

# Daniel J. Geiszler

<https://danny.bio> | [danny.geisz@gmail.com](mailto:danny.geisz@gmail.com) | Istanbul, Turkey

Updated 25 November 2024

## SKILLS

---

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

## EDUCATION

---

University of Michigan, Ann Arbor	Graduation: 19 Aug 2022
Ph.D., Bioinformatics	
<i>Computational Methods for Characterizing Post-translational and Chemical Modifications Found in Open Searches</i>	
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
<i>EMBO Postdoctoral Fellow – Proteome Informatics</i>	<b>Istanbul, Turkey</b>
<ul style="list-style-type: none"><li>Developed noise-robust method for post-translational modification localization utilizing machine learning and Bayesian statistics</li><li>Developed novel ion-level decoy generation method</li><li>Identified cell-type agnostic markers of cytokinesis in multi-cell line cell cycle phosphoproteomics data</li></ul>	
Koç Üniversitesi – Dr. Nurhan Özlü	15 Sep 2022 – 15 Sep 2023
<i>Marie Curie CoCirculation2 Postdoctoral Fellow – Proteome Informatics</i>	<b>Istanbul, Turkey</b>
<ul style="list-style-type: none"><li>Led efforts to identify urinary biomarkers of renal cell carcinoma in unenriched urine</li><li>Advised multiple biological teams on computational proteomics analysis techniques</li><li>Analyzed proteome interaction data to identify cell-surface markers of heterotypic cell-cell interactions</li></ul>	
University of Michigan Department of Pathology – Dr. Alexey Nesvizhskii	3 Jan 2018 – 31 Aug 2022
<i>Graduate Researcher – Proteome Informatics</i>	<b>Ann Arbor, MI, USA</b>
<ul style="list-style-type: none"><li>Published and maintained widely used software packages for mass tolerant proteomics searches</li><li>Developed methods for post-translational modification signature identification in mass spectra</li><li>Spearheaded computational collaborations for multiple inter-university, cross-functional projects in chemoproteomics</li></ul>	
College of Pharmacy – Dr. Heather Carlson	25 May 2016 – 5 Aug 2016
<i>Summer Researcher – Computational Structural Biology</i>	<b>Ann Arbor, MI, USA</b>
<ul style="list-style-type: none"><li>Analyzed thousands of apo and holo protein structure relationships from the PDB</li><li>Identified 50+ methods of comparing protein structure</li><li>Benchmarked methods of comparing protein structure</li></ul>	

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

## SCIENTIFIC SOFTWARE CONTRIBUTIONS

---

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

Creator

Technical support

Software maintenance

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

Technical support

Software maintenance

## 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 Issues

## 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).

## LANGUAGES

---

English (native)

Turkish (limited working proficiency)

Spanish (recoverable)

Java

Python

C++ (recoverable)