Sian Xiao (He/Him)

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Education

Southern Methodist University, Dallas, TX **Aug. 24, 2020 – Aug. 6, 2024**

- Ph.D. in Theoretical and Computational Chemistry GPA: 4.0/4.0
- Dissertation: Computational Study of Protein Dynamics and Allostery through Molecular Modeling and Machine Learning

Georgia Institute of Technology, Atlanta, GA **Aug. 21, 2022 – May. 1, 2025**

- M.S. in Computer Science, online GPA: 4.0/4.0
- Coursework: Software Dev Process, Computer Network, Data and Visual Analytics, Machine Learning for Trading, etc.

Beijing University of Chemical Technology, Beijing, China **Sep. 1, 2015 – Jul. 12, 2019**

- B.Eng. in Polymer Materials and Engineering GPA: 88.0/100

Work Experience

Goldman Sachs, Dallas, TX **Starting Jan. 13, 2025**

Quantitative Strategist (Prime Risk), Full-time

- The job duties will be similar to previous internship experience but not fully determined yet.

Southern Methodist University, Dallas, TX **Aug. 19, 2024 – Dec. 31, 2024**

Research Assistant, Full-time

- Conduct research on protein allostery mechanisms, specifically focusing on the ongoing *As*LOV2 study and collaborative work with Dr. Gennady Verkhivker on ABL Kinases.
- Prepare computational laboratory materials and provide technical support for the graduate-level course CHEM6344: Computer-Aided Drug.

Goldman Sachs, Dallas, TX **Jun. 10, 2024 – Aug. 16, 2024**

Quantitative Strategist (Prime Risk), Internship

- Analyze vulnerable market scenarios and funds vulnerable to them, to provide insights for manager from 5,000 hedge funds like Millennium.
- Automate the analysis process to cluster and analyze based on groups of clients and scenarios, which can be customized by users.
- Develop higher-level descriptors in risk factor decomposition to provide better explanation of market moves, focusing on Interest Rate.

Southern Methodist University, Dallas, TX **Aug. 24, 2020 – May. 31, 2024**

*Graduate Research Assistant – **AI for Science***

- Established and maintained one **public website** in **Django** for protein allosteric site prediction **(>85% accuracy, SOTA**).
- Developed, assessed, and benchmarked **deep learning** models to assist traditional simulations (**3 times faster**).
- Initiated automated and customized development workflow with **CI/CD** via GitHub Actions for the team.

Research

Protein Allostery Mechanism Explanation with Computational Approaches **Aug. 2022 – May. 2024**

- Wrote two review papers about the usage of emerging methods in protein allostery study to provide insights to this research field.
- Utilized molecular dynamics simulations and statistical methods to study the allosteric mechanism of *As*LOV2, SARS-COV-2 and ABL Kinases systems.

Protein Conformation Exploration **Sep. 2021 – Feb. 2023**

- Explored and benchmarked different models to assist conventional MD simulations to explore protein conformational spaces.
- Designed an efficient, open-source adaptive sampling algorithm based on structure embeddings and outlier dissimilarity that is 3 times faster than conventional MD simulations method.

Protein Allosteric Sites Prediction Server | http://passer.smu.edu **Jun. 2021 – Jun. 2023**

- Advanced the prediction accuracy of top 3 protein pockets and deployed the model to our Protein Allosteric Site Server (passer.smu.edu).
- The web server can handle job submission and protein visualization within web pages and already has more than 54,000 visits from more than 70 countries with more than 7,500 executions.