

Enes Kemal Ergin, PhD

Bioinformatician & Systems Engineer

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Google Scholar: [Enes K. Ergin](https://scholar.google.com/citations?user=eneskemalergin)

PROFILE

Computational biologist and systems engineer with a decade of experience in quantitative proteomics, multi-omics integration, and machine learning for pediatric cancer research. Builds tested, versioned, reproducible analysis pipelines and open-source tools, three first-author packages with full test suites, adopted in translational and clinical proteomics workflows. First and co-author on publications in *Nature Communications*, *EMBO Molecular Medicine*, *Journal of Proteome Research*, and *Bioinformatics*.

EDUCATION

PhD, Bioinformatics

2019 – 2025

University of British Columbia (UBC), Vancouver, BC

Four Year Doctoral Fellowship. Thesis: “Computational interrogation of proteoform dynamics in pediatric cancer”

MSc, Bioinformatics (transferred to PhD)

2017 – 2019

University of British Columbia (UBC), Vancouver, BC

Michael Cuccione Childhood Cancer Foundation Graduate Studentship.

BSc, Computer Science (Software Engineering)

2013 – 2017

North American University (NAU), Houston, TX

GPA 3.72; Exceptional Merit Scholarship; President’s Honor Roll.

EXPERIENCE

Founder

May 2026 – Present

Zenteomics | LinkedIn

- Computational proteomics practice focused on reproducible analysis and research software: contract analysis support, QC/reproducibility review, and tool development.
- Started and maintain [Awesome Proteomics](#), a curated community resource of tools, databases, workflows, and practitioner guides.
- Consulting on prior BCCHR projects and wrapping up several manuscripts.

Staff Bioinformatician

Jun 2025 – Jun 2026

BC Children’s Hospital Research Institute, Lange Lab

- Maintained a high-throughput clinical proteomics pipeline in R and Python; fully Dockerized and version-locked because outputs inform clinical decisions.
- Built modules for QC, normalization, imputation, and differential testing within Snakemake workflows on Compute Canada/Slurm.
- Contributed to Molecular Tumor Board reports for ACCESS/PROFYLE across 16+ pediatric centres.
- Administered Linux servers and HPC; trained researchers and mentored junior bioinformaticians.

Graduate Research Assistant

Sep 2017 – May 2025

University of British Columbia, Lange Lab

- Designed and published three first-author open-source tools ([QuEstVar](#), [ProteoForge](#), [SQuAPP](#)) with full test suites, versioning, and documentation.
- Built and deployed SQuAPP, an R/Shiny QC dashboard on Compute Canada that became the lab’s primary analysis tool for non-computational members.
- Eight publications including *Nature Communications* and *EMBO Molecular Medicine*; supervised a co-op student for one year; mentored four students.

Visiting Undergraduate Researcher

Nov 2015 – Sep 2016

Harvard Medical School, Churchman Lab

- Built CNNs for transcription factor binding prediction (~900 GB genomic data, TensorFlow) and alternative mRNA splicing prediction (Lua/Torch).
- ENCODE-DREAM Challenge participant; direct experience with NGS data structures and ML workflows.

Undergraduate Research Assistant

Sep 2015 – May 2017

North American University

- Led student activity in the Bioinformatics Lab and mentored four junior and sophomore students.
- Tutored newcomers with prepared tasks and facilitated weekly presentations on bioinformatics topics.
- Designed an open source bioinformatics curriculum with Open Source Society on GitHub.

Undergraduate Research Assistant

Aug 2014 – May 2015

Yeditepe University

- Worked remotely as a genomic data scientist investigating candidate inhibitor molecules.
- Queried NCBI PubMed and used virtual docking tools to evaluate molecular targets and likely inhibitors.

Undergraduate Research Assistant

Sep 2014 – Apr 2015

Texas Institute of Education and Research (TIBER)

- Worked as an experimental biologist on sinusitis bacteria drug development and testing.
- Prepared agar solutions and bacterial cultures, conducted liquid and solid drug tests, and maintained experimental records.

TEACHING

Teaching Assistant

Sep 2015 – May 2017

North American University

Co-taught four undergraduate computer science courses for classes of more than 60 students and shared responsibility for labs, supplementary sessions, exams, homework, and grading.

- COMP 3317 Algorithms
- COMP 3320 Programming Languages
- COMP 3322 Software Engineering
- COMP 2415 Systems Programming

Mathematics and Computer Science Tutor

Jan 2017 – May 2017

North American University

Tutored students in subjects ranging from college algebra and differential equations to CS1 and Data Mining.

