

# Daniel Graham Delafield

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## Education

### DOCTOR OF PHILOSOPHY | (MARCH 2023) | UNIVERSITY OF WISCONSIN-MADISON

- Primary Field: Chemistry
- Division: Analytical Chemistry
- GPA: 4.0

### MASTER OF SCIENCE | MAY 2018 | UNIVERSITY OF OKLAHOMA

- Primary Field: Chemistry
- Division: Analytical Chemistry
- GPA: 3.9

### BACHELOR OF SCIENCE | MAY 2016 | UNIVERSITY OF OKLAHOMA

- Major: Biochemistry
- Minor: Music
- Honors: Cum Laude

## Employment and Internships

- June 2021 – August 2021: **Summer Research Intern**, Genentech
  - Developed custom, full-stack desktop applications to automate and streamline immunogenicity assessment of drug candidates, which enabled > 99% reduction in analysis time.
  - Engineered custom user interfaces to enable high-throughput analysis of large tabular 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.
- 2019 – Present: **Ambassador**, Wisconsin Alumni Research Foundation
  - Identified novel scientific intellectual property from with a personal academic network of 300+ graduate students and 50+ principal investigators.
  - Implemented new outreach events, canvas campaigns, and network opportunities aimed towards educating investigators over intellectual property protection, management, and licensing.
  - Augmented the \$3 Billion+ WARF portfolio through addition of novel gene edited cell line technologies.

## Research Experience

### UNIVERSITY OF WISCONSIN-MADISON, LI LAB

- **Graduate Research/Teaching Assistant**, August 2018 – Present
  - Fabricated and validated PGC-enabled nano separation methodologies that provide up to 40% 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.
  - Deployed custom web-application based solutions for browsing, filtering, and sharing mass spectrometry data.
  - Implementation of informatics pipelines to establish inter- and intrasample quantitative accuracy in data-independent acquisition bottom-up proteomics.

- Performed custom informatic analysis of MALDI-MSI datasets to normalize multiplexed datasets, extract features of interest, and perform machine learning classification.
- Development of novel online multiplexed analysis of bottom-up, middle-down, and top-down glycoconjugate species utilizing capillary electrophoresis, porous graphitized carbon liquid chromatography, ion mobility spectrometry, and mass spectrometry.
- Leveraged custom liquid chromatography, capillary electrophoresis, and ion mobility to identify multiple conformations of active biomolecules.
- Trained and led small research teams of new graduate students and non-expert scientists in the areas of biomolecular analysis, bioinformatic processing, and project development.
- Maintained, serviced, and assisted in troubleshooting a variety of high-end mass spectrometers from all major vendors (Thermo, Bruker, Agilent).

## UNIVERSITY OF OKLAHOMA, WU LAB

- **Graduate Research/Teaching Assistant**, May 2016 – August 2018
  - Developed a three-dimensional method of glycopeptide purification and characterization allowing universal application, unbiased separation, and rapid recognition using HPLC, concurrent fractionation, Mass Spectrometry, and Differential Ion Mobility (FAIMS). Presented at ASMS, June 2017.
  - Demonstrated correlation between differential ion mobility detection and glycopeptide analytes based on backbone variation, glycan composition, and a combination thereof.
  - Analyzed post translationally modified glycoproteins of control and SLE patient serum immunoglobulin searching for correlations to immune response and glycan features based on our previous glycopeptide purification platform.
- **Honors Research Assistant**, January 2016 – May 2016
  - Conceptualized, designed, and constructed an online affinity capture technique for immunoprecipitation application involving intensive immunoglobulin purification, original apparatus design, and top-down mass spectrometry. ASMS, June 2016.
- **Undergraduate Research Assistant**, August 2015 – January 2016
  - Determined activity of novel biomass degrading enzymes from Great Lakes fungal samples through culturing, secretome extraction, enzymatic assays, concentration determination, electrophoresis, liquid chromatography and mass spectrometry. Published in JASMS, April 2017 (Online January 2017).

