cpd 1 + 2	Cpd 1 : DMSO	Cpd 2 : DMSO	Cpd 1+2 : DMSO
Adaptor/scaffold																			
QISRHNSTTSSTSSGGYR	3	669.2960	1	50.74	147.539	119.330	185.178	187.826	165.741	154.104	131.079	179.599	133.435	186.502	159.923	155.339	1.1	1.5	1.4
SNS*FSDERE	2	575.7063	4	53.02	521.329	289.928	623.955	691.552	372.023	448.509	574.969	846.168	405.629	657.754	410.266	710.569	1.3	1.3	2.2
SROGS*GVILROEE	2	769.8700	2	58.22	517,353	482,033	1,087,051	975,228	139,407	112,036	157,724	127,795	499.693	1,031,140	125,722	142,760	1.6	-3.2	-2.8
AASVPRQNS*ATESADSIE	2	908.3917	1	58.41	198.661	313.405	278.940	350.493	320.551	392.240	426.456	755.035	256.033	314.717	356.396	590.746	-1.1	1.7	2.8
TGPTLPRQNS*QLPAQVNGPSSQEE	3	886.0840	1	64.65	363.705	225.373	265.407	89.861	318,101	414.657	411.760	352.963	294.539	177.634	366.379	382.362	-2.1	1.6	1.6
RNT*LPAMDNSR	2	677.8006	2	57.60	362.827	249.602	798.945	674.969	317.697	287.543	338.065	359.473	306.215	736.957	302.620	348.769	1.9	1.2	1.4
SKS*QSSGSSATHPISVPGAR	3	674.3201	1	57.90	951.729	931.080	1,993.321	2,085.526	469.881	500.941	415.181	415.496	941.405	2,039.424	485.411	415.339	1.7	-1.6	-1.8
S*HTLSGGCGGGRS	3	480.8735	1	19.84			26.636	21,119					20.000	23.878	20.000	20.000	-1.7	1.2	1.2
MFES*QLSASQPTGGLPET*AR	3	712.6412	1	26.99	519,000	210,000	500,000	298,000	25,653	34,700		61,000	364,500	399,000	30,177	61,000	-1.2	-9.7	-4.8
RORLS*SLNLTDPDE	2	853.4173	2	65.76	1,563,173	1,238,359	1,505,274	2,033,658	2,095,257	2,573,178	1,933,259	2,116,532	1,400,766	1,769,466	2,334,218	2,024,896	-1.0	2.1	1.8
LSS*LNLTDPDE	2	633.2869	2	68.87	446,192	576,000	1,134,434	1,290,329	1,632,208	1,604,068	1,550,000	1,373,263	511,096	1,212,382	1,618,138	1,461,632	1.8	4.0	3.5
ERT*SLTQFPSSQEE	2	951.9097	1	62.93	260.963	261.392	429.882	449.704	268.500	290.082	135.256	183.720	261.188	499.793	279,191	159,488	1.3	1.3	-1.3
TSS*LTQFPSSQEE	2	809.3379	3	69.23	6,25E+5	878632	1,22E+6	1,44E+6	591876	538644	374346	378364	751,816	1,330,000	565,260	376,355	1.4	-1.1	-1.6
TLT*EPSVDFNHSDGTFPISTVQKTLQLE	3	1081.5099	4	78.19	348,763	336,000	1,575,393	1,521,678	244,000	192,000	71,200	62,600	342,382	1,548,536	218,000	66,900	3.5	-1.3	-4.2
Adhesion or extracellular matrix protein																			
RAS*SKGGGGYTCQSGSGWDE	2	1063.9156	2	59.26	217,197	232,254	376,079	424,647	165,667	180,744	318,169	324,201	226,626	400,363	173,206	321,165	1.4	-1.0	1.8
RAS*SKGKGGLTCQSGSGWDE	3	736.8194	3	60.70	373,364	360,398	149,295	118,635	249,377	353,135	148,038	55,440	366,881	133,965	301,256	101,739	-3.5	1.0	-2.9
RASS*SKGGGGYTCQSGSGWDE	3	709.6130	1	59.24	498,141	315,196	715,786	829,201	361,121	269,696	295,030	443,101	406,669	772,494	315,409	389,066	1.5	-1.0	1.1
GSQKPRPKS*EGFE	2	728.3353	1	49.42			47.577	51,554	37.877	34.478	29.928	26.459	20,000	49,566	36,178	28,194	1.9	2.3	1.7
