

# GW McElfresh | Computational Biology PhD

Oregon Health & Science University – Oregon National Primate Research Center

✉ [mcelfreshgw@gmail.com](mailto:mcelfreshgw@gmail.com) • 🌐 [gwmcelfresh.github.io](https://gwmcelfresh.github.io) • 🌐 [GWMcElfresh](https://GWMcElfresh.github.io)

🆔 [0000-0002-1948-7571](https://orcid.org/0000-0002-1948-7571) • Google Scholar: [GW McElfresh](https://scholar.google.com/citations?user=GWMcElfresh)

## Professional Summary

Computational biologist with expertise spanning single-cell and spatial transcriptomics, mathematical modeling, machine learning, and structural biology. I build analytical frameworks that turn high-dimensional biological data into actionable insights—from co-developing a widely-used rhesus macaque immune reference atlas to authoring open-source tools adopted across the single-cell sequencing community. Equally comfortable designing a stochastic model, deploying an HPC pipeline at scale, or collaborating with wet-lab immunologists to answer disease-relevant questions. Seeking to apply multiscale analytical expertise to challenging problems at the intersection of biology, data science, and translational research.

## Education

### University of Kansas

PhD, Computational Biology

Dissertation: *Multiscale analyses of cellular signaling and regulation in response to multiple stress conditions*

Advisor: J. Christian Ray, PhD

Lawrence, KS

2015–2020

### Drury University

B.S., Mathematics & Physics

Graduated with honors

Springfield, MO

2011–2015

## Research Experience

### Oregon National Primate Research Center / OHSU

Computational Biologist 3

Portland, OR

Dec 2024–Present

- Co-developed the **Rhesus Immune Reference Atlas (RIRA)**—the first immune-focused, multi-tissue single-cell atlas for rhesus macaques—integrating data across >15 tissues and providing a community-standard reference for reconciling transcriptional profiles with established immune lineages (*Cell Genomics*, 2025)
- Designed and deployed end-to-end scRNA-seq pipelines for studies of HIV/SIV, Tuberculosis, and Yellow Fever, enabling discovery of correlates of protection in NHP vaccine models
- Authored and maintain open-source R packages hosted on GitHub: [cellhashR](#) (scRNA-seq cell-hashing demultiplexing, widely adopted across the single-cell community) and [tcrClustR](#) (TCR repertoire clustering and analysis)
- Developed a supplemental alignment pipeline capturing allele-specific MHC-I regulation and other immune signals systematically missed by dominant scRNA-seq workflows
- Collaborated across multiple labs to translate high-dimensional data into biological hypotheses and manuscript-ready analyses

### Oregon National Primate Research Center / OHSU

Computational Biologist 2

Promoted to Computational Biologist 3, January 2025

Portland, OR

Nov 2020–Dec 2024

### University of Kansas, Ray Lab

Graduate Researcher

Lawrence, KS

2015–2020

- Characterized overlapping transcriptomic stress responses (stimulons) in *E. coli* using bulk RNA-seq, identifying shared gene programs across divergent stressors—co-first author on two resulting manuscripts
- Built stochastic and agent-based models of bacterial cell-cycle dynamics to reconstruct inheritance of stress signals across generations
- Developed and benchmarked template-based protein–protein docking approaches in collaboration with the Vakser Lab (KU), contributing to structural modeling best-practice guidelines

**University of Missouri, Zou Lab**

*Undergraduate Researcher*

Developed multi-target molecular docking methods for protein kinase inhibitor selectivity studies; presented at the University of Missouri Summer Undergraduate Research Symposium

**Columbia, MO**

*Summer 2014*

**Drury University, Deligkaris Lab**

*Undergraduate Researcher*

Derived and implemented a vibrational entropy correction for DNA–small molecule docking in AutoDock, improving binding free energy predictions; published as first author in *Computational Biology and Chemistry* (2018)

**Springfield, MO**

*2013–2015*

## Technical Skills

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**Transcriptomics:** Bulk RNA-seq, scRNA-seq (10X Genomics), spatial transcriptomics (NanoString GeoMx/CosMx); DESeq2, edgeR, kallisto/sleuth, Seurat, Scanpy, STAR

**Machine Learning:** PCA, UMAP, t-SNE; classification, clustering; CNNs, autoencoders, deep neural networks (TensorFlow, PyTorch); Bayesian & frequentist inference

**Mathematical Modeling:** Stochastic biochemical models (Gillespie, CME), agent-based models, dynamical systems, graph theory, network analysis

**Structural Biology:** Protein–protein docking (template-based & *ab initio*), small molecule docking (AutoDock, Vina), molecular dynamics, protein design (PyRosetta)

