

Erratum

Modeling circRNA expression pattern with integrated sequence and epigenetic features demonstrates the potential involvement of H3K79me2 in circRNA expression

Jia-Bin Chen, Shan-Shan Dong, Shi Yao, Yuan-Yuan Duan, Wei-Xin Hu, Hao Chen, Nai-Ning Wang, Xiao-Feng Chen, Ruo-Han Hao, Hlaing Nwe Thynn, Ming-Rui Guo, Yu-Jie Zhang, Yu Rong, Yi-Xiao Chen, Fu-Ling Zhou, Yan Guo and Tie-Lin Yang

Bioinformatics (2020) doi: 10.1093/bioinformatics/btaa567

In the originally published version of this manuscript, author affiliation 1 was incorrect.

The incorrect affiliation was as follows: “Key Laboratory of Biomedical Information Engineering of Ministry of Education, Biomedical Informatics & Genomics Center, School of Life Science

and Technology, Zhongnan Hospital of Wuhan University, Wuhan 430071, China.”

The correct affiliation should read: “Key Laboratory of Biomedical Information Engineering of Ministry of Education, Biomedical Informatics & Genomics Center, School of Life Science and Technology, Xi'an Jiaotong University, Xi'an 710049, P. R. China.”

This error has been corrected online.