

Shixiang Wang

王诗翔

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Research summary

I am a computational biologist working on cancer genomics. I use bioinformatics skills to decode the unfound patterns in cancer, and explore biomarkers for explaining the cancer heterogeneity and predicting the efficacy of cancer treatments, mainly in immunotherapy.

I am passionate about open science and developing open-source analysis toolkits. Because of this, currently I am a community member of OpenbioX¹, rOpenSci² and Bioconductor³. My long-term goal in academic field is being a master in a subfield of cancer bioinformatics and trying my best to continually boost the open-source bioinformatics ecosystem in China.

Research positions

2021 — present **Postdoctoral Researcher**, Experiment Research Department, Sun Yat-sen University Cancer Center⁴
Supervisor: Rui-Hua Xu⁵

Education

2016 — 2021 **PhD in Cancer Biology**, ShanghaiTech University & Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences
Supervisor: Xue-Song Liu⁶

2012 — 2016 **B.E. in Biomedical Engineering**, University of Electronic Science and Technology of China
Supervisor: Yang Xia

Major grants and funding

2022 — 2023 **General Project, China Postdoctoral Science Foundation**⁷ (¥ 80k), Developing new method for ecDNA identification and exploring its biomarker potential

Awards & honours

2021 **2021 Outstanding Graduate Award of Shanghai**, ShanghaiTech University

2020 **National Scholarship for Doctoral Students**, ShanghaiTech University

ShanghaiTech University Class A Postgraduate Academic Scholarship, ShanghaiTech University

Publications

Journal articles (fully reviewed, † for co-first)

- 2023 J18 **Accurate prediction of pan-cancer types using machine learning with minimal number of DNA methylation sites**
W. Ning, T. Wu, C. Wu, S. Wang, Z. Tao, G. Wang, X. Zhao, K. Diao, J. Wang, J. Chen, F. Chen, X. Liu
Journal of Molecular Cell Biology
- J17 **The repertoire of copy number alteration signatures in human cancer**
Z. Tao[†], S. Wang[†], C. Wu[†], T. Wu, X. Zhao, W. Ning, G. Wang, J. Wang, J. Chen, K. Diao, F. Chen, X. Liu
Briefings in Bioinformatics (representative work)
- 2022 J16 **Hiplot: a comprehensive and easy-to-use web service for boosting publication-ready biomedical data visualization**
J. Li[†], B. Miao[†], S. Wang[†], W. Dong[†], H. Xu[†], C. Si[†], W. Wang, S. Duan, J. Lou, Z. Bao, H. Zeng, Z. Yang, W. Cheng, F. Zhao, J. Zeng, X. Liu, R. Wu, Y. Shen, Z. Chen, S. Chen, M. Wang, H. Consortium
Briefings in Bioinformatics (representative work)
- J15 **Deciphering clonal dynamics and metastatic routines in a rare patient of synchronous triple-primary tumors and multiple metastases with MPTEvol**
Q. Chen, Q. Wu, Y. Rong, S. Wang, Z. Zuo, L. Bai, B. Zhang, S. Yuan, Q. Zhao
Briefings in Bioinformatics
- J14 **Quantification of neoantigen-mediated immunoediting in cancer evolution**
T. Wu, G. Wang, X. Wang, S. Wang, X. Zhao, C. Wu, W. Ning, Z. Tao, F. Chen, X. Liu
Cancer Research
- J13 **UCSCXenaShiny: an R/CRAN package for interactive analysis of UCSC Xena data**
S. Wang[†], Y. Xiong[†], L. Zhao[†], K. Gu[†], Y. Li, F. Zhao, J. Li, M. Wang, H. Wang, Z. Tao, T. Wu, Y. Zheng, X. Li, X. Liu
Bioinformatics (representative work)
- 2021 J12 **Ggct (γ-glutamyl cyclotransferase) plays an important role in erythrocyte antioxidant defense and red blood cell survival**
Z. He, X. Sun, S. Wang, D. Bai, X. Zhao, Y. Han, P. Hao, X. Liu
British Journal of Haematology
- J11 **Copy number signature analysis tool and its application in prostate cancer reveals distinct mutational processes and clinical outcomes**
S. Wang, H. Li, M. Song, Z. Tao, T. Wu, Z. He, X. Zhao, K. Wu, X. Liu
PLoS Genetics (representative work)
- J10 **Pan-cancer noncoding genomic analysis identifies functional CDC20 promoter mutation hotspots**
Z. He[†], T. Wu[†], S. Wang[†], J. Zhang[†], X. Sun, Z. Tao, X. Zhao, H. Li, K. Wu, X. Liu
iScience

