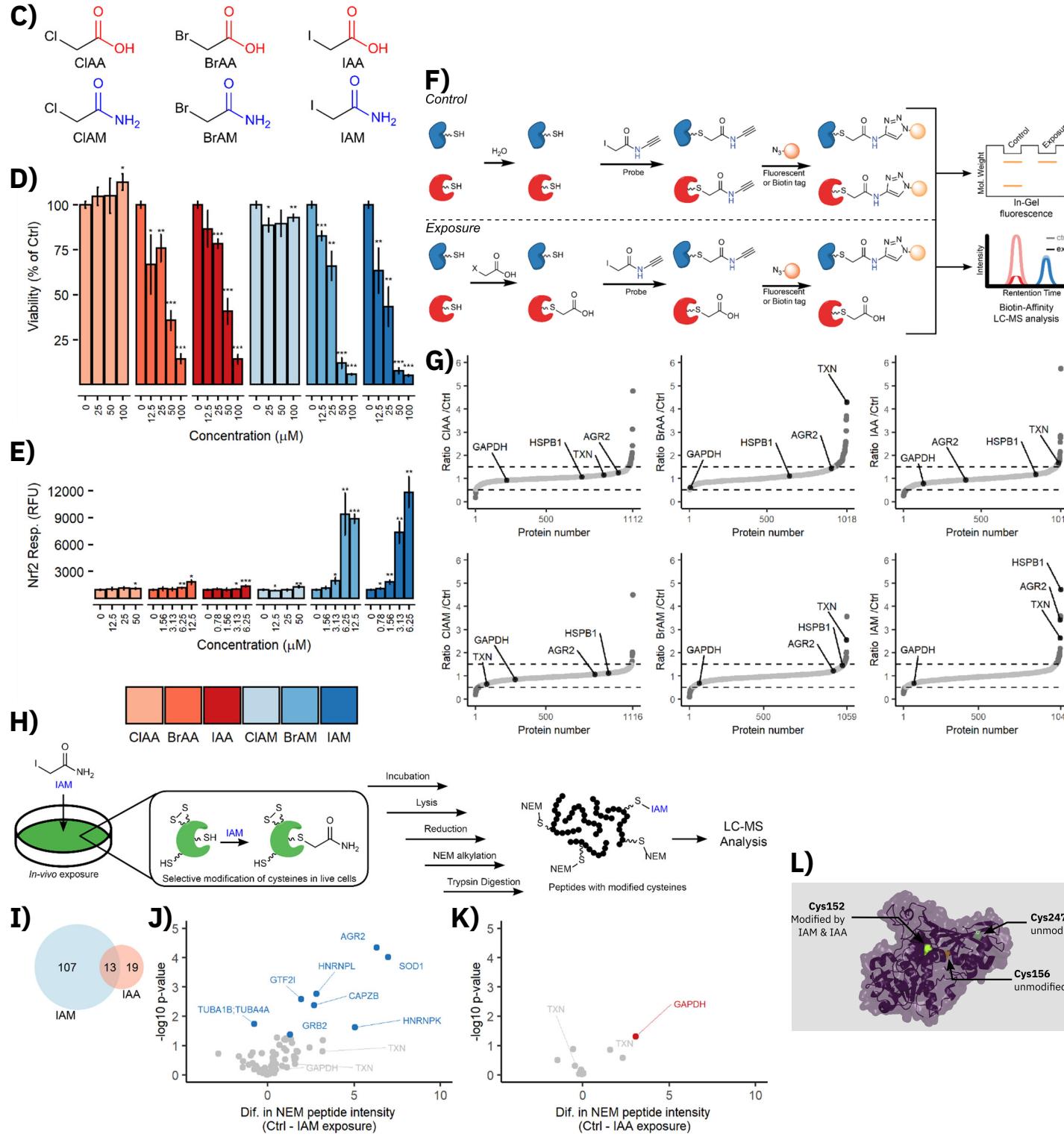
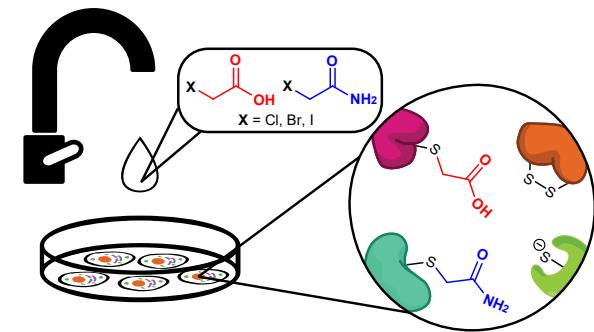


