Abstract of Presentation

Note: This paper should be typed in "Times New Roman" of 12pt.

Presentation Title(Should be no more than 20 words):

Mapping gene regulatory networks to understand transcription factor function in health and disease

Abstract :

Gene regulatory networks play a vital role in metazoan development and function as they control gene expression. Consequently, deregulation of these networks results in widespread changes in gene expression, which often lead to disease. Gene regulatory network deregulation is typically a consequence of the inappropriate (in)activation or expression of transcription factors (TFs), which are the core members of these regulatory networks. TFs function by integrating extra- and intracellular cues through protein-protein or protein-ligand interactions and translating these cues into gene expression output by binding to gene regulatory elements. Given their critical role as signal integrators, many TFs have so far been implicated in a wide range of pathologies including cancer and neurological diseases. Yet, they have traditionally been considered to be off-limit for drug development despite the availability of several successful drugs specifically targeting these regulatory proteins (e.g. tamoxifen targeting the estrogen receptor alpha TF in breast cancer). In recent years, several technologies have been developed (siRNA, TF decoys, TAT-fusion, nanoprobes) which promise to significantly improve our ability to drug target TFs. Consequently, there is renewed interest to examine TF function within the context of gene regulatory networks. Here, I will present the latest efforts of our lab to develop and apply novel resources and both experimental and bioinformatic tools to achieve a quantitative understanding of the regulatory mechanisms that control gene expression as part of the overall goal to understand TF function in health and disease.