Sheng Chen

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Education

Sun Yat-sen University, Guangzhou, China — 2021 – July 2025 (expected)
PhD Student in Computer Science and Technology

Sun Yat-sen University, Guangzhou, China — 2018 – 2020
M.Eng. in Software Engineering

Sun Yat-sen University, Guangzhou, China — 2014 – 2018
B.Eng. in Software Engineering

Experience

Sun Yat-sen University Guangzhou, China — 2021 – Present
PhD Candidate — Computer Science, AI for Life Science

AIxplorerBio Inc. Shanghai, China — 2022 – 2023
Director of AI — AI Platform AIxMTDD^{TM} for Dual-target Drug Design

Huawei Inc. Shenzhen, China — 2020 – 2021
Software Engineer — Huawei Cloud CodeArts Pipeline

Baidu Inc. Shenzhen, China — 2020
Intern — Automatic Vehicle Damage Assessment Algorithm

Publication

Journal/Conference	***Research Topic***	**Author Rank (Date)**
Nature Communications	*Cryo-EM Protein Complex Structure Modeling [1]*	1_{st} (2024)
Nature Communications	*Enzyme Functions Prediction [2]*	3_{rd} (2024)
Chemical Science	*Dual-target Drug Design [3]*	1_{st} (2024)
J. Chem. Inf. Model.	*Structure-Based Drug Design [4]*	co-1_{st} (2024)
IEEE BIBM	*Protein Side Chain Conformation Prediction [5]*	co-1_{st} (2023)
J. Comput. Chem.	*Protein Mutated Solubility Prediction [6]*	co-1_{st} (2023)
Briefings in bioinformatics	*Protein Intrinsic Disorder Prediction [7]*	3_{rd} (2023)
Bioinformatics	*B-Cell Epitopes Prediction [8]*	4_{th} (2023)
Briefings in Bioinformatics	*Protein-Metal-Iron Binding Site Prediction [9]*	2_{nd} (2022)
Briefings in Bioinformatics	*Protein-DNA Binding Site Prediction [10]*	2_{nd} (2022)
IEEE BIBM	*Cryo-EM Protein Structure Modeling [11]*	1_{st} (2021)
Nature Machine Intelligence	*Drug–Protein Interaction Prediction [12]*	3_{rd} (2020)
J. Chem. Inf. Model.	*Protein Design by Sequence Profile Prediction [13]*	1_{st} (2019)

Honors

Title	**Institution (Date)**
Tencent Scholarship	Tencent | SCSE, Sun Yat-sen University (2024)
Outstanding Poster of AI for Science doctoral student conference in GBA	Peking University (2024)
Champion of the Cryo-EM Protein Structure Modeling Challenge	National Protein Science Center | Alibaba | Intel (2022)
Outstanding Thesis	SCSE, Sun Yat-sen University (2020)

Philosophy

"Bridge, bridge across the realms of depth and sight"- inspired by Dylan Thomas's *Do not go gentle into that good night*.

References

[1] **Sheng Chen**, Sen Zhang, XiaoYu Fang, Liang Lin, Huiying Zhao, and Yuedong Yang. Protein complex structure modeling by cross-modal alignment between cryo-em maps and protein sequences. *Nature Communications*, 15(1):8808, 2024.

[2] Yidong Song, Qianmu Yuan, **Sheng Chen**, Yuansong Zeng, Huiying Zhao, and Yuedong Yang. Accurately predicting enzyme functions through geometric graph learning on esmfold-predicted structures. *Nature Communications*, 15(1):8180, 2024.

[3] **Sheng Chen**, Junjie Xie, Renlong Ye, David Daqiang Xu, and Yuedong Yang. Structure-aware dual-target drug design through collaborative learning of pharmacophore combination and molecular simulation. *Chemical Science*, 15(27):10366–10380, 2024.

[4] Junjie Xie†, **Sheng Chen**†, Jinping Lei, and Yuedong Yang. Diffdec: structure-aware scaffold decoration with an end-to-end diffusion model. *Journal of Chemical Information and Modeling*, 64(7):2554–2564, 2024.

[5] Deqin Liu†, **Sheng Chen**†, Shuangjia Zheng, Sen Zhang, and Yuedong Yang. Se (3) equivalent graph attention network as an energy-based model for protein side chain conformation. In *2023 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pages 120–123. IEEE, 2023.

[6] Jing Wang†, **Sheng Chen**†, Qianmu Yuan, Jianwen Chen, Danping Li, Lei Wang, and Yuedong Yang. Predicting the effects of mutations on protein solubility using graph convolution network and protein language model representation. *Journal of Computational Chemistry*, 45(8):436–445, 2024.

[7] Yidong Song, Qianmu Yuan, **Sheng Chen**, Ken Chen, Yaoqi Zhou, and Yuedong Yang. Fast and accurate protein intrinsic disorder prediction by using a pretrained language model. *Briefings in bioinformatics*, 24(4):bbad173, 2023.

[8] Yuansong Zeng, Zhuoyi Wei, Qianmu Yuan, **Sheng Chen**, Weijiang Yu, Yutong Lu, Jianzhao Gao, and Yuedong Yang. Identifying b-cell epitopes using alphafold2 predicted structures and pretrained language model. *Bioinformatics*, 39(4):btad187, 2023.

[9] Qianmu Yuan, **Sheng Chen**, Yu Wang, Huiying Zhao, and Yuedong Yang. Alignment-free metal ion-binding site prediction from protein sequence through pretrained language model and multi-task learning. *Briefings in bioinformatics*, 23(6):bbac444, 2022.

[10] Qianmu Yuan, **Sheng Chen**, Jiahua Rao, Shuangjia Zheng, Huiying Zhao, and Yuedong Yang. Alphafold2-aware protein–dna binding site prediction using graph transformer. *Briefings in Bioinformatics*, 23(2):bbab564, 2022.

[11] **Sheng Chen**, Sen Zhang, Xiongjun Li, Yubao Liu, and Yuedong Yang. Segem: A fast and accurate automated protein backbone structure modeling method for cryo-em. In *2021 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pages 24–31. IEEE, 2021.

[12] Shuangjia Zheng, Yongjian Li, **Sheng Chen**, Jun Xu, and Yuedong Yang. Predicting drug–protein interaction using quasi-visual question answering system. *Nature Machine Intelligence*, 2(2):134–140, 2020.

[13] **Sheng Chen**, Zhe Sun, Lihua Lin, Zifeng Liu, Xun Liu, Yutian Chong, Yutong Lu, Huiying Zhao, and Yuedong Yang. To improve protein sequence profile prediction through image captioning on pairwise residue distance map. *Journal of chemical information and modeling*, 60(1):391–399, 2019.