Abstract:

Genome wide association studies (GWAS) have successfully identified thousands of variants associated with hundreds of traits. Notably, the vast majority of variants are located outside of protein coding regions. This observation presents key challenges for pathogenic variant identification and for functional interpretation of trait-associated loci. In the past five years, it has become clear that GWAS variants are enriched in regulatory elements. Thus, there has been an unexpected convergence between the genetics and epigenetics fields. My talk will cover both the genetics and epigenetics of prostate cancer. Specifically, I will discuss using the powerful tools of genome editing to functionally identify causal variants, performing the first cistrome wide association study in prostate cancer, and performing in situ mutagenesis to identify functional enhancers.