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In vivo hydroxyl radical protein footprinting for the study of protein interactions in *Caenorhabditis elegans* --Manuscript Draft--

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Benjamin Werth, Senior Science Editor
Journal of Visualized Experiments

Dear Benjamin Werth,

Please find enclosed the manuscript entitled “*In vivo* hydroxyl radical protein footprinting for the study of protein interactions in *Caenorhabditis elegans*” authored by Jessica A. Espino and Lisa M. Jones which we are submitting to the *Journal of Visualized Experiments*. This manuscript highlights the use of the hydroxyl radical protein footprinting method *in vivo* fast photochemical oxidation of proteins (IV-FPOP) for studying protein structure in *C. elegans*, an animal model for human disease. FPOP utilizes an excimer laser to photolyze hydrogen peroxide to generate hydroxyl radicals for protein labeling. Mass Spectrometry is used to detect and quantitate protein labeling. In this manuscript, we describe the procedure for carrying out this new method. This includes a description for assembling a custom flow system to flow the worms in a single file. We feel the production of a video with the flow system construction and IV-FPOP method would greatly benefit the readers of JOVE who want to use the method.

Sincerely,

A handwritten signature in black ink that reads "Lisa Jones".

Lisa M. Jones
Associate Professor
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TITLE:

In Vivo Hydroxyl Radical Protein Footprinting for the Study of Protein Interactions in *Caenorhabditis elegans*

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KEYWORDS:

Caenorhabditis elegans, hydroxyl radical protein footprinting, FPOP, mass spectrometry, in vivo, proteomics

SUMMARY:

In vivo fast photochemical oxidation of proteins (IV-FPOP) is a hydroxyl radical protein footprinting technique that allows for mapping of protein structure in their native environment. This protocol describes the assembly and set-up of the IV-FPOP microfluidic flow system.

ABSTRACT:

Fast oxidation of proteins (FPOP) is a hydroxyl radical protein footprinting (HRPF) method used to study protein structure, protein-ligand interactions, and protein-protein interactions. FPOP utilizes a KrF excimer laser at 248 nm for photolysis of hydrogen peroxide to generate hydroxyl radicals which in turn oxidatively modify solvent-accessible amino acid side chains. Recently, we expanded the use of FPOP of in vivo oxidative labeling in *Caenorhabditis elegans* (*C. elegans*), entitled IV-FPOP. The transparent nematodes have been used as model systems for many human diseases. Structural studies in *C. elegans* by IV-FPOP is feasible because of the animal's ability to uptake hydrogen peroxide, their transparency to laser irradiation at 248 nm, and the irreversible nature of the modification. The assembly of a microfluidic flow system for IV-FPOP labeling, IV-FPOP parameters, protein extraction, and LC-MS/MS optimized parameters are described herein.

INTRODUCTION:

Protein footprinting coupled to mass spectrometry (MS) has been used in recent years to study protein interactions and conformational changes. Hydroxyl radical protein footprinting (HRPF) methods probe protein solvent accessibility by modifying protein amino acid side chains. The HRPF method, fast photochemical oxidation of proteins (FPOP)¹, has been used to probe protein structure in vitro², in-cell (IC-FPOP)³, and most recently in vivo (IV-FPOP)⁴. FPOP utilizes a 248 nm wavelength excimer laser in order to rapidly generate hydroxyl radicals by photolysis of hydrogen

peroxide to form hydroxyl radicals¹. In turn, these radicals can label 19 out of 20 amino acids on a microsecond time scale, faster than proteins can unfold. Although, the reactivity of each amino acid with hydroxyl radicals extends 1000-fold, it is possible to normalize side chain oxidation by calculating a protection factor (PF)⁵.

Since FPOP can oxidatively modify proteins regardless of their size or primary sequence, it proves to be advantageous for in-cell and in vivo protein studies. IV-FPOP probes protein structure in *C. elegans* similarly to in vitro and in-cell studies⁴. *C. elegans* are part of the nematode family and are widely used as a model to study human diseases. The ability of the worm to uptake hydrogen peroxide by both passive and active diffusion allows for the study of protein structure in different body systems. In addition, *C. elegans* are suited for IV-FPOP due to their transparency at the 248 nm laser wavelength needed for FPOP⁶. Coupling of this method to mass spectrometry allows for the identification of multiple modified proteins using traditional bottom-up proteomics approaches.

In this protocol, we describe how to perform IV-FPOP for the analysis of protein structure in *C. elegans*. The experimental protocol requires the assembly and set-up of microfluidic flow system for IV-FPOP adapted from Konermann et al⁷. After IV-FPOP, samples are homogenized for protein extraction. Protein samples are proteolyzed and peptides are analyzed by liquid chromatograph (LC) tandem MS, followed by quantification.

PROTOCOL:

1. *C. elegans* maintenance and culture

1.1. Grow and synchronize worms colonies to their fourth larvae (L4) stage following standard laboratory procedures⁸.

1.2. The day of IV-FPOP experiment, wash L4 worms from bacterial lawns (OP50 *E. coli*) with M9 buffer (0.02 M KH₂PO₄, 0.08 M Na₂HPO₄, 0.08 M NaCl, 1 mM MgSO₄).

1.3. Obtain 500 µL aliquots of ~10,000 worms per IV-FPOP sample.

2. Microfluidic flow system assembly

2.1. Start the flow system assembly by cutting a 2 cm piece of fluorinated ethylene propylene (FEP) tubing (1/16 in. outer diameter (o.d.) x 0.020 in. inner diameter (i.d.)).

2.2. Using a clean dissecting needle, widen the i.d. of the FEP tubing in order to make a small crater at one end only, ~50 mm in length. The crater should be big enough to fit two 360 µm o.d. pieces of fused silica.

NOTE: Do not widen the opposite end as this end will only be used to fit the outlet capillary.

2.3. With a ceramic cutter, cut two 15 cm pieces of 250 μm i.d. fused silica. These two pieces will become the infusing lines of the flow system.

2.4. Using self-adhesive tape, tape the two 250 μm i.d. capillaries together ensuring they are parallel to each other and their ends are 100% flushed.

NOTE: To ensure the fused silica ends are not crushed after cutting, and are straight and 100% flushed against each other, it is recommended to examine them using a magnifying glass or under a stereo microscope.

2.5. Insert the two taped capillaries into the handmade crater of the FEP tubing. Push the capillaries up to the very edge of the handmade crater.

CAUTION: To maintain the efficacy of the flow system, do not push past the handmade crater (**Figure 1a**).

2.6. Place a small dot of epoxy resin on a clean surface and mix with a dissecting needle.

2.7. Quickly, using the same needle, place a small drop of resin at the end of the infusing capillaries where they connect with the FEP tubing and allow the resin to dry, hanging outlet-side up, for a few minutes (**Figure 1a**).

2.8. While the resin dries, binding the FEP tubing and two capillaries together, cut a new 250 μm i.d. capillary. The new capillary will become the outlet capillary of the flow system. The desired length of the capillary can be calculated using the equation below:

$$\ell = \frac{f \times t}{\pi \left(\frac{i.d.}{2} \right)^2}$$

Where ℓ is length of the capillary to be cut in centimeters, t is the desired reaction time in minutes, f is the flow rate in mL/min, and i.d. is the inner diameter of the capillary in centimeters.

NOTE: After cutting the outlet capillary, examine the ends ensuring they are straight and not crushed.

2.9. Once the resin has dried, insert the new capillary through the FEP tubing outlet end. The inside ends of the outlet capillary and the two infusing capillaries should be flush against each other inside the FEP tubing, this creates the mixing-T (**Figure 1b**).

2.10. Bind the outlet capillary and FEP tubing with fresh epoxy resin as described in steps 2.6 and 2.7.

2.11. Allow the resin to dry overnight binding the flow system together. Set up the microfluidic

flow system the next day (**Figure 1c**).

3. Microfluidic flow system for in vivo FPOP

3.1. Insert four magnetic stirrers inside one 5 mL syringe. This syringe becomes the sample syringe. The magnetic stirrers prevent the worms from settling inside the syringe during IV-FPOP (**Figure 2A**).

3.2. Fill the two 5 mL syringes with M9. Make sure there are no air bubbles inside each syringe as they can affect the flow rate and mixing efficiency.

