
Nucleosome-positioning Long-range contacts at Topological boundaries

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Abstract

We shall discuss our recently published data together with unpublished stuffs highlighting a role of insulator proteins and their co-factors in functional long-range contacts. Our systematic analyses revealed hidden information in ChIP-Seq that may be used to predict long-range contacts in chromosomes. Further mathematical 'aggregation' of genome-wide Hi-C data confirms the relevance of such predicted long-range contact maps, defining a potent tool for determining contacts at a high resolution (\leq 500 bp). Such approach is currently being adapted for a broad usage by the research community of this tool as a package.

We will also present our published and unpublished results highlighting a role of the Histone-methyl transferase Mes4/NSD and dHypb/Set2 in transcription-dependent nucleosome positioning that controls progression of RNA polymerase through gene bodies. Our data further identifies Set2 as a key regulator of nucleosome positioning, involving the recruitment of chromatin remodelers to gene bodies.

Reference: Chromatin immunoprecipitation indirect peak highlight long-range interactions of insulator proteins and Pol II pausing. Liang J, Lacroix L, Gamot A, Cuvier O. 2014. [doi:10.1101/008888](https://doi.org/10.1101/008888)

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