KDS*LTQADE	2	550.2373	1	49.73	110,654	30,376	113,167	118,781	60,164	40,068	70,184	97,592	70,515	115,974	50,116	83,888	1.3	-2.1	1.5
Apoptosis																			
LNT*SFQKILKR	3	477.2452	10	60.43	34,558,120	34,741,804	133,146,536	129,618,856	2,736,639	3,538,319	1,850,589	1,740,997	34,649,962	131,382,696	3,137,479	1,795,793	2.9	-8.8	-15.7
IRSRRHS*SYPAGTEDDE	2	950.3973	2	52.46	356,980	350,383	163,989	134,439	69,706	58,098	43,358	50,301	353,682	149,214	63,902	46,830	-3.1	-4.4	-6.1
IRSRRHS*YPAGTEDDE	3	633.9342	5	52.44	2,001,427	1,766,358	928,487	863,698	422,918	356,226	233,913	218,047	1,883,893	896,093	389,572	225,980	-2.7	-3.9	-6.8
SRS*APPNLWAOR	3	511.9159	3	63.57	3,857,423	3,884,031	7,437,403	7,113,155	1,835,302	1,779,086	1,720,425	1,652,548	3,870,727	7,275,279	1,807,194	1,686,487	1.5	-1.7	-1.9
SRT*AS*LTSAASVDGNGR	2	876.8696	1	59.92	336,472	239,532	375,535	423,287	324,353	438,033	459,023	429,636	288,002	399,411	381,193	444,430	1.1	1.7	1.9
SRT*ASLT*ASASVDGNGR	3	584.9157	1	59.91	315,115	239,252	613,664	349,740	364,729	438,958	518,200	335,440	277,184	481,702	401,844	476,820	1.3	1.8	2.1
TAS*LTSAASVDGNGR	2	715.3198	3	60.37	989,808	680,853	632,000	535,000	387,402	496,526	419,386	664,822	794,427	583,500	441,964	542,104	-1.8	-1.4	-1.2
Cell cycle regulation																			
IROPs*VLTDDDDQTSVPHSAISDIMSSDOE	3	1151.8385	6	72.76	497,883	4,351,276	9,139,362	8,528,625	4,516,692	2,768,598	5,468,128	6,045,142	4,615,580	8,833,994	3,642,645	5,756,635	1.5	-1.0	1.5
IROPs*VLT*DDDDQTSVPHSAISDIMSSDOE	3	1178.4940	5	72.91	625,388	577,000	822,000	1,010,000	1,250,138	1,380,584	878,883	625,000	601,194	916,000	1,315,361	751,942	1.2	2.7	1.5
IROPs*VLT*DDDDQTSVPHSAISDIMSS*DOE	3	1205.1494	1	72.92	246,336	236,280	655,374	531,724	1,246,751	776,084	588,703	599,971	241,308	593,549	1,011,418	594,337	1.9	5.2	3.0
KFVQSSGRIIRQPS*VLTDDDDQTS*SVPHSA ISDIMSSDOE	4	1106.4917	1	71.64	85,483	104,026	116,606	74,059	124,416	181,067	80,663	111,146	94,755	95,333	152,742	95,905	-1.3	2.0	1.2
IROPs*VLTDDDDQTSVPHSAISDIM*SS*DOE	3	1183.8256	2	69.15	730,168	901,255	1,415,907	1,664,712	790,543	887,483	1,688,226	1,608,491	815,712	1,540,310	893,019	1,638,359	1.5	1.3	2.5
LGS*LSARSDSE	2	601.2587	1	57.68	906,236	762,925	641,587	597,289	697,624	674,765	490,655	681,071	834,581	619,438	686,195	585,863	-1.7	1.0	-1.2
LGS*LSARS*DSE	2	641.2419	1	58.03	51,322	72,142	187,737	66,211	233,855	253,135	71,210	103,417	111,732	126,974	243,495	87,314	-1.1	2.7	-1.0
RRT*LPQLNREE	2	716.8511	1	62.64	1,227,584	961,800	1,884,991	1,781,698	1,462,638	1,871,803	2,155,767	2,664,127	1,094,692	1,833,345	1,667,221	2,409,947	1.3	1.9	2.7
ROS*SGSATNVASTPDNR	2	614.4030	2	53.96	41,879	41,806		26,568	46,753	47,817	75,504		41,843	26,568	47,285	75,504	-2.0	1.4	2.2
NNNAS*ASFOE	2	902.2434	4	54.44	4,781,105	3,804,216	6,854,579	5,617,144	8,267,296	9,439,803	4,774,328	4,251,417	4,292,661	6,235,862	8,853,550	4,512,873	1.1	2.6	1.3
