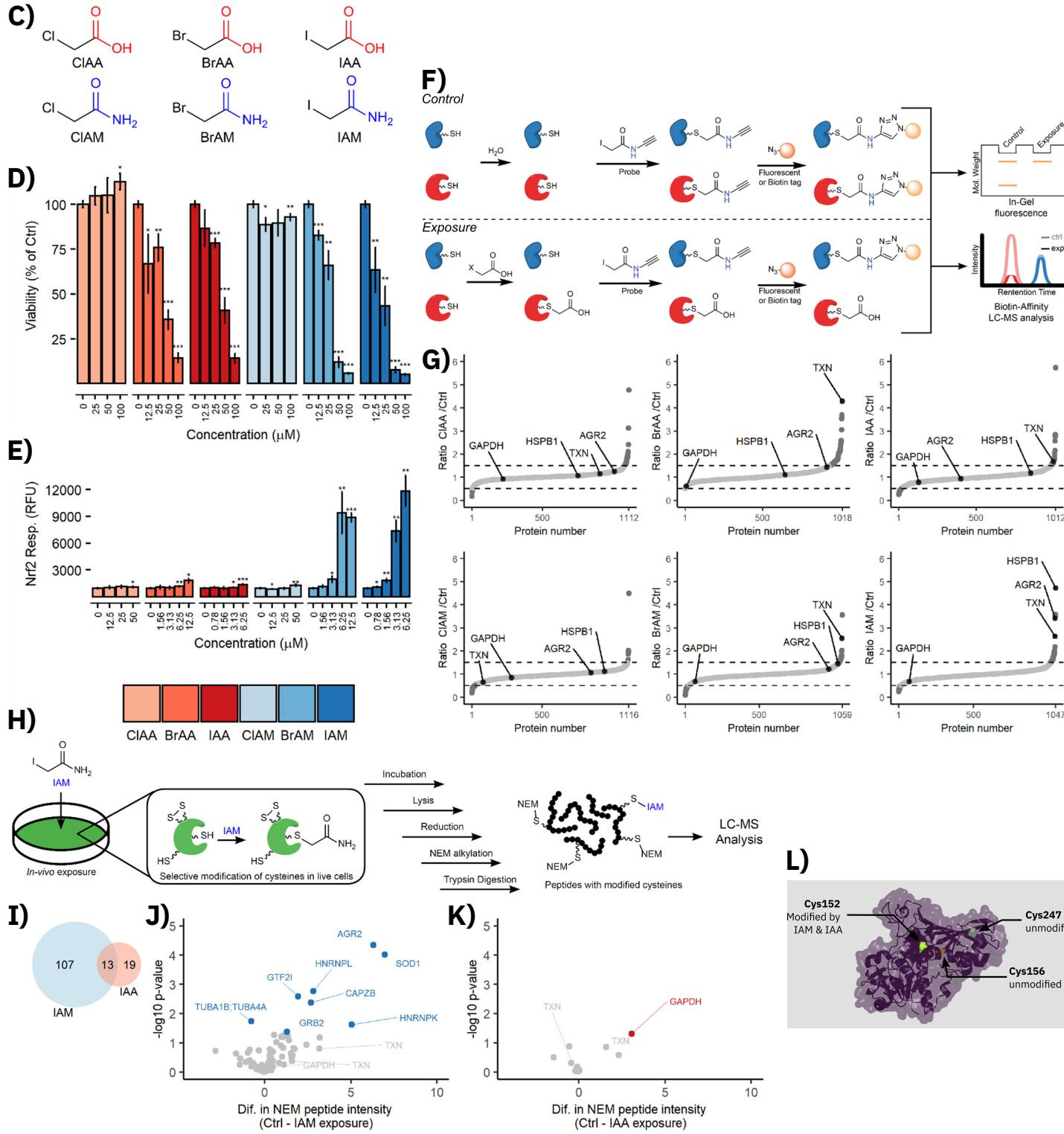


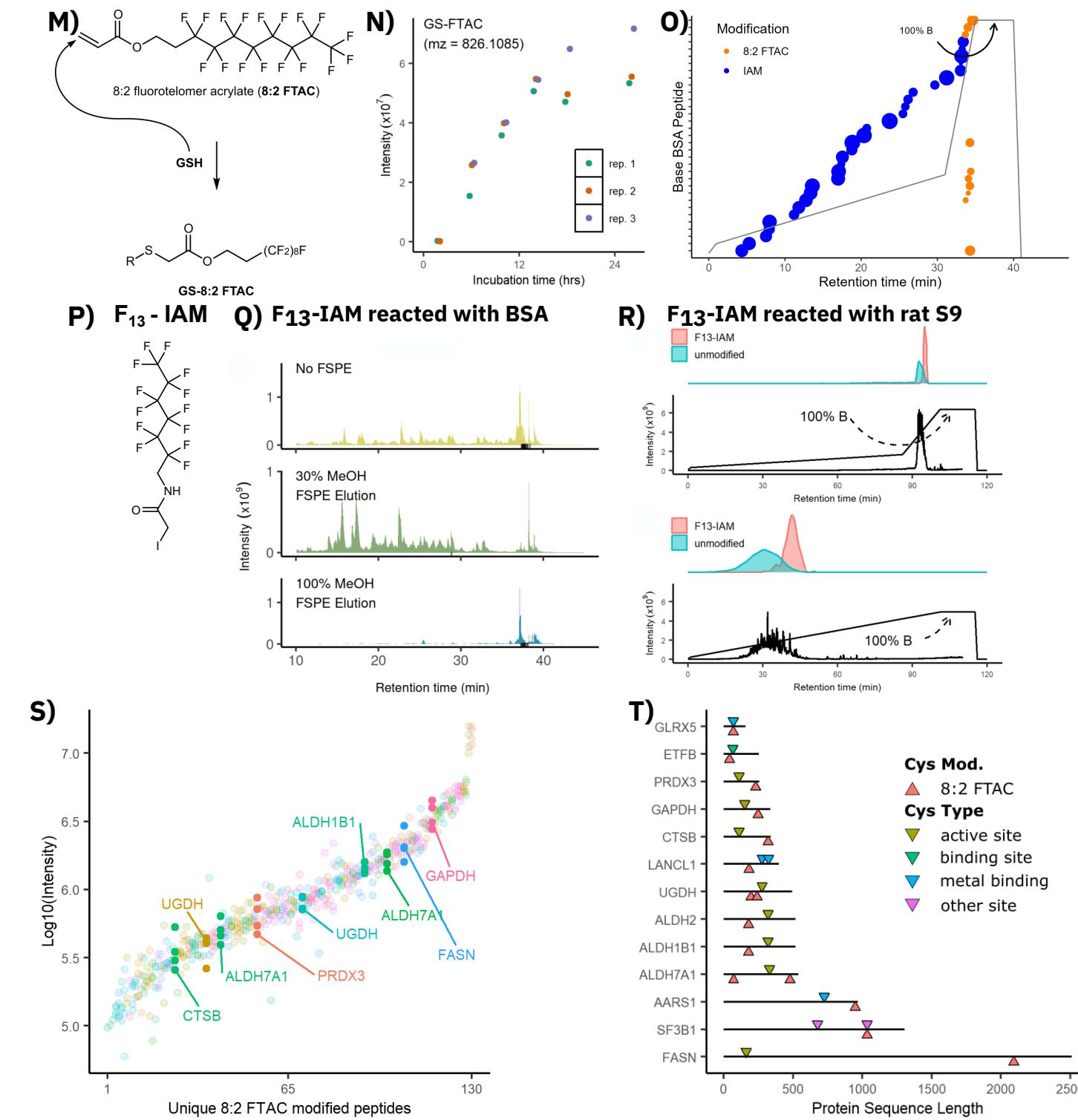
## Project 1: Profiling Proteome Thiol Reactivity of Monohaloacetic Acids and Monohaloacetamides

**C**) mHAAs and mHAMs investigated in this project **D**) MTT cytotoxicity  
**E**) Nrf2 luciferase reporter response **F**) Activity-based protein profiling (ABPP) **G**) Biotin affinity ABPP results **H**) Direct adduct monitoring **I**) Number of peptides with adducts **J**) Difference in NEM-modified peptides in the control group versus IAM **K**) and IAA **L**) IAA mod at Cys152 on GAPDH



