

ORAL PRESENTATION

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Ultra-high resolution mapping of protein-genome interactions using ChIP-exo

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With the advent of high-throughput and high resolution genome-wide protein-DNA detection assays, the interrelationships between chromatin and the transcription machinery are now becoming clearer. Here I will discuss our recent findings using MNase ChIP-seq to map nucleosome positions, and a novel ultra-high resolution mapping technique called ChIP-exo that we recently developed [1]. What is apparent from these studies is the following: firstly, transcription factors bind to many more locations in the genome than previously appreciated. Secondly, PICs form at the interface between nucleosomes and nucleosome-free promoter regions. Finally, Chromatin remodeling complexes target specific nucleosome positions, working in concert to organize nucleosomes at the beginning and end of genes. Many remodeler subunits interact asymmetrically with the nucleosome core across the genome, which may be important for the directional passage of RNA polymerase II.

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Reference

1. Rhee HS, Pugh BF: Comprehensive genome-wide protein-DNA interactions detected at single-nucleotide resolution. *Cell* 2011, **14**:1408.

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