



+ EDUCATION

- Washington University in St. Louis
2023
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
2019
BACHELOR OF SCIENCE
Bachelor of Science, Bioscience (Zhiyuan Honors Program)
 - 2019 Top 0.2% Bachelor Thesis: Rank #1 in Bioscience
 - 2019 Outstanding Graduate in Bachelor Degree

+ LINKS

Web Page

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

Twitter

<https://twitter.com/HaikuoLi>

+ PUBLICATIONS

- Cell Metabolism (accepted)
COMPREHENSIVE SINGLE-CELL TRANSCRIPTIONAL PROFILING DEFINES SHARED AND UNIQUE EPITHELIAL INJURY RESPONSES DURING KIDNEY FIBROSIS
Haikuo Li, Eryn E. Dixon, Haojia Wu, Benjamin D. Humphreys
- Nature Immunology
MAY 2022
NEW FUNCTIONS FOR BASOPHILS IDENTIFIED IN KIDNEY FIBROSIS
Haikuo Li, Benjamin D. Humphreys ([PDF](#))
- Innovations in Nephrology: Breakthrough Technologies in Kidney Disease Care (in press)
[BOOK CHAPTER] SINGLE-CELL TRANSCRIPTOMICS
Yoshiharu Muto*, **Haikuo Li***(equal contribution), Benjamin D. Humphreys
- Kidney360
JUL 2021
SINGLE CELL TECHNOLOGIES: BEYOND MICROFLUIDICS
Haikuo Li, Benjamin D. Humphreys ([PDF](#))
- Kidney International
DEC 2020
SURVEYING THE HUMAN SINGLE CELL LANDSCAPE
Haikuo Li, Benjamin D. Humphreys ([PDF](#))
- Phenomics (under review)
PROTEOMIC PORTRAIT OF HUMAN LYMPHOMA REVEALED PROTEIN MOLECULAR FINGERPRINT FOR DISEASE SPECIFIC SUBTYPES AND PROGRESSION
Xin Ku*, **Haikuo Li***(equal contribution), et al., Jie Jin#, Wei Yan#

+ WORK EXPERIENCE

- Dr. Benjamin Humphreys
Washington University in St. Louis
APR 2020 - PRESENT
GRADUATE RESEARCH ASSISTANT
 - 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

- Tim Peterson, Sid Puram, Benjamin Humphreys AUG 2019 - APR 2020
Washington University in St. Louis

PHD ROTATION EXPERIENCE

- 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

- Dr. Aaron Ring JUL 2018 - APR 2019
Yale University

VISITING UNDERGRADUATE RESEARCHER

- Modulating immune cytokines by protein engineering

- Dr. Wei Yan SEP 2016 - JUL 2018
Shanghai Jiao Tong University

UNDERGRADUATE RESEARCHER

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

- Dr. Manyuan Long JUN 2017 - AUG 2017
The University of Chicago

SUMMER INTERN

- Identification of mammalian positively selected genes by polygenic analysis

- Shandong Province Team JUL 2014 - FEB 2015

SCIENCE OLYMPIAD (MATHEMATICS)

- Top10 students selected to participate in the Chinese Mathematics Olympics

+ TEACHING EXPERIENCE

- Washington University in St. Louis AUG 2022 - PRESENT
ASSISTANT INSTRUCTOR

Structural bioinformatics of proteins (Bio4525)

- Washington University in St. Louis JAN 2022 - JUN 2022
PEER STUDY MENTOR

Genomics (Bio5488) and Python-based coding tutoring

- Washington University in St. Louis JAN 2021 - JUN 2021
ASSISTANT INSTRUCTOR

Genomics (Bio5488)

- Shanghai Jiao Tong University
UNDERGRADUATE TEACHING ASSISTANT

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

+ PRESENTATIONS

- Washington University in St. Louis MAY 2022
DBBS FRIDAY TALKS (MGG/CSB/HSG/IMSD PROGRAMS)
- REBUILDING A KIDNEY Spring Meeting APR 2022
LIGHTING TALK
- Washington University in St. Louis AUG 2021 - PRESENT
PHD PROGRAM THESIS COMMITTEE MEETINGS
- REBUILDING A KIDNEY Work in Progress DEC 2021
SMALL GROUP MEETING
- Washington University in St. Louis SEP 2020
PHD PROGRAM QUALIFYING EXAMINATION COMMITTEE MEETING
- SJTU Academic Festival FEB 2019
POSTER

Modulating the Tumor-Targeting Specificity of “Decoy-Resistant” Interleukin-18 by Protein Engineering ([PDF](#))
- Human Proteome Organization World Congress OCT 2018
POSTER

Clinical Proteomics Analysis using Data Independent Acquisition-Mass Spectrometry (DIA-MS) Identified Classifiers for Molecular Characterization of Lymphoma ([PDF](#))
- SJTU Academic Festival DEC 2017
POSTER

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.