

Siyuan Jiang

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EDUCATION

Tsinghua University, Tanwei College 2023 - 2027 (expected)
B.S. in Chemical Biology for Pharmaceutical Science Beijing, China

- GPA: 3.81/4.00
- Selected Courses:
Bioinformatics(A, Excellent Project), *Fundamentals of Programming (Python & C++)*(A, Excellent Project),
Chemical Biology(A), *AI in Healthcare*(A), *Medicinal Chemistry*(A)

RESEARCH EXPERIENCE

Wet Lab Member, iGEM Competition Aug 2024 - Oct 2024

Advisor: Prof. Chun Li

Department of Chemical Engineering, THU

- Developed an in-situ RNA quantification tool in yeast based on the ADAR protein, offering advantages over qPCR in speed, convenience, and non-destructive measurement.
- This tool facilitates a better understanding of real-time gene expression within living cells.
- Achievement: Awarded a Gold Medal at the 2024 iGEM Competition.

T-cell Specific In-situ CRISPR Screening System Jul 2025 - Oct 2025

Advisor: Prof. Xuebin Liao

School of Pharmaceutical Sciences, THU

- Addressed the limitations of traditional CRISPR screening, where scarce Hematopoietic Stem Cells (HSCs) impede in-situ studies.
- Leveraged infinitely proliferative mouse Embryonic Stem Cells (ESCs) with lineage-specific gene editing to establish an in-situ screening platform for immune cells.
- The platform aims to systematically dissect the dynamic regulation of T cell exhaustion and the metabolic-epigenetic coupling during memory T cell differentiation.

Spatiotemporal Evolution of the Gamma-Secretase Complex Jul 2025 - Now

Advisor: Prof. Yigong Shi

School of Life Sciences, THU

- Constructed eukaryotic phylogenetic trees for the gamma-secretase complex and traced the PS1 subunit from prokaryotic homologs to clarify its deep evolutionary origin.
- Batch-predicted approximately 1,500 structures with AlphaFold 3 and analyzed the stepwise assembly order of gamma-secretase subunits during evolution.
- Applied statistical methods and deep learning tools to identify mechanistically important residues in gamma-secretase and explore their potential association with Alzheimer's disease.

High-Throughput Screening of Functional Food-Derived Peptides Oct 2025 - Now

Advisor: Assoc. Researcher Yafei Yuan

School of Life Sciences, THU

- Developed a multi-stage screening pipeline for bioactive food-derived peptides targeting specific proteins, addressing the computational bottleneck of direct high-precision docking.
- Constructed and trained a lightweight pre-screening model to efficiently filter massive peptide libraries and enrich potential candidates for downstream analysis.
- Integrated AlphaFold 3 for high-precision structural validation of top candidates and finalized the study with wet-lab experimental assays to verify binding affinity.

RESEARCH INTERESTS

Protein Engineering, Design Models & Functional Evolution

My research interests center on **computational protein engineering**, especially model-driven protein design, virtual screening, evolutionary analysis, and functional redesign.

- **Protein Design Models:** I am interested in developing generative and predictive models for protein sequence, structure, and function. By integrating structural priors, evolutionary information, and experimental feedback, I hope to improve the reliability of computational protein design.
- **Virtual Screening & Functional Engineering:** I aim to build efficient screening pipelines for protein and peptide candidates, and to use evolutionary and functional analyses to guide rational modification of enzymes, binders, and other engineered proteins.

HONORS AND AWARDS

WeiGuang Program, Individual Excellence Award Jun 2025
An undergraduate research program initiated by the college to foster research skills.

Gold Award for the Practical Detachment, Tanwei College Jan 2025
Awarded for outstanding performance as the Team Leader of the 'Zhi-Shen-Qing-Lu' Social Practice delegation.

Comprehensive Excellence Award Nov 2024
Tsinghua University, University Scholarship (TOP 20%).

Gold Medal, iGEM Competition Oct 2024
The project was awarded in the premier international synthetic biology competition.

SELECTED PROJECTS

Machine Learning for Cancer Diagnosis using Plasma small RNAs Work Report
Developed a bioinformatics pipeline (Python, R, scikit-learn) to diagnose cancer from plasma small RNA-seq data. Implemented a robust feature selection method using L1-regularized regression over 100 stratified samples to identify stable biomarkers. The resulting 4-piRNA model for Colorectal Cancer (CRC) achieved a test AUC of 0.802. Also validated a novel "Rare Abundance Genes" (RAGs) strategy, building a scoring model that achieved an AUC of 0.971.

Protein-Peptide Interaction Prediction via Generative Docking & GNNs Course Project
Developed a generative-discriminative framework coupling diffusion-based docking (RAPiDock) with a Transformer-GNN scorer (ITN). Implemented multi-instance learning on 3D bipartite graphs to enable structure-aware, interpretable binding prediction. Outperformed sequence-based baselines in AUC and enrichment on pMHC I and SH3-peptide systems.

SKILLS

Programming Python, C++, R, Java, LaTeX
Frameworks PyTorch
Languages English (TOEFL 94)

HOBBIES

Sports Badminton (Member of the Tanwei College Team), Running, Swimming, Diving (Member of the Tsinghua University Diving Association)
Interests Rock Music, J-Pop, Sci-Fi Films (e.g., The Matrix, Star Wars)