Heqin Zhu

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Google Scholar

Research Interests

My research interests center on AI biology, with focus on fundamental challenges in RNA modeling and molecular design, including: **(1) Structure and function prediction; (2) Multimodal biological foundation model; (3) Unified molecular design.**

- **Structure and function prediction**: Structure-guided RNA foundation model: structRFM [I8] (Nature, Under Revision); IRES identification [I7]; RNA secondary structure prediction: BPfold [I6] (Nature Communications), NCfold [I9] (ICLR 2026).

Educations

Ph.D.	**University of Science and Technology of China (USTC)**, Biomedical Engineering • Advisor: Prof. Shaohua Kevin Zhou	09/2023 - 06/2026
MS	**Institute of Computing Technology (ICT), Chinese Academy of Sciences (CAS) & University of Chinese Academy of Sciences (UCAS)**, Computer Science and Technology • Advisor: Prof. Shaohua Kevin Zhou	09/2020 - 06/2023
BS	**University of Science and Technology of China (USTC)**, Computer Science and Technology • Hua Xia Talent Program in Computer Science and Technology	09/2016 - 06/2020

Awards and Honors

Chinese Academy of Sciences, President's Excellent Award, CAS	2026
Provincial Outstanding Graduate (Ph.D., Class of 2026), Anhui Province	2026
Outstanding Graduate (Ph.D., Class of 2026), USTC	2026
National Scholarship for Doctoral Students, Chinese Ministry of Education	2025
The Second Prize of the oral talk, The 3rd National Conference on Biomolecular Structure Prediction and Simulation	2025
Suzhou Industrial Park Scholarship, USTC	2025
Merit student award, UCAS & ICT	2023
Graduate Academic Scholarship, UCAS & ICT, USTC	2020 - 2025
Outstanding Student Award, USTC	2018 - 2019
Institute of Chemistry Excellence Scholarship, USTC	2017

Project and Internship

Structure-guided RNA Foundation Model - structRFM Paper | Code (35 stars)　Nature, Under Revision 08/2025

- First author
- Designed a structure-guided masked language modeling pre-training strategy (SgMLM) that selectively masks input tokens corresponding to canonical base pairs within local structural contexts.

- Achieved state-of-the-art results on fine-tuning downstream tasks: Zero-shot homology classification, secondary structure prediction, tertiary structure prediction, IRES identification, ncRNA classification, Splice site prediction.

RNA Secondary Structure Prediction Model - BPfold Paper ↗ | Code ↗ (35 stars) — Nature Communications 07/2025

- First author
- Introduced base pair motif energy to improve data coverage and quality for RNA structure prediction.
- Designed multi-modal fusion network BPfold (integrating sequence and energy matrix) to enhance prediction accuracy and generalization.

Tencent, JARVIS Lab, Research Intern — Shenzhen, China 07/2021 - 11/2021

- Developed depth-supervised feature fusion transformer for salient object detection [I3].

USTC Courses Resource GitHub ↗ ~16,000 stars, Open-source project — 2019 - Present

- Led and maintained open-source project for curating computer science learning resources.

Academic Activities

- **Academic Reviewer**: Neurips, MICCAI, TCSVT
- **Volunteer Activities**
  - Medical Augmented Reality Summer School (Suzhou, 2024)
  - Dushu Lake Symposium on Medical Image Computing (Suzhou, 2023)

Teaching Assistant

- Open Practice in Electronic Information (USTC, 2023)
- Biomolecular Structure Modeling (USTC, 2024)

Mentorship

I greatly enjoy partnering with these talented young researchers (including doctoral and master-s candidates I co-advised), and their efforts lead to a series of notable research achievements.

