

Daniel J. Geiszler

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SKILLS

Bioinformatics
Chemoproteomics
Algorithm development
Scientific computing
Proteomics
Post-translational modifications
Probability and statistics
Mass spectrometry
Test-driven development
Continuous integration (CI/CD)

EDUCATION

University of Michigan, Ann Arbor Ph.D., Bioinformatics <i>Computational Methods for Characterizing Post-translational and Chemical Modifications Found in Open Searches</i>	Graduation: 19 Aug 2022
California State University San Marcos B.S., Chemistry; B.S., Biotechnology; Minor, Mathematics	Graduation: 19 May 2017

EXPERIENCE

Koç Üniversitesi – Dr. Nurhan Özlü <i>EMBO Postdoctoral Fellow – Proteome Informatics</i>	16 Sep 2023 – Present Istanbul, Turkey
<ul style="list-style-type: none">Developed noise-robust method for post-translational modification localization utilizing machine learning and Bayesian statisticsDeveloped novel ion-level decoy generation methodIdentified cell-type agnostic markers of cytokinesis in multi-cell line cell cycle phosphoproteomics data	
Koç Üniversitesi – Dr. Nurhan Özlü <i>Marie Curie CoCirculation2 Postdoctoral Fellow – Proteome Informatics</i>	15 Sep 2022 – 15 Sep 2023 Istanbul, Turkey
<ul style="list-style-type: none">Led efforts to identify urinary biomarkers of renal cell carcinoma in unenriched urineAdvised multiple biological teams on computational proteomics analysis techniquesAnalyzed proteome interaction data to identify cell-surface markers of heterotypic cell-cell interactions	
University of Michigan Department of Pathology – Dr. Alexey Nesvizhskii <i>Graduate Researcher – Proteome Informatics</i>	3 Jan 2018 – 31 Aug 2022 Ann Arbor, MI, USA
<ul style="list-style-type: none">Published and maintained widely used software packages for mass tolerant proteomics searchesDeveloped methods for post-translational modification signature identification in mass spectraSpearheaded computational collaborations for multiple inter-university, cross-functional projects in chemoproteomics	
College of Pharmacy – Dr. Heather Carlson <i>Summer Researcher – Computational Structural Biology</i>	25 May 2016 – 5 Aug 2016 Ann Arbor, MI, USA
<ul style="list-style-type: none">Analyzed thousands of apo and holo protein structure relationships from the PDBIdentified 50+ methods of comparing protein structureBenchmarked methods of comparing protein structure	

GRANTS

European Molecular Biology Organization Postdoctoral Fellowship € 115,200 (ALTF 109-2023)	16 Sep 2023 – Present
Marie Skłodowska-Curie Action COFUND TÜBİTAK CoCirculation2 € 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

<i>A new statistical model for open search localization</i> TuPA International Proteomics Congress // 6th National Proteomics Congress	11 Oct 2024
<i>Illuminate Your Open Search: Comprehensive PTM Identification</i> TuPA International Proteomics Congress // 4th National Proteomics Congress	13 Oct 2022

ACADEMIC SERVICE

Computational Proteomics Workshop <i>Koç Üniversitesi</i>	25 Oct 2022 <i>Istanbul, TR</i>
<ul style="list-style-type: none">Designed a FragPipe user workshopTaught hands on computational proteomics workshop for experimentalists	
Bioinformatics Peer Mentorship Program <i>Mentee: Bradley Crone</i>	4 Sep 2018 – 31 Aug 2022 Ann Arbor, MI, USA
<ul style="list-style-type: none">Helped mentee acclimate to a new lifestyle and identified funding opportunities	
EMBO Practical Course on Quantitative Proteomics <i>European Molecular Biology Organization</i>	3 May 2021 Remote
<ul style="list-style-type: none">Designed post-translational modification analysis lesson planTaught hands-on post-translational modification workshop	
May Institute: Computation and statistics for mass spectrometry and proteomics <i>Northeastern University</i>	14 May 2021 Remote
<ul style="list-style-type: none">Facilitated a post-translational modification analysis workshop	
Ad hoc reviewer Cell Reports; Methods; Journal of Proteome Research; Nature Methods; Open Research Europe	

SCIENTIFIC SOFTWARE CONTRIBUTIONS

PTM-Shepherd (<https://ptmshepherd.nesvilab.org/>)

A tool for mass-tolerant search annotation

Roles: creator, technical support, software maintenance

FragPipe (<https://fragpipe.nesvilab.org/>)

A pipeline for analyzing mass-spectrometry proteomics data

Roles: contributor, technical support, software maintenance

EzRAG (<https://github.com/danielgeiszler/EzRAG/>)

A lightweight program for testing retrieval-augmented generation

Roles: creator

FragRAG (private)

A retrieval augmented generation-powered chatbot for FragPipe questions

Roles: creator

CERTIFICATIONS

Epigeum Research Integrity (2024)

Scholarly Publication; Professional Responsibilities; Communication, Social Responsibility, and Impact, Conflicts of Interest

ASMS 2023 13 Quantitative Proteomics: Case Studies Member Registration (2023)

Quantitative proteomics; SRM; DIA; Skyline; MSstats

Cultivating a Culture of Respect (2021)

Sexual- and Gender-based Misconduct; Equity

Responsible Conduct of Research and Scholarship (2021)

Ethical Research and Scholarship

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

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.

UNDER REVIEW

Proximity labeling and SILAC based proteomic approach identifies proteins at the interface of homotypic and heterotypic cancer cell interactions

Saner, N., Uzun, C., Akarlar, B., Ozkan, S. N., Ozturk, E., **Geiszler, D. J.**, Ozlu, N. (Under review). *Molecular & Cellular Proteomics*.

IN PREPARATION

A new statistical model for open search localization

Geiszler, D. J., Ozlu, N. (in preparation).

A multi-cell line phosphoproteomic atlas of cell cycle regulation

Ceyhan, C. S.,* **Geiszler, D. J.**,* Dittmann, A., Grossman, J., Ozlu, N. (in preparation).

*These authors contributed equally

Investigating the regulatory roles of protein palmitoylation during cell division

Ozkan, N. E., Yapici, G. N., **Geiszler, D. J.**, Ozlu, N. (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).

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).

SCIENTIFIC BLOG POSTS

Daniel Geiszler. (2025) *Retrieval Augmented Generation with DeepSeek*

<https://danny.bio/posts/20250125-retrieval-augmented-generation/RagSystem.html>

Daniel Geiszler. (2024) *How to Make a Rolling Blog Post with Continuous Integration*

<https://danny.bio/posts/20241221-rolling-blog-posts/>

Daniel Geiszler. (2024) *Machine Learning Basics*

<https://danny.bio/posts/20241219-machine-learning-basics/>

Daniel Geiszler. (2024) *Learning Pyro for Better Content Sorting*

https://danny.bio/posts/20241215-testing-pyro/testing_pyro.html

LANGUAGES

English (native)

Turkish (limited working proficiency)

Spanish (recoverable)

Java

Python

C++ (recoverable)