

CDB SEMINAR

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Friday, December 9, 2011 15:00~16:00 A7F CDB Seminar Room

The Functional interplay of Chromatin Insulators and Transcription

Summary

Insulators may maintain proper expression of eukaryotic genomes by defining the borders of chromatin domains marked by specific histone marks, and by blocking long-range interactions (e.g. enhancer-promoter communication) when interposed. In Drosophila, this task involves distinct insulator-binding proteins (IBPs) including dCTCF, BEAF-32, Su(Hw) and GAF that are essential for the activity of the known insulators. We shall present our Hi-Seq data for genome-wide ChIP-, RNA- and MNase/chromatin analyses- that functionally support both the enhancer-blocking and the barrier- function of insulators. In particular, high-resolution ChIP-Seq show that BEAF-32 binds to thousands of sites near promoters of thousands of genes that become positively regulated. This may involve CP190 and a key histone modifier, suggesting a direct mechanism how IBPs participate in specifying the epigenetic landscape of chromatin. In addition, we find that insulating activity is tightly linked to the regulation of the pausing stage of transcription, where insulators may together with the pausing machinery restrict the action of enhancers towards neighboring genes. Our results have important implications in understanding how IBPs may functionally interact with pausing to functionally compartmentalize interphasic chromosomes.

References:

Mol Cell Biol. 29, 3556-68 (2009) PLoS Biol. 6, 2896-910 (2008). Mol Cell. 6, 1013-24 (2000)

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