Science at the Edge Seminar Series

Quantitative Biology Graduate Program/ Gene Expression in Development and Disease



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The epigenomic landscape at base-pair resolution

I will describe new high-resolution methods for profiling the epigenomic landscape that we have applied to problems in chromatin dynamics, transcriptional regulation and chromosome segregation. These include methods for measuring nucleosome turnover, occupancy and positioning, DNA torsion, RNA polymerase stalling, transcription factor occupancy and dynamics, and centromere mapping.

Friday, April 17, 2015 at 11:30a.m. Room 1400 BPS

Refreshments at 11:15