Daniel Graham Delafield
Ph.D. Candidate

Professional 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 separation methodologies that provide up to 25% greater protein, peptide and glycopeptide identifications.
- Identified chromatographic conditions most suitable for glycopeptide label-free quantitation, isomeric resolution, or MS-based profiling depth.
- Utilized DIA-MS to identify 1,245 proteins across six dysregulation 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 custom liquid chromatography, capillary electrophoresis, and ion mobility to identify multiple conformations of active biomolecules.

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.

Contact

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Education

Ph.D. - Chemistry, (2023)
University of Wisconsin - Madison
GPA: 4.0

M.S. - Chemistry, 2018
University of Oklahoma
GPA: 3.9

B.S. - Chemistry, 2016
University of Oklahoma
Cum Laude

Please feel free to visit my personal website for an extensive work history and full portfolio of my scientific contributions.