JUNJIE XIA

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SUMMARY

- Computational and chemical biology expert with 4+ years of experience in single cell & spatial multi-omics
- Developed novel high-throughput NGS assays for integrated transcriptomics, proteomics & glycomics profiling
- Strong programming and analytical background with proficiency in Python, R, and statistical modeling
- Hands-on experience in antibody/protein conjugation, flow cytometry, microscopy, and NGS workflows

EDUCATION

PhD **University of Chicago** | Chicago, IL | Department of Chemistry   Sept 2021 – June 2026 (Expected)
Major courses: Chemical Biology, Fundamentals of Computational Biology,
               Machine Learning and Large-Scale Data Analysis
Honors: McCormick Fellowships (UChicago), Rising Stars in Measurement Sciences (2023, Merck),
               Olshansky Graduate Student Travel Award (UChicago)

BS **Zhejiang University** | Hangzhou, China | Department of Polymer Science   Sept 2017 – June 2021
Honors: National Scholarships for 2017-19 academic year (top 1% student)

RESEARCH EXPERIENCE

Institute for Genomics and Systems Biology, University of Chicago | Chicago, IL   Sept 2022 – Present
Graduate Researcher

- Conjugated over 80 antibodies and proteins with DNA oligos, followed by purification and validation using fluorescence-based flow cytometry and microscopy imaging to confirm binding specificity
- Applied spatial omics technology (Visium) with proximity ligation assay to simultaneously profile the transcriptome, proteome, and protein interactome in human tonsil tissue to study B cell development
- Found protein interaction-based biomarkers CD19-CD21 in Naïve B cells, revealing its spatiotemporal change during B cell maturation from primary follicle to germinal center
- Developed a novel NGS single-cell assay to jointly quantify mRNA, protein, glycan, and protein-specific glycosylation, enabling integrated multi-omics analysis of T cell differentiation
- Identified a new subset of terminally differentiated CD8+ T cells expressing CD45 with high poly-LacNAc modification, a new biomarker suggesting exhaustion and susceptibility to galectin-1-induced apoptosis
- Constructed a machine learning model using Elastic Net regression to predict protein and glycan abundance from single-cell mRNA expression profiles, achieving $R^2 = 0.72$ and MAE < 0.15
- Designed statistical algorithms to infer protein interactions from proximity proteomics, and built modular, object-oriented Python classes to streamline algorithm deployment
- Performed QC and alignment of bulk and single-cell RNA-seq data using FastQC, STAR, and downstream analysis via DESeq2, Scanpy, Seurat, and clusterProfiler
- Automated workflows using Bash scripting and executed high-throughput pipelines on SLURM-based HPC clusters via sbatch, srun, and job arrays
- Managed analysis workflow in Jupyter Notebooks, tracked versions using Git, and prepared 5+ public-facing code repository with documentation to support reproducibility and transparency

Dept. Of Chemistry, University of Chicago | Chicago, IL   Sept 2021 – Sept 2022
Graduate Researcher

- Employed non-compartmental PK models in Python to simulate drug ADME, and parameterized models with experimental data to optimize nanoparticle formulation and dosing strategy
- Applied survival analysis techniques including Kaplan–Meier curves and log-rank tests to assess antitumor efficacy in preclinical mouse study

Dept. Of Polymer Science and Engineering, Zhejiang University | Hangzhou, China   Sept 2019 – June 2021
Undergraduate Researcher

- Conducted Metropolis Monte Carlo simulation to model polymer chain conformation and properties

TECHNICAL SKILLS

Language: Python, R, Bash, C, Java
Workflow & Systems: SLURM, Git, Snakemake
Omics tools: Seurat, Scanpy, ScVI, DESeq2, clusterProfiler, Squidpy, CellChat, Monocle3

Data Types: Single-cell RNA-seq, spatial transcriptomics (Visium, Xenium), proteomics (OLINK), glycomics
Modeling & analysis: Bootstrapping, Monte Carlo, Principal component analysis, Regression modeling, Hypothesis testing, Bayesian methods, Random Forest, XGBoost, Lasso, Elastic Net Regression
Experiment: Antibody/Protein conjugation, Flow cytometry, Confocal microscope imaging, IHC, ELISA, Next generation sequencing (NGS) workflow
Interests: Leveraging data-driven insights to uncover hidden structure in complex systems

SELECT PUBLICATIONS (4 of 6)

Xia, J., Phan, H.V., Vistain, L., Chen, M., Khan, A.A., Tay, S. Computational prediction of protein interactions in single cells by proximity sequencing. PLoS Comput Biol 20, e1011915 (2024).

