

Rongxin Zhang

Ph.D. Candidate in Bioinformatics

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EDUCATION

Southeast University, *Ph.D. candidate* Sept. 2018 - present
State Key Laboratory of Bioelectronics
Department of Bioinformatics and System Biology
School of Biological Science and Medical Engineering, Nanjing, China
Nanjing Medical University, *Bachelor of Science* Sept. 2014 - June 2018
Department of Bioinformatics
School of Biomedical Engineering and Informatics, Nanjing, China

SKILLS

Programming: R, Python, PHP, et al. Software and website developing.
Proficiency in sequencing data analysis, such as RNA-seq, ChIP-seq, DNase-seq et al.
Data mining and statistical analysis and their application to medical or bioinformatics research.
Knowledge of biology and medicine.
Have good communication and teamwork skills.

RESEARCH EXPERIENCE

Designed and built two Bioinformatics databases, iCAN and Mir2Drug. (**Database Developing**)
Participated in a study to assess the risk of development of type 2 diabetes in the Chinese urban population by using machine learning approaches. (**Machine Learning Applied in Medicine**)
Identified Glioblastoma (GBM) samples from scRNA-seq data. (**Undergraduate Graduation Project**)
Analyzed the potential role of G-quadruplexes in the SARS-CoV-2 genome, the human 3D genome, and the human transcriptome. (**Epigenetic Project**)

AWARDS AND DISTINCTIONS

Outstanding Graduates of Nanjing Medical University
The Contest of LAN QIAO CUP (JAVA Programming Language Competition) [Third Prize]
China College Students Computer Design Competition (Software Development) [Second Prize]
Triple-A Students of Nanjing Medical University
Innovation Cup of Computer Design Competition [Second Prize]
Excellent Academic Poster (The 9th Jiangsu Provincial Bioinformatics Academic Conference)

PUBLICATIONS

[Google scholar](#)

- [1] **Zhang, R.**, Liu, Y., Zhang, X., Xiao, K., Hou, Y., Liu, H., & Sun, X. (2021). Detecting and Profiling Endogenous RNA G-Quadruplexes in the Human Transcriptome. *International journal of molecular sciences*, 22(15), 8012. <https://doi.org/10.3390/ijms22158012>
- [2] 李浩, 张荣鑫, 侯越 & 孙啸. (2021). 基因组G-四链体与疾病的关系. *生命的化学* (06), 1244-1251. [doi:10.13488/j.smhx.20200597](https://doi.org/10.13488/j.smhx.20200597)
- [3] **Zhang, R.**, Xiao, K., Gu, Y., Liu, H., & Sun, X. (2020). Whole Genome Identification of Potential G-Quadruplexes and Analysis of the G-Quadruplex Binding Domain for SARS-CoV-2. *Frontiers in genetics*, 11, 587829. <https://doi.org/10.3389/fgene.2020.587829>
- [4] Hou, Y., **Zhang, R.**, & Sun, X. (2019). Enhancer LncRNAs Influence Chromatin Interactions in Different Ways. *Frontiers in genetics*, 10, 936. <https://doi.org/10.3389/fgene.2019.00936>
- [5] Hou, Y., Li, F., **Zhang, R.**, Li, S., Liu, H., Qin, Z. S., & Sun, X. (2019). Integrative characterization of G-Quadruplexes in the three-dimensional chromatin structure. *Epigenetics*, 14(9), 894-911. <https://doi.org/10.1080/15592294.2019.1621140>
- [6] Xiong, X. L., **Zhang, R. X. (co-first author)**, Bi, Y., Zhou, W. H., Yu, Y., & Zhu, D. L. (2019). Machine Learning Models in Type 2 Diabetes Risk Prediction: Results from a Cross-sectional Retrospective Study in Chinese Adults. *Current medical science*, 39(4), 582-588. <https://doi.org/10.1007/s11596-019-2077-4>
- [7] Zuo, J., Li, J., **Zhang, R.**, Xu, L., Chen, H., Jia, X., Su, Z., Zhao, L., Huang, X., & Xie, W. (2017). Institute collection and analysis of Nanobodies (iCAN): a comprehensive database and analysis platform for nanobodies. *BMC genomics*, 18(1), 797. <https://doi.org/10.1186/s12864-017-4204-6>
- [8] Wang, X., Jiang, H., Wu, W., **Zhang, R.**, Wu, L., Chen, H., Li, P., Nie, Y., Shao, J., Li, Y., Lin, X., Lv, S., Wang, Q., & Hu, J. (2017). An Integrating Approach for Genome-Wide Screening of MicroRNA Polymorphisms Mediated Drug Response Alterations. *International journal of genomics*, 2017, 1674827. <https://doi.org/10.1155/2017/1674827>