

Justice (Hsiu-Yi) Lu

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Summary

Computational biologist with a strong foundation in microbiology, applying large-scale multi-omics analysis, protein structural modeling, and machine learning to tackle fundamental questions in cell biology and disease. Experienced in single-cell and bulk transcriptomics, proteomics, protein structure–function studies, and scalable ML workflows.

Work Experience

Graduate Student Researcher, Duke University, Hiroaki Matsunami Lab

2020 - Present

- Designed and implemented scalable single-cell, bulk RNA-seq, and proteomics pipelines to identify genetic regulators of protein expression, accelerating in vitro screening and target discovery.
- Built deep learning models (CNNs) in PyTorch, integrating AlphaFold-predicted protein structures, ESM features and transcriptomic data to predict receptor–ligand interactions, uncovering structural features driving ligand selectivity.
- Developed and deployed geLine, an interactive web application for large-scale gene co-expression and maturation trajectory analysis, empowering researchers to explore developmental programs across cell types.
- Mentored trainees in both computational and experimental projects, fostering independent design and test skills.

ML Data Science Intern, Kriya Therapeutics

2023

- Engineered scalable ML pipelines for high-throughput drug target prediction, increasing 10× data throughput.
- Optimized data preprocessing and model training workflows using Python, scikit-learn, and cloud computing resources.
- Partnered with biology teams to incorporate omics-derived features into predictive models, improving biological relevance.

Research Technician II, Duke University, John Rawls Lab

2017 - 2019

- Conducted studies on host–microbe interactions in zebrafish, uncovering protective gut responses to pathogenic bacteria.
- Performed a genetic screen identifying novel regulators of lipid metabolism and adipose tissue morphogenesis, with implications for metabolic disease biology.

Education

Duke University (Expected graduation, Fall 2025)

2019 - Present

Ph.D. in Molecular Genetics and Microbiology (Advisor: Hiroaki Matsunami)

- IBIEM Computational Biology Fellow | Taiwan-Duke Fellowship Recipient

Purdue University, B.S in Biological Science

2013 - 2016

Selected Publications (* First author)

- Identifying Key Regulators in Odorant Receptor Trafficking.
Lu, HY*, & Matsunami, H. **Journal of Neuroscience** (in revision)
- Physiology of olfactory sense.
Lu, HY*, Meesa, P. & Matsunami, H., **Digital Technologies in Olfaction**, 7-14 (2025)
- Role of iRhom2 in Olfactory Sensory Neurons: Implications for Odorant Receptor Regulation.
Azzopardi, S*, **Lu, HY***, Monette, S., Rabinowitsch, A., Salmon, J., Matsunami, H., & Blobel, C. **IJMS** (2024)
- Sex steroid hormones synthesis, metabolism and the effects on the mammalian olfactory system.
Abaffy, T., **Lu, HY.**, & Matsunami, H. **Cell and tissue research** (2023).
- An odorant receptor that senses four classes of musk compounds
Yoshikawa, K., Deguchi, J., Jieying, H., **Lu, HY.**, & Matsunami, H. **Current Biology** (2022).
- Enteroendocrine cells sense bacterial tryptophan catabolites to activate enteric and vagal neuronal pathways.
Ye L, Bae M, Cassilly CD, Jabba SV, Thorpe DW, Martin AM, **Lu HY.**, ... & Rawls JF. **Cell Host Microbe** (2021).

Skills

Computer Programming Language: Python, R, Bash, Git

Bioinformatics: omics analysis (single-cell/bulk RNA-seq, proteomics), protein modeling, AlphaFold, ESM, Boltz, Dash

ML & Data Science: PyTorch, CNNs, regression/classification, scikit-learn, Pandas, NumPy, Scikit-learn, SciPy

Collaboration: Bench-to-computation project design, cross-disciplinary communication

Interest: Building pipelines and tools for optimization. Using data driven approach to solve complex biological questions