

Ziwei Xue



Ph.D., Postdoctoral Fellow at The European Molecular Biology Laboratory (EMBL)

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EDUCATION



Zhejiang University-University of Edinburgh Institute (ZJE), Haining, Zhejiang, China

- B.S. in Biomedical Science Sep 2017 – Jun 2021
 - Dual degree awarded by Zhejiang University and the University of Edinburgh
 - First-Class Honours Degree
- Ph.D. in Bioinformatics Sep 2021 – Jun 2026
 - Dual doctoral degree awarded by Zhejiang University and the University of Edinburgh
 - **Thesis:** Integrative Analysis of Large-scale Immunomics Data
 - **Supervisor:** Dr. Wanlu Liu

PROFESSIONAL APPOINTMENTS



The European Molecular Biology Laboratory (EMBL), Heidelberg, Germany

dkfz. The German Cancer Research Center (DKFZ), Heidelberg, Germany

- Postdoctoral Fellow, Alliance Interinstitutional Postdoc Program **Starting** Oct 2026
 - **Host supervisors:** Dr. Oliver Stegle at EMBL and Dr. Michael Platten at Heidelberg University
 - **Project:** Decoding Spatially Constrained Cellular Plasticity in Malignant Gliomas through Integrative Spatial Transcriptomics and Deep Regulatory Modeling

RESEARCH INTERESTS

I am interested in multi-omics data analysis, focusing on **artificial intelligence (AI)**-based approaches to gain deeper insights into the **phenotypic diversity and plasticity of immune and malignant cells in cancer and autoimmune diseases**. My work centers on developing methods for integrating multi-modal next-generation sequencing datasets encompassing **genomics, transcriptomics, metabolomics, and immunomics** at **bulk, single-cell, and spatial resolutions**, with the goal of elucidating immune system dynamics and regulatory programs under diverse disease conditions. My current research extends these approaches to **spatial transcriptomics and deep regulatory modeling of malignant gliomas**.

PUBLICATIONS

Selected Publications, *first or co-first authors ✉ corresponding authors

- [1] **Xue, Z.***, Wu, L.*, Tian, R., Gao, B., Zhao, Y., Bing, H., Zhao, B., Li, Y., Zhu, K., Wang, L., Yao, J.✉, Liu, W.✉ & Lu, L.✉ Integrative mapping of human CD8+ T cells in inflammation and cancer. *Nature Methods* **22**, 435–445. (2025)
- [2] **Xue, Z.** scAtlasVAE: A deep learning framework for generating a human CD8+ T cell atlas. *Nature Reviews Cancer* **25**, 319. (2025)
- [3] **Xue, Z.***, Wu, L.*, Gao, B.*, Tian, R., Chen, Y., Qi, Y., Dong, T., Bai, Y., Zhao, Y., He, B., Wang, L., Liu, Z., Yao, H., Lu, L., Liu, W.✉ A pan-disease and population-level single-cell TCRαβ repertoire reference. *Cell Discovery* **11**, 82. (2025)
- [4] Tian, R.*, **Xue, Z.***, Chen, Y., Qi, Y., Zhang, J., Yuan, J., Ruan, D., Lin, J., Liu, J., Wang, D., Ye, Y., Liu, W.✉ Integrating Cross-Sample and Cross-Modal Data for Spatial Transcriptomics and Metabolomics with SpatialMETA. *Nature Communications*, **16**, 8855. (2025)
- [5] Wu, L.*, **Xue, Z.***, Jin, S., Zhang, J., Bai, Y., Jin, X., Wang, C., Wang, L., Wang, J.Q., Lu, L. & Liu, W.✉ huARdb: human Antigen Receptor database for interactive clonotype-transcriptome analysis at the single-cell level. *Nucleic Acids Research* **50**, D1244-D1254. (2022)
- [6] Tian, R.*, **Xue, Z.***, Ruan, D., Chen, P., Xu, Y., Dai, C., Shen, W., Ouyang, H., Liu, W., & Lin, J.✉ MSdb: An integrated expression atlas of human musculoskeletal system. *iScience*, **26**, 106933. (2023)

