



## 余华 博士

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

医学科技创新中心组学与大数据平台负责人

### ● 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 Cell Reports、Nature Communications、Nature Immunology、Nature Metabolism、Protein & Cell、Genome Biology、Bioinformatics 等高水平杂志上共发表 SCI 学术论文 26 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 16 篇，发表当年影响因子累计 276，全部文章累计被引用 2200 余次，H 指数 16，第一作者论文单篇最高引用 360 余次，代表性成果受邀在国际干细胞协会年会（ISSCR）上做口头学术报告，其中三篇论文被选为杂志封面论文，二篇论文被 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**##\*, Jing Zhao#, Yuxuan Shen, Qiao Lu, Yuheng Liu, Guanglei Xie, Shu hui Chang, Tingying Ge, Nan Li, Ming Chen, Hu Li, Jin Zhang\*, Xi Wang\*. The dynamic landscape of enhancer-derived RNA during mammalian early embryo development. *Cell Reports*, 2024, 43(4):114077. <https://doi.org/10.1016/j.celrep.2024.114077>.

[2] **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(1):6365. <https://doi.org/10.1038/s41467-021-26576-2>.

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[10] **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>.

[11] **Hua Yu#**, Jianxin Chen#, Xue Xu, Yan Li, Huihui Zhao, Xiuxiu Li, Wei Zhou, Wei Wang\* and Yonghua Wang\*. A systematic prediction of multiple drug-target interactions from chemical, genomic and pharmacological data. *PLoS ONE*, 2012, 7(5): e37608. <https://doi.org/10.1371/journal.pone.0037608>.

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ijk, Jifeng Tang, Hanneke M. A. Witsenboer, Shancen Zhao, Zhensheng Li, Aimin Zhang\*, Daowen Wang\*, Chengzhi Liang\*. Genome sequence of the progenitor of wheat A subgenome Triticum Urartu. *Nature*, 2018, 557:424-428. <https://doi.org/10.1038/s41586-018-0108-0>.

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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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