Vistain, L., Keisham, B., **Xia, J.,** Phan, H.V. & Tay, S. Proximity sequencing for the detection of mRNA, extracellular proteins and extracellular protein complexes in single cells. Nat Protoc 19, 3568–3589 (2024).

Jiang, X., Lee, M., **Xia, J.,** Luo, T., Liu, J., Rodriguez, M., Lin, W. Two-Stage SN38 Release from a Core–Shell Nanoparticle Enhances Tumor Deposition and Antitumor Efficacy for Synergistic Combination with Immune Checkpoint Blockade. ACS Nano 16, 21417–21430 (2022).

Li, Y., Jiang, X., Luo, T., **Xia, J.,** Lee, M., Weichselbaum, R., Lin, W. TLR3 agonist nanoscale coordination polymer synergizes with immune checkpoint blockade for immunotherapy of cancer. Biomaterials 290, 121831 (2022).

MANUSCRIPTS IN SUBMISSION/REVIEW

Xia, J., Keisham, B., Pang, J. M., Padhi, A., Wang, H., Vasquez, M. G., Huang, L. M., Tay, S. Single-cell measurement of glycoforms, proteins and mRNA reveals dynamic glycan remodeling during T cell differentiation. *In review.*

Wang, H.[#], **Xia, J.[#],** Rahman, P.M.S.M.R., Keisham, B., Padhi, A., Deng, Y., Li, Y., Vistain, L., Kim, S., Vasquez, M. G., Khan, A.A., Clark, M.R., Tay, S. Spatial proximity sequencing maps developmental dynamics in germinal center. *In review.*

PATENTS & INTELLECTUAL PROPERTY

Tay, S., **Xia, J**. *Integrated Multi-Omics Profiling.* Provisional Patent Application No. 63/880,541, filed 2025.

CONFERENCE PRESENTATIONS

Poster, Merck-UChicago Lectureship, "Integrated profiling of proteins, glycoforms and mRNA in single cells reveals dynamic glycan remodeling during T cell differentiation." 2025

Poster, The Chicago BioEngineering Conference 2024, "Computational prediction of protein interactions in single cells by proximity sequencing." 2024

Poster, Merck Rising Stars in Measurement Sciences Symposium, "Spatial profiling of proteins, protein complexes and mRNA in human tonsil by proximity sequencing" 2023

LEADERSHIP AND SERVICE

Department of Chemistry, University of Chicago, Teaching Assistant   2021 – 2022
- Taught and supported over 50 undergraduate students in General Chemistry through weekly discussion sections
- Facilitated hands-on laboratory experiments and ensured proper safety and technique
- Held regular office hours to provide individual support and reinforce key concepts

PROFESSIONAL EXPERIENCE

Department of Biomedicine and Healthcare, Kaitai Capital, Venture Capital Analysis Intern   June 2021– Sept 2021
- Evaluated scientific and clinical data on cell-based therapies, including gene-edited CAR-T (e.g., PD-1 knockout), TCR-T for solid tumors, and gene therapies targeting CNS disorders
- Researched >15 biotech and pharma companies with a focus on epigenetic therapeutics; analyzed drug targets, mechanisms of action, and market competition to support the Cytosinlab Therapeutics investment decision
- Benchmarked nucleic acid aptamer-drug conjugates (ApDCs) against antibody-drug conjugates (ADCs)
- Supported 3 investment committee pitch decks and prepared 10+ internal review and due diligence memos; contributed to due diligence checklists, interview frameworks, and 10+ founder meeting summaries
- Developed internal tools in Excel and Python to streamline evaluation of clinical-stage assets, automating data extraction and risk stratification across therapeutic areas