

YUANYUAN ZHANG

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- Expected graduation date: 2026.8

🎓 EDUCATION

Purdue University , West Lafayette, IN, US	2021.9 – 2026.8
<i>Ph.D student</i> in Computer Science, GPA: 3.8/4.0	
University of Chinese Academy of Sciences , Beijing, China	2018.8 – 2021.6
<i>Master</i> in Computer Science	
Sichuan University , Sichuan, China	2014.9 – 2018.6
<i>Bachelor</i> in Computer Science and Technology	

⭐ EXPERIENCE

Samsung America , Seattle WA, US	2025.5 – 2025.8
<i>Research intern</i>	
<i>Research area: Large Language Model post-training, Chain-Of-Thought reasoning on scaled model</i>	
<i>Research project: LLMAD-mini</i>	
<ul style="list-style-type: none">• Developed novel LLM-based log anomaly detection method that provides root cause analysis beyond detection, achieving 97% F1 score with 8B model (beating 235B baselines).• Proposed novel hierarchical Chain-of-Thought knowledge distillation from teacher model to student model significantly reducing training cost while maintaining performance.• Achieved 3.2x improvement in reasoning quality and 16x improvement in root cause diagnosis compared to larger LLMs, reducing debugging time by 60% in production tests	
Noble Lab and Wang Lab, University of Washington Seattle, WA, US	2024.6 – 2024.8
<i>Research intern</i> Advisor: Prof. William Stafford Noble and Sheng Wang	
<i>Research area: Generative AI, Self-supervised foundation model</i>	
<i>Research project: HiCFoundation</i>	
<ul style="list-style-type: none">• developed a contrastive based masked autoencoder for Hi-C data.• integrated vision transformer as network architecture.	
<i>Research project: CryoNeRF</i>	
<ul style="list-style-type: none">• worked on NeRF application on cryo-EM 3D image• designed heterogeneity-aware encoder for cryo-EM heterogeneity problem• utilized hash encoding to effectively encode the query coordinates.	

KiharaLab, Purdue University West Lafayette, IN, US	2022.5 – Present
<i>Research assistant</i> Advisor: Prof. Daisuke Kihara	
<i>Research area: AI for science, Generative AI</i>	
<i>Research project: Flow-All</i>	
<ul style="list-style-type: none">• developed a conditioned rectified flow matching algorithm for cryo-EM 3D density image denoising.	
<i>Research project: DAQ-Atom</i>	
<ul style="list-style-type: none">• developed a 3D-MUNet based architecture on 3D density map segmentation for protein structure evaluation.	
<i>Research project: Distance-AF</i>	
<ul style="list-style-type: none">• proposed a fine-tuning pipeline based on AlphaFold2 integrating distance constraints.• designed multi-task loss to optimize structure prediction	

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

SELECTED PUBLICATIONS

- **Zhang, Y.**, Bai, Y., Zhu, J., Hao, H. & Min, S. (2025) LLMAD-mini: Efficient Distilling Chain-of-Thought for Interpretable Log Anomaly Reasoning and Detection using Large Language Model. [\[Large Language Model\]](#)
- Jiang, Y.*, Li, X.* **Zhang, Y.***, Han, J., Xu, Y., Pandit, A., ... & Liu, J. (2025). PoseX: AI Defeats Physics Approaches on Protein-Ligand Cross Docking. *(Accepted by ICLR 2026)* <https://arxiv.org/abs/2505.01700>
- **Zhang, Y.**, Wang X. , Terashi G. , & Kihara D. (2025) Flow-All: A generalized flow-matching model for 3D structure modeling on low resolution cryo-EM maps. *(In submission)* [\[Generative AI\]](#), [\[AI for Science\]](#)
- Liu, X.*, **Zhang, Y.***, Lu, Y., Yin, C., Hu, X., Liu, X., ... & Wang, X. (2025). Biomedical Foundation Model: A Survey. <https://arxiv.org/abs/2503.02104>
- Wang, X.*, **Zhang, Y.***, Ray, S., Jha, A., Fang, T., Hang, S., ... & Wang, S. (2024). A generalizable Hi-C foundation model for chromatin architecture, single-cell and multi-omics analysis across species. *bioRxiv*. *Nature Methods* (Accepted). <https://www.biorxiv.org/content/10.1101/2024.12.16.628821v1.abstract> [\[Generative AI\]](#), [\[AI for Science\]](#)
- **Zhang, Y.**, , Zhang, Z., Kagaya, Y., Terashi, G., Zhao, B., Xiong, Y., & Kihara, D. (2025). Distance-AF improves predicted protein structure models by AlphaFold2 with user-specified distance constraints. *Communications Biology*, 8(1), 1392. <https://www.nature.com/articles/s42003-025-08783-5> [\[AI for Science\]](#)
- Terashi, G., Wang X., **Zhang Y.**, Zhu H., Park J. & Kihara D. (2025) DMcloud: Macromolecular Structure Modeling Using Local Structure Fitting for Medium to Low Resolution cryo-EM maps. *Under review by Nature Methods*. [\[Generative AI\]](#), [\[AI for Science\]](#)
- Hu, M., Ma, C., **Zhang, Y.**, ... & Zhou, B. (2025). A Survey of Scientific Large Language Models: From Data Foundations to Agent Frontiers. *arXiv preprint arXiv:2508.21148*. <https://arxiv.org/abs/2508.21148>
- Xu, Z., Wu, F., **Zhang, Y.**, & Zhao, Y. (2024). Retrieval-reasoning large language model-based synthetic clinical trial generation. *(Accepted by 2025 SIGKDD)* <https://arxiv.org/abs/2410.12476> [\[Large Language Model\]](#)
- 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. *Nature Biotechnology*. (Under 1st review) <https://www.biorxiv.org/content/10.1101/2025.01.10.632460v1> [\[Generative AI\]](#), [\[AI for Science\]](#)
- **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 to Nature Methods* [\[AI for Science\]](#)
- **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.
- 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.**, Ibtehaz, N., Erkine, 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.

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

SKILLS

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