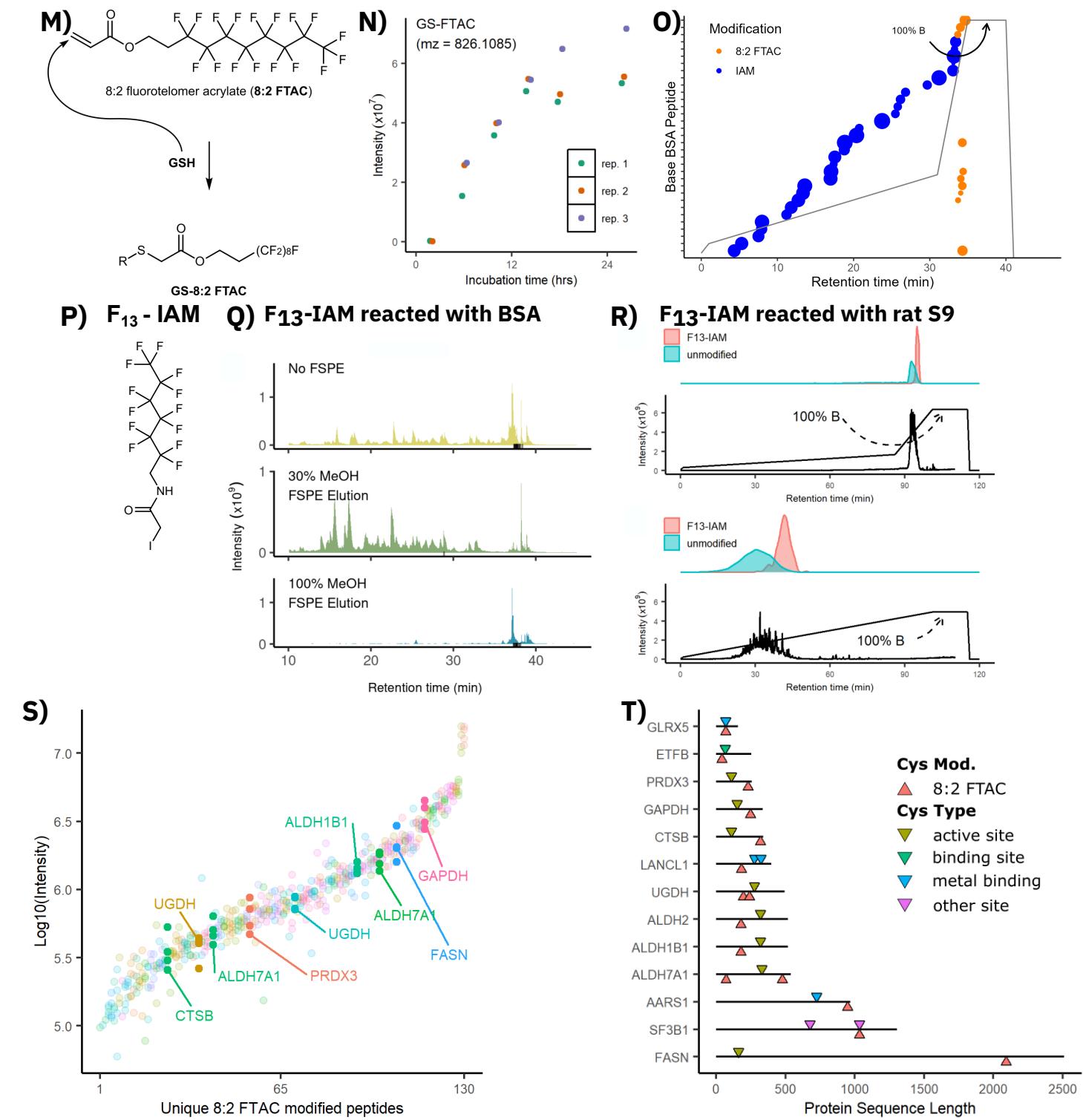
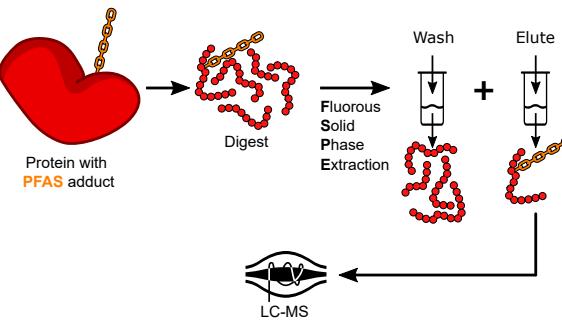
## **Project 1:** Profiling Proteome Thiol Reactivity of Monohaloacetic Acids and Monohaloacetamides