3.3. Connect a Luer adapter to each 5 mL syringe ensuring they are finger tight and secured in place.

3.4. Attach each syringe to a single 3-2 valve. The syringe should be attached to the middle port of the valve (**Figure 2B**).

3.5. Secure each 5 mL syringe to the dual syringe pump and adjust the mechanical stop collar to prevent over pressure to the syringe from the pusher block. Keep in mind the addition of the magnetic stirrers when setting the stop collar.

3.6. Attach each infusing capillary end of the homemade microfluidic flow system to the top port of each 3-2 valve using a super flangeless nut, FEP sleeve, and super flangeless ferrule (**Figure 2B**).

3.7. To the remaining opened port of the 3-2 valve (bottom port), attach a 10 cm 450 μm i.d. capillary using a super flangeless nut, FEP sleeve, and super flangeless ferrule (**Figure 2B**). These capillaries become the withdrawing sample capillaries.

3.8. Start the pump flow and check all connections of the microfluidic flow system for visual leaks. Flow at least three syringe volumes using the experimental flow rate. The final flow rate is dependent on the laser irradiation window, laser frequency, and a zero-exclusion fraction volume.

NOTE: For this protocol, a final flow rate of 375.52 $\mu\text{L}/\text{min}$ was calculated from a laser irradiation window of 2.55 mm, 250 μm i.d. fused silica, zero exclusion fraction, and 50 Hz frequency.

3.8.1. The flow path is marked by the arrows on the 3-2 valve handle. Each syringe can be refilled manually by moving the valve handle from the expelling position to the withdrawing position.

NOTE: Leaks at the 3-2 valve can be fixed by re-screwing the super flangeless nut or replacing any of the valve connections (super flangeless nut, FEP sleeve, or super flangeless ferrule). Leaks at the mixing-T require a reassembly of the microfluidic flow system (steps 2.1 to 2.11).

175 3.9. Move the microfluidic flow system to the experimental bench and secure the outlet capillary
176 to the radiating stage using a 360 μm o.d. stainless steel union (**Figure 2C,D**).
177

178 3.10. Using a long-reach lighter, burn the coating of the fused silica at the laser irradiation
179 window. Clean the burned coating using lint-free tissue and methanol.
180

181 NOTE: Alternate between burning cycles and methanol cleaning cycles to avoid over-heating the
182 capillary as excess heat can melt and/or break the capillary.
183

184 3.11. Position the magnetic stirrer block above the 5 mL syringe containing the magnetic stirrers.
185 Adjust the speed and position of the magnetic stirrer block so that the magnetic stirrers inside
186 the 5 mL syringe are rotating slowly and constantly.
187

188 **4. In vivo FPOP**

189
190 4.1. Turn on the KrF excimer laser and allow the thyatron to warm-up.
191

192 CAUTION: The laser emits visible and invisible radiation at 248 nm wavelength that can damage
193 eyes. Proper eye protection should be worn before turning on the laser and opening the beam
194 exit window.
195

196 4.2. Measure the laser energy at a frequency of 50 Hz for at least 100 pulses by placing the optical
197 sensor at the beam exit window.
198

199 NOTE: For this protocol, a 2.55 mm irradiation window was used with a laser energy of 150 ± 2.32
200 mJ.
201

202 4.3. Obtain approximately 10,000 worms (500 μL) and manually withdraw the sample into the
203 sample syringe.
204

205 4.4. Fill the sample syringe with 2.5 mL of M9 buffer for a final sample volume of 3 mL. Make sure
206 that no air bubbles are introduced into the sample syringe.
207

208 4.5. Fill the second syringe with 3 mL of 200 mM H_2O_2 , again ensuring no air bubbles are
209 introduced into the syringe.
210

211 4.6. At the end of the outlet capillary, place a 15 mL conical tube wrapped in aluminum foil
212 containing 6 mL of 40 mM N'-Dimethylthiourea (DMTU), 40 mM N-tert-Butyl- α -phenylnitrone
213 (PBN), and 1% dimethyl sulfoxide to quench excess H_2O_2 , hydroxyl radicals, and inhibit
214 methionine sulfoxide reductase activity, respectively.
215

216 4.7. Start the excimer laser from the software window, wait for the first pulse, and start the
217 sample flow from the dual syringe.
218

NOTE: Samples should be run in biological duplicates in technical triplicates under 3 samples conditions: laser irradiation with H₂O₂ (sample), no laser irradiation with H₂O₂ *and* no laser irradiation *no* H₂O₂ (controls), totaling to 9 samples per biological set.

4.8. Collect the entire sample in the 15 mL tube, while actively monitoring the sample flow for any visual leaks as some back pressure from the sample syringe can sometimes build-up.

4.9. Following IV-FPOP, pellet worms by centrifugation at 805 x *g* for 2 min. Remove quench solution, add 250 µL of lysis buffer (8 M urea, 0.5% SDS, 50 mM HEPES, 50 mM NaCl, 1 mM EDTA, 1 mM phenylmethylsulfonyl fluoride [PMSF]). Transfer the sample to a clean microcentrifuge tube, flash freeze, and store at -80 °C until sample digestion.

5. Protein extraction, purification, and proteolysis

5.1. Thaw frozen samples on ice and homogenize by sonication for 10 s, followed by a 60 s ice incubation. Multiple rounds of sonication may be required, homogenate can be observed under a stereomicroscope by placing a 2 µL sample aliquot on a microscope slide. Sample homogenization is complete when small to no pieces of worms are seen.

5.2. Centrifuge homogenized worms at 400 x *g* for 5 min at 4 °C and collect the supernatant into a clean microcentrifuge tube.

5.3. Determine sample protein concentrations using a bicinchoninic acid assay (BCA assay) using the manufacturer's instructions.

NOTE: Sample concentration can be determined using any biochemical protein concentration assay of choice. Keep in mind reagent compatibility with lysis buffer (8 M urea, 0.5% SDS, 50 mM HEPES, 50 mM NaCl, 1 mM EDTA, 1 mM PMSF). Additionally, a buffer dilution may be necessary.

5.4. Obtain 100 µg of protein from each sample and place in clean microcentrifuge tubes.

5.5. Add dithiothreitol (DTT) to a 10 mM final concentration to reduce disulfide bonds in all samples. Vortex, spin down, and incubate samples at 50 °C for 45 min.

5.6. Cool samples to room temperature for 10 min.

5.7. Add iodoacetamide (IAA) to a 50 mM final concentration to alkylate reduced residues. Vortex, spin down, and incubate samples for 20 min at room temperature protected from light.

5.8. Immediately after alkylation, precipitate the protein sample by adding 4 volumes of 100% pre-chilled acetone and incubate at -20 °C overnight.

5.9. The next day, pellet protein precipitate by centrifugation at 16,000 x *g* for 10 min. Wash sample pellet with 90% acetone, remove supernatant, and allow pellet to dry for 2–3 min.

5.10. Re-suspend the protein pellet in 25 mM Tris-HCl (1 µg/µL). Add trypsin at a final protease to protein ratio of 1:50 (w/w) and digest samples at 37 °C overnight.

5.11. The next day quench the trypsin digestion reaction by adding 5% formic acid.

NOTE: A minimum of 0.5 µg of peptides per sample is needed for LC-MS/MS analysis (steps 6.1-6.5). Determine sample peptide concentrations using a quantitative colorimetric peptide assay (see the **Table of Materials**) as described by the manufacturer's protocol.

6. High performance liquid chromatography-tandem mass spectrometry (LC-MS/MS)

6.1. Use the following LC mobile phases: water in 0.1% FA (A) and ACN in 0.1% FA (B).

6.2. Load 0.5 µg of peptides onto a trap column (180 µm × 20 mm) containing C18 (5 µm, 100 Å) and wash sample with 99% solvent A and 1% B for 15 min at 15 µL/min flow rate.

6.3. Separate peptides using an in-house packed column (0.075 mm i.d. × 20 mm) with C18 reverse phase material (5 µm, 125 Å).

6.4. Use the following analytical separation method: the gradient was pumped at 300 nL/min for 120 min: 0–1 min, 3% B; 2–90 min, 10–45% B; 100–105 min, 100% B; 106–120 min, 3% B.