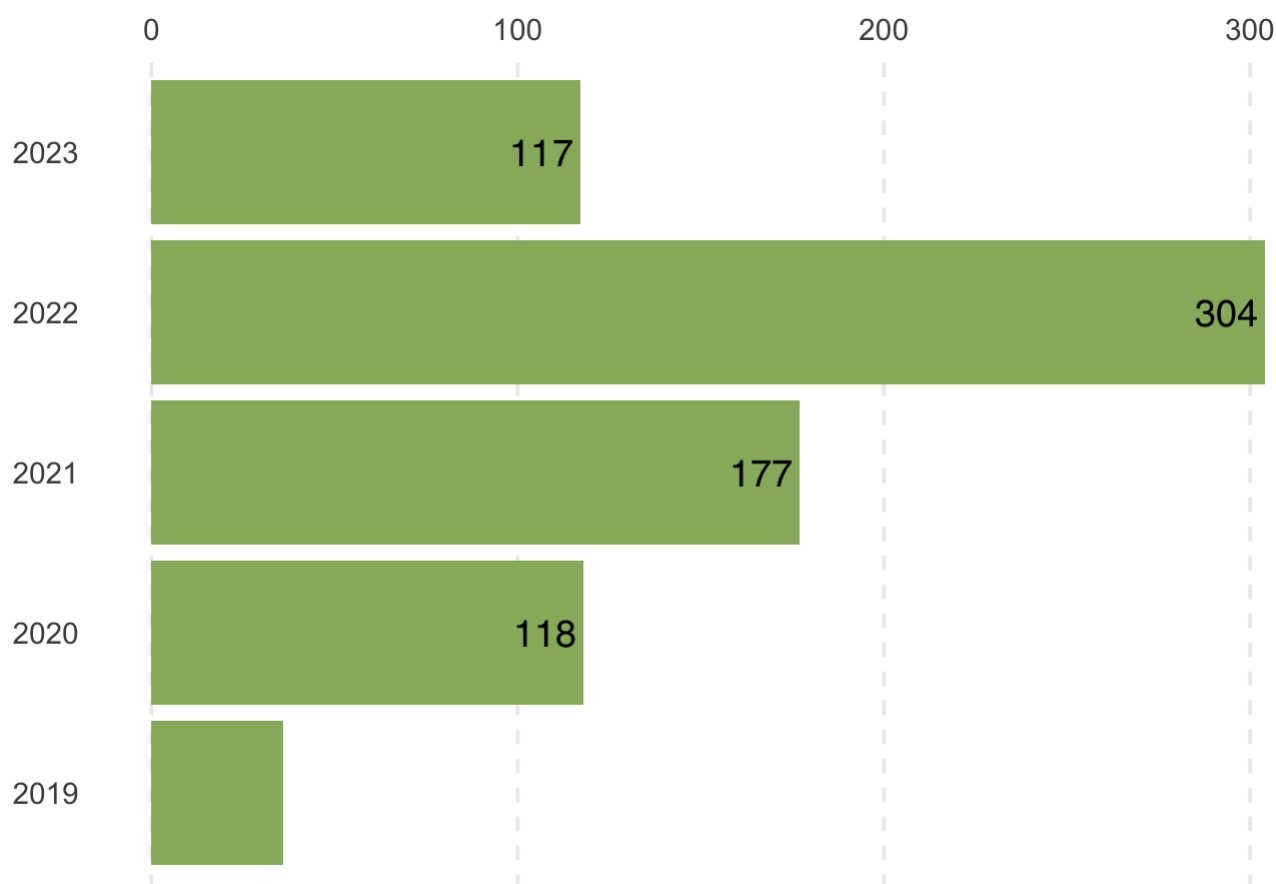
J09	Association of CSMD1 with Tumor Mutation Burden and Other Clinical Outcomes in Gastric Cancer X. Wang [†] , S. Wang [†] , Y. Han, M. Xu, P. Li, M. Ke, Z. Teng, P. Huang, Z. Diao, Y. Yan, Q. Meng, Y. Kuang, W. Zheng, H. Liu, X. Liu, B. Jia International Journal of General Medicine
2020	J08 Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis S. Wang, Z. Tao, T. Wu, X. Liu Bioinformatics (representative work)
2019	J07 Can tumor mutational burden determine the most effective treatment for lung cancer patients? S. Wang, Z. He, X. Wang, H. Li, T. Wu, X. Sun, K. Wu, X. Liu Lung Cancer Management
J06	Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction S. Wang, Z. He, X. Wang, H. Li, X. Liu eLife (representative work)
J05	The predictive power of tumor mutational burden in lung cancer immunotherapy response is influenced by patients' sex S. Wang, J. Zhang, Z. He, K. Wu, X. Liu International Journal of Cancer (representative work)
J04	Ras downstream effector GGCT alleviates oncogenic stress Z. He [†] , S. Wang [†] , Y. Shao [†] , J. Zhang [†] , X. Wu, Y. Chen, J. Hu, F. Zhang, X. Liu iScience
J03	Sex Differences in Cancer Immunotherapy Efficacy, Biomarkers, and Therapeutic Strategy S. Wang [†] , L. An Cowley [†] , X. Liu Molecules
J02	The UCSCXenaTools R package: a toolkit for accessing genomics data from UCSC Xena platform, from cancer multi-omics to single-cell RNA-seq S. Wang, X. Liu Journal of Open Source Software
2018	J01 APOBEC3B and APOBEC mutational signature as potential predictive markers for immunotherapy response in non-small cell lung cancer S. Wang [†] , M. Jia [†] , Z. He, X. Liu Oncogene (representative work)

