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特聘教授、博士生导师

非编码 RNA 功能研究与转化应用实验室独立 PI

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● 教育和工作背景:

2010 年，安徽科技学院，生物技术专业，理学学士；

2013 年，西北农林科技大学，生物信息学专业，理学硕士；

2017 年，中国科学院遗传与发育生物学研究所，生物信息学专业，理学博士；

2017/08—2018/03，南通大学医学院，讲师；

2018/04—2021/06，浙江大学医学院，博士后；

2021/09—2022/11，西湖大学生命科学学院，助理研究员；

2022/12—2023/02，西湖实验室，副研究员；

2022/03—至今，南昌大学基础医学院，特聘教授、博士生导师。

● 研究兴趣及领域:

课题组长期致力于通过干湿相结合的研究策略（一方面开发新型计算生物学方法及工具，另一方面开展生物学实验）对非编码 RNA 功能及作用机制进行系统性研究及应用转化，发现驱动胚胎干细胞命运决定及癌症发生发展的关键非编码 RNA 分子，筛选靶向关键非编码 RNA 的小分子及大分子药物。近年来，课题组在 Nature Communications、Nature Metabolism、Protein & Cell、Genome Biology、Bioinformatics 等高水平杂志上共发表 SCI 学术论文 22 篇，开发生物信息学软件 7 款，其中第一作者或通讯作者（含共同）论文 14 篇，发表当年影响因子累计 197，全部文章累计被引用 2200 余次，H 指数 13，第一作者论文单篇最高引用次数 351，代表性研究成果受邀在国际干细胞协会年会（ISSCR）上做口头学术报告，其中两篇论文被选为杂志封面论文，一篇论文被 Science News 等多家知名媒体专题报道。

● 学术兼职:

Bioinformatics 杂志审稿人。

● 代表性论文:

(#) 共同第一作者; (*) 通讯作者

- [1] **Hua Yu#**, Zhen Sun#, Tianyu Tan#, Hongru Pan#, Jing Zhao, Ling Zhang, Jiayu Chen, Yuqing Zhu, Lang Chen, Yuyan Xu, Shaorong Gao, George Q. Daley, Jin Zhang*. rRNA Biogenesis Regulates Mouse 2C-like State by 3D Structure Reorganization of Peri-Nucleolar Heterochromatin. *Nature Communications*, 2021 12(6365). <https://doi.org/10.1038/s41467-021-26576-2>.
- [2] Zhen Sun#, **Hua Yu#**, Jing Zhao#, Tianyu Tan, Hongru Pan, Bo Gao, Yuqing Zhu, Lang Chen, Cheng Zhang, Li Zhang, Anhua Lei, Yuyan Xu, Xianju Bi, Xin Huang, Cristina Correia, Ming Chen, Qiming Sun, Li Shen, Longfei Wang, Yu Feng, Jianlong Wang, Xiaohua Shen, Hu Li, Hao Wu, George Q. Daley, Jin Zhang*. LIN28 coordinately promotes nucleolar/ribosomal functions and represses the 2C-like transcriptional program in pluripotent stem cells. *Protein & Cell*, 2021. <https://doi.org/10.1007/s13238-021-00864-5>.
- [3] Jing Zhao#, Ke Yao#, **Hua Yu#**, Ling Zhang, Yuyan Xu, Lang Chen¹, Zhen Sun, Yuqing Zhu, Chen Zhang, Yuli Qian, Zhuyan Ji, Min Zhang, Jie Chen, Cristina Correia, Taylor Weiskittel, Dan Zhang, Hu Li, Wei Xie, Zeping Hu*, Jin Zhang* Metabolic reprogramming during mouse early embryo development. *Nature Metabolism*, 2021 3(1). <https://doi.org/10.1038/s42255-021-00464-x>.
- [4] Lin Yang, Yuqing Zhu#, **Hua Yu#**, Xiaolong Cheng, Sitong Chen, Yulan Chu, He Huang, Jin Zhang*, Wei Li*. scMAGeCK links genotypes with multiple phenotypes in single-cell CRISPR screens. *Genome Biology*, 2020 21(19). <https://doi.org/10.1186/s13059-020-1928-4>.
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- [6] **Hua Yu#***, Lu Lu#, Bingke Jiao, Chengzhi Liang*. Systematic discovery of novel and valuable plant gene modules by large-scale RNA-seq samples. *Bioinformatics*, 2018, bty642. <https://doi.org/10.1093/bioinformatics/bty642>.
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- [8] **Hua Yu#***, Lu Lu#, Ming Chen, Chen Li*, Jin Zhang*, Genome-wide discovery of hidden genes mediating known drug-disease association using KDDANet. *npj Genomic Medicine*, 2021 6(50). <https://doi.org/10.1038/s41525-021-00216-6>.

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● 荣誉及奖励

1. 西湖实验室“开拓学者”计划入选者。
2. 浙江大学优秀博士后。
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