Instructor

Feb 2015 – Apr 2015

North American University

Taught introductory Python programming to 35 students, faculty, and staff; this was the first course taught solely by a student at NAU. ([GitHub](#))

PUBLICATIONS

Peer-Reviewed Articles and Thesis

1. **Ergin, E. K.**, Conrrero, A., Ferguson, K. M., Lange, P. F. (2026). ProteoForge: An Imputation-Aware Framework for Differential Proteoform Discovery in Bottom-Up Proteomics, doi: [10.1021/acs.jproteome.5c01235](https://doi.org/10.1021/acs.jproteome.5c01235), *Journal of Proteome Research*.
2. **Ergin, E. K.** (2025). Computational interrogation of proteoform dynamics in pediatric cancer. PhD thesis, University of British Columbia, Vancouver, BC, Canada. Supervisor: Philipp F. Lange.
3. Barnabas, G. D., Bhat, T. A., Goebeler, V., Leclair, P., Azzam, N., Melong, N., Anderson, C., Gom, A., An, S., **Ergin, E. K.**, Shen, Y., Conrrero, A., Mungall, A. J., Mungall, K. L., Maxwell, C. A., Reid, G. S. D., Hirst, M., Jones, S., Chan, J. A., Senger, D. L., Berman, J. N., Parker, S. J., Bush, J. W., Strahlen-dorf, C., Deyell, R. J., Lim, C. J., Lange, P. F. (2025). Proteomics and personalized PDX models identify treatment for a progressive malignancy within an actionable timeframe, doi: [10.1038/s44321-025-00107-w](https://doi.org/10.1038/s44321-025-00107-w), *EMBO Molecular Medicine*.
4. **Ergin, E. K.**, Myung, J. J. K., Lange, P. F. (2024). Statistical Testing for Protein Equivalence Identifies Core Functional Modules Conserved across 360 Cancer Cell Lines and Presents a General Approach to Investigating Biological Systems, doi: [10.1021/acs.jproteome.4c00131](https://doi.org/10.1021/acs.jproteome.4c00131), *Journal of Proteome Research*.
5. Lorentzian, A. C., Rever, J., **Ergin, E. K.**, Guo, M., Akella, N. M., Rolf, N., Lim, C. J., Reid, G. S. D., Maxwell, C. A., Lange, P. F. (2023). Targetable lesions and proteomes predict therapy sensitivity through disease evolution in pediatric acute lymphoblastic leukemia, doi: [10.1038/s41467-023-42701-9](https://doi.org/10.1038/s41467-023-42701-9), *Nature Communications*.
6. **Ergin, E. K.**, Uzozie, A. C., Chen, S., Su, Y., Lange, P. F. (2022). SQuAPP: Simple Quantitative Analysis of Proteins and PTMs, doi: [10.1093/bioinformatics/btac628](https://doi.org/10.1093/bioinformatics/btac628), *Bioinformatics*.
7. Uzozie, A. C., **Ergin, E. K.**, Rolf, N., Tsui, J., Lorentzian, A., Weng, S. H., Nierves, L., Smith, T., Lim, C. J., Maxwell, C., Reid, G. S. D., Lange, P. F. (2022). PDX models reflect the proteome landscape of pediatric acute lymphoblastic leukemia but divert in select pathways, doi: [10.1186/s13046-021-01835-8](https://doi.org/10.1186/s13046-021-01835-8), *Journal of Experimental and Clinical Cancer Research*.
8. Weng, S. H.*, Demir, F.*, **Ergin, E. K.**, Dirnberger, S., Uzozie, A., Tuscher, D., Nierves, L., Tsui, J., Huesgen, P. F., Lange, P. F. (2019). Sensitive determination of proteolytic proteoforms in limited microscale proteome samples, doi: [10.1074/mcp.TIR119.001560](https://doi.org/10.1074/mcp.TIR119.001560), *Molecular and Cellular Proteomics*.
9. Kocabas, F., **Ergin, E. K.** (2016). Identification of small molecule binding pocket for inhibition of Crimean-Congo hemorrhagic fever virus OTU protease, doi: [10.3906/biy-1501-56](https://doi.org/10.3906/biy-1501-56), *Turkish Journal of Biology*.

