

Xin Dong

Ph.D. in Biology

Sycamore Research Institute of Life Sciences, Shanghai, China

School of Life Sciences and Technology, Tongji University, Shanghai, China

✉ dongxin@tongji.edu.cn; xindongnov@gmail.com | 🎓 Scholar

EDUCATION

- Sep. 2018 – Jul. 2024** **Ph.D. in Biology**
School of Life Sciences and Technology, Tongji University, China
Advisor: Dr. Chenfei Wang
- Sep. 2014 – Jun. 2018** **B.S. in Biotechnology**
College of Life Sciences, Shandong Normal University, China

WORK EXPERIENCES

- Sep. 2025 – Present Research Scientist Sycamore Research Institute of Life Sciences, Shanghai
- Jul. 2024 – Sep. 2025 Research Assistant School of Life Sciences and Technology, Tongji University

RESEARCH EXPERIENCES

Research Scientist, Sycamore Research Institute of Life Sciences, Shanghai (Sep. 2025 – Present)

- Data Analysis for cancer treatments and fundamental researches.

Research Assistant, School of Life Sciences and Technology, Tongji University (Jul. 2024 – Sep. 2025)

- Developed computational methods for analyzing high-dimensional biological datasets in developmental biology.

Graduate Student, Tongji University (Sep. 2018 – Jul. 2024, Advisor: Dr. Chenfei Wang)

- Developed computational methods for integrating public single-cell epigenomic and transcriptomic data to infer transcription regulator activity and gene regulatory networks, with applications in lineage tracing and cell-type-specific network inference.
- Co-developed a comprehensive web resource for exploring single-cell transcriptome profiles of the tumor microenvironment, enabling systematic comparison across cancer types, patients, and treatment conditions.
- Developed a pipeline that processes the epigenome data to readable results with a single command line. It integrates states-of-the-art tools for cistrome NGS data and chooses the appropriate analysis parameters.
- Developed and maintained the Cistrome Data Browser, which hosts many public cistrome sequence datasets. It offers a user-friendly interface to access the data quality and the results of downstream analysis.

PUBLICATIONS

Asterisk (*) denotes the Co-first Authors and Hashtag (#) denotes the Corresponding Authors.

- Tang, K.*, Han, Y.*, Sun, D., **Dong, X.**, Han, T., Wei, H., Shao, W., Hu, J., Liu, Z., Zhang, L., Li, T., Zhang, P., Wu, Q.# & Wang, C#. Reference-guided computational framework identifies microenvironment metabolic subtypes and targets using pan-cancer single-cell datasets. *Genome Medicine* 17, 150 (2025).
- Jiang, R., Chen, J., Pei, L., Huang, S., Feng, M., Ouyang, Z., Yuan, M., Zhu, Y., Yao, S., He, F., Zhang, H., **Dong, X.**, Xie, P.# & Wei, K.# Myosin inhibition enhances cardiomyocyte cell cycle activity through SIRT1-NFAT-mediated H3K9me3 modification. *European Journal of Cell Biology* 104, 151504 (2025).
- Sun, F.*, Li, H.*, Sun, D.*, Fu, S.*, Gu, L.*, Shao, X.*, Wang, Q.*, **Dong, X.***, Duan, B.*, Xing, F.*, Wu, J.*, Xiao, M.#, Zhao, F.#, Han, J.-D. J.#, Liu, Q.#, Fan, X.#, Li, C.#, Wang, C.# & Shi, T.# Single-cell omics: experimental workflow, data analyses and applications. *SCIENCE CHINA Life Sciences* 68, 5–102 (2025).
- Chang, Z.*, Xu, Y.*, **Dong, X.***, Gao, Y. & Wang, C.# Single-cell and spatial multiomic inference of gene regulatory networks using SCRIPPro. *Bioinformatics* 40, btae466 (2024).

