Xie, Yang
Email: tvtxieyang@outlook.com
Website: https://xieeeee.github.io/

Education

- University of California San Diego, Ph.D., 2018-2024.

Field of study: Biomedical Science, School of Medicine

- Fudan University, B.S., 2014-2018

Field of study: Biological Sciences, School of Life Sciences

Personal statement

I am a postdoctoral scientist at the New York Genome Center developing and applying single-cell multiomic technologies to understand how epigenomic regulation encodes cellular identity, developmental potential, and disease susceptibility. I have interdisciplinary training spanning experimental genomics, chromatin biology, and computational modeling. During my Ph.D. with Dr. Bing Ren, I led the development of scalable single-cell epigenomic platforms (Droplet Paired-Tag and Droplet Hi-C) that enabled high-throughput interrogation of chromatin state and genome organization in complex tissues—regulatory layers that were previously difficult to measure at scale. These tools helped establish a foundation for studying the heterogeneity of gene regulation in a multimodal framework. In my postdoctoral work, I have served as a major contributor to multi-investigator grants and consortium efforts, building strong collaborative relationships across experimental and computational teams. I have led integrative analyses in the adult human brain and in metabolic diseases (including heart failure and liver steatosis) to identify cell-type-specific, disease-associated regulatory programs and interpret the functional impact of noncoding variants. Moving forward, I will leverage these strengths to advance predictive models that mechanistically link chromatin state to future transcriptional outcomes and perturbation responses, while strengthening my independent research profile through targeted training in machine learning and quantitative modeling. This mentored phase will position me to transition to independence with a research program at the interface of single-cell multiomics and AI-driven predictive epigenomics.

Positions, Scientific Appointments

2025 - Now	Postdoctoral Research Associate, New York Genome Center, New York, NY
2024 - 2025	Postdoctoral Research Associate, University of California San Diego, San Diego, CA

Honors

2015 - 2018	Fellow, Tan School of Innovation, Fudan University, Shanghai, China
2018	Award for Outstanding Undergraduate in Shanghai, Shanghai, China
2017	Fosun Pharma Scholarship for Life Science, Shanghai, China

Contributions to Science

1. **Development of novel single-cell epigenomic profiling methods.** My research has addressed key technical and conceptual limitations in single-cell epigenomics by developing scalable multi-omic technologies and applying them to uncover regulatory mechanisms underlying cellular identity and disease. Early in my work, I led the development of Droplet Paired-Tag and Droplet Hi-C, which enable high-throughput, single-cell profiling of histone modifications, chromatin architecture, and transcription. These methods substantially reduced experimental complexity while improving data quality and accessibility, providing a practical foundation for large-scale, multimodal interrogation of gene regulation in heterogeneous tissues. Using these tools, I revealed cell-type-specific repressive regulatory programs in the mouse cortex and resolved dynamic structural variation in glioblastoma under drug treatment, establishing new frameworks for studying chromatin regulation at scale.

a. Chang L*, **Xie Y***, Taylor B, et al. Droplet Hi-C enables scalable, single-cell profiling of chromatin architecture in heterogeneous tissues. *Nat Biotechnol*. 2025;43(10):1694-1707. doi:10.1038/s41587-024-02447-1
b. **Xie Y***, Zhu C*, Wang Z, et al. Droplet-based single-cell joint profiling of histone modifications and transcriptomes. *Nat Struct Mol Biol*. 2023;30(10):1428-1433. doi:10.1038/s41594-023-01060-1

2. **Characterization of disease associated gene regulatory programs.** Building on these technologies, I applied single-cell multimodal profiling to human disease to enable mechanistic interpretation of noncoding genetic risk variants. In human heart failure, I led integrative analyses of single-cell transcriptomic, chromatin accessibility, histone modification, and 3D genome organization data across multiple disease etiologies, revealing cardiomyocyte-specific erosion of chromatin compartmentalization and identifying transcriptional regulators driving pathological progression. In metabolic liver disease (MASLD/MASH), I analyzed multimodal data from over two million cells across the disease spectrum and demonstrated that steatosis and steatohepatitis are governed by distinct regulatory programs, linking the majority of disease-associated risk loci to putative effector genes. Together, these studies illustrate how multimodal epigenomics enables insights into disease mechanisms that are inaccessible through transcriptome-only approaches.
   a. **Xie Y***, Tucciarone L*, Farah EN*, Chang L*, et al. Single cell multiomics and 3D genome architecture reveal novel pathways of human heart failure. Preprint. *medRxiv*. 2025;2025.05.08.25327176. Published 2025 May 9. doi:10.1101/2025.05.08.25327176 (Revised at *Science*)
   b. Elison W*, Chang L*, **Xie Y***, et al. Single cell multiomics reveals drivers of metabolic dysfunction-associated steatohepatitis. Preprint. *medRxiv*. 2025;2025.05.09.25327043. Published 2025 May 11. doi:10.1101/2025.05.09.25327043 (Revised at *Nature*)

3. **Prediction of epigenomic dynamics and noncoding variants effect.** In addition to the contributions mentioned above, I have combined multimodal epigenomic profiling with computational and machine-learning approaches to move beyond descriptive atlases toward predictive models of gene regulation and disease risk. Using the adult human brain as a model system, I identified repressive chromatin features associated with regional and laminar specialization across cell types, and applied sequence-based deep learning models to prioritize the functional impact of noncoding variants linked to neuropsychiatric disorders in a cell-type-specific manner. Collectively, these work advance a predictive understanding of how epigenomic regulation encodes cellular identity, constrains developmental trajectories, and shapes disease susceptibility.
   a. **Xie, Y.***, Chang L*, Zhong G, et al. Single-Cell Atlas of Transcription and Chromatin States Reveals Regulatory Programs in the Human Brain. *bioRxiv*. Published online 2026. doi:10.64898/2026.02.02.703166 (Under review at *Cell*)
   b. Chang L*, Li K*, **Xie Y***, Zhong G*, et al. Single-cell Multiome Analysis of Chromatin State and Transcriptome in the Human Basal Ganglia. *bioRxiv*. Published online 2026. doi:10.64898/2026.02.03.703645 (Under review at *Cell*)

Complete List of Published Work in My Bibliography:
https://www.ncbi.nlm.nih.gov/myncbi/yang.xie.7/bibliography/public/

Teaching Experience & Mentorship

- Graduate Instructional Apprentice, *The Cell*, Division of Biological Sciences, UC San Diego, Fall 2021
- Mentoring undergraduate student: Bohan Huang (General Biology, UC San Diego, 2023-2026), Melissa Vu (Biology, UC San Diego, 2023-2026)