

D. Graham Delafield

Ph.D., Chemistry

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Profile

I have over 9 years of industrial and academic proteomics research experience, with a focus on analytical characterization of protein sequence, modification, structure, and function. Seeing first-hand the utility of *in silico* predictions and hypothesis generation for protein and systems biology, I have sought to blend computational and wet-lab methodologies to enable models and approaches beneficial to the life sciences. I am an ambitious problem solver who excels communication, collaboration, and leadership.

Experience

SCIENTIST | Calico Life sciences | July 2023 - Present

- Conceived and validated a high-throughput (>24x) automated platform to screen affinity and selectivity of >7,000,000 computationally designed peptide drug candidates against targets of interest.
- Coupled quantitative proteomics methodologies and dataset integration to identify and present on- and off-target interactions of up to 15 therapeutic drugs in parallel.
- Initiated novel mass-spectrometry chemoproteomics pipelines that facilitate 200-fold higher intact mass screening and quantitative assessment of covalent fragment libraries (~1,000 compounds) in a single run.

GRADUATE RESEARCH ASSISTANT | University of Wisconsin-Madison | AUGust 2018-May 2023

- Fabricated and validated PGC-enabled nano-LC separation methodologies that provide up to 40% greater protein, peptide and glycopeptide identifications. *
- 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. *

RESEARCH INTERN | Genentech | 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.

Education

PH.D., CHEMISTRY | University of Wisconsin-Madison | May 2023

M.S., CHEMISTRY | University of Oklahoma | May 2018

B.S., BIOCHEMISTRY | University of Oklahoma | May 2016

Skills & Abilities

PROTEOMICS

Bottom-up and top-down protein characterization, PTM identification, regular use of UniProt and PDB.

MASS SPECTROMETRY & LIQUID CHROMATOGRAPHY

Expertise in instrumentation from all major vendors. Biological discovery and high-throughput quantitation. RPLC, SEC, PGC, IEX. HPLC, nano-LC.

COMPUTER SCIENCE

Python (advanced), R, SQL, Rust, JS, HTML, CSS. Supervised and unsupervised ML. Application development, web development.

*Publications, posters, and presentations may be viewed on my personal website.