

Haikuo Li

Postdoctoral Research Associate @ Yale University

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EDUCATION

PhD Student, Program in Molecular Genetics and Genomics

8/2019 – 12/2023

Washington University in St. Louis, MO, United States

- Thesis mentor: Benjamin D. Humphreys, M.D., Ph.D.
- Thesis committee: Ting Wang, Samantha Morris, Jeffrey Millman, Allegra Petti, Michael Meers

Bachelor of Science, Bioscience (Zhiyuan Honors Program)

9/2015 – 6/2019

Shanghai Jiao Tong University, Shanghai, China

- 2019 Top 0.2% Bachelor Thesis: Rank #1 in Bioscience
- 2019 Outstanding Graduate in Bachelor Degree, Shanghai

Visiting Student, Immunobiology

6/2018 – 4/2019

Yale University, New Haven, CT, United States

- Research supervisor: Aaron M. Ring, M.D., Ph.D.

PUBLICATIONS

First-author research articles

1. **Li, H.**, Li, D., Ledru, N., Xuanyuan, Q., Wu, H., Asthana, A., Byers, L.N., Tullius, S.G., Orlando, G., Waikar, S.S. & Humphreys, B.D. (2024). Transcriptomic, epigenomic, and spatial metabolomic cell profiling redefines regional human kidney anatomy. *Cell Metabolism*, 36(5), 1105-1125. (URL)
 - Featured Content of the *Cell Metabolism* journal website
2. **Li, H.**, Dixon, E. E., Wu, H., & Humphreys, B. D. (2022). Comprehensive single-cell transcriptional profiling defines shared and unique epithelial injury responses during kidney fibrosis. *Cell Metabolism*, 34(12), 1977–1998. (PDF)
 - Research featured by NIH NIDDK annual report (PDF)
 - Research Highlights by *Nature Review Nephrology* (URL)
 - Research Highlights by *Kidney International* (URL)
3. **Li, H.**, & Humphreys, B. D. (2024). Spatially resolved metabolomic dataset of distinct human kidney anatomic regions. *Data in Brief*, 54, 110431. (URL)
4. **Li, H.**, & Humphreys, B. D. (2024). Protocol for multimodal profiling of human kidneys with simultaneous high-throughput ATAC and RNA expression with sequencing. *STAR Protocols*, 5(3), 103049. (URL)
5. **Li, H.**, & Humphreys, B. D. (2022). Mouse kidney nuclear isolation and library preparation for single-cell combinatorial indexing RNA sequencing. *STAR Protocols*, 3(4), 101904. (PDF)
6. Ku, X.*, Wang, J.*, **Li, H.*** (co-first author), Meng, C., Yu, F., Yu, W., Li, Z., Zhou, Z., Zhang, C., Hua, Y., Yan, W., Jin, J. (2022). Proteomic Portrait of Human Lymphoma Reveals Protein Molecular Fingerprint of Disease Specific Subtypes and Progression. *Phenomics*, 3(2), 148-166. (PDF)

7. Wang, J.*, Ku, X.*, Ma, Q.*, **Li, H.*** (co-first author), Huang, S., Mao, L., Yu, F., Jin, J. & Yan, W. (2023). Hsa_circ_0007099 and PIP4K2A coexpressed in diffuse large B-cell lymphoma with clinical significance. *Genes & Diseases*, 11(4), 101056. (PDF)

First-author review/commentary articles

8. Li, H., & Humphreys, B. D. (2024). Multimodal characterization of sexual dimorphism in the mammalian kidney. *Kidney International*, 105(4), 653-655. (URL)
9. Li, H., & Humphreys, B. D. (2024). Targeting de novo lipogenesis to mitigate kidney disease. *The Journal of Clinical Investigation*, 134(4). (PDF)
10. **Li, H.**, & Humphreys, B. D. (2022). New functions for basophils identified in kidney fibrosis. *Nature Immunology*, 23(6), 824-825. (PDF)
11. **Li, H.**, & Humphreys, B. D. (2021). Single cell technologies: Beyond microfluidics. *Kidney360*, 2(7), 1196-1204. (PDF)
12. **Li, H.**, & Humphreys, B. D. (2020). Surveying the human single-cell landscape. *Kidney International*, 98(6), 1385-1387. (PDF)

First-author book chapter

13. Muto, Y*., **Li, H.*** (co-first author), & Humphreys, B. D. (2022). Single Cell Transcriptomics. In *Innovations in Nephrology: Breakthrough Technologies in Kidney Disease Care* (pp. 87-102). Cham: Springer International Publishing. (PDF)