## Publications

- **D.G. Delafield**, H.N. Miles, W.A. Ricke, L. Li (2022). "Higher Temperature Porous Graphitic Carbon Separations Differentially Impact Distinct Glycopeptide Classes." *Journal for the American Society for Mass Spectrometric*. Published online November 30, 2022. 10.1021/jasms.2c00249
- **D.G. Delafield**, C. Kaminsky, G. Liu, L. Li. "High-End Ion Mobility Mass Spectrometry: A Current Review of Analytical Capacity in Omics Applications and Structural Investigations." *Trends in Analytical Chemistry*. Published online August 24, 2022. 10.1016/j.trac.2022.116761.
- **D.G. Delafield**, H.N. Miles, Y. Liu, W.A. Ricke, L. Li, (2021). "Complementary Proteome and Glycoproteome Access Revealed Through Comparative Analysis of Reversed Phase and Porous Graphitic Carbon Chromatography." *Analytical Bioanalytical Chemistry*. Invited contribution to the topical paper collection featuring **Promising Early-Career (Bio-)Analytical Researchers**. Published online February 9, 2022. 10.1007/s00216-022-03934-7.
- **D.G. Delafield**<sup>†</sup>, H.N. Miles<sup>†</sup>, L. Li, (2021). "Recent Developments and Applications of Quantitative Proteomics Strategies for High-Throughput Cancer Biomolecular Analyses in Cancer Research. *RSC Chemical Biology*. Published online May 15, 2021. 10.1039/D1CB00039J. († Co-First Authors)
- **D.G. Delafield**, Li, L., (2020) "Recent Advances in Analytical Approaches for Glycan and Glycopeptide Quantitation." *Molecular & Cellular Proteomics*. Published online June 23, 2020. 10.1074/mcp.R120.002095.
- **D.G. Delafield**, H.N. Miles, L. Li. "Inclusion of Porous Graphitic Carbon Chromatography Yields Greater Protein Identification, Compartment and Process Coverage, and Enables More Reflective Protein-Level Label-Free Quantitation." (In Preparation)

- **D.G. Delafield**, H.N. Miles, W.A. Ricke, L. Li. "Sample Agnostic Spectral Libraries Reveal Underlying Molecular Pathways in Aggressive Metastatic Prostate Cancer." (In Preparation)
- **D.G. Delafield**, N. Truettner, H.N. Miles, W.A. Ricke, L. Li, "Capsule Network Retention Time Correction Facilitates Prostatic Tumorigenesis Discovery Through Porous Graphitic Carbon DIA-MS." (In Preparation)
- **D.G. Delafield**, H.N. Miles, W.A. Ricke, L. Li. "Six-plex Isobaric Labeling Reveals Glycosylation Dysregulation Across Benign, Metastatic, and Tumorigenic Prostate Cancer." (In Preparation)
- **D.G. Delafield**<sup>†</sup>, X. Zhong<sup>†</sup>, L. Li. "Sample Agnostic Spectral Libraries Improve Profiling Depth in Data Independent Analysis of Cerebrospinal Fluid." (In Preparation) († Co-First Authors)
- **D.G. Delafield**<sup>†</sup>, X. Zhong<sup>†</sup>, L. Li. "Enhanced Proteomic Coverage Enabled through BoxCar DIA and Sample Agnostic Spectral Libraries." (In Preparation) († Co-First Authors)
- Y. Liu, **D.G. Delafield**, L. Li "Comprehensive Mass Spectrometric Characterization of Neuropeptidome in Nervous System of the Atlantic Blue Crab, *Callinectes sapidus*," *Analytical Chemistry*, to be submitted.
- G. Li, C. Jeon, M. Ma, Z. Zheng, **D.G. Delafield**, E. Romanova, J. Sweedler, B. Ruotolo, L. Li, "Site-specific Chirality-conferred Structural Compaction Differentially Rescues the Cytotoxicity of A $\beta$ 42" *Angewandte Chemie* (In Submission)
- M. Ma, Q. Yu, **D.G. Delafield**, Y. Cui, Z. Li, W. Wu, X. Shi, A. Gutierrez, P.R. Westmark, M. Xu, C.J. Westmark, L. Li. "On-tissue Spatial Proteomics Integrating MALDI-MS Imaging with Shotgun Proteomics Reveals Soy Consumption-induced Biomarkers in a Fragile X Syndrome Mouse Model". *Nature Communications*. (Under revision)
- H. Zhang, **D.G. Delafield**, L. Li. (2023) "Mass spectrometry imaging: the rise of spatially resolved single-cell omics." *Nature Methods*. (Accepted)
- Y Shi, Z. Li, B. Wang, Z. Ye, H. Ye, **D.G. Delafield**, X. Shi, Z. Chen, F. Ma, L. Li (2022) "Enabling Global Analysis of Protein Citrullination and Homocitrullination via Biotin Thiol Tag-Assisted Mass Spectrometry." *Analytical Chemistry*. Published online December 13, 2022. 10.1021/acs.analchem.2c03844.
- N. Wang, N. Wang, S. Yu, H. Zhang, S. Tang, D. Wang, W. Lu, H. Li, **D.G. Delafield**, Y. Kong, X. Wang, C. Shao, L. Lv, G. Wang, R. Tan, N. Wang, H. Hao, H. Ye (2022) "Cyclic Immonium Ion of Lactyllysine Reveals Widespread Lactylation in the Human Proteome," *Nature Methods*. Published online June 28, 2022. 10.1038/s41592-022-01523-1.
- Z. Li, D. M. Tremmel, F. Ma, Q. Yu, M. Ma, **D.G. Delafield**, Y. Shi, B. Wang, S. A. Mitchell, A. K. Feeney, V. S. Jain, S. D. Sackett, J. S. Odorico, L. Li (2020) "Proteome-wide and Matrisome-specific Alterations during Human Pancreas Development and Maturation," *Nature Communications*. Published online February 15, 2021. 10.1038/s41467-021-21261-w.
- Ruiz, M., Y. Yang, C. A. Lochbaum, **D. G. Delafield**, J. J. Pignatello, L. Li and J. A. Pedersen (2019). "Peroxy monosulfate Oxidizes Amino Acids in Water without Activation." *Environmental Science and Technology*. 53, 10845-10854.
- Li, G., **D.G. Delafield**, L. Li (2019). "Improved Structural Elucidation of Peptide Isomers and Their Receptors Using Advanced Ion Mobility-Mass Spectrometry." *Trends in Analytical Chemistry*. Published online, June 4, 2019. 10.1016/j.trac.2019.05.048.
- Ma, H., **D. G. Delafield**, Z. Wang, J. You and S. Wu (2017). "Finding Biomass Degrading Enzymes Through an Activity-Related Quantitative Proteomics Platform (ACPP)." *Journal of American Society for Mass Spectrometry*. 28, 655-663.

