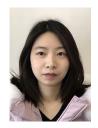
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Education

2018 – 2022 Ph.D. candidate, City University of Hong Kong
Biomedical Sciences. Supervisor: Dr. Xin WANG, Dr. Xin DENG

2013 – 2016 M.S. Zhejiang University

Plant Protection. Supervisor: Prof. Zhicheng SHEN

2009 – 2013 **B.S. Soochow University**Horticulture

Research Interest

■ Integrative analysis of multi-omics data

Integrate transcriptomics, single cell transcriptomics, epigenetics, proteomics, metabolomics, microbiomics data to investigate the mechanism of human diseases

■ Biomarker development

Identifying clinical prognostic and predictive biomarkers of cancer or disease

Epigenetics modification

Investigate the epigenomics regulatory network as well as the evolution of epigenomics modification in prokaryotes

Publications

- **Tan, M.**, Ma, J., Yang, X., . . . Qiu, X., Wang, X., Zhang, L. Quantitative proteomics reveals differential immunoglobulin-associated proteome (IgAP) in patients of acute myocardial infarction and chronic coronary syndromes. *Journal of Proteomics*. 2021. (IF: 3.5)
- Izumi, D., Zhu, Z., Chen, Y., . . . **Tan, M.**, . . . Wang, X., Goel, A. Assessment of the Diagnostic Efficiency of a Liquid Biopsy Assay for Early Detection of Gastric Cancer. *JAMA network open.* 2021. (IF: 8.5)
- Shao, X., **Tan, M.**, Xie, Y., . . . Wang, X., Deng, X. Integrated regulatory network in Pseudomonas syringae reveals dynamics of virulence. *Cell Reports*. 2021. (**IF: 9.4**)
- Feng, Z., Zhou, F., **Tan, M.**, . . . Wang, X., Deng, X., He, M. Targeting m⁶ a modification inhibits herpes virus 1 infection. *Genes & Diseases*. 2021. (**IF: 7.1**)
- Gao, F., Wang, W., **Tan, M.**, . . . Vermeulen, L., Wang, X. Deepcc: A novel deep learning-based framework for cancer molecular subtype classification. *Oncogenesis*. 2019. (**IF: 6.1**)

Ongoing Project

The intestinal microenvironment in sepsis

Use multi-omics data (single cell RNA-seq, bulk tissue RNA-seq, microbiomics, metabolomics, lipidomics) to investigate the changes of mouse sepsis at microenvironment level

Evolution of bacteria m⁶A modification

Investigate the conservative modified genes and evolution characteristics of $\mathrm{m}^6\mathrm{A}$ modification in bacteria

Ongoing Project (continued)

RNA binding protein

Identify the bind RNAs and binding mode of a novel RNA binding protein in prokaryotes based on CLIP-seq data