Other publications

14. Wilson, P. C., Verma, A., Yoshimura, Y., Muto, Y., **Li, H.**, Malvin, N. P., ... & Humphreys, B. D. (2024). Mosaic loss of Y chromosome is associated with aging and epithelial injury in chronic kidney disease. *Genome biology*, 25(1), 36. (PDF)
15. Cheng, Z. et al. (special journal issue; [author list alphabetically ordered](#)) (2023). RNA-seq: questions and answers. *STAR Protocols*. (URL)

SOFTWARE DEVELOPMENT

MALDIpy: Single-cell analysis of MALDI-MS imaging mass spectrometry data (first contributor)

- `pip install MALDIpy` (<https://pypi.org/project/MALDIpy/>)

RESEARCH EXPERIENCE

Postdoctoral Research Associate, Rong Fan Lab	2/2024 – present
Biomedical Engineering, School of Engineering & Applied Science, Yale University	
Research Associate, Benjamin Humphreys Lab	12/2023 – 1/2024
Division of Nephrology, Washington University in St. Louis	
PhD Student, Benjamin Humphreys Lab	4/2020 – 12/2023

Division of Nephrology, Washington University in St. Louis

- Multiomics characterization of kidney physiology: developing an anatomically stratified human kidney atlas with single-cell combinatorial indexing multiomics sequencing
- Multiomics characterization of kidney pathology: studying mouse models of kidney fibrosis with single-cell combinatorial indexing RNA-seq and spatially resolved transcriptomics
- Studying metabolic mechanisms that drive kidney fibrosis
- Studying cell fate determination in kidney injury & regeneration and regional differentiation
- Method development: single-cell combinatorial indexing (split-pool barcoding) library generation and unique data analysis; computational pipeline of analyzing spatially resolved metabolomics data

PhD Rotation Student, Tim Peterson, Sidharth Puram, Benjamin Humphreys Labs

8/2019 – 4/2020

Washington University in St. Louis

- Peterson Lab: Understanding the intracellular effects of Cationic Amphipathic Drugs on organelles
- Puram Lab: Studying head and neck cancer by CITE-seq
- Humphreys Lab: Characterizing kidney injury and repair markers by RNAscope

Visiting Student, Aaron Ring Lab

6/2018 – 4/2019

Department of Immunobiology, Yale University

- Modulating immune cytokines by protein engineering
- Bench supervisor: Ting Zhou, Ph.D.

Undergraduate Researcher, Wei Yan Lab

9/2016 – 7/2018

Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University

- Identification of biomarkers of lymphoma with mass spectrometry; clinic proteomics
- Bench supervisor: Xin Ku, Ph.D.

Summer Intern, Manyuan Long Lab

6/2017 – 8/2017

Department of Ecology and Evolution, The University of Chicago

- Identification of mammalian positively selected genes by polygenic analysis

Science Olympiad (Mathematics), Shandong Province Team, China

7/2014 – 2/2015

- Top10 students selected to participate in the Chinese Mathematics Olympics

SKILLS

Wet lab experiment

- Extensive experience in single-cell and single-nucleus library generation from diverse technologies, including 10X Genomics, sci-RNA-seq, SHARE-seq and INTACT, as well as multimodal profiling including RNA-seq, ATAC-seq, Hi-C, CUT&RUN, CARLIN and CITE-seq
- Extensive experience in molecular biology technologies such as cloning, vector construction, qPCR, immunohistology, and in-situ hybridization
- Extensive experience in tissue culture including primary cell isolation, immunocytochemistry and Seahorse metabolic measurement
- Strong experience in animal work such as mouse kidney disease surgery (UUO/IRI) and tumor implantation
- Strong experience in clinical sample management and processing such as human kidney dissection

- Strong background in protein chemistry including mass spectrometry sample preparation & recombinant protein preparation and protein liquid chromatography

Computational workflow

- Extensive experience in using Python, R, Shell and Jupyter
- Extensive experience in single-cell sequencing data preprocessing and analysis including UMAP visualization, data integration, sample demultiplexing, cell trajectory inference, fate mapping, gene activity prediction and multimodal analysis at the million-cell level.
- Extensive experience in spatially resolved transcriptomics and metabolomics analysis
- Strong experience in analysis of bulk RNA-seq, proteomics and metabolomics data
- Extensive experience in data mining and discovering biological insights
- Strong training background in mathematics