Additional Peer-reviewed Publications, *first or co-first authors ✉ corresponding authors

- [7] Liu, Z.*, Jiang, S.*, Hu, T.*, **Xue, Z.***, Chen, Y., Ruan, D., Xia, H., Feng, Y., Hao, J., Li, W., Zhou, T., Fang, B., Wu, J., Liu, W.✉ DestinyNet: A deep learning framework integrating lineage tracing and single-cell sequencing information for fate clustering, flow, and prediction. *Patterns*. (2025)
- [8] Tian, R.*, Yu, Z.*, **Xue, Z.**, Wu, J., Wu, L., Cai, S., Gao, B., He, B., Zhao, Y., Yao, J., Lu, L. & Liu, W.✉ Evaluation of T Cell Receptor Construction Methods from scRNA-Seq Data. *Genomics, Proteomics & Bioinformatics*. (2024)

- [9] Guo, Y.*, **Xue, Z.**, Gong, M., Jin, S., Wu, X. & Liu, W.[✉] CRISPR-TE: a web-based tool to generate single guide RNAs targeting transposable elements. *Mobile DNA* **15**, 3. (2024)
- [10] Su, Y.*, Yu, Z., Jin, S., Ai, Z., Yuan, R., Chen, X., **Xue, Z.**, Guo, Y., Chen, D., Liang, H., Liu, Z. & Liu, W.[✉] Comprehensive assessment of mRNA isoform detection methods for long-read sequencing data. *Nature Communications* **15**, 3972. (2024)
- [11] Li, Z.*, Xu, H.*, Li, J.*, Xu, X.*, Wang, J., Wu, D., Zhang, J., Liu, J., **Xue, Z.**, Zhan, G., Tan, B.C.P., Chen, D., Chan, Y-S., Ng, H.H., Liu, W., Hsu, C-H., Zhang, D., Shen, Y. & Liang, H.[✉] Selective binding of retrotransposons by ZFP352 facilitates the timely dissolution of totipotency network. *Nature Communications*. **14**, 3646. (2023)
- [12] Xiang, X.*, Tao, Y.*, DiRusso, J., Hsu, F.M., Zhang, J., **Xue, Z.**, Pontis, J., Trono, D., Liu, W.[✉] & Clark, A.[✉], Human reproduction is regulated by retrotransposons derived from ancient Hominidae-specific viral infections, *Nature Communications*, **13**, 463. (2022)
- [13] Jin, S.*, **Xue, Z.***, Zhang, J., Wang, Z., Zhang, J., Chen, D.*, Liu, W.[✉], & Lin, J.[✉] Identification of SRSF3 target mRNAs using inducible TRIBE. *Biochemical and Biophysical Research Communications* **578**, 21-27. (2021)
- [14] Guo, Y.*, **Xue, Z.**, Yuan, R., Li, J., Pastor, W. & Liu, W.[✉] RAD: a web application to identify region associated differentially expressed genes. *Bioinformatics* **37**, 2741-2743. (2021)

RESEARCH SOFTWARE & DATASETS

- **scAtlasVAE**: deep generative framework for constructing and interrogating a human CD8+ T cell atlas 2025
 - Associated publication: *Nature Methods, Nature Reviews Cancer*;
- **TCR-DeepInsight**: Identification of disease-associated cTrGx-TCRs 2025
 - Associated publication: *Cell Discovery*;
- **spatialMETA**: a method for integrating spatial multi-omics data 2025
 - Associated publication: *Nature Communications*
- **huARdb**: human antigen receptor database for interactive clonotype-transcriptome analysis at the single-cell level 2022
 - Associated publication: *Nucleic Acids Research*;
- **MSdb**: integrated expression atlas and visualization resource for the human musculoskeletal system 2023
 - Associated publication: *iScience*;
- **RAD**: web application for identifying region-associated differentially expressed genes 2021
 - Associated publication: *Bioinformatics*;
- **CRISPR-TE**: web-based tool for designing guide RNAs targeting transposable elements 2024
 - Associated publication: *Mobile DNA*

