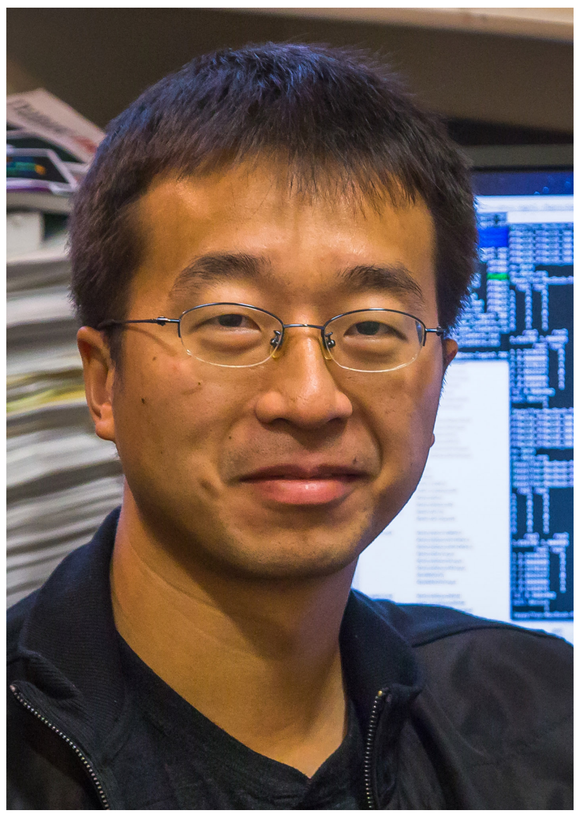
2015年1月16日(周五)上午10:00-11:00

同济大学医学楼1101会议室

Genome-wide analysis of RNA-protein interactions in regulated transcription and splicing



Yu Zhou, Ph.D.

Postdoc Fellow
in Prof. Xiang-Dong Fu's lab
University of California,
San Diego

Next-Generation Sequencing (NGS) has revolutionized biological studies from basic research to translational medicine. Whole-exome sequencing has discovered mutations in many RNA binding proteins (RBPs) that are tightly associated with different diseases. However the functions of RBPs and the underlying mechanisms are still largely unknown. In this talk, I will present our works on exploring the functional roles and mechanisms of classical RBPs in gene transcription and alternative spicing regulation using various NGS techniques. Specifically, I will first focus on our findings of RBP binding-targets identification across the genome by CLIP-seq and quantitative determination of splicing isoforms by RASL-seq. Using these techniques, we have uncovered the positional rules of PTB protein in regulating splicing and microRNA targeting, and the competition/cooperation between SR proteins in regulated splicing. Moreover, with ChIP-seq and GRO-seq, we recently discovered the function of SRSF2 in transcriptional pause-release. Lastly, I will introduce our newly developed DRB releasing assay to measure Pol II elongation rates, by which we identified several potential positive and negative determinants at different levels in the regulation of transcriptional elongation and acceleration.

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