SOFTWARE

ProteoForge (Python)	2026
Imputation-aware differential proteoform discovery (robust linear models, permutation testing).	
Publication Manuscript analysis	
QuEstVar (Python)	2024
Equivalence-testing framework, 60k+ comparisons/min across 360 datasets.	
Publication Manuscript analysis	
SQuAPP (R/Shiny)	2022
Web-based QC and analysis dashboard deployed on HPC; lab's primary analysis tool.	
Publication	
Proteomics & Mass Spectrometry	
PepVet (R)	2026
Interpretable, protein-level digestion-quality scoring for mass spectrometry (length, coverage, hydrophobicity, ionizability, proteotypicity).	
<i>Interpretable, Protein-Level Digestion Quality Scoring for Mass Spectrometry in R</i> (paper in preparation)	
XICGuard (Python)	2026
Validate, extract, and score Spectronaut XIC evidence from the command line.	
<i>Private repository</i>	
mzValidate (Zig)	2026
Validator for open proteomics data formats, starting with mzML; written in Zig for portability, speed, and strict conformance checking.	
mzarc (Zig)	2026
Domain-specific compression for mass spectrometry data; tuned for fast random access and strong compression ratios on large spectral datasets.	
loqulate (R)	2025
Limit-of-detection and limit-of-quantitation calculator for mass spectrometry calibration curves.	
PXAudit (Python)	2026
CLI auditing PRIDE proteomics datasets on a 7-tier FAIR ladder plus a quantification-readiness axis; queries the PRIDE Archive REST API with local JSON caching.	
PXSeek (Python)	2024
CLI to query, filter, and retrieve ProteomeXchange dataset metadata with local caching.	
HarmonizePy (Python)	2025
Pure-Python port of HarmonizR for missing-value-aware batch-effect correction in proteomics and multi-omics data.	
Systems & Performance (Zig)	
z-fasta (Zig)	2026
FASTA toolkit indexing the human genome $\sim 23\times$ faster than samtools; $O(1)$ region extraction, byte-for-byte verified against samtools and bedtools.	
ZigR (R/Zig)	2026
High-performance bridge for integrating Zig into R; fast, portable, and memory-safe.	
z-toml (Zig)	2026
TOML v1.1.0 parser for Zig 0.16; single-pass, dependency-free, corpus-validated.	
zebrac (Zig)	2026
Linux performance benchmark using <code>perf_event_open</code> to compare commands; hardware counters, peak RSS, statistical significance, terminal UI.	
z-oci (Zig)	2026
Pure-Zig OCI/Docker Registry API v2 client.	
ZagPlot (Zig)	2025
Dependency-free, pure-Zig plotting library and CLI; SVG output.	

PRESENTATIONS

Oral Presentations

1. **Ergin, E. K. (2023)**. Exploring Stable Proteome in Cancer Cell Line Atlas with QuEstVar, Trainee Omics Group (TOG), Jun 2023.
2. **Ergin, E. K. (2023)**. InPACCT: Integrated Proteomics Analysis of Curated Childhood Tumours, Canadian National Proteomics Network, May 2023.

3. **Ergin, E. K. (2020).** Normalization in Proteomics: Past, Present, and Future, Trainee Omics Group (TOG), May 2020.

Workshop Presentations

1. **Ergin, E. K. (2023).** Proteomics Workshop – Common Downstream Analysis Pipeline, Trainee Omics Group (TOG), Jul 2023.

Poster Presentations

1. Jenane, L., Nierves, L., **Ergin, E. K.**, Lange, P. F. (2024). Characterization of a New Type of Neoantigen in T-Cell Acute Lymphoblastic Leukemia (T-ALL) by Cell Surface Terminomics, US HUPO 2024, Portland, OR, USA.
2. Yadegari, M., **Ergin, E. K.**, Lange, P. F. (2023). Detection of Shed Surface Proteins and Processed Oncoproteoforms in Biofluids, Canadian Cancer Research Conference 2023, Halifax, NS, Canada.
3. **Ergin, E. K.**, Rostin, K., Lange, P. F. (2023). InPACCT: Integrated proteomics analyses of curated childhood tumours, Canadian National Proteomics Network, Regina, SK, Canada.
4. **Ergin, E. K.**, Lange, P. F. (2023). Stable Proteome in Cancer Cell Lines with Combined Testing, Canadian National Proteomics Network, Regina, SK, Canada.
5. Rostin, K., **Ergin, E. K.**, Lange, P. F. (2023). Insightful, Integrated Analyses of Public Pediatric Cancer Proteomics with InPACCT, BIG 23 Research Day, Vancouver, BC, Canada.
6. Weng, S. H., Demir, F., **Ergin, E. K.**, Dirnberger, S., Uzozie, A., Tuscher, D., Nierves, L., Tsui, J., Huesgen, P. F., Lange, P. F. (2019). Sensitive determination of proteolytic proteoforms in limited samples, 2019 Pathology Day, Vancouver, BC, Canada.
7. Ji, J., Thibodeau, M., **Ergin, E. K.**, Culibrk, L., Smith, T. (2018). SWI/SNF Chromatin Remodeling Complex in Clear Cell Ovarian Cancer. Stat540 Group Project Poster Session.

