

Haikuo Li

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Education

Washington University in St. Louis

8/2019 – present

Ph.D. Program in *Molecular Genetics and Genomics*, Division of Biology and Biomedical Sciences

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

Shanghai Jiao Tong University

9/2015 – 6/2019

Bachelor of Science, Bioscience (Zhiyuan Honors Program)

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

Research Interests

Single-cell multiomics; Systems biology; Fibrosis and regeneration; Metabolisms; Translational medicine

Research & Training Experiences

Benjamin Humphreys Lab, Washington University in St. Louis

4/2020 – present

PhD Student, advised by *Benjamin D. Humphreys*

- 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 Rotations, Washington University in St. Louis

8/2019 – 4/2020

PhD Rotation Student, advised by *Tim R. Peterson*, *Sidharth V. Puram*, *Benjamin D. Humphreys*

- 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

Aaron Ring Lab, Department of Immunobiology, Yale University

7/2018 – 4/2019

Visiting Undergraduate Researcher, advised by *Aaron M. Ring*

- Modulating immune cytokines by protein engineering

Wei Yan Lab, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University

9/2016 – 7/2018

Undergraduate Researcher, advised by *Wei Yan*

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

Manyuan Long Lab, Department of Ecology and Evolution, The University of Chicago

6/2017 – 8/2017

Summer Intern, advised by *Manyuan Long*

- 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

Publications

Comprehensive single-cell transcriptional profiling defines shared and unique epithelial injury responses during kidney fibrogenesis

Cell Metabolism (invited for revision after peer review)

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

New functions for basophils identified in kidney fibrosis ([PDF](#))

Nature Immunology, 2022

Haikuo Li, Benjamin D. Humphreys

Single-cell transcriptomics (book chapter) *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 (PDF)

Kidney360, 2021

Haikuo Li, Benjamin D. Humphreys

([Twitter Discussion #1](#)) ([Twitter Discussion #2](#)) ([Twitter Discussion #3](#))

Surveying the Human Single Cell Landscape (PDF)

Kidney International, 2020

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([News #1](#)) ([News #2](#))

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#

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)

Presentations & Posters

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

8/2021, 4/2022

REBUILDING A KIDNEY Work in Progress | small group meeting

12/2021

PhD Program Qualifying Examination Committee Meeting

9/2020

POSTER (PDF) | Modulating the Tumor-Targeting Specificity of “Decoy-Resistant” Interleukin-18 by Protein Engineering
SJTU Academic Festival 2019

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

Human Proteome Organization World Congress 2018

POSTER (PDF) | Detecting Positively Selected Genes among Mammalian Species Using Phylogenetic Analysis of Maximum Likelihood
SJTU Academic Festival 2017

Academic Honors

Top 0.2% Bachelor Thesis of Shanghai Jiao Tong University (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, Guangdong

2018

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

2015

Silver medal, Chinese Mathematical Olympiad (CMO), Chongqing

2014

Other Activities

Member, ASN (American Society of Nephrology)	8/2020 – Present
Peer Study Mentor, Genomics (Bio5488), Washington University in St. Louis School of Medicine	1/2022 – 4/2022
Teaching Assistant, Genomics (Bio5488), Washington University in St. Louis School of Medicine	1/2021 – 5/2021
Teaching Assistant, College Genetics Course, Shanghai Jiao Tong University	2/2019 – 6/2019
Teaching Assistant, College Macrobiology Course, Shanghai Jiao Tong University	2/2018 – 6/2018
Vice President, Students' Union of Zhiyuan Honors Program, Shanghai Jiao Tong University	6/2017 – 3/2018
Teaching Assistant, College Biochemistry Course, Shanghai Jiao Tong University	9/2017 – 1/2018

Personal Statement

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.