James Lee

New York, NY | (858) 210-1206 | james.hyojae.lee@gmail.com

 jameshyojaelee.github.io | linkedin.com/in/jameshyojaelee/

EDUCATION

New York University   New York, NY

Master of Science in Bioinformatics and Systems Biology   Sept 2024-May 2025

- Cumulative GPA: 3.82/4.0

University of California San Diego   La Jolla, CA

Bachelor of Science in General Biology   Aug 2015-Jul 2021

Bachelor of Science in Political Science – Data Analytics   Aug 2015-Jul 2021

- Leave of absence (Jan 2017-Jan 2019) for mandatory military service in South Korea

RESEARCH EXPERIENCE

New York Genome Center - Sanjana Lab   New York, NY

Research Assistant   Jun 2025-Present

Graduate Research Assistant   Aug 2024-May 2025

- Lead in vivo Cas13 CRISPR screen to investigate novel genetic regulators in MASLD/MASH

- Design and optimize genome-wide screens in primary immune cells to identify novel genetic regulators

- Establish reproducible analysis pipelines for large-scale bulk and single-cell RNA-seq analysis for iterative screen library design

Scale Biosciences   San Diego, CA

Research Associate   Jan 2023-Jul 2024

- Co-developed and optimized single-cell RNA assay using combinatorial indexing, capable of sequencing up to 4 million cells with high sensitivity in one experiment, enabling the detection of rare sub-populations that are typically lost in standard-throughput assays

- Co-developed single-cell protein assay in collaboration with Biolegend, allowing phenotyping of 1.2 million cells in one experiment

- Designed and implemented Nextflow pipelines for internal single-cell data analysis, enabling faster assay development and optimization

UC San Diego, Moores Cancer Center   La Jolla, CA

Staff Research Associate (Part-time) - Stupack Lab   Jan 2023-Oct 2023

- Leveraged single-cell omics to demonstrate that liposomal doxorubicin, unlike platinum-taxane, uniquely reprograms ovarian cancers via MHC-II upregulation, providing a rationale for improved chemo-immunotherapy strategies

Research Assistant/Staff Research Associate - Chen Lab   Feb 2020-Nov 2022

- Investigated tumor microenvironment changes in pancreatic ductal adenocarcinoma, uncovering significant changes in tumor-infiltrating lymphocytes and macrophage polarization upon SUMOylation inhibition

PUBLICATIONS

*Co-first authorship

Peer-Reviewed Publications

- Chen, X., …, **Lee, H. J.**, et al. (2026) Ovarian Tumor FAK Inhibition Releases Omega-3 Fatty Acids Stimulating GATA6 Peritoneal Macrophage CXCL13 Production Enhancing Immunotherapy. *Accepted in Cell Reports*.

- **Lee, H. J.***, Chen, X.*, Ozmadenci, D.* et al. (2025). Liposomal doxorubicin, but not platinum-taxane, supports MHC-II expression and immune maturation in the ovarian cancer tumor microenvironment. *Cancers.*

- Erdem, S.*, **Lee, H. J.***, Suryanarayanan, J.*, et al. (2024). Inhibition of SUMOylation Induces Adaptive Anti-Tumor Immunity Against Pancreatic Cancer through Multiple Effects on the Tumor Microenvironment. *Molecular Cancer Therapeutics*.

- Weitz, J.*, Hurtado de Mendoza, T.*, …, **Lee, H. J.**, et al. (2022). An Ex Vivo Organotypic Culture Platform for Functional Interrogation of Human Appendiceal Cancer Reveals a Prominent and Heterogenous Immunological Landscape. *Clinical Cancer Research*.

Preprints

- Li, K.*, Courelli, A.*, **Lee, H. J.,** et al. (2024) SUMO Inhibition Plus CD40 Agonism Increases Anti-Tumor Immunogenicity Through Interferon Mediated Macrophage Activation. *bioRxiv*.

PRESENTATIONS

- Croteau, J., Zhang, F., Zorzetto-Fernandes, A. L., Gong, H., **Lee, H. J.**, et al. (2024). *Ultra-high parameter, instrument-free, protein profiling by sequencing using TotalSeq™ -A antibodies at scale*. Poster at the AGBT General Meeting, Orlando, FL 2024. [Poster]

- **Lee, H. J.** (2022) *Orthotopic mouse PDAC model and scRNA-seq to strategize potential combination therapies*. UC San Diego Department of Surgery Symposium, San Diego, CA. [Talk]

COMPUTATIONAL PROJECTS

- scPerturb-CMap: integrates Broad Connectivity Map data to rank existing compounds that are most likely to reverse pathological cell states within single-cell RNA-seq datasets, enabling rapid, data-driven **drug repurposing prediction** for bench validation

SKILLS

- **Computational Biology**: Python, R, Bash, AWS, HPC, Git, Nextflow, Snakemake, SQL, scikit-learn, PyTorch, scRNA-seq analysis (Scanpy/Seurat), CRISPR screen analysis (MAGeCK/SCEPTRE/PertPy)

- **Wet lab:** Flow Cytometry, Fluorescence Microscopy, Mammalian Cell Culture, Viral Transduction

- **In vivo**: Xenograft model, retro-orbital/tail-vein/intraperitoneal/subcutaneous injection