Elliot MacKrell, Ph.D.

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[GitHub Portfolio](#) • [Personal Website](#) • [LinkedIn](#)

Education

California Institute of Technology   Pasadena, CA
Ph.D. Chemical Engineering   2016-2024
Thesis (Defended 6/20/24): *Global Analysis of Protein Synthesis and Degradation in Escherichia coli*

University of Florida   Gainesville, FL
B.S. Chemical Engineering   2016
Minor: Biomolecular Engineering

Research Experience

California Institute of Technology, Division of Chemistry and Chemical Engineering   2016-Present
Postdoctoral Scholar (2024-Present); Ph.D. Candidate - NSF Graduate Fellow (2016-2024); Advisor: Prof. David A. Tirrell

- Discovered global regulatory roles of protein degradation by combining chemoproteomic analysis, linear modeling, text mining, and machine learning to identify 186 novel protease substrate candidates in *Escherichia coli*.
- Developed a predictive machine learning model for *in vivo* protein stability in *E. coli*, achieving 87.5% accuracy in the experimental validation of 8 substrates.
- Engineered and deployed an open-source interactive application for filtering, normalization, differential expression analysis, and pathway enrichment analysis of mass spectrometry–based proteomics data. ([repository](#)) ([publication](#))
- Identified DNA repair factors recruited to colibactin-induced DNA interstrand cross-links in *Xenopus* egg extracts via differential expression analysis and time-series clustering of chromatin mass spectrometry data. ([preprint](#))

EMD Serono, Department of Translational Medicine and Global Clinical Development   2022
Bioinformatics Co-op; Supervisor: Dr. Irina Kalatskaya

- Developed Shiny application for visualizing cell type–specific transcript abundance, identifying differentially expressed genes, and conducting gene set enrichment analysis in clinical samples across autoimmune disease states.
- Established pipeline and Shiny application for the real-time analysis of text mining data from PubMed to identify genes, pathways, and diseases of therapeutic interest through information-theoretic and statistical approaches.

Harvard Medical School, Wellman Center for Photomedicine, Massachusetts General Hospital   2015
NSF REU Fellow; Advisor: Prof. Robert Redmond

- Investigated the effects of photocrosslinking on ex vivo tissue biomechanics via cyclic uniaxial tensile testing.

Johns Hopkins University School of Medicine, Department of Radiation Oncology   2014
NSF REU Fellow; Advisor: Prof. Robert Ivkov

- Evaluated the anti-tumor immune response generated by magnetic nanoparticle hyperthermia and ionizing radiation treatments in a mouse model for cancer.

University of Florida, Department of Chemistry   2012-2015
Undergraduate Research Assistant; Advisor: Prof. Brent S. Sumerlin

- Developed an amphiphilic and pH-responsive copolymer for site-specific drug delivery in plants by functionalizing polysuccinimide with hydrophilic molecules.

Publications

Altshuller, M., He, X., **MacKrell, E. J.**, Wernke, K. M., Wong, J.W. H., Sellés Baiget, S., Wang, T. Y., Chou, T. F., Duxin, J. P., Balskus, E. P., Herzon, S. B., Semlow, D. R. "The Fanconi anemia pathway repairs colibactin-induced DNA interstrand cross-links." **bioRxiv, 2024.** https://doi.org/10.1101/2024.01.30.576698

Jones, J.J., **MacKrell, E.J.**, Wang, T.Y., Lomenick, B., Roukes, L.M., and Chou, T.F. "tidyproteomics: An open-source R package and data object for quantitative proteomics post analysis and visualization." **BMC Bioinformatics, 2023,** *24,* 239. https://doi.org/10.1186/s12859-023-05360-7

Hill, M.R., **MacKrell, E.J.**, Forsthoefel, C.P., Jensen, S., Chen, M., Moore, G., He, Z.L. and Sumerlin, B.S. "Biodegradable and pH-Responsive Nanoparticles Designed for Site-Specific Delivery in Agriculture." **Biomacromolecules**, **2015**, *16*, 1276-1282. https://doi.org/10.1021/acs.biomac.5b00069

Manuscripts in preparation

MacKrell, E. J., Lomenick, B., Chou, T. F., and Tirrell, D. A. "Global protease substrate identification reveals instability of diverse regulators in *Escherichia coli.*" Manuscript in preparation.

MacKrell, E. J., Lomenick, B., Chou, T. F., and Tirrell, D. A. "MazF activates the cold shock response in *Escherichia coli.*" Manuscript in preparation.

Technical Skills

Bioinformatics and statistics: Mass spectrometry-based proteomics analysis, RNA-seq analysis, Machine learning, Text mining, Cloud computing, Shiny application development, Linear modeling, Regulatory network analysis, Gene set enrichment, Bayesian inference

Programming languages: Python, R, SQL, Bash, JavaScript, CSS, HTML

Machine learning: Scikit-learn, PyTorch, XGBoost

Data analysis and visualization: Pandas, NumPy, Matplotlib, Seaborn, Jupyter Notebook, Shiny, Bioconductor, tidyverse

Cloud and development tools: Docker, AWS, Git, Visual Studio Code, RStudio

Software suites: GeneData Profiler, Proteomics analysis suites (MaxQuant, Proteome Discoverer), Clarivate CBDD

Laboratory skills: Molecular cloning, Cell culture, Genome editing (Recombination, CRISPR-Cas9), Immunoblotting, Confocal microscopy, Proteomics sample preparation

Awards and Honors

CEMI Pilot Grant, California Institute of Technology	2018
CEMI Fellow, California Institute of Technology	2016-2024
NSF Graduate Research Fellowship, California Institute of Technology	2016-2021
Yao Su Student Research Prize, HST Summer Institute	2015
NSF REU Fellowship, Harvard-MIT Division of Health Sciences and Technology (HST)	2015
Collins Engineering Scholarship, University of Florida	2015
NSF REU Fellowship, Johns Hopkins University Institute for NanoBioTechnology (INBT)	2014
University Scholars Program, University of Florida	2013