# **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 Openbiox 1, 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: Prof. Rui-Hua Xu5; Cooperate with Prof. Qi Zhao6

## **Education**

2016 - 2021

PhD in Cancer Biology, ShanghaiTech University 7 & Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences8 Supervisor: Prof. Xue-Song Liu9

2012 — 2016

B.E. in Biomedical Engineering, University of Electronic Science and Technology of China

Supervisor: Prof. Yang Xia

# Major grants and funding

2022 - 2023China Postdoctoral Science Foundation 10 (¥ 80k), General Project 2024 - 2026

National Natural Science Foundation of China 11 (¥ 300k), Young Scientists Fund

#### **Awards & honours**

2021 2021 Outstanding Graduate Award, Shanghai Tech 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, * for corresponding)
2023	J19	Unveiling the interplay between mutational signatures and tumor microenvironment: a pan-cancer analysis
		L. Luo, S. Li, C. Wei, J. Ma, L. Qian, Y. Chen, S. Wang <sup>*</sup> , Q. Zhao <sup>*</sup> <u>Frontiers in Immunology</u>
	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 <sup>†</sup> , S. Wang <sup>†</sup> , C. Wu <sup>†</sup> , T. Wu, X. Zhao, W. Ning, G. Wang, J. Wang, J. Chen, K. Diao, F. Chen, X. Liu <u>Briefings in Bioinformatics (representative work)</u>
2022	J16	Hiplot: a comprehensive and easy-to-use web service for boosting publication- ready biomedical data visualization
		J. Li <sup>†</sup> , B. Miao <sup>†</sup> , S. Wang <sup>†</sup> , W. Dong <sup>†</sup> , H. Xu <sup>†</sup> , C. Si <sup>†</sup> , 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 <u>Briefings in Bioinformatics (representative work)</u>
	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 <u>Briefings in Bioinformatics</u>
	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 <u>Cancer Research</u>
	J13	UCSCXenaShiny: an R/CRAN package for interactive analysis of UCSC Xena data
		S. Wang <sup>†</sup> , Y. Xiong <sup>†</sup> , L. Zhao <sup>†</sup> , K. Gu <sup>†</sup> , Y. Li, F. Zhao, J. Li, M. Wang, H. Wang, Z. Tao, T. Wu, Y. Zheng, X. Li, X. Liu <u>Bioinformatics (representative work)</u>
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

Pan-cancer noncoding genomic analysis identifies functional CDC20 promoter

 $Z.\;He^{\dagger},\,T.\;Wu^{\dagger},\,S.\;Wang^{\dagger},\,J.\;Zhang^{\dagger},\,X.\;Sun,\,Z.\;Tao,\,X.\;Zhao,\,H.\;Li,\,K.\;Wu,\,X.\;Liu$ 

2 Last updated: October, 2023

mutation hotspots

<u>iScience</u>

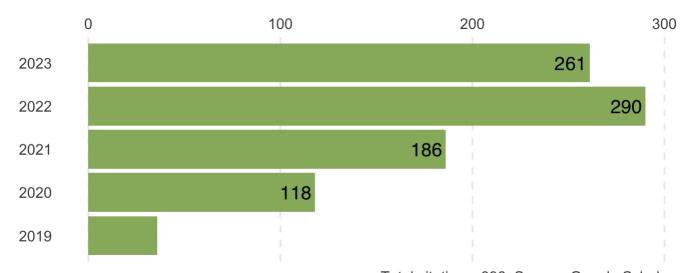
J10

PLoS Genetics (representative work)