- Ren, P.* , Shi, X.* , Yu, Z., **Dong, X.**, Ding, X., Wang, J., Sun, L., Yan, Y., Hu, J., Zhang, P., Chen, Q., Zhang, J., Li, T. & Wang, C.# Single-cell assignment using multiple-adversarial domain adaptation network with large-scale references. *Cell Reports Methods*, 3, 100577 (2023).
- Han, Y.* , Wang, Y.* , **Dong, X.***, Sun, D., Liu, Z., Yue, J., Wang, H., Li, T.# & Wang, C.# TISCH2: expanded datasets and new tools for single-cell transcriptome analyses of the tumor microenvironment. *Nucleic Acids Research*, 51, D1029-D1037 (2022).
- Shi, X.* , Yu, Z.* , Ren, P., **Dong, X.**, Ding, X., Song, J., Zhang, J., Li, T.# & Wang, C.# HUSCH: an integrated single-cell transcriptome atlas for human tissue gene expression visualization and analyses. *Nucleic Acids Research*, 51, D1425-D1431 (2022).
- **Dong, X.***, Tang, K.* , Xu, Y., Wei, H., Han, T. & Wang, C. # Single-cell gene regulation network inference by large-scale data integration. *Nucleic Acids Research*, 50, e126 (2022).
- Xu, R.* , Li, S.* , Wu, Q.* , Li, C.* , Jiang, M.* , Guo, L., Chen, M., Yang, L., **Dong, X.**, Wang, H., Wang, C.#, Liu, X.#, Ou, X.# & Gao, S.# Stage-specific H3K9me3 occupancy ensures retrotransposon silencing in human pre-implantation embryos. *Cell Stem Cell*, 29, 1051-1066.e8 (2022).
- Sun, D.* , Wang, J.* , Han, Y.* , **Dong, X.**, Ge, J., Zheng, R., Shi, X., Wang, B., Li, Z., Ren, P., Sun, L., Yan, Y., Zhang, P., Zhang, F.#, Li, T.# & Wang, C.# TISCH: a comprehensive web resource enabling interactive single-cell transcriptome visualization of tumor microenvironment. *Nucleic Acids Research*, 49, D1420-D1430 (2021).
- Zheng, R.* , **Dong, X.***, Wan, C., Shi, X., Zhang, X.# & Meyer, C.A.# Cistrome Data Browser and Toolkit: analyzing human and mouse genomic data using compendia of ChIP-seq and chromatin accessibility data. *Quantitative Biology*, 8, 267-276 (2020).
- Chen, C.-H., Zheng, R., Tokheim, C., **Dong, X.**, Fan, J., Wan, C., Tang, Q., Brown, M., Liu, J.S., Meyer, C.A. # & Liu, X.S.# Determinants of transcription factor regulatory range. *Nature Communications*, 11, 2472 (2020).
- Li, S.* , Wan, C.* , Zheng, R., Fan, J., **Dong, X.**, Meyer, C.A.# & Liu, X.S.# Cistrome-GO: a web server for functional enrichment analysis of transcription factor ChIP-seq peaks. *Nucleic Acids Research*, 47, W206–W211 (2019).

CONFERENCES

- 2024 Poster Speaking, Human Cell Atlas Asia 2024, Hong Kong SAR, China
- 2024 Poster Speaking (Awarded), The 2nd Bioinformatics Conference of Yangtze River Delta, Shanghai, China
- 2023 Poster Speaking, The WLA Research Conference on Cells and Genes, Shanghai, China
- 2023 Poster Speaking, The 11st National Conference on Bioinformatics and Systems Biology, Guangzhou, China
- 2023 Poster Speaking, Human Cell Atlas Asia 2021 Meeting, online
- 2021 Poster Speaking, The 10th National Conference on Bioinformatics and Systems Biology, Chengdu, China

AWARDS AND DISTINCTIONS

- 2024 Outstanding Graduates Awards of Shanghai
- 2023 The 17th Academic Pioneer (Top 0.05%), Tongji University
- 2019 Outstanding Graduate Student Scholarship, Tongji University
- 2017 Outstanding Graduates Awards of Shandong Province