

# Siyuan Jiang

 siyuanj |  jiang-sy23@mails.tsinghua.edu.cn |  188 1131 1636

## EDUCATION

---

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

- GPA: 3.80/4.00
- Selected Courses:  
*Bioinformatics*(A, Excellent Project), *Fundamentals of Programming (Python & C++)*(A, Excellent Project), *Organic Chemistry A(1)(2)*(A-), *Chemical Biology*(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 science, 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*

- Investigated the evolutionary pathway of how the subunits of the gamma-secretase complex assembled into a functional tetramer.
- Analyzed the absence of the complex in certain species and explored which proteins may have functionally replaced its role.
- Constructed phylogenetic trees for individual subunits and the complete tetramer to trace their evolutionary history.

**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, successfully enriching 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

---

## Computational Protein Design & Structural Biology

My research interests lie in **AI-driven protein sequence design** and **structure prediction**, with a specific focus on functional scaffolding.

- **Enzyme Engineering:** My goal is to replace empirical trial-and-error with computational methods to rationally design protein scaffolds and linkers. By spatially organizing multi-enzyme cascades, I seek to enhance substrate channeling and significantly improve reaction rates.
- **Structural Biology:** I am interested in designing auxiliary protein scaffolds to stabilize proteins. With the help of prediction tools, we can accelerate the high-resolution structure determination process.

# 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-Lü' 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

Research 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)