**Programming:** Python (expert: pandas, numpy, scipy, scikit-learn, TensorFlow, PyTorch), R (advanced: Bioconductor), MATLAB, Mathematica, C++, bash, Perl, SQL, FORTRAN

**Infrastructure:** Git/GitHub/BitBucket, Docker, Singularity/Apptainer, SLURM/PBS HPC

**Data Formats:** LaTeX, Markdown, YAML, XML, SBML, HTML/CSS, Parquet, JSON, SQL

**Lab Skills:** RNA-seq library preparation (Illumina), bacterial molecular genetics, microbiology culture & quantification, aseptic technique

## Selected Publications

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†: Co-first / first authorship

**2025:** Mahyari E, Boggy GJ, **McElfresh GW**, et al. Enhanced interpretation of immune cell phenotype and function through a rhesus macaque single-cell atlas. *Cell Genomics*, 5(5).

**2025:** Bimber BN, Sunshine J, **McElfresh GW**, et al. Viral escape mutations do not account for non-protection from SIVmac239 challenge in RhCMV/SIV vaccinated rhesus macaques. *Frontiers in Immunology*, 15: 1444621.

**2023:** Wang H, **McElfresh GW**†, et al. Signatures of antibiotic tolerance and persistence in response to divergent stresses. *bioRxiv* 2023.02.05.527212.

**2022:** Boggy GJ, **McElfresh GW**, et al. BFF and cellhashR: analysis tools for accurate demultiplexing of cell hashing data. *Bioinformatics*, 38(10), 2791–2801. [doi:10.1093/bioinformatics/btac213](https://doi.org/10.1093/bioinformatics/btac213)

**2020:** Chakravarty D, **McElfresh GW**, et al. How to choose templates for modeling of protein complexes. *Proteins*, 88(9), 1070–1081. [doi:10.1002/prot.25875](https://doi.org/10.1002/prot.25875)

**2018:** **McElfresh GW**†, Deligkaris C. A vibrational entropy term for DNA docking with AutoDock. *Computational Biology and Chemistry*, 73, 9–14. [doi:10.1016/j.compbiolchem.2018.03.027](https://doi.org/10.1016/j.compbiolchem.2018.03.027)

**2018:** **McElfresh GW**†, Ray JCJ. Intergenerational Cellular Signal Transfer and Erasure. In: *The Interplay of Thermodynamics and Computation in Natural and Artificial Systems*.

Full list: [Google Scholar](https://scholar.google.com/citations?user=UWUWUWUWUW) | [ORCID 0000-0002-1948-7571](https://orcid.org/0000-0002-1948-7571)

## Selected Presentations

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**2022:** **McElfresh GW** et al. Integration of Spatial and Single Cell Transcriptomics Identifies Novel Pathologically Relevant Markers in SIV- and *M. tuberculosis*-infected Rhesus Macaques. *Nonhuman Primate Models for AIDS*.

**2021:** **McElfresh GW** et al. Single Cell Transcriptomic Profiling of Early Tuberculosis Infection and Granuloma Formation in Rhesus Macaque. *Nonhuman Primate Models for AIDS*.

**2019: McElfresh GW**, Drawert B, Ray JCJ. Discrete timescales of effects that stress signals have on the cell cycle. *q-bio Conference*.

**2018: McElfresh GW**, Drawert B, Ray JCJ. Reconstructing the Role of Inheritance in Stress Signaling. *Modeling of Protein Interactions*.

**2014: McElfresh GW**, Deligkaris C. Inclusion of Empirical Entropic Contributions to Binding Free Energy of Ligand-DNA Systems During Docking. *ACS Midwest Regional Meeting*.

## Teaching Experience

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### University of Kansas

*Lab Teaching Assistant — Bioinformatics*

Led hands-on computational labs covering sequence alignment, phylogenetics, and transcriptomic analysis pipelines

**Lawrence, KS**

*F2018, F2019, S2020*

### University of Kansas

*Discussion Leader & Primary Grader — Genetics*

**Lawrence, KS**

*Summer 2017*

### University of Kansas

*Lab Teaching Assistant — Intro Cellular & Molecular Biology*

**Lawrence, KS**

*F2016, F2017*

### University of Kansas

*Lab Teaching Assistant — Intro Organismal Biology*

**Lawrence, KS**

*S2016*

### University of Kansas

*Lab Teaching Assistant — Intro Principles of Biology*

**Lawrence, KS**

*F2015*

## Awards & Honors

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**2019:** Graduate Research Award, University of Kansas

**2015:** Outstanding Physics Student Researcher, Drury University

## Service

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**Reviewing:** Peer reviewer, *Nature Communications*

**Open Source:** Contributor and maintainer, cellhashR, RIRA, CellMembrane, and other open-source tools