

Daniel J. Geiszler

<https://danny.bio> | danny.geisz@gmail.com | Campbell, CA, USA

Updated 29 March 2025

SKILLS

Data Science

Bioinformatics
Machine learning
Probability and statistics
Scientific computing

Technical

Computational proteomics
Chemoproteomics
Post-translational modifications
Proteogenomics, multi-omics integration
Mass spectrometry

Software development

Algorithm development
Test-driven development
Continuous integration (CI/CD)
Java, Python, R, C++, Bash
Git/GitHub

EDUCATION

University of Michigan, Ann Arbor

Graduation: Aug 2022

Ph.D., Bioinformatics

Computational Methods for Characterizing Post-translational and Chemical Modifications Found in Open Searches

California State University San Marcos

Graduation: May 2017

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

Structural Biology in the Drug Design Process

EXPERIENCE

Koç Üniversitesi – Dr. Nurhan Özlü

2022 – Present

Marie Curie CoCirculation2 Postdoctoral Fellow – Proteome Informatics

Istanbul, Turkey

- Collaborated in cross-functional teams with biologists, leading bioinformatics efforts in 4 projects to create tailored workflows for complex proteomics projects spanning bulk proteomics, protein-protein interactions, and phosphoproteomics
- Utilized machine learning and Bayesian statistics to develop noise-robust method for post-translational modification localization that achieved near-theoretically optimal performance
- Led bioinformatics efforts to identify 13 universal markers of cytokinesis in a multi-cell line, multi-cell phase experiment with factorial design and identified ontology-enriched patterns across cell cycle phases

University of Michigan Department of Pathology – Dr. Alexey Nesvizhskii

Jan 2018 – Aug 2022

Graduate Researcher – Proteome Informatics

Ann Arbor, MI, USA

- Published and maintained widely used software packages with more than 75,000 downloads for mass tolerant proteomics searches
- Developed automated methods to mine for post-translational modification signature identification in mass spectra that increase identified peptides by up to 100% in some cases

- Spearheaded collaborations for inter-university, cross-functional projects in engineering chemoproteomics probe fragmentation patterns resulting in 2 publications
- Provided end-user support for FragPipe, promptly troubleshooting hundreds of IT and configuration issues
- Integrated 110 cancer patient transcriptomic and proteomic samples with multi-omics approaches to identify neo-antigens as part of the Clinical Proteomics Tumor Analysis Consortium

Department of Chemistry and Biochemistry – Dr. Katherine Kantardjieff

Jun 2015 – 2017

Student Researcher – Computational Structural Biology

San Marcos, CA, USA

- Computationally analyzed protein structure and function for Ewing sarcoma
- Designed butyrylcholinesterase-selective inhibitors to treat Alzheimer's disease
- Collected and elucidated X-ray diffraction data for lactate dehydrogenase

College of Pharmacy – Dr. Heather Carlson

May 2016 – Aug 2016

Summer Researcher – Computational Structural Biology

Ann Arbor, MI, USA

- Analyzed biophysical relationships of thousands of apo and holo protein structure relationships from the PDB
- Identified and benchmarked 4 functional methods of comparing protein structure to determine optimal algorithms

Department of Biology – Dr. Matthew Escobar

Jun 2014 – May 2016

Student Researcher – Plant Molecular Biology

San Marcos, CA, USA

- Used molecular biology techniques to generate 18 transcript-suppressed *A. thaliana* mutants and validated with quantitative PCR
- Performed protein activity and concentration assays to measure reactive oxygen species

GRANTS

European Molecular Biology Organization Postdoctoral Fellowship €115,200 (ALTF 109-2023)	Sep 2023 – Present
Marie Skłodowska-Curie Action COFUND TÜBİTAK CoCirculation2 €70,200 (121C367)	Sep 2022 – Sep 2023
Proteome Informatics of Cancer Training Program \$73,968 (T32 CA 140044) 48648	Sep 2018 – Aug 2021
Training Program in Bioinformatics \$23,844 (T32 GM 070449)	Sep 2017 – 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	Oct 2024
<i>Illuminate Your Open Search: Comprehensive PTM Identification</i> TuPA International Proteomics Congress // 4th National Proteomics Congress	Oct 2022

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 with 75,000 downloads

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

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)