6.5. Perform data acquisition of peptides in positive ion mode nano-electrospray ionization (nESI) using a high-resolution mass spectrometer.

NOTE: For this protocol, an ultra-performance LC (UPLC) instrument couple to a high-resolution mass spectrometer was utilized. Data dependent acquisition was utilized. The m/z scan range for MS1 was 3750–1500 at 60,000 resolution and 60 s dynamic exclusion. Ions with charge states of +1 and >6 were excluded. An automatic gain control (AGC) target of 5.5e5 was used with a maximum injection time of 50 ms and an intensity threshold of 5.5e4. Ions selected for MS2 were subjected to higher-energy collisional dissociation (HCD) fragmentation using 32% normalized collision energy. Fragment ions were detected in the spectrometer with 15,000 resolution and a 5.0e4 AGC target.

7. Data analysis

7.1. Search tandem MS files with a bottom-up proteomics analysis software against the *C. elegans* database.

7.2. Set the protein analysis search parameters as follow: one trypsin missed cleavage, 375–1500 m/z peptide mass range, fragment mass tolerance of 0.02, and precursor mass tolerance of 10 ppm. Carbamidomethylation is set as a static modification and all known hydroxyl radical side-chain modifications^{9,10} as dynamic. Peptide identification is established at 95% confidence

(medium) and residue at 99% confidence (high). The false discovery rate (FDR) is set a 1%.

7.3. Export data to an electronic database and summarize the extent of oxidation per peptide or residue using the equation below¹¹:

$$\frac{\sum \text{EIC area modified}}{\sum \text{EIC area}}$$

NOTE: Where EIC area modified is the extracted ion chromatographic area (EIC) of the peptide or residue with an oxidative modification, and EIC area is the total area of the same peptide or residue with and without the oxidative modification.

REPRESENTATIVE RESULTS:

In the microfluidic flow system used for IV-FPOP, H₂O₂ and the worms are kept separated until just prior to laser irradiation. This separation eliminates breakdown of H₂O₂ by endogenous catalase and other cellular mechanisms¹². The use of a 250 µm i.d. capillary shows a total sample recovery between 63–89% across two biological replicates, while the 150 µm i.d. capillary only shows 21–31% recovery (**Figure 3A**). The use of a larger i.d. capillary (250 µm) leads to better worm flow during IV-FPOP and single worm flow (**Figure 3B**) when compared to a smaller i.d. capillary (150 µm) (**Figure 3C**). The 150 µm i.d. capillary does not allow for single worm flow (**Figure 3C**) and multiple worms are seen flowing together at the laser irradiating window which decreases the amount of laser exposure per single worm.

IV-FPOP is a covalent labeling technique that probes solvent accessibility in *C. elegans*. **Figure 4A** shows a representative extracted ion chromatograms (EIC) of a FPOP modified and unmodified peptide. The hydroxyl radical label changes the chemistry of oxidatively modified peptides, thus making FPOP modified peptides more polar. In reverse phase chromatography, IV-FPOP modified peptides have earlier retention times than unmodified peptides. MS/MS fragmentation of isolated peptides allows for the identification of oxidatively modified residues (**Figure 4B**).

IV-FPOP has shown to oxidatively modified a total of 545 proteins across two biological replicates within *C. elegans* (**Figure 5A,B**). An advantage of IV-FPOP as a protein footprinting method relies on the technique's ability to modify proteins in a variety of body systems within the worms (**Figure 5C**). This method would allow to probe protein structure and protein interactions regardless of body tissue or organ within the worm. Further, tandem MS analysis confirms IV-FPOP probes solvent accessibility in vivo. The oxidation pattern of the heat shock protein 90 (Hsp90) in complex with the myosin chaperon protein UNC-45 was analyzed (**Figure 6**). MS/MS analysis for Hsp90 shows four oxidatively modified residues (**Figure 6C,D**), the normalized extent of FPOP modification (ln(PF))⁵ indicates Hsp90's residue M698 to be less solvent accessible than residues R697, E699, and E700 when bound to UNC-45 (**Figure 6C**). These differences in oxidation are validated by literature solvent accessible surface area (SASA) calculations (PDB 4I2Z¹³). Residue M698 has a SASA value of 0.03 which is consider to be a buried residue when compared to residues R697, E699, and E700 with higher SASA values (**Figure 6C**).¹⁴

FIGURE LEGENDS:

Figure 1. In vivo FPOP microfluidic flow system schematic. (A) The two infusing lines (orange) of the IV-FPOP flow system are shown inside the FEP tubing (yellow), the correct binding position of the epoxy resin is represented by the light blue circle. (B) Complete assembled mixing-T formed by the three 250 μm i.d. capillaries. The correct resin binding position of the outlet capillary to the FEP tubing is represented by the light blue circle. (C) The complete assembled flow system for in vivo covalent labeling of *C. elegans*. Prior to FPOP, worms are kept separated from H_2O_2 until just prior to labeling; the laser irradiation window is shown in light blue and the laser beam is represented by the purple lightning bolt. Figures are not to scale. This figure has been modified from Espino et al.⁴.

Figure 2. Microfluidic system during IV-FPOP. (A) Representative picture of *C. elegans* inside the 5 mL syringe. Without stirring, the worms settle at the bottom of the syringe (left). The magnetic stirrers and stirrer block keep the worms in suspension during the IV-FPOP experiments (right). (B) Representative picture of a 5 mL syringe, infusing capillary, and withdrawing capillary connected to the 3-2 valve. The 3-2 valve handle is shown in the withdrawing position. (C) Microfluidic flow system during IV-FPOP, the magnetic stirrer block is position above the worms' 5 mL syringe. (D) Outlet capillary secured to the radiating stage.

Figure 3. Comparison of *C. elegans* flow and recovery using two i.d. capillaries. (A) Percent recovery of worms after IV-FPOP for two biological replicates (BR) with 250 (gray) and 150 (black) μm i.d. capillaries. Error bars are calculated from the standard deviation across technical triplicates. *C. elegans* flowing through the laser irradiating window through a 250 μm (B) and 150 μm (C) i.d. capillaries. The worms are more tightly compacted in the smaller capillary. The 150 μm i.d. capillary shows clumping of worms. This figure has been modified from Espino et al.⁴.

Figure 4. Representative LC-MS/MS results following IV-FPOP. (A) EIC of a FPOP modified peptide (red) and unmodified (blue). The selected peptide belongs to the actin-1 protein. (B) MS/MS spectrum of doubly charged unmodified actin-1 peptide 317-327. (C) MS/MS spectrum of doubly charged FPOP modified actin-1 peptide 317-327, in this example P323 was oxidatively modified (γ_5^+ ion, red).

Figure 5. IV-FPOP oxidatively modifies proteins within *C. elegans*. (A) Venn diagram of oxidatively modified proteins in the presence of 200 mM hydrogen peroxide at 50 Hz across two biological replicates (BR), BR1 is in blue and BR2 is in yellow. (B) Venn diagram of oxidatively modified proteins identified in irradiated samples, hydrogen peroxide control, and worm-only control in BR2 across technical triplicates. (C) Pie chart of oxidatively modified proteins within different *C. elegans* body systems. This figure has been modified from Espino et al.⁴.

Figure 6. Correlating IV-FPOP modifications to solvent accessibility. (A) Myosin chaperon protein UNC-45 (gray) (PDB ID 4I2Z¹³) highlighting two modified peptides identified by LC/MS/MS analysis, 669–680 and 698–706 (green, left inset). UNC-45 is bound to the Hsp90 peptide fragment (blue). Oxidatively modified residues within this fragment are shown in sticks (red), and

UNC-45 is rendered as a surface (right inset). (B) Tandem MS spectra of UNC-45 peptide 669–680 (top) and 698–706 (bottom) showing b- and y-ions for the loss of CO₂, an FPOP modification. (C) The calculated ln(PF) for the Hsp90 oxidatively modified residues, R697, M698, E699, and E700. Calculated SASA values for Hsp90 are denoted above each residue. (D) Tandem MS spectra for R697, M698, E699, and E700 showing a +16 FPOP modification. This figure has been modified from Espino et al.⁴.

