Daniel J. Geiszler

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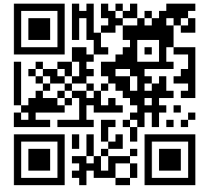
EDUCATION

University of Michigan, Ann Arbor	Graduation: 19 Aug 2022

Ph.D., Bioinformatics
*Computational Methods for Characterizing Post-translational and Chemical
Modifications Found in Open Searches*

California State University San Marcos	Graduation: 19 May 2017

B.S., Chemistry; B.S., Biotechnology; Minor, Mathematics

EXPERIENCE

Koç Üniversitesi – Dr. Nurhan Özlü — 16 Sep 2023 – Present
EMBO Postdoctoral Fellow – Proteome Informatics — **Istanbul, Turkey**

- Developed noise-robust method for post-translational modification localization utilizing machine learning and Bayesian statistics
- Worked alongside biologists to extract meaning from complex experimental designs
- Implemented continuous integration via GitHub Actions

Koç Üniversitesi – Dr. Nurhan Özlü — 15 Sep 2022 – 15 Sep 2023
Marie Curie CoCirculation2 Postdoctoral Fellow – Proteome Informatics — **Istanbul, Turkey**

- Led efforts to identify urinary biomarkers of renal cell carcinoma in unenriched urine
- Advised multiple biological teams on computational proteomics analysis techniques

University of Michigan Department of Pathology – Dr. Alexey Nesvizhskii — 3 Jan 2018 – 31 Aug 2022
Graduate Researcher – Proteome Informatics — **Ann Arbor, MI, USA**

- Published and maintained widely used software packages for mass tolerant proteomics searches
- Developed methods for post-translational modification signature identification in mass spectra
- Spearheaded computational collaborations for multiple inter-university, cross-functional projects in chemoproteomics

University of Michigan Department of Biological Chemistry – Dr. Philip Andrews — 5 Sep 2017 – 21 Dec 2017
Rotation Student – Computational Protein Crosslinking — **Ann Arbor, MI, USA**

- Investigated structural changes in the Hsp-CHIP-Tau complex via cleavable crosslinkers
- Devised strategies to adapt existing proteomics software to handle crosslinking technology

Department of Chemistry and Biochemistry – Dr. Katherine Kantardjieff — 1 Jun 2015 – 18 May 2017
Student Researcher – Computational Biology — **San Marcos, CA, USA**

- Computationally analyzed chimeric protein structure and function with end goal of drug design
- Collected and elucidated X-ray diffraction data for lactate dehydrogenase
- Engineered *in silico* a selective enzyme inhibitor with attention to ADME/T properties

College of Pharmacy – Dr. Heather Carlson — 25 May 2016 – 5 Aug 2016
Summer Researcher – Computational Structural Biology — **Ann Arbor, MI, USA**

- Analyzed thousands of apo and holo protein structure relationships from the PDB
- Identified 50+ methods of comparing protein structure
- Benchmarked methods of comparing protein structure

FUNDING

European Molecular Biology Organization Postdoctoral Fellowship € 115,200 (ALTF 109-2023)	16 Sep 2023 – Present
Marie Sklodowska-Curie Action COFUND TÜBİTAK CoCirculation2 Postdoctoral Fellowship € 70,200 (121C367)	15 Sep 2022 – 15 Sep 2023
Proteome Informatics of Cancer Training Program $73,968 (T32 CA 140044) 48648	1 Sep 2018 – 31 Aug 2021
Training Program in Bioinformatics $23,844 (T32 GM 070449)	5 Sep 2017 – 31 Aug 2018

HONORS AND AWARDS

Rackham Graduate Travel Award
2021

Proteomics Data Mining Challenge 2020 winning team
2020

IREU Summer Scholarship Recipient
2017

Magna Cum Laude – CSUSM
2017

Outstanding Chemistry Graduate
2017

HyperCube Scholar in Computational Chemistry
2016

Outstanding Senior at CSUSM
2016

INVITED TALKS

Illuminate Your Open Search: Comprehensive PTM Identification TuPA International Proteomics Congress // 4th National Proteomics Congress	13 Oct 2022

ACADEMIC SERVICE

Computational Proteomics Woskhop *Koç Üniversitesi*	25 Oct 2022 ***Istanbul, TR***

- Designed a FragPipe user workshop
- Taught hands on computational proteomics workshop for experimentalists

Bioinformatics Peer Mentorship Program *Mentee: Bradley Crone*	4 Sep 2018 – 31 Aug 2022 **Ann Arbor, MI, USA**

- Helped mentee acclimate to a new lifestyle and identified funding opportunities

EMBO Practical Course on Quantitative Proteomics *European Molecular Biology Organization*	3 May 2021 **Remote**

- Designed post-translational modification analysis lesson plan
- Taught hands-on post-translational modification workshop

May Institute: Computation and statistics for mass spectrometry and proteomics *Northeastern University*	14 May 2021 **Remote**

- Facilitated a post-translational modification analysis workshop

Ad hoc reviewer
    Cell Reports; Methods; Journal of Proteome Research; Nature Methods; Open Research Europe

OTHER PROFESSIONAL ACTIVITIES

Technical support and open-source software maintenance
    FragPipe (https://fragpipe.nesvilab.org/)
    PTM-Shepherd (https://ptmshepherd.nesvilab.org/)

