

# YUANYUAN ZHANG

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- Expected intern time: May 12,2025 - August 11,2025

## 🎓 EDUCATION

<b>Purdue University</b> , West Lafayette, IN, US	2021.9 – present
<i>Ph.D student</i> in Computer Science, GPA: 3.8/4.0 Area: Computational Biology, Machine Learning, Deep Learning	
<b>University of Chinese Academy of Sciences</b> , Beijing, China	2018.8 – 2021.6
<i>Master student</i> in Computer Science Area: Natural Language Processing, Machine Learning, Deep Learning	
<b>Sichuan University</b> , Sichuan, China	2014.9 – 2018.6
<i>Bachelor student</i> in Computer Science and Technology	

## 🏆 HONORS AND AWARDS

D.E. Shaw DESRES Doctoral Fellowship, New York, US	2024.3
Graduate Student Scholarship of ICT CAS (Top 1%), Beijing, China	2018.9-2021.6
Outstanding Graduate of Sichuan University (Top 1%) Chengdu, China	2018.6
Outstanding Student of Sichuan University (Top 3%), Chengdu, China	2015.9-2018.6
National Endeavor Fellowship (Top 1%), Sichuan University, Chengdu, China	2016.9-2017.6

## 👥 EXPERIENCE

<b>NobleLab and WangLab, University of Washington</b> Seattle, WA, US	2024.6 – 2024.8
<i>Summer intern</i> Advisor: Prof. William Stafford Noble and Sheng Wang <i>Masked autoencoder on Hi-C image reconstruction.</i> <ul style="list-style-type: none"><li>• Develop a Foundation Model based on MAE to high-throughput chromosome conformation capture(Hi-C) analysis.</li></ul> <i>Neural radiance field(NeRF) on cryo-EM structural reconstruction</i> <ul style="list-style-type: none"><li>• CryoNeRF: develop a neural radiance fields (NeRF)-based framework to reconstruct 3D cryo-EM structures on Euclidean 3D space.</li></ul>	
<b>KiharaLab, Purdue University</b> West Lafayette, IN, US	2022.5 – Present
<i>Research assistant</i> <i>Flow-matching on Cryo-EM map denosing</i> <ul style="list-style-type: none"><li>• FlowModeler-All Atom: A computational tool using Flow-Matching model to automatically build all-atom structure modeling with AlphaFold.</li></ul> <i>3D volume segmentation on Cryo-EM map using MUnet</i> <ul style="list-style-type: none"><li>• DAQ-ATOM: Estimating atomic structure with Deep Learning of 3D-MUNet to help experimental researchers to revise their deposited structures.</li></ul> <i>Protein structure prediction based on AlphaFold2</i> <ul style="list-style-type: none"><li>• Distance-AF: Accurately predict protein structures with distance constraints using AlphaFold2 using transformer and invariant point attention.</li></ul>	
<b>Department of Computer Science, Purdue University</b> West Lafayette, IN, US	2021.9 – Present
Teaching assistant for CS38003, CS50023, CS25100	

**Key Laboratory of Network Data Science and Technology, CAS Beijing, China** 2019.8 – 2021.6

*Research assistant*

Sentiment analysis and knowledge graph network by Deep Learning

**Xiaomi Co., Ltd.** Beijing, China

2019.3 – 2019.7

*Machine Learning Algorithm Intern*

Optimize recommendation algorithm based on feeds information

**Institute of Automation, CAS Beijing, China**

2016-6 – 2017.3

*Research Intern*

Intelligent education based on Deep Learning

## PUBLICATIONS

- Wang, X.\*, **Zhang, Y.\***, Ray, S., Jha, A., Doulatov, S., Wang S. & Noble, W. (2024). A generalizable Hi-C foundation model for chromatin architecture, single-cell and multi-omics analysis across species. Hi-C and Multi-omics Analysis.(Under first review of Science)
- Qu, H., Wang, X., **Zhang, Y.**, Wang, S., Noble, W. S., & Chen, T. (2025). CryoNeRF: reconstruction of homogeneous and heterogeneous cryo-EM structures using neural radiance field. bioRxiv, 2025-01.
- **Zhang, Y.**, Wang, X., Li, S., Terashi, G., Nakamura, T. & Kihara, D. (2024). DAQ-ATOM score for protein models evaluation from high-resolution Cryo-EM maps.(In submission)
- **Zhang, Y.**, Wang, X., Zhang, Z., Huang, Y., & Kihara, D. (2024). Assessment of Protein–Protein Docking Models Using Deep Learning. Protein-Protein Docking: Methods and Protocols, 149-162.
- **Zhang, Y.**, Zhang, Z., Kagaya, Y., Terashi, G., Zhao, B., Xiong, Y., & Kihara, D. (2023). Distance-AF: Modifying Predicted Protein Structure Models by AlphaFold2 with User-Specified Distance Constraints. bioRxiv, 2023-12.
- Wang, X., **Zhang, Y.**, Yu, S., Liu, X., & Wang, F. Y. (2018). Computerized adaptive English ability assessment based on deep learning. In Image and Video Technology: PSIVT 2017 International Workshops, Wuhan, China, November 20-24, 2017, Revised Selected Papers 8 (pp. 158-171). Springer International Publishing.
- Wang, X., **Zhang, Y.**, Yu, S., Liu, X., Yuan, Y., & Wang, F. Y. (2017, October). E-learning recommendation framework based on deep learning. In 2017 IEEE international conference on systems, man, and cybernetics (SMC) (pp. 455-460). IEEE.
- Farheen, F., Broyles, B. K., **Zhang, Y.**, Ibtihaz, N., Erkin, A. M., & Kihara, D. (2024). Predicting transcriptional activation domain function using Graph Neural Networks. bioRxiv, 2024-05.
- Bou Abdallah, F., Fish, J., Terashi, G., **Zhang, Y.**, Kihara, D., & Arosio, P. (2024). Unveiling the stochastic nature of human heteropolymer ferritin self assembly mechanism. Protein Science, 33(8), e5104.
- Gagliardi, L., Raffo, A., Fugacci, U., Biasotti, S., Rocchia, W., Huang, H., Amor, B.B., Fang, Y., **Zhang, Y.**, Wang, X. and Christoffer, C., 2022. SHREC 2022: Protein–ligand binding site recognition. Computers & Graphics, 107, pp.20-31.
- Lensink, M. F., Brysbaert, G., Raouraoua, N., Bates, P. A., Giulini, M., Honorato, R. V., ..., **Zhang, Y.**, ...& Wodak, S. J. (2023). Impact of AlphaFold on structure prediction of protein complexes: The CASP15 CAPRI experiment. Proteins: Structure, Function, and Bioinformatics, 91(12), 1658-1683.

## SKILLS

- **Expertise:** Python, Deep Learning, Machine Learning, Pytorch, TensorFlow
- **Capable:** Hadoop, Spark, C, C++, Java, Matlab