

**主辦單位：生命科學與技術學院****報告人：Prof. Michael Q. Zhang****清華大學/University of Texas at Dallas****主持人：岳銳 教授****時間：2018年11月21日 (周三) , 10:00-11:00 am****地點：醫學樓二樓報告廳****報告題目：****Dissecting Functional Regulatory Structures of the Genome from 1D to 3D****報告人簡介：**

Michael got his B.S. in Mech. Eng. from USTC and joined the first CUSPEA (initiated by T.D. Lee) group studying physics in USA in 1981. After getting Statistical Physics PhD from Rutgers University in 1987, he became a postdoc at the Courant Institute of Mathematics at NYU until he became a Genome Research fellow at CSHL in 1991. He started his Computational Genomics Lab there in 1996 and became full professor in 2002. He became guest professor of Tsinghua University in 2009 and moved to The University of Texas at Dallas as the Cecil H. and Ida Green Distinguished endowed chair Professor in 2010. He is currently the director of Center for Systems Biology at UT Dallas and the co-director of Center for Synthetic and Systems Biology at Tsinghua U.

In this lecture, Michael will briefly review technology development in studying cis-regulatory structures and functional genomics/epigenomics in his lab. Then introduce their recent developments in biochemical (BL-Hi-C), biophysical (Super-resolution imaging) and Bioinformatics (Functional DNA loop quantitation and prediction) technologies, in particular on a new methodology CAPTURE -- "In Situ Capture of Chromatin Interactions by Biotinylated dCas9" and its application for in situ capture of individual constituents of the enhancer cluster controlling human  $\beta$ -globin genes, which establishes evidence for composition-based hierarchical 3D regulatory organization.