DISCUSSION:

The current benchmark for the study of in vivo protein-protein interactions (PPI) is fluorescence resonance energy transfer (FRET). In its most simple form, this technique studies PPI by energy transfer between two molecules when they are in close proximity to one another¹⁵. Unlike MS techniques, FRET does not have the resolution to characterize conformational changes and interaction sites at the amino-acid level. MS based techniques have been increasingly utilized for the study of PPI¹⁶. IV-FPOP is a HRP method that allows for the in vivo protein structural analysis in *C. elegans*. In order to successfully label *C. elegans* by IV-FPOP, it is important to properly assemble the microfluidic flow system to reduce sample loss. The 250 µm i.d. capillary has shown to maximize sample recovery when compared to smaller i.d. capillaries⁴. Larger i.d. capillaries have not been tested, however the microfluidic flow system is designed using a capillary with the same i.d. as a commercially available flow cytometry system for the sorting of *C. elegans*.¹⁷ The worm sample size is also important, a sample size of less than ~10,000 per sample prior to FPOP does not yield protein concentrations high enough for LC-MS/MS analysis. Higher samples sizes (>10,000 worms) can also be used by adjusting the initial starting volume (step 4.5).

Proper assembly of the microfluidic flow system is important. Leaks in the sample pathway result in an inconsistent flow of the worms or H₂O₂. The ferrules, sleeves, and 3-2 valves can be reused from multiple IV-FPOP experiments if properly cleaned after each experiment. However, we recommend to assemble a new microfluidic flow system for every biological replicate. If the microfluidics is properly assembled, the worms and H₂O₂ will mix at the mixing-T with minimal back pressure. As quality control (QC) of the microfluidic flow system, we recommend testing the mixing efficiency by using colored dyes. It is important to monitor the motion of the magnetic stirrers inside the worm syringe during IV-FPOP, improper sample mixing at the worm syringe or the mixing-T can result in back pressure causing leaks. In addition, poor mixing conditions lead to large sample losses, poor laser exposure of worms at the laser window, and clogging.

C. elegans maintenance is important in order to decrease background oxidation. We recommend growing the worms at low temperatures under low stress conditions as high temperatures can affect total background oxidation. A control sample set of worms only, no H₂O₂ and no laser irradiation, is recommended for all IV-FPOP experiments to account for background oxidation due to laboratory maintenance. One of the current limitations of this technique is total number of oxidatively modified peptides identified and the total number of residues oxidized per peptide in order to gain higher protein structural information. Although not recommended, an increase in oxidative modifications could be achieved by using higher concentrations of hydrogen peroxide. An increase in hydrogen peroxide could significantly alter important biological pathways as well as lead to oxidation-induced unfolding. If the hydrogen peroxide concentration for IV-FPOP is

increased, it is recommended to test worm viability and background oxidation as concentrations higher than 200 mM have not been tested.

The LC-MS/MS protocol described can be optimized and modified to meet the MS QC of other laboratories. The use of 2D-chromatography techniques has been previously shown to increase the identification of oxidatively modified peptides and proteins¹⁸. Nonetheless, protein enrichment techniques that target a specific protein of interest are not recommended, including but not limited to antibody precipitation or pull-down assays. These techniques can bias towards one protein conformer if the epitope/binding site of the protein has been oxidatively modified by IV-FPOP. New developments in footprinting radical reagents, such as sulfate radical anion¹⁰ or trifluoromethylation¹⁹ could increase the versatility of IV-FPOP. Although the only labeling reagent tested in vivo thus far is hydrogen peroxide, other laser-activated radicals could be optimized. The use of other radicals should prove to be compatible with worm viability, cell permeable, and the 248 nm laser wavelength. Owing to the use of *C. elegans* as a model system for many human diseases, IV-FPOP has the potential to have a strong impact in studying the role of protein structure in disease pathogenesis.

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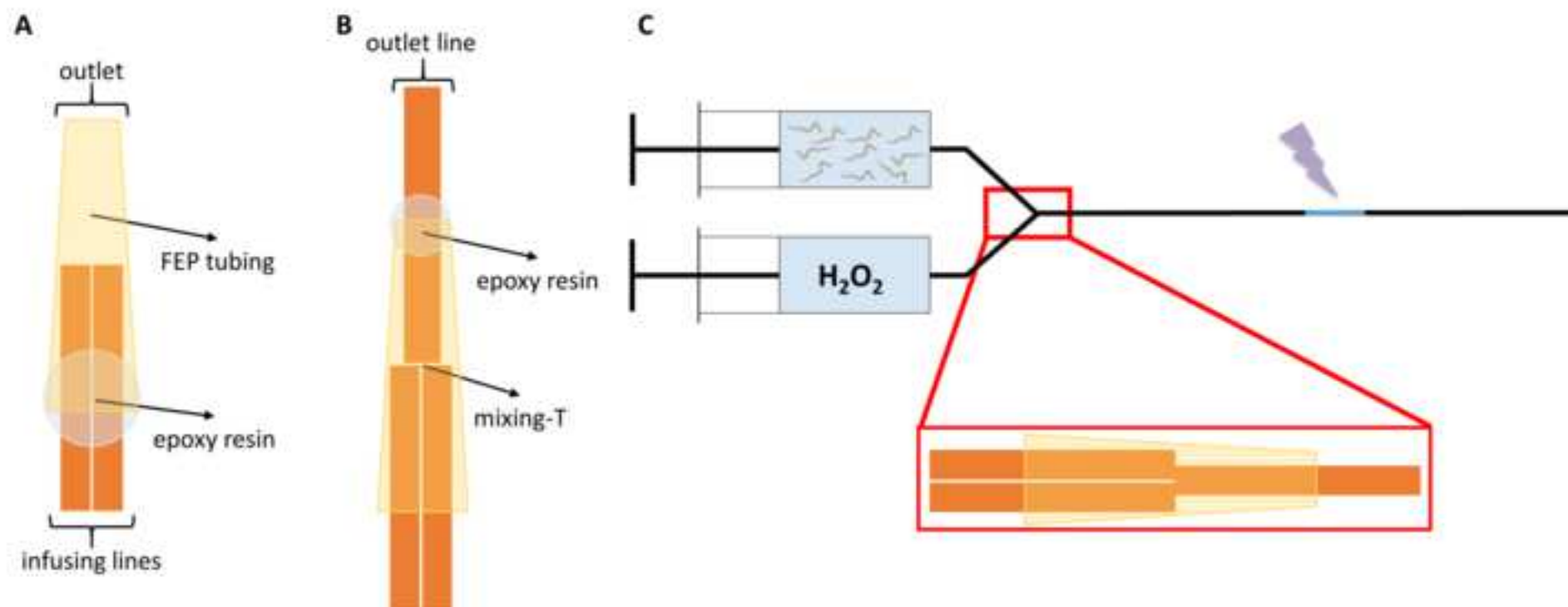
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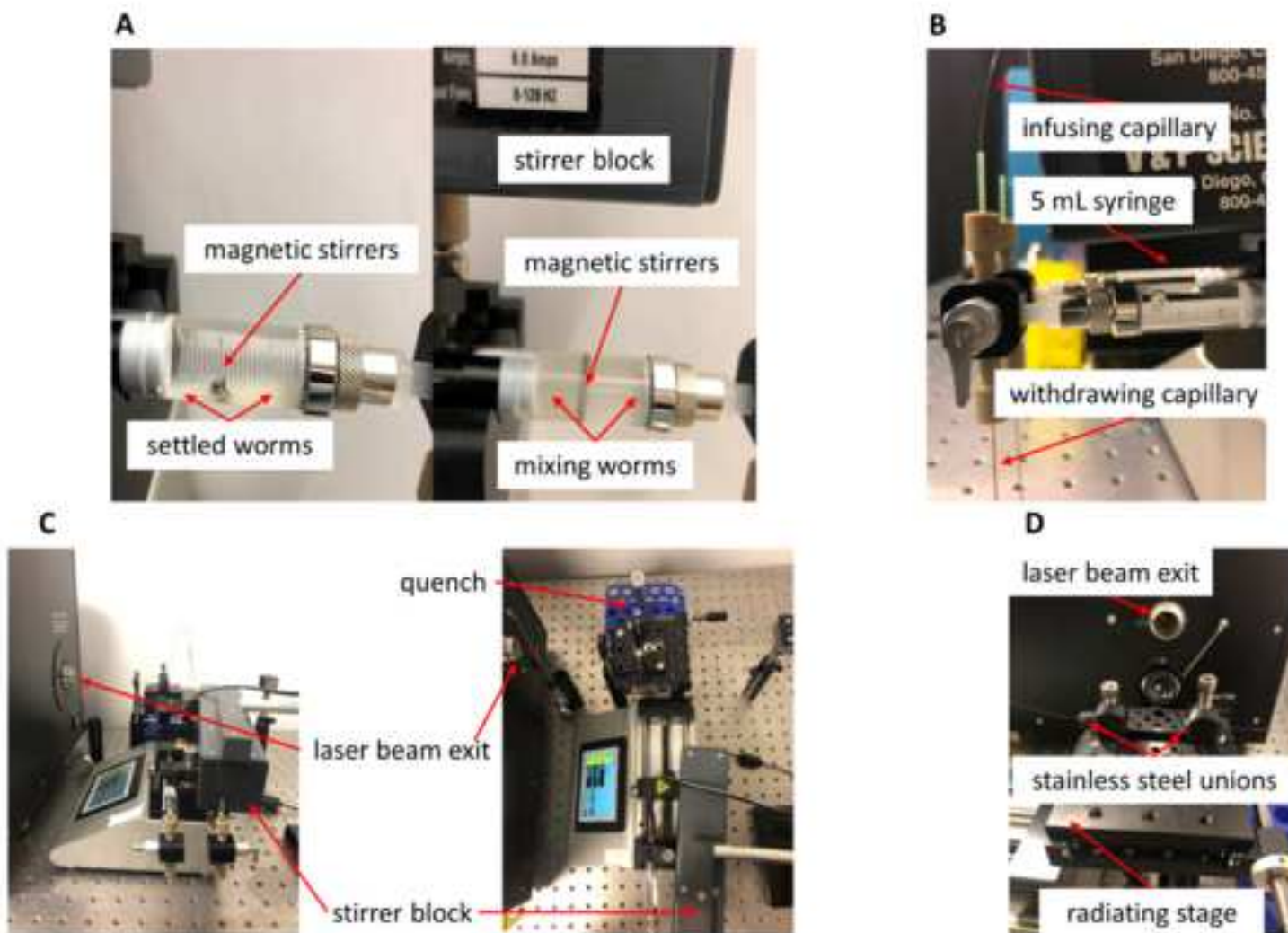
This publication was written in partial fulfillment of JAE Ph.D. thesis. The authors declare no conflict of interest.

