

# Xiao LIANG 梁 潇

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## EDUCATION

Fudan University, PhD program at School of Basic Medical Sciences	09/2018 – 06/2023
Westlake University, Joint PhD program at School of Life Sciences	09/2018 – 06/2023
University of Helsinki, Exchange program at Department of Chemistry	08/2016 – 12/2016
Wuhan University, Undergraduate program at College of Chemistry and Molecular Science	09/2014 – 06/2018

## CAREER

<b>Center for Infectious Disease Research, School of Medicine, Westlake University</b>	07/2023 –
Working with Professor Dr. Ren SUN, I perform on-demand mass spectrometry analysis of proteomics and metabolomics for the Center, and collaborate to develop new technologies for immunomics profiling and medical diagnosis. Additionally, I coordinate the establishment and maintenance of a core facility housing two advanced mass spectrometers at the Center.	
<b>Laboratory for Proteomic Big Data, School of Life Sciences, Westlake University</b>	09/2018 – 06/2023
At my Ph.D. stage, I was supervised by Professor Dr. Tiannan GUO to investigate the molecular mechanisms of COVID-19 and long COVID, and also to develop a list of mass spectrometry technologies for protein analytics. I also intern at Westlake Omics Co., a spin-off of my research group, to provide consulting and informatics services of proteomics.	

## SELECTED HONORS & AWARDS

Outstanding Graduate Certificate, Fudan University	03/2023
Dean's Award, Westlake University	01/2022
Best Posters From Asia, Human Proteome Organization Conference	11/2021 & 12/2022
National Scholarship for Postgraduates	10/2019
First prize at National Students Innovation and Entrepreneurship Training Competition	11/2017
Program Exchange Student Scholarship, Wuhan University	09/2016

## MEMBERSHIPS

Human Proteome Organization (HUPO) Early Career Researcher Initiative, member	12/2022 – 03/2025
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## SELECTED PUBLICATIONS

Twelve published papers with over 1,600 citations in total. Please refer [here](#) for a complete list. #, first and co-first authors; \*, correspondence.

7. **Liang, X.#**, Sun, R.; Wang, J.; Zhou, K., Li, J., *et al.*, Proteomics Investigation of Diverse Serological Patterns in COVID-19. *Molecular & Cellular Proteomics* 2023, 22(2): 100493. I led a medical project to define and analyze the diversity of serum antibody titers in COVID-19.
6. **Liang, X.#\***, Wang, Y., & Guo, T. Proteomics approaches to long COVID: current status and outlooks. *Life Medicine* 2023, Inad023. I wrote a technological review on proteomics methods for long COVID analytics.
5. Wang, J.#; **Liang, X.#**; Zheng, Y.#; Zhu, Y.#; Zhou, K.#, *et al.*, Pulmonary and Renal Long COVID at Two-year Revisit. *iScience* 2024, 110344. I led a translational medicine project to integrate high-dimensional clinical, imaging and multi-omics data of COVID-19 survivors for two years, and thereby predict the long COVID symptoms in lungs and kidneys with machine learning, achieving independently verifiable biomarker results with an accuracy of over 90%.
4. Gao, X.#, Sun, R.#, Jiao, N.#, **Liang, X.#**, *et al.*, Integrative multi-omics deciphers the spatial characteristics of host-gut microbiota interactions in Crohn's disease. *Cell Reports Medicine* 2023, 4(6), 101050. I collaborated on a translational medicine project to profile the multi-omics host response landscape of Crohn's disease.
3. Bao, J.#; Liu, S.#; **Liang, X.#**; Huang, W.#; Wang, C., *et al.*, A simple prediction model for COVID-19 liver dysfunction in patients with normal hepatic biochemicals. *Life Science Alliance* 2022, 6(1): e202201576. 2022. I collaborated on a translational medicine project to analyze liver injuries during COVID-19 based on clinical data and proteomics.
2. Yan, H.#; **Liang, X.#**; Du, J.#; He, Z.; Wang, Y., *et al.*, Proteomic and metabolomic investigation of serum lactate dehydrogenase elevation in COVID-19 patients. *Proteomics* 2021, 21 (15), 2100002. I collaborated on a medical project to investigate lactate dehydrogenase overexpression in COVID-19 patients based on multi-omics.
1. Ge, W.#; **Liang, X.#**; Zhang, F.#; Hu, Y.#; Xu, L., *et al.*, Computational optimization of spectral library size improves DIA-MS proteome coverage and applications to 15 tumors. *Journal of Proteome Research* 2021, 20 (12), 5392-5401. I collaborated on a mass spectrometry methodological project to develop a bioinformatics software with improved proteome identification performances.

## PATENTS

3. Guo, T., **Liang, X.**, Chen, C., Shi, Y. A analytical method to enhance body fluid proteome depth. ZL202210399034.7 [Chinese patent]
2. Guo, T., **Liang, X.**, Shi, Y., Wang, Y. A method to eliminate peptide carry-overs in liquid chromatography. ZL202210103388.2 [Chinese patent]
1. Guo, T., **Liang, X.**, Zhu, Y. Protein/peptide carriers enhances proteomics efficiency. ZL202010762585.6 [Chinese patent]

## SELECTED TALKS

2. Two-year Characterization of Pulmonary and Renal long COVID. *HUPO* 2022, Cancun, Mexico.
1. Multi-omics Characterization of COVID-19 Reveals Risk Factors for One-year Sequelae. *HUPORReconnect* 2021, Online.