

# 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

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**Graduate Student Researcher**, Duke University, Hiroaki Matsunami Lab 2020 - Present

- Applied single-cell, bulk RNAseq and proteomic analysis pipeline and identified gene candidates to enhance olfactory receptor cell surface expression for *in vitro* genetic screen.
- Developed convolutional neural network (CNN) models to predict receptor–ligand binding from protein structures, integrating structural biology with machine learning.
- Created geLine, a web tool for gene co-expression analysis and maturation trajectory tracing, enabling researchers to interrogate maturation trajectories across cell type.
- 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

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**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)

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- 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

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**Computer Programming Language:** Python, R, Bash, Git

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

**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