## Presentations

- **Delafield, D.G.**; Miles, H.N.; Liu, T.N.; Ricke, W.A.; Li, L. "Revealing Systematic Proteomic Remodeling through Library-Free DIA-MS Analysis of a Novel Progressive Prostate Cancer Cell Model" US HUPO 2023 (poster)
- **Delafield, D.G.**; Li, L. "Evaluation of Porous Graphitic Carbon at Elevated Temperatures for Glycopeptide Analyses: Impacts on Signal Suppression, Reduced Identification and Quantitative Inaccuracies" ASMS 2022 (poster).
- **Delafield, D.G.**; Zhong, X.; Yu, Q.; Sauer, C.S.; Zetterberg, H.; Li, L. "Sample Agnostic Spectral Libraries: An Open Framework for Enhanced Data Independent Analysis Profiling Depth" Wisconsin Proteomics Symposium 2022 (oral)

- **Delafield, D.G.;** Xia, J.; Li, L. “High Resolution Demultiplexing Ion Mobility: A New Paradigm for Intact Glycopeptide Structural Assignment” ASMS 2021 (poster).
- **Delafield, D.G.;** Cui, Y.; Li, L. “Uncovering Glycoprotein Structural and Compositional Heterogeneity Through Capillary Electrophoresis-Ion Mobility Mass Spectrometry” ACS Fall Meeting 2021 (**oral**).
- **Delafield, D.G.;** Li, L. “Enhancing Glycopeptide Detection, Identification, and Structural Characterization through PGC-Incorporated LC-MS” Pittcon 2021 (**oral**).
- **Delafield, D.G.;** Li, L. “Enhancing Glycopeptide Detection, Identification, and Structural Characterization through PGC-Incorporated LC-IMS” ASMS 2020 (poster).
- **Delafield, D.G.;** Li, G.; Li, L. “Pursuit of Bottom-Up, Middle-Down, and Top-Down Glycoconjugate Analysis Enabled Through Online CE-ESI-IMS” ASMS 2019 (poster).
- **Delafield, D.G.;** Wang, Z.; Baird, M.A.; Shvartsburg, A.; Wu, S. “Characterization Analysis of Glycopeptides Through Arrival Time Correlation using Concurrent RPLC Fraction Monitoring and FAIMS Filtering” ASMS 2018 (poster).
- **Delafield, D.G.,** N-Glycopeptide Feature Identification by Revealing Trends Between Analyte Composition and Compensation Field Through FAIMS-Coupled MS Platform” US HUPO 2018 (**oral**).
- **Delafield, D.G.;** Wang, Z.; Baird, M.A.; Shvartsburg, A.; Smith, K.; Wu, S. “Three-Dimensional Platform for N-Linked Glycopeptide Separation and Analysis” ASMS 2017 (poster).
- **Delafield, D.G.;** Wang, Z.; Woodard, T. Wu, S. “Magnetic Resin Microreactor for Affinity-Capture Top-Down Mass Spectrometry” ASMS 2016 (poster).

