报 告 人：**Zhe Ji, PhD**

Assistant Professor
Northwestern University

主 持 人：杨 鹏

时　　间：**2017 年 1 月 17 日 10:00-11:00**

地　　点： 医学楼 1102

Education

Postdoc Cancer Systems Biology, Harvard Medical School, Boston, MA

Postdoc Computational Biology, Broad Institute of MIT and Harvard, Cambridge, MA

Ph.D Computational Genomics, Rutgers University, Newark, NJ

B.S. Biotechnology, Nanjing University, China

Research focus

Our group uses high-throughput genomic technologies and computational modeling to examine the regulation of gene transcription and RNA translation underlying oncogenic processes. We aim at revealing novel cancer therapeutic strategies for precision medicine and immunotherapy.

Reference

Miotto, B.*, Ji, Z.* and Struhl, K. (2016). Selectivity of ORC binding sites and the relation to replication timing, fragile sites, and deletions in cancers. Proc Natl Acad Sci U S A, 113, E4810-E4819.

Ji, Z., Song, R., Huang, H., Regev, A. and Struhl, K. (2016). Transcriptome-scale RNase-footprinting of RNA-protein complexes. Nature Biotechnology, 34 (4), 410-413.

Ji, Z.*, Song, R.*, Regev, A. and Struhl, K. (2015). Many lncRNAs, 5'UTRs, and pseudogenes are translated and some are likely to express functional proteins. eLife, 4: e08890.

Hoque, M.*, Ji, Z.*, Zheng, D., Luo, W., Li, W., You, B., Park, J.Y., Yehia, G., and Tian, B. (2013). Analysis of alternative cleavage and polyadenylation by 3' region extraction and deep sequencing. Nature Methods 10, 133-139.