JIATAO LIANG

Postdoctoral Researcher

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EDUCATION

PhD Harvard University: Chemistry and Chemical Biology — Feb 2025

BS University of California, Berkeley: Chemical Biology — May 2019
Highest Honors

BA University of California, Berkeley: Statistics — May 2019
Highest Honors

HONORS AND AWARDS

UC Berkeley Chemistry Department Citation — 2019
Awarded in highest recognition of distinguished undergraduate work to a single graduating senior

RESEARCH EXPERIENCE

University of Pennsylvania, Philadelphia, PA — 2025-current
Postdoctoral Researcher, Advisor: Yoseph Barash

- Implementation of generative machine learning models for the acceleration of directed evolution of non-canonical nucleic acid ribozymes
- Application of computational bioinformatics on long non-coding RNAs to explore biological mechanism towards therapeutic applications
- Consultation for a large language model using contrastive learning to extract key chemical features of small molecules and probes from scientific literature

Harvard University, Cambridge, MA — 2019-2025
Doctoral Candidate, Advisor: Matthew Shair
Supported by Blavatnik Biomedical Accelerator and Deerfield Lab1636

- Independently designed and synthesized small molecule inhibitors of ADAR1, an RNA-editing enzyme implicated in cancer pathogenesis
- Conceived and developed novel assays to quantify inhibition profiles of synthesized compounds
- Interpreted assay results in context of *in silico* docking simulations to establish structure-activity relationships and inform future work
- Collaborated with virtual biotech 3DC in directing contract research organizations in design, synthesis, and assay of key molecules to interrogate inhibition of ADAR1
- Dissertation: Development of Inhibitors of ADAR1

Lawrence Berkeley National Laboratory, Berkeley, CA — 2017-2019
Undergraduate Research Assistant, Advisor: Yi Liu

- Explored the stability and reactivity of *para*-azaquinodimethane moiety in extended conjugated systems for use in organic electronic applications

Plexxikon, Inc., Berkeley, CA 2018
Medicinal Chemistry Summer Intern

- Synthesized over forty compounds for the inhibition of kinases implicated in oncology
- Interpreted structural biology data and assay results to inform future work

TEACHING EXPERIENCE

Harvard University, Cambridge, MA Spring 2021
Head Teaching Fellow

- Courses taught: Organic Chemistry of Life (CHEM27) with Prof. Emily Balskus
- Responsibilities include setting and implementing course policy, managing fifteen junior teaching fellows, interfacing with other course staff, giving review lectures, and holding office hours.

Harvard University, Cambridge, MA 2020
Teaching Fellow

- Courses taught: Organic Chemistry of Life (CHEM 27) with Prof. Emily Balskus and Principles of Organic Chemistry (CHEM17) with Prof. Christina Woo
- Responsibilities include holding office hours, leading discussion sections, and proctoring exams.

PUBLICATIONS

Anderson, C.L., … Liang, J., *et al.* **Solution-processable and functionalizable ultra-high molecular weight polymers via topochemical synthesis**. *Nat Commun* **12**, 6818 (2021).
https://doi.org/10.1038/s41467-021-27090-1

Anderson, C.L., Liang, J., *et al*. **A highly substituted pyrazinophane generated from a quinoidal system: Via a cascade reaction**. *Chemical Commun* **56**, 4472–4475 (2020).
https://doi.org/10.1039/d0cc00916d

Jones, H.T., … Liang, J., *et al.* **A Dataset for Distilling Knowledge Priors from Literature for Scientific Discovery.** *NeurIPS*. (2025).
https://doi.org/10.48550/arXiv.2508.10899

PRESENTATIONS

Harvard Chemistry ChemTalks Series

- Speaker September 2021

Harvard Chemistry and Chemical Biology Symposium

- Poster presentation March 2022, 2023

SKILLS AND EXPERIENCE

- Planning and executing multi-step chemical syntheses, with focus in heterocyclic systems
- Analysis of structural biology data on platforms such as Molecular Operating Environment (MOE) and Pymol, including generation of homology models based on both published structures and computationally generated AlphaFold models
- Coding in Python, Java, and R, including scripting workflows for processing, analyzing, and visualizing biological data from RNASeq