Ao Chang, Ph.D.: Motif-informed RNA language pre-training using Mamba — 2025 - 2026

Haobin Chen, MS: Using LLM and agent to retrieve lncRNA knowledge from literature — 2025 - 2026

Duofan Tu, MS: Building medical agent for diagnosis — 2024 - 2026

Feng Zhang, MS: IRES identification in circlular RNAs — 2024 - 2026

- IRESeek: structure-informed deep learning method for accurate identification of internal ribosome entry sites in circular RNAs

Xiaoqian Zhou, MS: Anatomical landmark detection in medical images — 2022 - 2024

- Hybrid attention network: An efficient approach for anatomy-free landmark detection

Zhen Huang, MS: Anatomical landmark detection in x-ray images — 2021 - 2023

- Pele scores: pelvic x-ray landmark detection with pelvis extraction and enhancement

Invited Talks

Structure-centric AI for RNA modeling, Course on Digital Healthcare Technology and Applications, USTC — Dec 2025

Deep generalizable prediction of RNA secondary structure via base pair motif energy, The 3rd National Conference on Biomolecular Structure Prediction and Simulation — May 2025

Universal one-shot detection of anatomical landmarks, Academic Forum for Graduates, Institute of Computing Technology. Mar 2023

Technical Skills

Deep Learning: PyTorch, LLM, Diffusion Model, Multi-modality Fusion,

Programming & Tools: C++, Python, Git, VIM, Latex, HTML, Office, Matplotlib

References

S. Kevin Zhou, Professor, University of Science and Technology of China skevinzhou@ustc.edu.cn
Peng Xiong, Professor, University of Science and Technology of China xiongxp@ustc.edu.cn
Wanxiang Shen, Professor, Zhejiang University shenwx25@zju.edu.cn

Selected Publications

I=Representative, J=Journal, C=Conference

# denotes co-first author and * denotes co-corresponding author. For full list, please refer to Google Scholar.

Representative Papers

[I9] **Heqin Zhu**#, Ruifeng Li#, Ao Chang, Mingqian Li, Hongyang Chen*, Peng Xiong*, and S. Kevin Zhou*. "Toward Accurate RNA Non-Canonical Structure Prediction: The NC-Bench Benchmark and the NCfold Framework." (ICLR 2026). [bioRxiv; Code]

[I8] **Heqin Zhu**, Ruifeng Li, Feng Zhang, Fenghe Tang, Tong Ye, Xin Li, Yunjie Gu, Peng Xiong*, and S. Kevin Zhou*. "A fully open structure-guided RNA foundation model for robust structural and functional inference." (Nature, Under Revision). [bioRxiv; Code]

[I7] Feng Zhang#, **Heqin Zhu**#, Jiayin Gao, Jie Hu, Ke Chen, Shaohua Kevin Zhou*, and Peng Xiong*. "IRESeek: structure-informed deep learning method for accurate identification of internal ribosome entry sites in circular RNAs." NAR Genomics and Bioinformatics 7, no. 4 (2025): lqaf210. (NAR Genomics and Bioinformatics). [Paper;Code]

[I6] **Heqin Zhu**, Fenghe Tang, Quan Quan, Ke Chen, Peng Xiong*, and S. Kevin Zhou*. "Deep generalizable prediction of RNA secondary structure via base pair motif energy." Nature Communications 16, (2025): 5856. (Nat. Commun., 2025). [Paper; Code]

[I5] **Heqin Zhu**, Quan Quan, Qingsong Yao, Zaiyi Liu, and S. Kevin Zhou. "Uod: Universal one-shot detection of anatomical landmarks." In International Conference on Medical Image Computing and Computer-Assisted Intervention, pp. 24-34. Cham: Springer Nature Switzerland, 2023. (MICCAI 2023). [Paper; Code]

[I4] **Heqin Zhu**, Qingsong Yao, and S. Kevin Zhou. "Datr: Domain-adaptive transformer for multi-domain landmark detection." arxiv preprint arxiv:2203.06433 (2022). (Preprint). [Paper; Code]