Preprints (not reviewed, † for co-first, # for corresponding)

2022	P3 Onlinemeta: A Web Server For Meta-Analysis Based On R-shiny Y. Yi, A. Lin, C. Zhou, J. Zhang [#] , S. Wang [#] , P. Luo [#] bioRxiv
	P4 The repertoire of copy number alteration signatures in human cancer Z. Tao [†] , S. Wang [†] , C. Wu [†] , T. Wu, X. Zhao, W. Ning, G. Wang, J. Wang, J. Chen, K. Diao, F. Chen, X. Liu bioRxiv
2021	P2 ezcox: An R/CRAN Package for Cox Model Batch Processing and Visualization S. Wang, X. Liu, J. Li, Q. Zhao

Revisiting neoantigen depletion signal in the untreated cancer genome

S. Wang[†], X. Wang[†], T. Wu[†], Z. He, H. Li, X. Sun, X. Liu
 bioRxiv

Cited by

data from Google Scholar (<https://scholar.google.com/citations?user=FvNp0NkAAAAJ>)

Talks

2020

T1

BioC Asia 2020⁸, Online

Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis⁹

Poster presentations

2020

P1

BioC Asia 2020¹⁰

Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis¹¹

2019

P2

ShanghaiTech University, BioForum 2019, Shanghai, China

Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction

Teaching experience

2019

Teaching assistant, Cancer Biology, ShanghaiTech University
Teacher: Xue-Song Liu

Service

2019 — present

Reviewer Briefings in Bioinformatics¹², Frontiers in Immunology¹³, Frontiers in Oncology¹⁴, Frontiers in Cell and Developmental Biology¹⁵

Links

1. <https://github.com/openbiox>
2. <https://ropensci.org/>
3. <https://www.bioconductor.org/>
4. <http://english.sysucc.org.cn/>
5. http://english.sysucc.org.cn/info_19.aspx?itemid=154
6. https://slst.shanghaitech.edu.cn/lxs_en/main.htm
7. <https://jj.chinapostdoctor.org.cn/website/index.html>
8. <https://biocasia2020.bioconductor.org/>
9. <https://www.youtube.com/watch?v=nzAxPDTznm4>
10. <https://biocasia2020.bioconductor.org/>
11. <https://f1000research.com/posters/9-1217>
12. <https://academic.oup.com/bib>
13. <https://www.frontiersin.org/journals/immunology>
14. <https://www.frontiersin.org/journals/oncology>
15. <https://www.frontiersin.org/journals/cell-and-developmental-biology>