

Haikuo Li

✉ haikuo.li@wustl.edu | 🏠 <https://haikuoli.github.io> | 🐦 Twitter

Education

Washington University in St. Louis

8/2019 – 2024 (expected)

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 technologies; Proteomics; Kidney Fibrosis; Tissue regeneration; Cancer

Research Experiences

Humphreys Lab, Washington University in St. Louis

4/2020 – 2024 (expected)

Ph.D. Thesis Lab, advised by [Benjamin D. Humphreys](#)

- Characterizing models of kidney fibrosis by sci-RNA-seq3
- Establishing a single-cell atlas of tissue fibrosis

Rotation Projects, Washington University in St. Louis

8/2019 – 4/2020

First-year rotation researches, 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 markers by RNAscope

Ring Lab, Department of Immunobiology, Yale University

7/2018 – 4/2019

Visiting undergraduate intern, advised by [Aaron M. Ring](#)

- Modulating immune cytokines by protein engineering

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

9/2016 – 7/2018

Undergraduate Researcher, advised by [Wei Yan](#)

- Discovery of lymphoma classifiers via mass spectrometry; clinic proteomics

Publications

Surveying the Human Single Cell Landscape ([PDF](#))

Kidney International 2020

Haikuo Li, Benjamin D. Humphreys

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

Pending

Haikuo Li, Jinghan Wang, Wenjuan Yu, Fang Yu, Zhongqi Li, Xin Ku, Jie Jin, Wei Yan

Undergraduate Research Description

Ring Lab, Department of Immunobiology, Yale University

7/2018 – 4/2019

Zhou et al. (*Nature* 2020) showed that IL-18BP, a high-affinity IL-18 decoy receptor, is frequently upregulated in diverse human and mouse tumors and limits the anti-tumor activity of IL-18 in mice. At Ring Lab, I participated experiments involved in this study. Using directed evolution, we engineered a ‘decoy-resistant’ IL-18 (DR-18) which showed promising immunotherapeutic efficacy.

Besides, I conducted my thesis research independently (2019 Top 0.2% Bachelor Thesis ([PDF](#)) of Shanghai Jiao Tong University): we aimed to further improve the tumor-targeting specificity of DR-18, balancing its therapeutic efficacy and potential toxicity. Here, we proposed two assays, pro-peptide assay and pH-sensitive assay: the former assay leveraged the unique property of IL-18 that precursor peptide processing is required for its maturation. The latter assay harnessed the extracellular acidity of tumor and aimed to construct a low-pH favorable variant. Both assays were developed and evaluated in vitro, ex vivo, and in vivo.

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

9/2016 – 7/2018

At Yan Lab, I completed a proteomic study as the first author. Development of molecular classifiers of lymphoma for precision medicine practice, in together with the traditional lymphoma classification, has been highly demanded. In this study, we leveraged Data Independent Acquisition (DIA) mass spectrometry method on 109 lymph node samples from clinical patients, covering a comprehensive suite of lymphoma subtypes including B-NHL, T-NHL, HL, Lymphadenitis, Tumor metastatic lymph node, and Non-neoplastic lymph node. We generated a lymphoma-associated proteomic profiling data resource, quantified and validated significant classifiers of different disease subgroups, and provided classifiers correlating with the aggressive and prognostic characteristics of lymphoma.

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

6/2017 – 8/2017

My summer research at UChicago (advised by [Manyuan Long](#)) focused on evolutionary biology. Here, we used phylogenetic analysis to discover positively selected genes among mammalian species.

Posters

Clinical Proteomics Analysis using Data Independent Acquisition-Mass Spectrometry (DIA-MS)

Identified Classifiers for Molecular Characterization of Lymphoma ([PDF](#)) *Human Proteome Organization World Congress 2018*

Haikuo Li, Jinghan Wang, Wenjuan Yu, Fang Yu, Zhongqi Li, Xin Ku, Jie Jin, Wei Yan

Modulating the Tumor-Targeting Specificity of

“Decoy-Resistant” Interleukin-18 by Protein Engineering ([PDF](#))

SJTU Academic Festival 2019

Haikuo Li, Ting Zhou*, Aaron M. Ring*

Detecting Positively Selected Genes among Mammalian Species

Using Phylogenetic Analysis of Maximum Likelihood ([PDF](#))

SJTU Academic Festival 2017

Haikuo Li, Jianhai Chen*, Manyuan Long*

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 of Chinese Ministry of Education, Guangdong

2018

Top 0.1% in Chinese University Entrance Examination

2015

Bronze medal, Chinese Mathematical Olympiad (CMO), Chongqing

2014

Other Activities

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

Presidium, 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