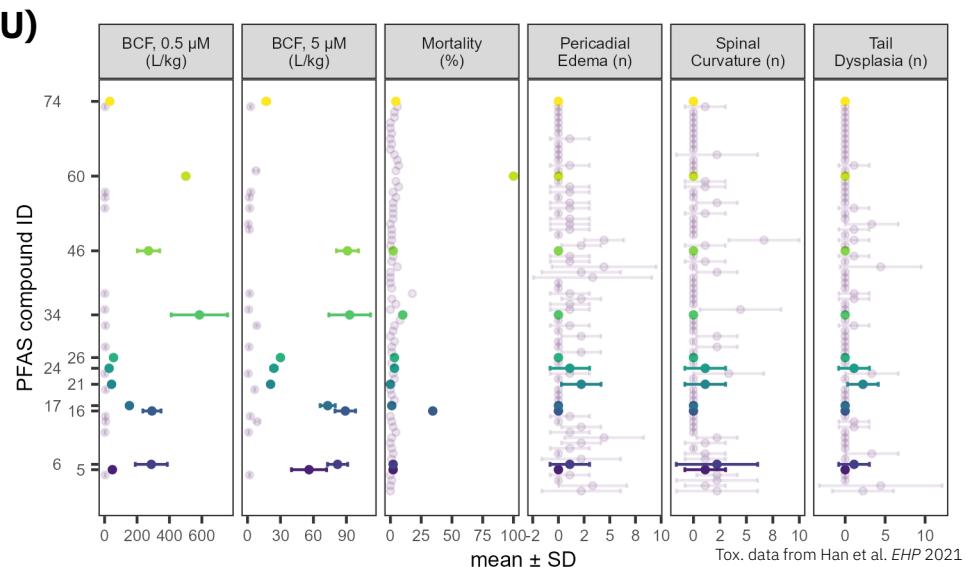
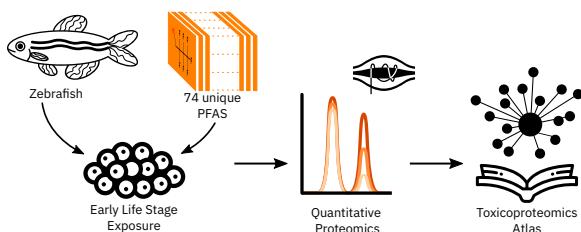
## Project 2: Development of Fluorous Solid Phase Extraction for the Enrichment of Long-Chain PFAS modified peptides

**M**) Reaction of 8:2 FTAC with GSH **N**) Monitoring GS-FTAC formation **O**) Retention time of IAM vs. 8:2 FTAC modified peptides **P**) F<sub>13</sub>-IAM probe **Q**) TIC of eluants from FSPE stages **R**) Comparison of nLC gradients **S**) Hep G2 lysate peptides with 8:2 FTAC modification **T**) Location of detected 8:2 FTAC mods. vs. annotated residues



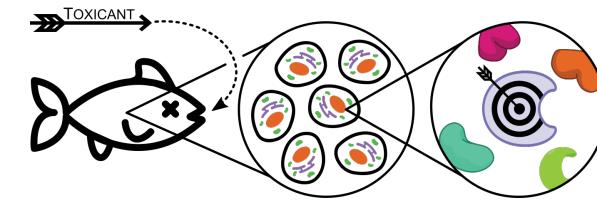
### Project 3: Toxicoproteomics Atlas of Per- and Polyfluoroalkyl Substances in Early-Life Stages Zebrafish (*Danio rerio*)

**U)** Phenotypic toxicity results reported by Han et al. *EHP* 2021; significant results coloured  
**V)** Structure of sulfonamides in 74 PFAS chemical library  
**W)** Heatmap of significant up and down regulated proteins, both protein groups and PFAS compounds were clustered using hierarchical clustering. Note only proteins with an absolute log<sub>2</sub> fold-change (FC) greater than 2 and p-value less than 0.05 were considered.