**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 DBP adducts **J)** Difference in NEM-modified peptides in the control group versus IAM **K)** and IAA **L)** IAA mod at Cys152 on GAPDH



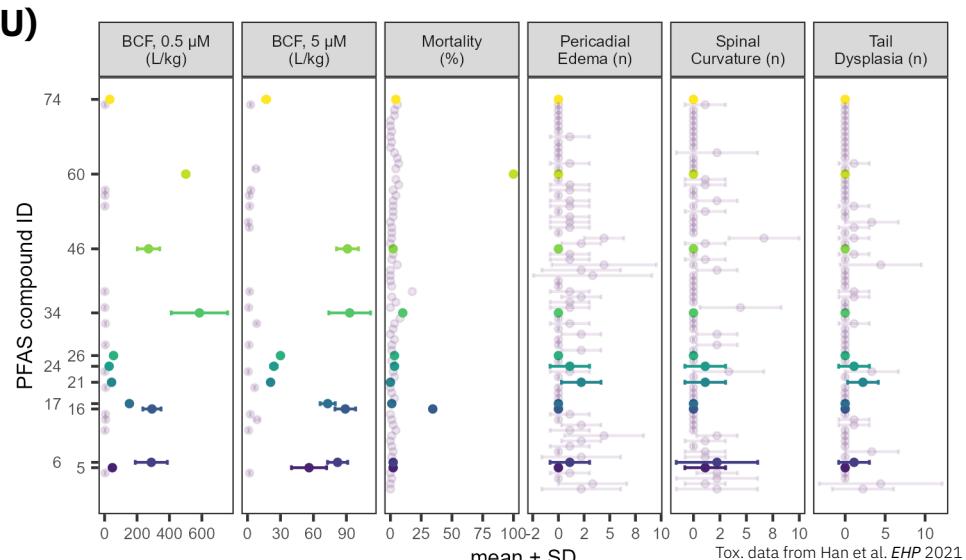
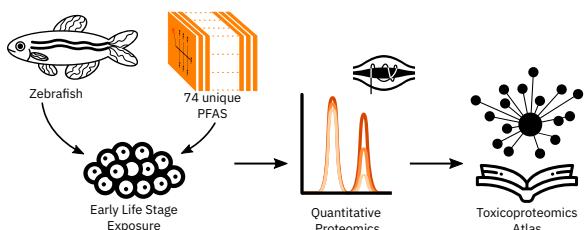
**Project 2:** Development of Fluorous Solid Phase Extraction for the Enrichement of Long-Chain PFAS modified peptides

**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 residue positions.



### 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 included.

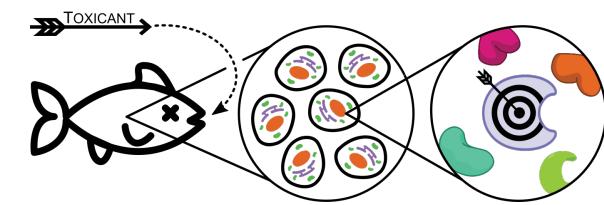


### Chemical Proteomics Methods for Elucidating the Physical Protein Targets of Environmental Contaminants

David Hall

Final Oral Exam

Dec. 9th 2022



Full slides available at:  
[davidrosshall.github.io/phd-defence-talk](https://davidrosshall.github.io/phd-defence-talk)

**A)** Scheme of general bottom-up proteomics from model organism – single cells to complex vertebrates – through to protein identification via nLC-MS/MS **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.