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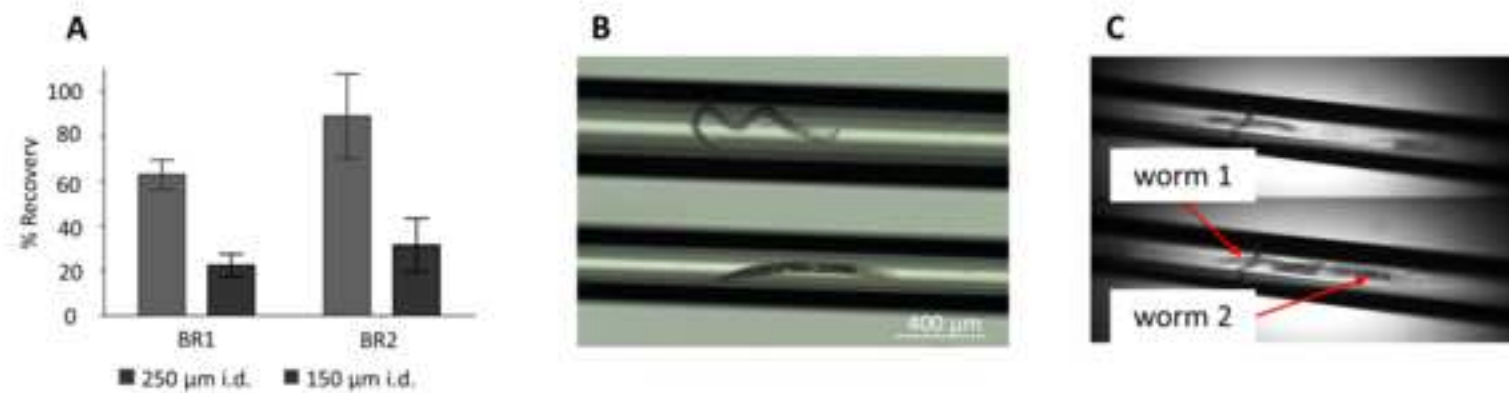
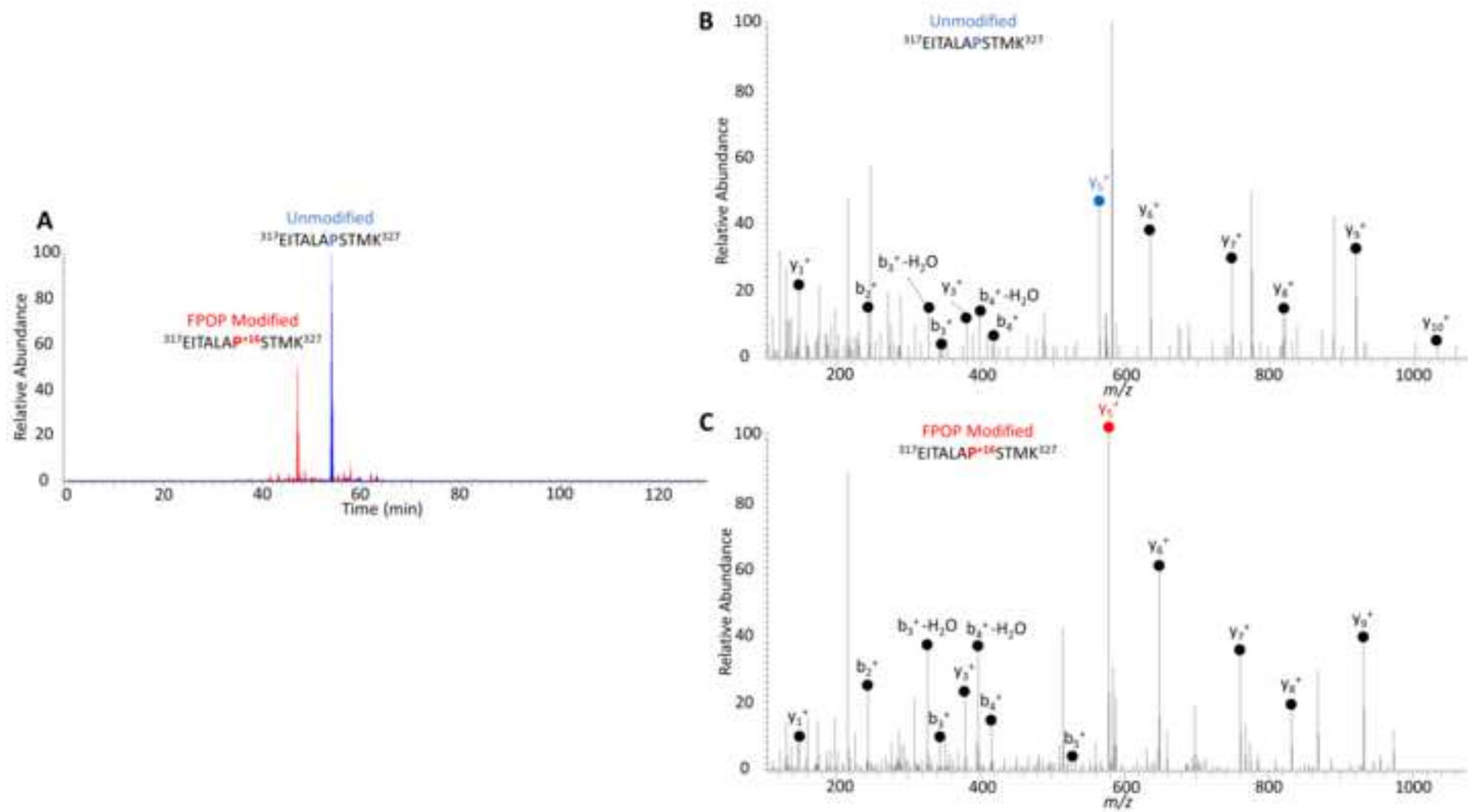