NNNAS*AS*FOE	2	642.2265	3	53.58	5,295,456	2,242,092	5,360,044	5,133,962	242,482	278,985	150,869	174,659	3,768,774	5,247,003	260,734	162,764	1.1	-11.6	-18.8
NRS*AEEGEALAE	2	642.7591	1	55.41	321,847		352,504	364,986	229,292	368,844	20,006	281,865	321,847	358,745	299,068	150,936	-1.2	1.2	-1.7
TSHLQPLNQRRT*SSVVEE	3	763.7168	2	57.04	9,565,713	8,570,666	4,014,013	3,640,047	2,537,487	2,349,513	1,033,699	1,767,235	9,068,190	3,827,030	2,443,500	1,400,467	-3.1	-3.0	-5.3
QRTSS*VVEE	2	557.7427	3	51.21	9,393,272	3,903,982	12,780,931	11,584,579	4,661,044	4,014,189	2,127,761	4,233,702	6,648,627	12,182,755	4,337,617	3,180,732	1.4	-1.2	-1.7
Cell development/differentiation																			
SRHTSHS*SSLGSGESPFSR	3	682.9678	1	60.31	554,774	506,741	603,193	744,328	616,554	745,099	278,594	345,657	530,758	673,761	680,827	312,126	-1.0	1.6	-1.4
Chaperone																			
SOIRSRTPS*ASNDQOQE	3	666.9556	58	52.44	2,478,398	2,492,744	1,011,563	927,928	1,670,416	1,751,090	134,553	140,255	2,485,571	969,746	1,710,753	137,404	-3.3	-1.2	-14.7
Chromatin, DNA-binding, DNA repair or DNA replication protein																			
AFS*HSGVSLDGGDE	2	740.2989	3	61.15	1,580,449	1,434,620	729,739	842,831	1,369,713	1,517,138	315,680	392,803	1,507,535	786,285	1,443,426	354,242	-2.5	1.2	-3.5
AFSHS*GVHSLDGGDEVDSQALQE	3	784.0046	1	66.60	1,706,770	1,390,587	1,097,057	1,117,019	1,981,652	2,231,135	525,298	529,841	1,548,679	1,107,038	2,106,394	527,570	-1.8	1.7	-2.4
HREDS*DVEMVE	2	713.2715	2	58.80	566,844	416,822	732,126	565,654	424,017	381,738	345,864	410,407	491,833	648,890	402,878	378,136	1.0	1.0	-1.1
RARLAS*NLQWVSCPTQYSE	3	782.0232	2	69.64	740,472	628,026	176,344	144,176	290,614	271,508	65,352	45,400	684,249	160,260	281,061	55,376	-5.5	-2.0	-10.0
Cytoskeletal protein																			
RVASASGSCDVPSFNFRHPRGS*HLDSHRR	4	810.1276	1	60.07	81,472	241,206	55,889	162,817	148,558	149,933	175,556	281,852	161,339	109,353	149,246	228,704	-1.9	1.2	1.7
GRNTPGKPMREDT*MF	3	562.5764	1	47.22	33,159		69,349	71,884					33,159	70,617	20,000	20,000	1.6	-1.3	-1.3
LGS*FGSITROQE	2	701.8220	1	67.62	340,000	384,818	1,330,000	827,000	648,610	539,985	414,080	486,000	362,259	1,078,500	594,298	450,040	2.3	2.1	1.5
SAT*LSGGSATNLSAATAALKADRSKNPE	4	741.3716	3	72.95	1,224,606	1,000,809	1,071,955	789,429	667,252	408,430	518,094	643,437	1,112,708	990,692	537,841	580,766	-1.5	-1.7	-1.6
NLAGWRPRQGS*LIIE	3	592.9650	2	72.20	39,778,480	35,480,112	42,671,552	39,350,472	17,672,536	26,147,154	16,517,955	28,238,938	37,629,296	41,011,012	21,909,845	22,378,447	-1.2	-1.4	-1.4
KRRS*STVAPADPGAESE	3	655.9727	5	52.92	1,059,377	958,155	785,358	778,206	850,766	853,716	1,409,272	1,231,949	1,008,766	781,782	852,241	1,320,611	-1.7	1.1	-1.1
KRRS*STVAPADPGAESE	3	682.6282	4	53.92	269,232	240,545	815,420	685,883	410,427	432,153	269,770	377,256	254,889	750,652	421,290	323,513	2.3	2.1	