## Funding

- Creating a Region-Specific Biomolecular Atlas of the Brain in Alzheimer’s Disease (1R01AG078794-01, September 2022)
  - Role: Contributing Author
  - Funding Amount: \$3,780,730
- Acquisition of a Dual-Source, High-Performance, Ion Mobility, Quadrupole Time-of-Flight Mass Spectrometry System for Biomedical Research at UW-Madison (1S10OD028473-01A1, May 2021)
  - Role: Primary Author
  - Funding Amount: \$1,275,704

## Skills

- **Proteomics, -omics**
  - High-throughput bottom-up, top-down, and middle-down proteomics.
  - Label-free and isobaric labeling relative quantitation.
  - Glycan, glycopeptide, glycoprotein identification and characterization.
  - Phosphoproteomics.
  - PTM identification and localization.
  - Small molecule absolute quantification.
- **Mass Spectrometry**
  - Expertise in all major vendors: ThermoFisher, Bruker, Agilent, Waters.
  - Data-dependent acquisition.
  - Data-independent acquisition.
  - Parallel reaction monitoring.
  - CID, HCD, ETD.
- **Liquid-Chromatography, Separations**
  - Reversed-phase liquid chromatography.
  - Porous graphitic carbon.
  - Ion exchange chromatography.
  - Size exclusion chromatography.

- Capillary electrophoresis – CZE and microfluidic CZE.
- Ion mobility (TIMS, DTIMS, FAIMS).
- **Computer Science**
  - Python
  - R
  - SQL
  - Rust
  - Javascript
  - HTML
  - CSS
  - High throughput analysis, process automation, machine learning, web development.
- **Professional**
  - Written communication.
  - Oral communication.
  - Project management.
  - Public speaking.
  - Manuscript authorship

## Awards and Honors

- **2023:** Gary Parr Memorial Award for Outstanding Bioanalytical Graduate Research
- **2022:** Luminex Summer Fellowship
- **2022:** Chemistry Department Travel Award
- **2022:** Department of Chemistry Harold Hay Fellowship
- **2019:** Student Research Travel Grant
- **2018:** Honored Instructor Award
- **2018:** ASMS Travel Grant
- **2017:** Head Teaching Assistant
- **2017:** Certificate of Distinction in Teaching
- **2017:** College of Arts & Sciences Travel Grant
- **2016:** Scott Laing Outstanding Undergraduate Research Award
- **2016:** Honors Research Assistant
- **2016:** Outstanding Senior Man Award
- **2016:** J. Lee Burke Outstanding Student Achievement Award

## Teaching Experience and Community Involvement

- **Teaching Assistant**, August 2018-May 2019
  - Formulated and delivered bi-weekly lesson plans based on outlined course objectives.
  - Assisted in exam writing and proofing.
  - Aided student groups in the development of unique experiment design and result presentation.
- **Head Teaching Assistant**, August 2017-May 2018
  - Coordinated teaching schedules, materials, and lesson plans for 57 Teaching Assistants across 71 classes.
  - Served as primary contact between professors of record and 2,000+ undergraduate students.
  - Led teaching assistants through development of weekly instruction, grading expectations, and lesson preparation.
  - Reviewed and rewrote exam material based on learning objectives.
- **Teaching Assistant**, August 2016-May 2017
  - Designed interactive lessons based on course learning objectives.
  - Promoted individual and group demonstration of knowledge.
  - Created, submitted, explained, and graded weekly assignments.
- **Norman North High School**, 2015-2017

- Formulated and implemented lesson plans for groups small and large.
- Assisted team members in goal-based teaching strategies.
- Adapted learning concepts to promote growth and retention.

## **Professional Affiliations**

- **American Society for Mass Spectrometry (ASMS)**
- **United States Human Proteome Organization (U.S. HUPO)**