PATENTS & COPYRIGHTS

- **Patents**
 - Lu, L., Liu, W., Wu, L., **Xue, Z.** Single-cell visualization methods based on single-cell immune profiling data (ZL202111026323.4, Valid authorization)
 - Liu, W., Lu, L., **Xue, Z.**, Wu, L. Data processing methods, apparatuses, devices, and computer-readable storage media (202310802339.2, Pending)
- **Copyrights of computer software**
 - Wu, L.,**Xue, Z.**, Liu, W. & Lu, L. A large-scale single-cell transcriptome cross-atlas integration deep learning software based on variational neural networks (2025SR1043543)
 - Lin, J., Tian, R., **Xue, Z.**, Ruan, D., Liu, W. An analysis and visualization software for musculoskeletal multi-modality data (2023SR1142549)
 - **Xue, Z.**, Wu, L., Liu, W. & Lu, L. A visualization software for single-cell immune profiling data (2022SR0296997)
 - Guo, Y., **Xue, Z.**, Liu, W. RAD: a web application to identify region associated differentially expressed genes (2021SR1099956)

AWARDS & SCHOLARSHIPS

- **Alliance Interinstitutional Postdoc Program** 2026
 - **Project**: Decoding Spatially Constrained Cellular Plasticity in Malignant Gliomas through Integrative Spatial Transcriptomics and Deep Regulatory Modeling
- **Chu Kochen Scholarship of Zhejiang University** (竺可桢奖学金) 2025
- **National Scholarship of China** (国家奖学金) 2025

	▪ Student of Distinction of the International Campus (浙江大学国际校区先锋学子) 2025 ▪ QiuShi Rising Star Ph.D. student Program of Zhejiang University (求是新星培养计划) 2024
CONFERENCES & PRESENTATIONS	▪ The 1st ZiJuan Youth Scholars Forum Dec 2023 • Invited talk: Integrative and transfer learning of large-scale immunogenomics datasets ▪ 14th National Conference on Bioinformatics and Systems Biology Oct 2025 • Invited talk: AI-Driven Integration of Single-Cell Immunomics Reveals T Cell Phenotypic Plasticity and TCR Diversity ▪ Annual Meeting of the American Association of Immunologists (AAI) May 2025 • Poster: Unified integration of pan-cancer single-cell and spatial transcriptomics ▪ Human Cell Atlas Asia Meeting Dec 2024 • Poster: Integrative Mapping of Human CD8+ T Cell in Inflammation and Cancer • Poster: A pan-disease and population-level single-cell TCRαβ repertoire reference atlas
INTERNSHIP	▪ Internship, Tencent AI for Life Sciences Lab Jun 2025 - Sep 2025 • Technical Research - Machine Learning Direction ▪ Internship, Tencent AI Lab Aug 2022 - Sep 2022 • Rhinobird Exchange Program
MENTORING & SUPERVISION	▪ Undergraduate course mentoring, BMI3 Biomedical Informatics 3, ZJE Institute, Zhejiang University 2021–2023 • Mentored undergraduate students in English-taught biomedical informatics coursework, including project design, data analysis, and scientific presentation. ▪ Research mentoring in computational immunology and single-cell multi-omics 2021–2026 • Provided day-to-day guidance for junior trainees on single-cell data processing, immune repertoire analysis, reproducible coding practice, and manuscript-oriented figure generation.
PROFESSIONAL SERVICES	▪ Ad hoc reviewer: <i>Science Advances, BioData Mining, Immunological Research, Scientific Data</i> ▪ Conference committee members of Unravelling T-cell recognition, University of Oxford, UK