PROJECTS

Zenteomics Community Resources

Awesome Proteomics

May 2026

Zenteomics initiative: a curated list of proteomics tools, databases, workflows, and learning resources, with expert guides and practitioner pipelines.

[Website](#) | [LinkedIn](#) | [GitHub](#)

Earlier Projects

Open Source Bioinformatics Curriculum

Jun 2016

Developed an open source bioinformatics curriculum with contributions from the open source community.

[GitHub](#)

Scholar Development Center

Feb 2016

Created a non-profit community organization under the Raindrop Foundation to support Turkish undergraduate students in Texas pursuing academia or industry.

Essential Algorithms in Python

Sep 2014 – Present

Implemented algorithms from *A Practical Approach to Computer Algorithms* by Rod Stephens and extended the repository with additional algorithms and number-theory implementations.

AWARDS

- Four Year Doctoral Fellowship Award 2019 – 2023
- Michael Cuccione Childhood Cancer Foundation Graduate Studentship 2018 – 2019
- North American University Exceptional Merit Scholarship 2012 – 2017
- North American University President's Honor Roll 2015 – 2017
- North American University Outstanding Student of the Year 2015

MEMBERSHIPS

- ISCB (International Society of Computational Biology) Aug 2016 – Present
- ACM (Association for Computing Machinery) Feb 2013 – Present

LEADERSHIP

- NAU Future Leaders Club, Founder and Director Apr 2015 – May 2017
- Student Government, VP of Unity and Social Justice Sep 2014 – May 2017
- Student Government, VP of Finance Nov 2014 – Apr 2015
- NAU ACM, Vice President Sep 2015 – May 2016
- NAU ACM, Secretary Feb 2013 – Sep 2014
- NAU Kazakh Student Association, Club Advisor Sep 2016 – May 2017

SKILLS

- **Languages:** Python, R, Zig, Rust; Bash/Shell, SQL, C/C++
- **Data & Storage:** DuckDB, PostgreSQL, SQLite; Parquet, Arrow; NumPy, Pandas, Polars
- **Workflows & Reproducibility:** Snakemake, Nextflow, Docker; Jupyter, Quarto; Git/GitHub, CI/CD, semantic versioning, automated testing
- **Statistics & Methods:** Equivalence testing (TOST), permutation tests, robust linear models; multiple-testing correction; missing-value imputation; batch-effect correction; limma, MSstats, DESeq2
- **Proteomics & MS:** Bottom-up proteomics, peptide-level quantification, PTM analysis; QC, normalization, differential testing; proteoform deconvolution; ProteomeXchange/PRIDE
- **ML, DL & PLM:** PyTorch, scikit-learn, TensorFlow; HuggingFace, ESM, AlphaFold; CNNs/deep learning
- **Genomics & Sequence:** FASTA/FASTQ tooling, NGS data structures; Biopython; transcription-factor binding and splicing prediction
- **Software Engineering:** Code review, documentation/SOPs; memory-mapped I/O, SIMD, custom binary formats; R Shiny dashboards
- **HPC & Infrastructure:** Compute Canada/Slurm, Linux server administration, job schedulers, large-scale batch processing
- **Platforms:** Unix/Linux, macOS, Windows

CERTIFICATES

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| ▪ Neural Networks and Deep Learning, Coursera | Nov 2017 |
| ▪ Statistics for Genomic Data Science, With Distinction, Coursera | Nov 2016 |
| ▪ Command Line Tools for Genomics Data Science, With Distinction, Coursera | Oct 2016 |
| ▪ Machine Learning, Coursera | Aug 2016 |
| ▪ Bioconductor for Genomic Data Science, With Distinction, Coursera | Jul 2016 |
| ▪ Algorithms for DNA Sequencing, With Distinction, Coursera | May 2016 |
| ▪ Bioinformatics Methods I and II, With Distinction, Coursera | Dec 2015 |
| ▪ Introduction to Genomic Technologies, With Distinction, Coursera | Oct 2015 |
| ▪ Python for Genomic Data Science, With Distinction, Coursera | Oct 2015 |
| ▪ Introduction to R, Honor Certificate, EdX | Sep 2015 |
| ▪ Getting and Cleaning Data, Coursera | Mar 2015 |
| ▪ R Programming, With Distinction, Coursera | Feb 2015 |
| ▪ Introduction to R, DataCamp | Jan 2015 |
| ▪ Data Scientist's Toolbox, With Distinction, Coursera | Dec 2014 |
| ▪ Programming for Everybody (Python), With Distinction, Coursera | Jun 2014 |