Figure4

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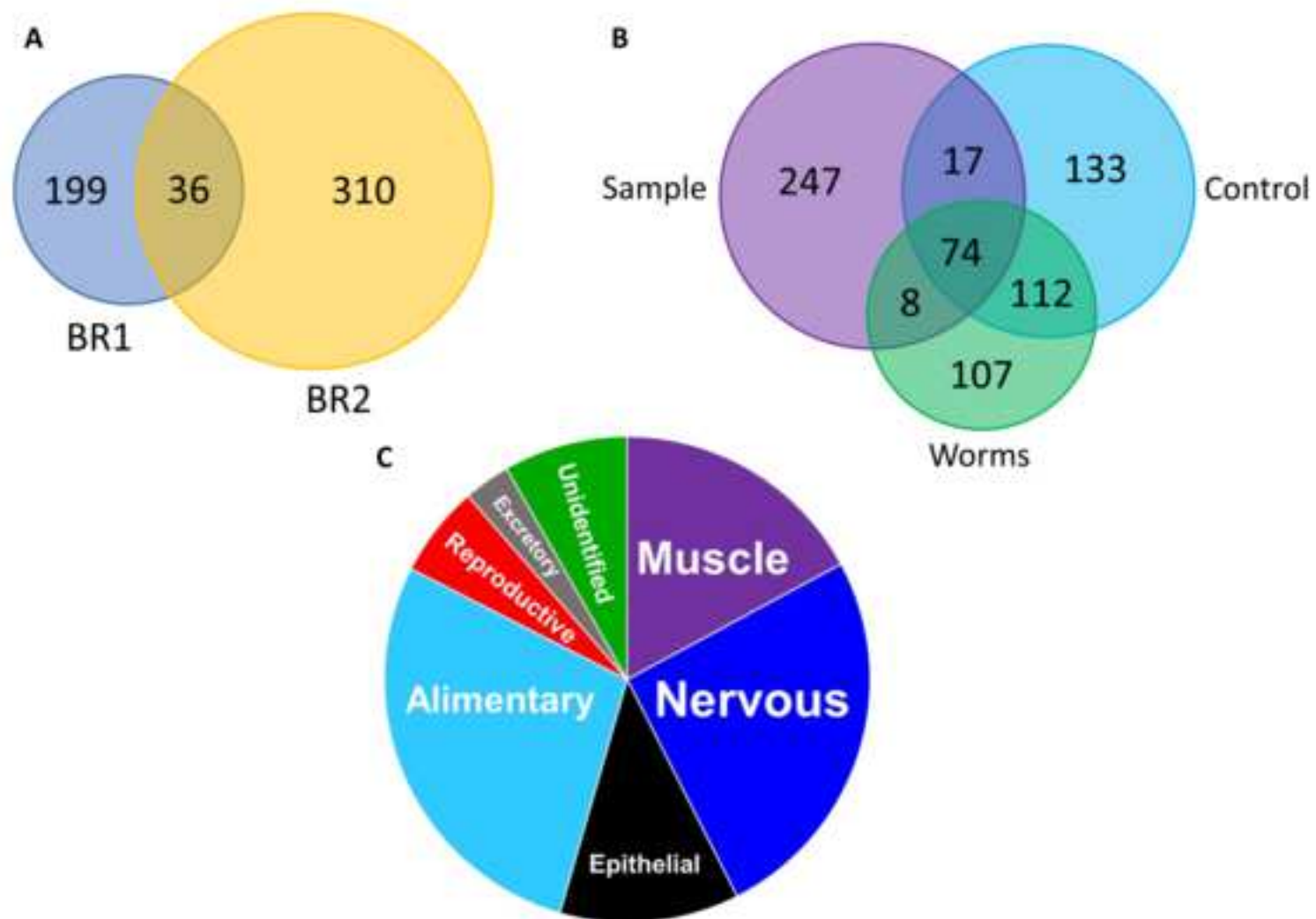
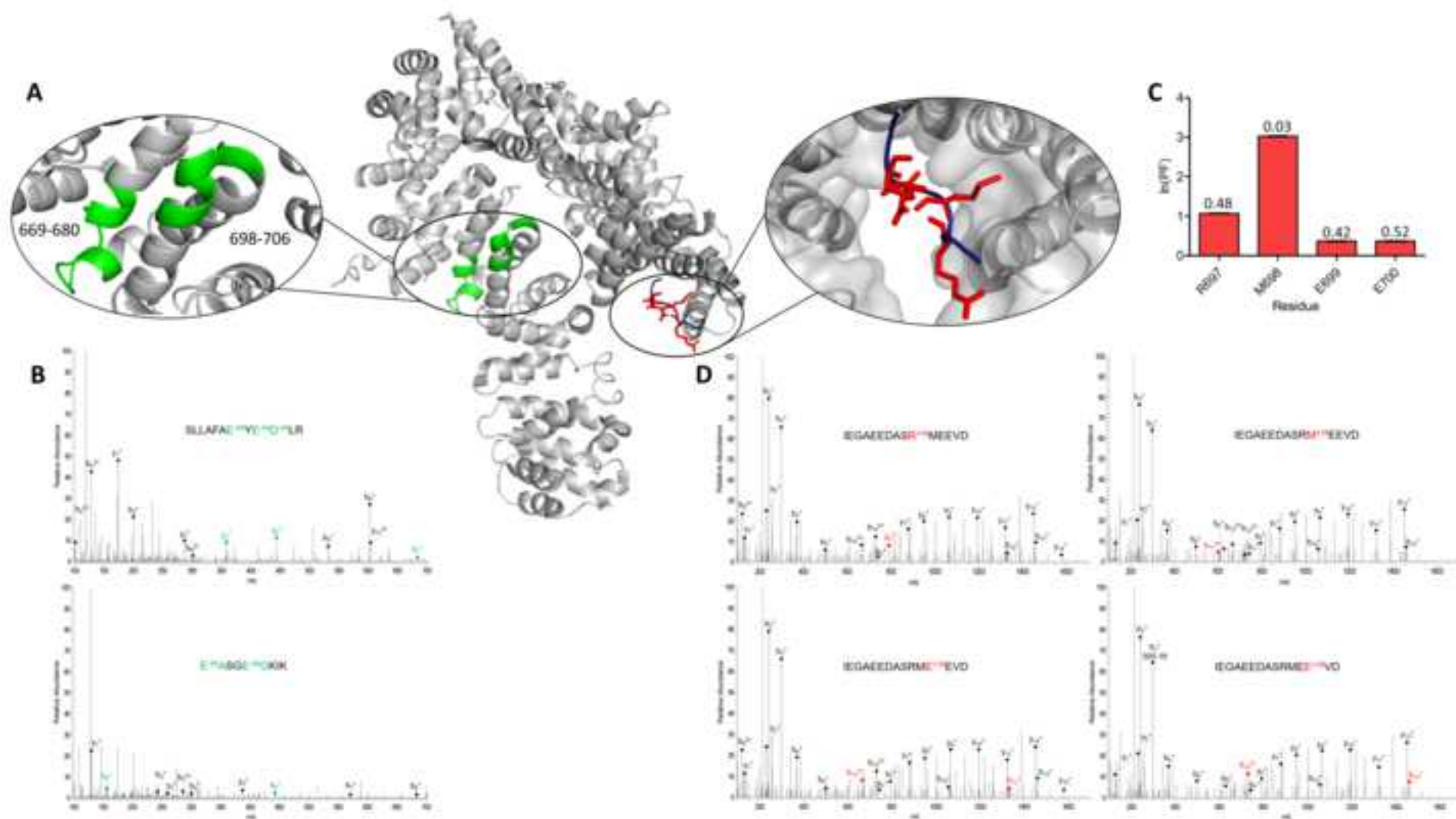


Figure6



Name of Material/Equipment

15mL Conical Centrifuge Tubes

5 mL Gas Tight Syringe, Removable Luer Lock

60 Sonic Dismembrator

Acetone, HPLC Grade

Acetonitrile with 0.1% Formic Acid (v/v), LC/MS Grade

ACQUITY UPLC M-Class Symmetry C18 Trap Column, 100Å, 5 µm, 180 µm x 20 mm, 2G, V/M, 1/pkg

