

# James Lee

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## EDUCATION

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### New York University

New York, NY

Master of Science in Bioinformatics and Systems Biology

Sept 2024-May 2025

### University of California San Diego

La Jolla, CA

Bachelor of Science in General Biology

Jan 2019-Jul 2021

Bachelor of Science in Political Science – Data Analytics

Jan 2015-Jul 2021

## RESEARCH

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\*Co-first authorship

### Peer-Reviewed Publications

- **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

- Chen, X.\*, ..., **Lee, H. J.**, et al. (2025) [Ovarian Tumor FAK Inhibition Releases Omega-3 Fatty Acids Stimulating GATA6 Peritoneal Macrophage CXCL13 Production Enhancing Immunotherapy.](#) *bioRxiv*.
- 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*.

### Published Conference Abstracts

- Courelli, A., Li, K., **Lee, H. J.**, et al. (2024) [Abstract B043: Synergy of Subsumstat and anti-CD40 improves survival by augmenting tumor macrophage infiltration.](#) *Cancer Research*.

## RESEARCH EXPERIENCE

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### New York Genome Center

New York, NY

Research Assistant - Sanjana Lab

June 2025 – Present

Graduate Research Assistant - Sanjana Lab

Aug 2024 – June 2025

- Design and execute genome-wide screens in human primary NK cells to identify novel genetic regulators
- Co-lead in vivo Cas13 CRISPR screens in mouse models to investigate various diseases
- Established single-cell CRISPR analysis pipeline to identify genetic regulators in autism spectrum disorder

## Scale Biosciences (Now part of 10x Genomics)

San Diego, CA

Research Associate

Jan 2023 – Jul 2024

- Co-developed [single-cell RNA assay](#) using combinatorial indexing, capable of sequencing up to 4 million cells without losing sensitivity
- Co-developed [TotalSeq PhenoCyte](#) single-cell protein assay in collaboration with Biolegend
- Independently designed and implemented bioinformatics pipelines for internal scRNA-seq data analysis, enabling assay optimization

## UC San Diego, Moores Cancer Center

La Jolla, CA

Staff Research Associate II- Stupack Lab

Jan 2023 – Oct 2023

- Conducted scRNA-seq analysis to show liposomal doxorubicin uniquely reprograms ovarian tumors via MHC-II upregulation, providing a rationale for improved chemo-immunotherapy sequencing

Staff Research Associate I - Chen Lab

Aug 2021 – Nov 2022

- Investigated tumor microenvironment changes in pancreatic ductal adenocarcinoma, uncovering significant changes in tumor-infiltrating lymphocytes and macrophage polarization upon SUMOylation inhibition
- Evaluated the immunomodulatory effects of SUMOylation inhibition in CAR-T

Research Assistant - Chen Lab

Feb 2020 – Jul 2021

## PRESENTATIONS

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- 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]

## SKILLS

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- **Computational Biology:** Python, R, Bash, scRNA-seq analysis (Scanpy/Seurat), CRISPR screen analysis (SCEPTRE/PertPy), SQL, BioConductor, Machine Learning (scikit-learn, PyTorch, TensorFlow), AWS, HPC, Git, BLAST
- **Molecular Biology:** Single-cell RNA-seq, Bulk RNA-seq, NGS Library Preparation, CRISPR Screens
- **Cell Biology:** Flow Cytometry, Fluorescence Microscopy, Mammalian Cell Culture, Viral Transduction
- **In vivo:** Xenograft model, retro-orbital/tail-vein/intraperitoneal/subcutaneous injection, colony management