



Hong Kong RNA Club



RNA Enthusiast Spotlight (May 2023)



Dr. Jilin ZHANG is an assistant professor in the Department of Biomedical Sciences at the City University of Hong Kong (CityU). In 2022, he joined cityU as a junior faculty member.

Dr. ZHANG's group at CityU primarily applies and develops novel computational approaches to study the interaction between RNA binding proteins (RBPs) and non-coding RNAs. His team currently focuses on revealing molecular mechanisms that determine the binding specificity and diversity between RBPs and RNAs, particularly for the structured long non-coding RNAs. His group is also developing new tools to analyze high-throughput sequencing assays that probe the RNA secondary structures, including HTR-SELEX and SHAPE-MaP.

In addition, Dr. ZHANG's laboratory has enthusiastically engaged in addressing biological questions through integrative analyses of single-cell omics and numerous genomics data. Please find more information on the CityU website: <https://www.cityu.edu.hk/bms/profile/jilinzhang.htm> and the group's website: www.jzlab.net

Recent representative publications

S. Fan, W. Sun, L. Fan, N. Wu, W. Sun, H. Ma, S. Chen, Z. Li, Y. Li, J. Zhang, J. Yan, The highly conserved RNA-binding specificity of nucleocapsid protein facilitates the identification of drugs with broad anti-coronavirus activity. *Comput Struct Biotechnol J* 20, 5040-5044 (2022).

Z. Wang, J. Zhang, X. Xu, C. Witt, Y. Deng, G. Chen, G. Meng, S. Feng, L. Xu, T. Szekely, G. Zhang, Q. Zhou, Phylogeny and sex chromosome evolution of Palaeognathae. *J Genet Genomics* 49, 109-119 (2022).

A. Jolma, J. Zhang, E. Mondragón, E. Morgunova, T. Kivioja, Y. Yin, F. Zhu, G. Bourenkov, Q. Morris, T. R. Hughes, L. J. Maher III, J. Taipale, Binding specificities of human RNA binding proteins towards structured and linear RNA sequences. *Genome Research* 30, 962-973 (2020).

To decode the functional map of genomic sequences, it is crucial to know how sequences are utilized *in vivo*. Dr. ZHANG is excited about the recent advance in sequencing techniques and computational biology, which has dramatically empowered our ability to address various biological questions at unprecedented scale and depth. He believes that RNAs play broad and essential regulatory roles in biological processes, where RBPs and RNA secondary structures can form distinct functional modules to exert diverse functions in the sub-cellular compartments.

Dr. ZHANG believes "It is never too late to learn". As a principal investigator and a mentor, Dr. Zhang always encourages his students to tackle problems and find the answers to their questions by themselves. He envisions that the modular structures of regulatory RNAs will remain a challenging research topic and that elucidating the underlying principles will significantly impact non-heritable transcriptome engineering. What's more, he believes that Kong Kong is becoming an international hub that attracts many talented students/PIs to join the local RNA community to do spectacular RNA research.



Written by Jilin Zhang, Edited by Hill Lam Lau (HKRNAClub Team)

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