

## Zhengqing Ouyang

Howard Hughes Medical Institute and Program in Epithelial Biology  
Department of Genetics and Center for Genomics and Personalized Medicine  
Stanford University School of Medicine

*SeqFold: Accurate genome-scale RNA structure reconstruction integrating experimental measurements provides insights into gene regulation*

Regulatory information in RNA is encoded not only in its primary sequence, but also in its structure with complex base pairing patterns. Virtually every step in the gene expression program, from transcription to splicing and translation, is influenced by RNA structure. Precise mapping of RNA structure is essential for understanding the functions of RNAs, especially for the large set of functionally uncharacterized non-coding RNAs (ncRNAs) (Wan et al. 2011). Experimental methods for RNA structure determination, although quite accurate, are traditionally only applicable to analyze a single RNA per experiment, and limited in the length of the probed RNA. Computational methods, aiming at predicting RNA structure from primary sequence, have been developed and can be applied to a large number of RNAs with the increasing computational power. However, in silico algorithms have variable accuracy, and may be limited by the scope of applicability under real experimental conditions.