

HAIKUO LI



CONTACTS

haikuo.li@wustl.edu



Washington University in St. Louis



LINKS

Web Page:

<https://haikuoli.github.io/>

Twitter:

<https://twitter.com/HaikuoLi>

EDUCATION

Ph.D., Washington University in St. Louis

2023

Program in Molecular Genetics and Genomics, Division of Biology and Biomedical Sciences

- Thesis Mentor: Benjamin D. Humphreys, M.D., Ph.D.

Bachelor of Science, Shanghai Jiao Tong University

2019

Bachelor of Science, Bioscience (Zhiyuan Honors Program)

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

PUBLICATIONS

Comprehensive single-cell transcriptional profiling defines shared and unique epithelial injury responses during kidney fibrosis, Cell Metabolism (accepted)

Haikuo Li, Eryn E. Dixon, Haojia Wu, Benjamin D. Humphreys

New functions for basophils identified in kidney fibrosis, Nature Immunology

May 2022

Haikuo Li, Benjamin D. Humphreys ([PDF](#))

[book chapter] Single-cell transcriptomics, Innovations in Nephrology: Breakthrough Technologies in Kidney Disease Care (in press)

Yoshiharu Muto*, **Haikuo Li*** (equal contribution), Benjamin D. Humphreys

Single Cell Technologies: Beyond Microfluidics, Kidney360

Jul 2021

Haikuo Li, Benjamin D. Humphreys ([PDF](#))

Surveying the Human Single Cell Landscape, Kidney International

Dec 2020

Haikuo Li, Benjamin D. Humphreys ([PDF](#))

Proteomic portrait of human lymphoma revealed protein molecular fingerprint for disease specific subtypes and progression, Phenomics (under review)

Xin Ku*, **Haikuo Li*** (equal contribution), et al., Jie Jin#, Wei Yan#

WORK EXPERIENCE

Graduate Research Assistant, Dr. Benjamin Humphreys, Washington University in St. Louis

Apr 2020 - Present

- Developing a single-cell atlas of kidney fibrosis with single-cell multimodal profiling
- Studying metabolic mechanisms that drive kidney fibrogenesis
- Developing single-cell combinatorial indexing (split-pool barcoding) platforms

PhD Rotation Experience, Tim Peterson, Sid Puram, Benjamin Humphreys, Washington University in St. Louis

Aug 2019 - Apr 2020

- 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 Undergraduate Researcher, Dr. Aaron Ring, Yale University

Jul 2018 - Apr 2019

- Modulating immune cytokines by protein engineering

Undergraduate Researcher, Dr. Wei Yan, Shanghai Jiao Tong University

Sep 2016 - Jul 2018

- Identification of biomarkers of lymphoma with mass spectrometry; clinic proteomics

Summer Intern, Dr. Manyuan Long, The University of Chicago

Jun 2017 - Aug 2017

- Identification of mammalian positively selected genes by polygenetic analysis

Science Olympiad (Mathematics), Shandong Province Team

Jul 2014 - Feb 2015

- Top10 students selected to participate in the Chinese Mathematics Olympics
-

TEACHING EXPERIENCE

Assistant Instructor, Washington University in St. Louis

Aug 2022 - Present

Structural bioinformatics of proteins (Bio4525)

Peer study mentor, Washington University in St. Louis

Jan 2022 - Jun 2022

Genomics (Bio5488) and Python-based coding tutoring

Assistant Instructor, Washington University in St. Louis

Jan 2021 - Jun 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

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

Sep 2022

POSTER, PhD Program Retreat

Sep 2022

Cell profiling defines metabolic dysregulation in kidney fibrosis ([PDF](#))

DBBS Friday Talks (MGG/CSB/HSG/IMSD programs), Washington University in St. Louis

May 2022

Lighting talk, REBUILDING A KIDNEY Spring Meeting

Apr 2022

PhD Program Thesis Committee Meetings, Washington University in St. Louis

Aug 2021 - Present

small group meeting, REBUILDING A KIDNEY Work in Progress

Dec 2021

PhD Program Qualifying Examination Committee Meeting, Washington University in St. Louis

Sep 2020

POSTER, SJTU Academic Festival

Feb 2019

Modulating the Tumor-Targeting Specificity of "Decoy-Resistant" Interleukin-18 by Protein Engineering ([PDF](#))

POSTER, Human Proteome Organization World Congress

Oct 2018

Clinical Proteomics Analysis using Data Independent Acquisition-Mass Spectrometry (DIA-MS) Identified Classifiers for Molecular Characterization of Lymphoma ([PDF](#))

POSTER, SJTU Academic Festival

Dec 2017

Detecting Positively Selected Genes among Mammalian Species Using Phylogenetic Analysis of Maximum Likelihood ([PDF](#))

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, 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, as well as language tutoring

- 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
 - 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 (Silver medal in 2014 CMO)
-

HONORS AND OTHER ACTIVITIES

Member, ASN (American Society of Nephrology) (8/2020-Present)

Top 0.2% Bachelor Thesis of Shanghai Jiao Tong University (2019)
[Thesis PDF](#)

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, Guangdong (2018)

Top 0.1% in Chinese University Entrance Examination (681 points) (2015)

Silver medal, Chinese Mathematical Olympiad (CMO), Chongqing (2014)

Vice President, Students' Union of Zhiyuan Honors Program, Shanghai Jiao Tong University (6/2017-3/2018)

ABOUT ME

- In high school, I was most interested in mathematics and won the Silver Medal in 2014 Chinese Mathematics Olympics. At that point, I learned that biology had entered a big data era and required multidisciplinary approaches such as mathematical modelling and statistics to solve cutting-edge genomic problems. Therefore, I chose bioscience as my undergraduate major at Shanghai Jiao Tong University (SJTU). At SJTU, I was mainly trained in biochemistry and systems biology and led a first-author project in which we identified biomarkers for lymphoma patients with mass spectrometry-based proteomics. I worked as an undergraduate researcher at Yale University Department of Immunobiology in my 4th year to broaden my knowledge in immunology. At WashU DBBS, I matriculated in the Program in Biochemistry, Biophysics and Structural Biology with my background in proteomics. During my first-year PhD training at WashU, I learned that advances in single-cell genomics improved our understanding of tissue heterogeneity and underlying cellular events in disease, and therefore, I transferred to the Program in Molecular Genetics and Genomics with huge passion in using single-cell technologies to better precision medicine.
- Since joining the Humphreys Lab in 2020, I have developed deep expertise in both wet-lab (single-cell library generation, technology development, mouse surgery, tissue culture, microscope imaging etc.) and dry-lab skills (single-cell data preprocessing, analysis, visualization and computational modelling), and have completed four first author review or commentary articles on single-cell technology development and applications. My thesis projects aim to decipher cellular events that drive kidney fibrosis with high-throughput single-cell multiomics approaches. We specifically selected single-cell combinatorial indexing (sci) as the platform, leveraging its unique advantage in ultra-high throughput, sample multiplexing capacity and low costs, compared to the current popular 10X Genomics solution. My first project has led to a first author research article under peer review by Cell Metabolism, in which we used sci-RNA-seq to study metabolic dysregulation in kidney fibrosis. My second ongoing project will develop a large-scale human cell atlas of kidney fibrosis with a multimodal sci-based method and seeks to provide potential therapeutic targets to ameliorate kidney fibrosis.