[I3] **Heqin Zhu**, Xu Sun, Yuexiang Li, Kai Ma, S. Kevin Zhou*, and Yefeng Zheng*. "DFTR: Depth-supervised fusion transformer for salient object detection." arxiv preprint arxiv:2203.06429 (2022). (Preprint). [Paper; Code]

[I2] **Heqin Zhu**, Qingsong Yao, Li Xiao, and S. Kevin Zhou. "Learning to Localize Cross-Anatomy Landmarks in X-Ray Images with a Universal Model." BME Frontiers 2022 (2022): 9765095. (BMEF 2022). [Paper; Code]

[I1] **Heqin Zhu**, Qingsong Yao, Li xiao, and S. Kevin Zhou. "You only learn once: Universal anatomical landmark detection." In Medical Image Computing and Computer Assisted Intervention, pp. 85-95. Springer International Publishing, 2021. (MICCAI 2021). [Paper; Code]

Journal Papers

[J4] Quan Quan#, Qingsong Yao#, **Heqin Zhu**, and S. Kevin Zhou. "IGU-Aug: Information-guided unsupervised augmentation and pixel-wise contrastive learning for medical image analysis." IEEE Transactions on Medical Imaging (2024). (TMI 2024).

[J3] Quan Quan#, Qingsong Yao#, **Heqin Zhu**, Qiyuan Wang, and S. Kevin Zhou. "Which images to label for few-shot medical image analysis?." Medical Image Analysis 96 (2024): 103200. (MIA 2024).

[J2] Huang Zhen#, Han Li#, Shitong Shao, **Heqin Zhu**, Huijie Hu, Zhiwei Cheng, Jianji Wang, and S. Kevin Zhou. "PELE scores: pelvic X-ray landmark detection with pelvis extraction and enhancement." International Journal of Computer Assisted Radiology and Surgery 19, no. 5 (2024): 939-950. (IJCARS 2024).

[J1] Pengbo Liu, Hu Han, Yuanqi Du, **Heqin Zhu**, Yinhao Li, Feng Gu et al. "Deep learning to segment pelvic bones: large-scale CT datasets and baseline models." International Journal of Computer Assisted Radiology and Surgery 16 (2021): 749-756. (IJCARS 2021).

Conference Papers

[C4] Fenghe Tang, Chengqi Dong, Wenxin Ma, Zikang Xu, **Heqin Zhu**, Zihang Jiang, Rongsheng Wang, Yuhao Wang, Chenxu Wu, and Shaohua Kevin Zhou. "U-Bench: A Comprehensive Understanding of U-Net through 100-Variant Benchmarking." arXiv preprint arXiv:2510.07041 (2025). (Under review).

[C3] Xinyi Wang, Zikang Xu, **Heqin Zhu**, Qingsong Yao, Yiyong Sun, and S. Kevin Zhou. "SIX-Net: Spatial-Context Information miX-up for Electrode Landmark Detection." In International Conference on Medical Image Computing and Computer-Assisted Intervention, pp. 338-348. Cham: Springer Nature Switzerland, 2024. (MICCAI 2024).

[C2] Fenghe Tang, Ronghao Xu, Qingsong Yao, Xueming Fu, Quan Quan, **Heqin Zhu**, Zaiyi Liu, and S. Kevin Zhou. "Hyspark: Hybrid sparse masking for large scale medical image pre-training." In International Conference on Medical Image Computing and Computer-Assisted Intervention, pp. 330-340. Cham: Springer Nature Switzerland, 2024. (MICCAI 2024).

[C1] Yuanyuan Lyu, Haofu Liao, **Heqin Zhu**, and S. Kevin Zhou. "A 3 DSegNet: anatomy-aware artifact disentanglement and segmentation network for unpaired segmentation, artifact reduction, and modality translation." In International Conference on Information Processing in Medical Imaging, pp. 360-372. Cham: Springer International Publishing, 2021. (IPMI 2021).