ACQUITY UPLC M-Class System

Aluminum Foil

Aqua 5 µm C18 125 Å packing material

Centrifuge

Delicate Task Wipers

Dissecting Needle

Dithiothreitol (DTT)

DMSO, Anhydrous

Epoxy instant mix 5 minute

Ethylenediaminetetraacetic acid (EDTA)

EX350 excimer laser (248 nm wavelength)

FEP Tubing 1/16" OD x 0.020" ID

Formic Acid, LC/MS Grade

HEPES

HV3-2 VALVE

Hydrochloric Acid

Hydrogen Peroxide

Iodoacetamide (IAA)

Legato 101 syringe pump

Luer Adapter Female Luer to 1/4-28 Male Polypropylene

Magnesium Sulfate

Methanol, LC/MS Grade

Microcentrifuge

N,N'-Dimethylthiourea (DMTU)

NanoTight Sleeve Green 1/16" ID x .0155" ID x 1.6"

NanoTight Sleeve Yellow 1/16" OD x 0.027" ID x 1.6"

N-tert-Butyl- α -phenylnitrone (PBN)
OmniPur Phenylmethyl Sulfonyl Fluoride (PMSF)
Orbitrap Fusion Lumos Tribrid Mass Spectrometer
PE50-C pyroelectric energy meter
Pierce Quantitative Colorimetric Peptide Assay
Pierce Rapid Gold BCA Protein Assay Kit
Pierce Trypsin Protease, MS Grade
Polymicro Cleaving Stone, 1" x 1" x 1/32"
Polymicro Flexible Fused Silica Capillary Tubing, Inner Diameter 250 μ m, Outer Diameter 350 μ m, TSP250350

Polymicro Flexible Fused Silica Capillary Tubing, Inner Diameter 450 μ m, Outer Diameter 670 μ m, TSP450670

Polymicro Flexible Fused Silica Capillary Tubing, Inner Diameter 75 μ m, Outer Diameter 375 μ m, TSP075375
Potassium Phosphate Monobasic
Proteome Discover (bottom-up proteomics software)
Rotary Magnetic Tumble Stirrer
Rotary Magnetic Tumble Stirrer, accessory kit for use with Syringe Pumps
Scissors
Self-Adhesive Label Tape
Snap-Cap Microcentrifuge Flex-Tube Tubes
Sodium Chloride
Sodium Dodecyl Sulfate (SDS)
Sodium Phosphate Dibasic Heptahydrate
Stereo Zoom Microscope
Super Flangeless Ferrule w/SST Ring, Tefzel (ETFE), 1/4-28 Flat-Bottom, for 1/16" OD
Super Flangeless Nut PEEK 1/4-28 Flat-Bottom, for 1/16" & 1/32" OD
Super Tumble Stir Discs, 3.35 mm diameter, 0.61 mm thick
Tris Base
Universal Base Plate, 2.5" x 2.5" x 3/8"
Urea
VHP MicroTight Union for 360 μ m OD
Water with 0.1% Formic Acid (v/v), LC/MS Grade
Water, LC/MS Grade

Company	Catalog Number	Comments/Description
Fisher Scientific	14-959-53A	any brand is sufficient
SGE Analytical Science	008760	2 minimum
Fisher Scientific	FM3279	This item is no longer available. Any low-volume sonicator will be sufficient
Fisher Scientific	A929-4	4 L quantity is not necessary
Fisher Scientific	LS120-500	
Waters	186007496	
Waters		
Fisher Scientific	01-213-100	any brand is sufficient
Phenomenex		
Eppendorf	022625501	
Fisher Scientific	06-666A	
Fisher Scientific	50-822-525	only a couple are needed
AmericanBio	AB00490-00005	
Invitrogen	D12345	
Loctite	1365868	
Fisher Scientific	S311-100	
GAM Laser		
IDEX Health & Sciene	1548L	
Fisher Scientific	A117-50	
Fisher Scientific	BP310-500	
Hamilton	86728	2 minimum
Fisher Scientific	A144S-500	
Fisher Scientific	H325-100	any 30% hydrogen peroxide is sufficient
ACROS Organics	122270050	
KD Scientific	788101	
IDEX Health & Sciene	P-618L	2 minimum
Fisher Scientific	M65-500	
Fisher Scientific	A454SK-4	4 L quantity is not necessary
Thermo Scientific	75002436	
ACROS Organics	116891000	
IDEX Health & Sciene	F-242X	
IDEX Health & Sciene	F-246	

ACROS Organics	177350250	
Sigma-Aldrich	7110-OP	any protease inhibitor is sufficient
Thermo Scientific		other high resolution instruments (e.g. Q exactive Orbitrap or Orbitrap Fusion) ca
Ophir Optonics	7Z02936	
Thermo Scientific	23275	
Thermo Scientific	A53225	
Thermo Scientific	90058	
Molex	1068680064	any capillary tubing cutter is sufficient
Polymicro Technologies	1068150026	
Polymicro Technologies	1068150625	
Polymicro Technologies	1068150019	
Fisher Scientific	P382-500	
Thermo Scientific	OPTON-30799	
V&P Scientific, Inc.	VP 710D3	
V&P Scientific, Inc.	VP 710D3-4	
Fisher Scientific	50-111-1315	any scissors are sufficient
Fisher Scientific	15937	one roll is sufficient
Fisher Scientific	05-402	any brand is sufficient
Fisher Scientific	S271-500	
Fisher Scientific	15-525-017	
Fisher Scientific	S373-500	
Fisher Scientific	03-000-014	a magnifying glass is sufficient
IDEX Health & Sciene	P-259X	
IDEX Health & Sciene	P-255X	
V&P Scientific, Inc.	VP 722F	
Fisher Scientific	BP152-500	
Thorlabs Inc.	UBP2	
Fisher Scientific	U5378	
IDEX Health & Sciene	UH-436	2 minimum
Fisher Scientific	LS118-500	
Fisher Scientific	W6-4	

n be used

JoVE60910. *In vivo* hydroxyl radical protein footprinting for the study of protein interactions in *Caenorhabditis elegans*.


Editorial comments

- Textual Overlap: Significant portions show significant overlap with previously published work. Please re-write lines 27-33, 289-294, 316-320 to avoid this overlap.

 Text has been edited.

- Protocol Detail:

1) 2.2: mention needle gauge

 We are unavailable to provide a needle gauge as it is not provided by the manufacturer. However, we list the company and part number of the needle use in the table of materials.

- Protocol Numbering: All steps should be lined up at the left margin with no indentations.

 We deleted indentations.

- Discussion: JoVE articles are focused on the methods and the protocol, thus the discussion should be similarly focused. Please ensure that the discussion covers the following in detail and in paragraph form (3-6 paragraphs): 1) modifications and troubleshooting, 2) limitations of the technique, 3) significance with respect to existing methods, 4) future applications and 5) critical steps within the protocol.

 The discussion has been modified to include the editor's comment.

- Figures:

1) Fig 3: Define error bars.

 Error bars have been defined (Lines 373-374) (Lines 412-413 with track changes on).

- Commercial Language: JoVE is unable to publish manuscripts containing commercial sounding language, including trademark or registered trademark symbols (TM/R) and the mention of company brand names before an instrument or reagent. Examples of commercial sounding language in your manuscript are GAM Laser Inc, Waters Acquity, Thermo Scientific Orbitrap, Lumos Fusion MS, Proteome Discover (Software Version 2.2), Thermo Scientific, Excel

1) Please use MS Word's find function (Ctrl+F), to locate and replace all commercial sounding language in your manuscript with generic names that are not company-specific. All commercial products should be sufficiently referenced in the table of materials/reagents. You may use the generic term followed by "(see table of materials)" to draw the readers' attention to specific commercial names.

 We have removed the commercial language mentioned above.


JoVE60910. *In vivo* hydroxyl radical protein footprinting for the study of protein interactions in *Caenorhabditis elegans*.

- Please define all abbreviations at first use.

 All abbreviations have been defined.

- Lines 48, 64, 80-81, 290, 293, and 295. (Lined 60, 78-79, 95-96, 310, 314, 316 with track changes on).