	J09	Association of CSMD1 with Tumor Mutation Burden and Other Clinical Outcomes in Gastric Cancer
		X. Wang <sup>†</sup> , S. Wang <sup>†</sup> , 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 <u>International Journal of General Medicine</u>
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 <u>Lung Cancer Management</u>
	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 <a href="International Journal of Cancer">International Journal of Cancer</a> (representative work)
	J04	Ras downstream effector GGCT alleviates oncogenic stress
		Z. He <sup>†</sup> , S. Wang <sup>†</sup> , Y. Shao <sup>†</sup> , J. Zhang <sup>†</sup> , X. Wu, Y. Chen, J. Hu, F. Zhang, X. Liu <u>iScience</u>
	J03	Sex Differences in Cancer Immunotherapy Efficacy, Biomarkers, and Therapeutic Strategy
		S. Wang <sup>†</sup> , L. An Cowley <sup>†</sup> , X. Liu <u>Molecules</u>
	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 <sup>†</sup> , M. Jia <sup>†</sup> , Z. He, X. Liu Oncogene (representative work)
		Preprints (not reviewed, † for co-first, * for corresponding)
2023	P5	TCCIA: A Comprehensive Resource for Exploring CircRNA in Cancer Immunotherapy
		S. Wang <sup>†</sup> , Y. Xiong <sup>†</sup> , Y. Zhang <sup>†</sup> , H. Wang, M. Chen, J. Li, P. Luo, Y. Luo, M. Hecht, B. Frey, U. S Gaipl, X. Li, Q. Zhao, H. Ma, J. Zhou bioRxiv
2022	P4	The repertoire of copy number alteration signatures in human cancer
		Z. Tao <sup>†</sup> , S. Wang <sup>†</sup> , C. Wu <sup>†</sup> , T. Wu, X. Zhao, W. Ning, G. Wang, J. Wang, J. Chen, K. Diao, F. Chen, X. Liu bioRxiv

Р3 Onlinemeta: A Web Server For Meta-Analysis Based On R-shiny Y. Yi, A. Lin, C. Zhou, J. Zhang<sup>\*</sup>, S. Wang<sup>\*</sup>, P. Luo<sup>\*</sup> bioRxiv 2021 P2 ezcox: An R/CRAN Package for Cox Model Batch Processing and Visualization S. Wang, X. Liu, J. Li, Q. Zhao arXiv 2020 P1 Revisiting neoantigen depletion signal in the untreated cancer genome S. Wang<sup>†</sup>, X. Wang<sup>†</sup>, T. Wu<sup>†</sup>, Z. He, H. Li, X. Sun, X. Liu bioRxiv

### Cited by



Total citations: 898; Source: Google Scholar

#### **Talks**

T1 2020 BioC Asia 202012, Online

> Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis 13

## Poster presentations

2020 Р1 BioC Asia 202014

> Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis15

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, Shanghai Tech University

Teacher: Xue-Song Liu

2023 Supervisor, Open Source Promotion Plan 202316

Student: Shensuo Li

#### Service

2021 — present Review Editor in in Cancer Immunity and Immunotherapy Frontiers 17

2019 — present Reviewer Briefings in Bioinformatics 18, Journal of Translational Medicine 19, STAR

Protocols20, Frontiers in Immunology21, Frontiers in Oncology22, Frontiers in Cell

and Developmental Biology23

# Links

- 1. https://github.com/openbiox←
- 2. <a href="https://ropensci.org/">https://ropensci.org/</a>
- 3. <a href="https://www.bioconductor.org/">https://www.bioconductor.org/</a> ←
- 4. http://english.sysucc.org.cn/←
- 5. <a href="http://english.sysucc.org.cn/info">http://english.sysucc.org.cn/info</a> 19.aspx?itemid=154€
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- 13. <a href="https://www.youtube.com/watch?v=nzAxPDTznm4+">https://www.youtube.com/watch?v=nzAxPDTznm4+</a>
- 14. <a href="https://biocasia2020.bioconductor.org/">https://biocasia2020.bioconductor.org/</a> ←
- 15. https://f1000research.com/posters/9-1217 ←
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- 17. https://www.frontiersin.org/←
- 18. <a href="https://academic.oup.com/bib↔">https://academic.oup.com/bib↔</a>
- 19. <a href="https://translational-medicine.biomedcentral.com/←">https://translational-medicine.biomedcentral.com/←</a>

- 20. https://www.cell.com/star-protocols/home ←
- 21.  $\underline{\text{https://www.frontiersin.org/journals/immunology}} \leftarrow$
- 22.  $\underline{\text{https://www.frontiersin.org/journals/oncology}} \leftarrow$
- 23. <a href="https://www.frontiersin.org/journals/cell-and-developmental-biology">https://www.frontiersin.org/journals/cell-and-developmental-biology</a> →