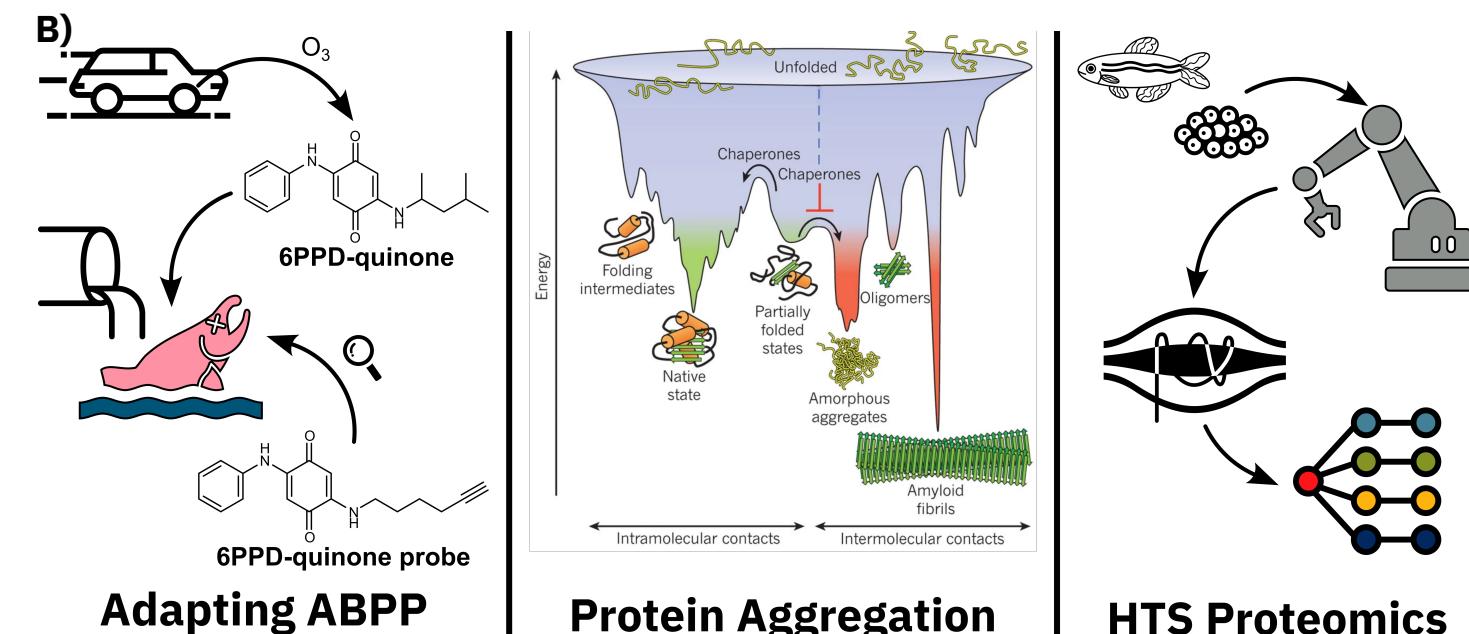
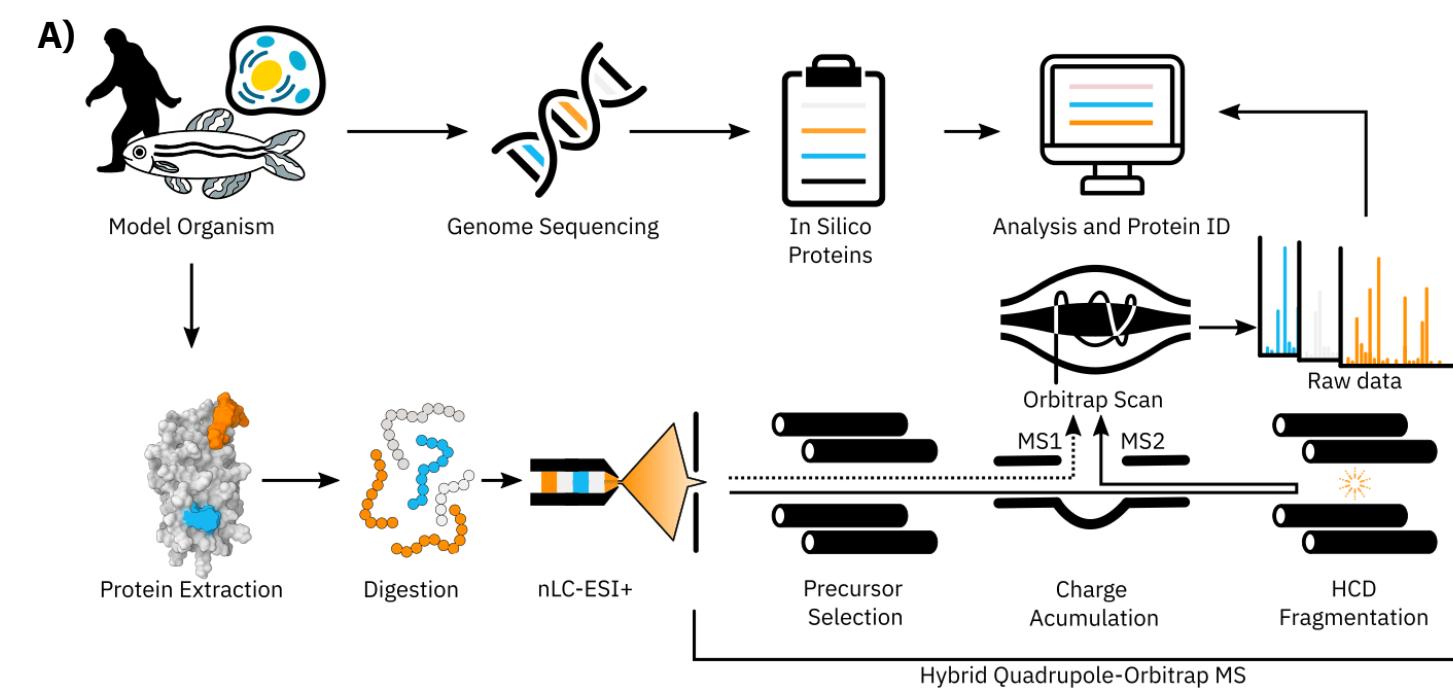


### Chemical Proteomics Methods for Elucidating the Physical Protein Targets of Environmental Contaminants

David Hall  
Dec. 9th 2022



**A)** Scheme of general bottom-up proteomics from model organism, from complex vertebrates to single cells, through to protein identification **B)** Potential next steps from this thesis work: adapting ABPP to investigate new compounds, exploring exposomics effects on protein aggregation, and adapting proteomics for high-throughput screening.



Aggregation figure from Ulrich et al. *Nature Reviews*