- If your figures and tables are original and not published previously or you have already obtained figure permissions, please ignore this comment. If you are re-using figures from a previous publication, you must obtain explicit permission to re-use the figure from the previous publisher (this can be in the form of a letter from an editor or a link to the editorial policies that allows you to re-publish the figure). Please upload the text of the re-print permission (may be copied and pasted from an email/website) as a Word document to the Editorial Manager site in the "Supplemental files (as requested by JoVE)" section. Please also cite the figure appropriately in the figure legend, i.e. "This figure has been modified from [citation]."

 Re-print permission has been uploaded with resubmission. In addition, we have edited all figure captions as described by JoVE and the previous publisher.

Comments from Peer-Reviewers

Reviewer #1

Manuscript Summary:

Overall, this is an outstanding description of the protocol for performing IV-FPOP of *C. elegans*. The step-by-step instructions are largely clear and unambiguous. The figures are well-designed and add significantly to the clarity of the manuscript. Safety hazards are noted. Overall, I recommend this manuscript with minor revision to clarify particular areas.

Major Concerns:

None

Minor Concerns:

Figure 2A: Images of the syringe barrel should be taken against a flat, featureless background to prevent the light diffracting effects that are currently obscuring the contents of the syringe.

✚ We appreciate all of the reviewer's comments and concerns. We have retaken the picture.

Authors need to define the laser fluence or range of fluences used to generate sufficient FPOP signal. Specifying the laser fluence used to generate results in Figures 4-6 is also desirable.

✚ We added a note indicating the laser irradiation window and energy used in this protocol (Lines 165-166 and 199-200) (Lines 182-184 and 218-219 with track changes on).

Authors may wish to define the acronym FEP.

✚ We have defined FEP at first use (Lines 80-81) (Lines 95-96 with track changes on).

JoVE60910. *In vivo* hydroxyl radical protein footprinting for the study of protein interactions in *Caenorhabditis elegans*.

Reviewer #2:

Manuscript Summary:

The manuscript describes the application of *in vivo* hydroxyl radical protein footprinting using a KrF excimer laser to study the effect oxidatively modified amino acids have on protein protein interaction in *C.elegans*. The method provides an adaptation of existing technology to the study of whole organism systems. This is useful in view of the fact that *C.elegans* serves as an excellent model organism for various disease states, in particular neurological disease. The authors describe the assembly of the microfluidic system in great detail, and highlight the pitfalls a user may encounter during installation.

Major Concerns:

Apart from the details provided for the step by step assembly of the microfluidic system, the submitted paper contains the information and a number figures that have already been published in sufficient detail in *Anal Chem* 2019,91,19, 6577-6584. Although in the current submission the emphasis is on the assembly of the apparatus, provides no information that is not available in the original *Anal Chem* paper.

✚ We appreciate all of the reviewer's comments and concerns. We know most of the figures used in this protocol have been published, however our main focus for this manuscript is to provide potential readers with a visualized version of our IV-FPOP method. Since our *Anal Chem* publication of the IV-FPOP, and also in-cell FPOP, multiple groups have shown interests in both methods and the possibility to do these experiments in their laboratories. Due to this we have focused on the protocol and the major pitfall of the method, in addition to areas of improvement.

Reviewer #3:

Manuscript Summary:

This manuscript describes the assembly and implementation of IV-FPOP on *C. elegans*; in particular, a microfluidic set-up with online irradiation that allows the living organism to be footprinted. Representative analyses for selected proteins are shown with tandem MS data interrogating their solvent accessibility.

This work is of great benefit to the wider community and will allow others to set up and develop similar microfluidic systems for IV-FPOP. Such set-ups will hopefully explore different living systems and expand to complementary photochemical probes.

The manuscript is well written and appropriately conveys the described method. I recommend this manuscript for publication in JoVE with the following minor revisions to be addressed, where possible.

Major Concerns:

None

Minor Concerns:

1. In the abstract the authors comment on the study of protein aggregates in neurodegenerative diseases such as Parkinson's and Alzheimer's (Lines 29-32). Given that there is no mention made of these proteins (alpha-synuclein and amyloid beta) in the manuscript among identified peptides, and that these statements are not elaborated in the introduction section -- this is purely speculative and should be removed, as it gives the initial impression that these proteins are discussed in some way. For retention in the manuscript, the authors should make mention of these proteins/diseases in the introduction and also note the published FPOP work on amyloid beta aggregates to support the utility of IV-FPOP for studying these diseases.

✚ We appreciate all of the reviewer's comments and concerns. Because of their comment and what could lead to misinterpretation of our protocol we have edited the abstract in order to avoid any confusion for the reader, deleting the mention on the study of neurodegenerative diseases such as Parkinson's and Alzheimer's.

2. The authors should clarify their statement regarding hydroxyl radical insertion (Lines 47-48), making mention of the 3-order of magnitude range of reactivity.

✚ We have added a sentence in order to clarify the difference is amino acid reactivity to hydroxyl radicals (Lines 46-48) (Lines 58-60 with track changes on).

3. (Line 84) The authors should clarify the "~50 mm" number, as currently written this implies that the crater should be that much in diameter rather than length.

JoVE60910. *In vivo* hydroxyl radical protein footprinting for the study of protein interactions in *Caenorhabditis elegans*.

✚ We have edited the sentence to reflect the 50 mm measurement indicates length rather than diameter (Line 84) (Line 101 with track changes on).

4. (Lines 118 and 161-163) Could the authors give some typical values for flow rates and outlet capillary lengths. This will greatly help readers setting up the instrumentation for the first time.

✚ We have added a note indicating the typical final flow rate use in IV-FPOP to the protocol (Lines 165-166) (Lines 182-184 with track changes on).

5. (Line 191) Should this say "'Before' turning on the laser..."?

✚ Sentence has been edited (Line 193) (Line 213 with track changes on).

6. (Line 340 and Figure 5A) Are the authors able to comment on the total number of proteins identified in the Worms-only control for these BRs. If possible, could the authors also show the overlap between both controls and the sample for one of the BRs -- 3-way Venn diagram. This will help put into context the utility of the method for identifying surface-accessibility *in vivo*.

✚ We have edited figure 5 to include the reviewer's suggestion in the number of oxidatively modified proteins in all conditions.

7. (Lines 344-345) The authors state that IV-FPOP probes solvent accessibility similar to *in vitro* studies. Could the authors provide a reference for this statement -- if the authors are referring to their comparison of SASA from PDB 4I2Z and MS/MS data for UNC-45, this should be made clearer. The current form implies that *in vitro* FPOP data correlate with the IV-FPOP data herein.

✚ We have removed the statement "similar to *in vitro* FPOP" in the representative results section to avoid any confusion for the reader. Additionally, we added text to indicate the correlation between IV-FPOP experimental oxidation and SASA calculations using the PDB 4I2Z (Line 346-349) (Lines 385-388 with track changes on).

8. (Lines 349 and 396) Are these $\ln(\text{PF})$ values calculated from PDB 4I2Z? If so, please state this in the Figure 6 caption. Is it possible to show the $\ln(\text{PF})$ for both in crystal structure and IV-FPOP for comparison?

✚ The $\ln(\text{PF})$ is calculated from the extent of oxidation. We can then correlated this to the calculated SASA values if a crystal structure is available. We have added the calculated SASA values of the Hsp90 fragment to **Figure 6C** to show that as $\ln(\text{PF})$ increases SASA decreases (Line 346-349) (Lines 385-388 with track changes on).

9. (Figure 6B) If possible, could the corresponding unmodified MS/MS from the controls be shown for either of these peptides. This would show representative changes for multiply oxidized peptides.

JoVE60910. *In vivo* hydroxyl radical protein footprinting for the study of protein interactions in *Caenorhabditis elegans*.

✚ Unfortunately, for these peptides only the oxidized MS/MS was detected. Because this is a methods/protocol manuscript and want to show representative peptide changes of oxidized and unoxidized, we have included **Figure 4A-C**. Changes in peptide chemistry during reverse-phase LC and fragmentation are described.

10. (Line 428) Could the authors clarify that 2D-chromatography increases the 'identification' of oxidatively modified proteins.

✚ This sentence has been edited to address the reviewer's concern (Line 446) (Line 492 with track changes on).



Jessica Espino Perez <jespino@umaryland.edu>

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