

## Summary

Investigational proteomics researcher with 8 years of experience employing liquid-chromatography-mass spectrometry in tandem with statistical and high-throughput computer programming languages to further elucidate the human proteome. Interested in combining technical innovation with health-focused applications, I offer strong written and oral communication, proficient and innovative problem solving, and punctual delivery.

## Work Experience

### Graduate Research Assistant, University of Wisconsin-Madison, 2018-Present

- Fabricated and validated PGC-enabled nano-LC separation methodologies that provide up to 40% greater protein, peptide and glycopeptide identifications.\*
- Identified chromatographic conditions most suitable for label-free glycopeptide quantitation, isomeric resolution, and MS-based profiling depth.\*
- Utilized DIA-MS to identify 1,242 dysregulated proteins across six diagnostic patterns correlated with early, mid, and late-stage prostate cancer.\*
- Coupled machine learning with DIA-MS to quantify >9,300 cerebrospinal fluid proteins and elucidate 1,642 putative neurological disease markers across patient cohorts.\*
- Leveraged traditional and microfluidic capillary electrophoresis for small molecule quantitation, isomeric separation, and protein attribute characterization.

### Research Intern, Genentech BAS-O3M, June 2021-August 2021

- Developed custom, full-stack desktop applications to automate and streamline immunogenicity assessment of drug candidates, enabling >99% reduction in analysis time.
- Engineered custom user interfaces to enable high-throughput analysis of large proteomic datasets, providing a 500-fold increase in data utilization.
- Constructed analysis pipelines leading to the discovery of constitutive immunogenic signatures that enable reliable quality control in immunopeptidomic workflows.

## Skills

### Proteomics, -omics

High throughput bottom-up, top-down and middle-down proteomics. Label-free and isobaric tagging relative quantitation. Glyco- and phosphoproteomics.

### Liquid-Chromatography, Separations

Reversed-phase (C18, C4), porous graphitic carbon, ion exchange, size exclusion. Capillary electrophoresis. Ion mobility - TIMS, DTIMS, FAIMS.

### Mass Spectrometry

Expertise in Thermo, Agilent, Waters, and Bruker instruments. ESI and MALDI.

### Computer Science

*Back-end:* Python, C, SQL, R, Rust. *Front-end:* Javascript, HTML, CSS. High-throughput analysis, process automation, machine learning, web development.

### Professional

Written and verbal communication, project management, public speaking, grant and manuscript authorship.

## Education

**Ph.D.**, Chemistry, University of Wisconsin-Madison, 2018-2023

**M.S.**, Chemistry, University of Oklahoma, 2016-2018

**B.S.**, Biochemistry, University of Oklahoma, 2011-2016

*\*Full record of scientific publications, posters, and oral presentations may be seen on my personal website.*