



BİLKENT UNIVERSITY
MOLECULAR BIOLOGY AND GENETICS
DEPARTMENTAL SEMINAR

“Combining computational, structural, and systems biology to study oncogenesis”

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Somatic mutations within the human genome are the root of most cancers. The impact of cancer causing mutations on cellular processes remains however largely elusive. Here, I will present a research program that aims to identify cancer driver mutations in coding and non-coding regions on proteins, protein complexes and protein interaction networks. Key to these efforts will be the development of a new protein interaction network that holds the most comprehensive list of protein binding sites, stores knowledge on mutually exclusive interactions and provides tailored interaction networks for alternative protein isoforms. Using this new database, the impact of coding and non-coding mutations from whole cancer genome sequencing efforts of the International Cancer Genomics Consortium will be predicted. Furthermore, two novel structural proteomics approaches will be described for probing the structure and alterations of protein complexes in cancerous cells. The proposed combination of algorithms, data and methods will lead to an enhance understanding of cancer genotype-phenotype relationships and will identify new target genes for personalized cancer therapies.

Date-Time : Wednesday, December 2, 2015 – at 15:40
Place : SBZ-14
Host : Isık Yulug