GRAHAM DELAFIELD Ph.D. Candidate, Chemistry

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Summary

Investigational proteomics researcher with 7 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 1,245 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.