CERTIFICATIONS

ASMS 2023 13 Quantitative Proteomics: Case Studies Member Registration (Upcoming)
    Quantitative proteomics; SRM; DIA; Skyline; MSstats

Cultivating a Culture of Respect (2021)
    Sexual- and Gender-based Misconduct; Equity

NIH Research Responsibility and Ethics (2017)
    Fraud, Fabrications, and Plagiarism; Data Store, Ownership, and Peer Review; Animal Use and Care;
    Human Subjects Research and IRBs; Conflict of Interest; Research in the Global Workplace; Dual Use
    Issues

Responsible Conduct of Research and Scholarship (2021)
    Ethical Research and Scholarship

PUBLICATIONS

Detecting diagnostic features in MS/MS spectra of post-translationally modified peptides
Geiszler, D. J., Polasky, D. A., Yu, F., Nesvizhskii, A. I. Nature Communications (2023).

Solid-phase compatible silane-based cleavable linker enables custom isobaric quantitative chemoproteomics
Burton, N. R, Polasky, D. P., Shikwanna, F., Ofori, S., Yan, T., **Geiszler, D. J.**, da Veiga Leprevost, F.,
Nesvizhskii, A. I., Backus, K. M. Journal of the American Chemical Society (2023).

MSFragger Labile Mode: A Flexible Method to Improve PTM Search in Proteomics
Polasky, D. A., **Geiszler, D. J**., Yu, F., Teo, G. C., Nesvizhskii, A. I. (2023). Molecular & Cellular Proteomics,
22(5), 100538.

Multiattribute Glycan Identification and FDR Control for Glycoproteomics
Polasky, D. A., **Geiszler, D. J**., Yu, F., Nesvizhskii, A. I. (2022). Molecular & Cellular Proteomics, 21(3), 100205.

*Enhancing Cysteine Chemoproteomic Coverage Through Systematic Assessment of Click Chemistry Product
Fragmentation*
Yang, T., Palmer, A. B., **Geiszler, D. J**., Polasky, D. A., Boatner, L. M., Burton, N. R., Armenta, E., Nesvizhskii,
A. I., Backus, K. M. (2022). Analytical Chemistry, 94(9), 3800-3810.

*PTM-Shepherd: analysis and summarization of post-translational and chemical modifications from open search
results*
Geiszler, D. J., Kong, A. T., Avtonomov, D. M., Yu, F., da Veiga Leprevost, F., & Nesvizhskii, A. I. (2021).
Molecular & Cellular Proteomics, 20, 100018.

Identification of modified peptides using localization-aware open search
Yu, F., Teo, G. C., Kong, A. T., Haynes, S. E., Avtonomov, D. M., **Geiszler, D. J.**, & Nesvizhskii, A. I. (2020).
Nature Communications, 11(1), 1-9.

Integrated proteogenomic characterization of clear cell renal cell carcinoma
Clark, D. J., [39 authors], **Geiszler, D.**, [39 authors]. (2019). Cell, 179(4), 964-983.

Clear cell renal cell carcinoma biomarkers in unenriched urine
Geiszler, D. J., Nazlı Ezgi Özkan, Gamze Bur Yapici, Murat Can Kiremit, Nurhan Ozlu. Manuscript in
preparation.

A statistical model for localization of post-translational modifications in noisy spectra

Geiszler, D. J., Nurhan Ozlu. Manuscript in preparation.

PRESENTATIONS AND OTHER WORK

A new statistical model for open search localization
Daniel J. Geiszler, Nurhan Ozlu [Poster]. American Society for Mass Spectrometry (2024). (Upcoming)

The Urinary Post-Translational Modification Landscape and Applications in Clear Cell Renal Cell Carcinoma Biomarker Discovery
Daniel J. Geiszler, Nazli Ozkan, Gamze Yapici, Meral Kiremit, Nurhan Ozlu [Poster]. American Society for Mass Spectrometry (2023).

Computational Methods for Characterizing Post-translational and Chemical Modifications Found in Open Searches **Daniel J. Geiszler**. [Dissertation]. University of Michigan (2022).

Automated modification-specific spectral feature detection
Daniel J. Geiszler, Daniel A Polasky, Fengchao Yu, Alexey I. Nesvizhskii. [Poster]. American Society for Mass Spectrometry (2021).

Multi-Level Post-Translational Modification Classification with PTM-Shepherd
Daniel J. Geiszler, Andy T. Kong, Dmitry M. Avtonomov, Felipe da Veiga Leprevost, Hui-Yin Chang, Fengchao Yu, Alexey I. Nesvizhskii. [Poster]. American Society for Mass Spectrometry (2020).

Exploring the Open Proteome: Proteomics Open Search Analysis with PTM-Shepherd
Daniel J Geiszler, Andy T Kong, Dmitry M Avtonomov, Felipe V Leprevost, Guo Ci Teo, Hui-Yin Chang, Alexey I Nesvizhskii. [Poster]. American Society for Mass Spectrometry (2019).

Structural Biology in the Drug Design Process
Daniel J. Geiszler. [Thesis]. California State University San Marcos (2017).

Crystal Structure of Chicken Muscle Lactate Dehydrogenase
Daniel J. Geiszler, Katherine Kantardjieff. [Poster]. Department of Chemistry and Biochemistry Symposium (2017).

LANGUAGES

English (native)	Java
Turkish (limited working proficiency)	Python
Spanish (recoverable)	C++ (recoverable)