TEACHING EXPERIENCE

1. Trainee Supervisory Experience

Rotation Project Bench Mentor, Washington University in St. Louis 9/2023-11/2023

- Rachel W. (Ph.D. student in CSB/DBBS): Functional analysis of human kidney single-cell multiomics

Peer Study Mentor, Washington University in St. Louis 3/2023-6/2023

- Jenna U. (Ph.D. student in MGG/DBBS): Genomics (Bio5488) and Python-based coding tutoring

Rotation Project Bench Mentor, Washington University in St. Louis 12/2022-1/2023

- Qiao X. (Ph.D. student in BIDS/DBBS): Spatially resolved metabolomics analysis and package development

Bench Mentor, Washington University in St. Louis 9/2022-7/2023

- Dian L. (Ph.D. student in CSB/DBBS): Single-cell multimodal integration on human kidney physiology

Peer Study Mentor, Washington University in St. Louis 1/2022 – 6/2022

- Julie C. (Ph.D. student in HSG/DBBS): Genomics (Bio5488) and Python-based coding tutoring

2. Course Instructor Assistant

Assistant Instructor, Washington University in St. Louis 8/2022 – 6/2023

- Structural bioinformatics of proteins (Bio4525)

Assistant Instructor, Washington University in St. Louis 1/2021 – 6/2021

- Genomics (Bio5488)

Undergraduate Teaching Assistant, Shanghai Jiao Tong University

- College Genetics Course (2/2019–6/2019)
- College Macrobiology Course (2/2018–6/2018)
- College Biochemistry Course (9/2017–1/2018)

PRESENTATIONS & POSTERS

Oral Talk Speaker, American Society of Nephrology Annual Meeting (ASN Kidney Week) 11/2023

Retreat Talk (MGG/CSB/HSG/IMSD programs), Washington University in St. Louis 9/2023

POSTER (PDF) | PhD program retreat, Washington University in St. Louis 9/2023

- Transcriptomic, epigenomic and spatial metabolomic cell profiling redefines regional human kidney anatomy

Project Talk, CZI Single-Cell Biology Annual Meeting	11/2022
Speaker, Nephrology Division Research Seminars, Washington University in St. Louis	9/2022
Retreat Talk (MGG/CSB/HSG/IMSD programs), Washington University in St. Louis	9/2022
POSTER (PDF) PhD program retreat, Washington University in St. Louis	9/2022
• Cell profiling defines metabolic dysregulation in kidney fibrosis	
DBBS Friday Talks (MGG/CSB/HSG/IMSD programs), Washington University in St. Louis	5/2022
REBUILDING A KIDNEY Spring Meeting lighting talk	4/2022
PhD Program Thesis Committee Meeting, Washington University in St. Louis	8/2021, 4/2022, 4/2023, 12/2023
REBUILDING A KIDNEY Work in Progress small group meeting	12/2021
PhD Program Qualifying Examination Committee Meeting	9/2020
POSTER (PDF) SJTU Academic Festival (Best Poster Award)	2/2019
• Modulating the Tumor-Targeting Specificity of “Decoy-Resistant” Interleukin-18 by Protein Engineering	
POSTER (PDF) Human Proteome Organization World Congress	10/2018
• Clinical Proteomics Analysis using Data Independent Acquisition-Mass Spectrometry (DIA-MS) Identified Classifiers for Molecular Characterization of Lymphoma	
POSTER (PDF) SJTU Academic Festival (Best Poster Award)	12/2017
• Detecting Positively Selected Genes among Mammalian Species Using Phylogenetic Analysis of Maximum Likelihood	

HONORS & ACTIVITIES

Award for Outstanding Students Abroad [highest award granted by the Chinese government to students overseas (LINK)]	2023
Member, NCFDD (National Center for Faculty Development & Diversity)	2023 - present
Member, ASN (American Society of Nephrology)	2020 - present
Top 0.2% Bachelor Thesis of Shanghai Jiao Tong University (URL) (Thesis PDF)	2019
Outstanding Graduate in Bachelor Degree, Shanghai	2019
Academic Excellence Scholarship (First-class), Shanghai Jiao Tong University	2016, 2017, 2018
Rank #1 Student Presentation, National Biology Education Conference of Chinese Ministry of Education	2018
Vice President, Students' Union of Zhiyuan Honors Program, Shanghai Jiao Tong University	2017 - 2018
Top 0.1% in Chinese University Entrance Examination (681 points)	2015
Bronze medal, Chinese Mathematical Olympiad (CMO)	2014