

Abstract Submitted
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New insights into nucleosome unwrapping RAZVAN CHEREJI, ALEXANDRE MOROZOV, Rutgers University — Eukaryotic genomes are organized into arrays of nucleosomes, in which stretches of 147 base-pairs (bp) of DNA are wrapped around octameric histones. Recently, a new approach for direct mapping of nucleosome centers at bp resolution was developed [Brogaard et al., Nature 486, 496-501 (2012)] and some intriguing results appeared. About 40% of the inter-dyad distances are smaller than 147 bp, which imply massive nucleosome unwrapping, genome-wide, in vivo. The histogram of the inter-dyad distances presents small oscillations which indicate a step-wise unwrapping of the nucleosomal DNA from the histone. We present a statistical mechanics model for the nucleosome unwrapping, which is able to take into account sequence-dependent binding energies, sequence-independent potential barriers and wells, effective two-body interactions between the nucleosomes, competition between different species, cooperative-binding, and other important factors which dictate the nucleosome distribution along the DNA. We are able to reproduce the distribution of the inter-dyad distances, which cannot be obtained if there is no nucleosome unwrapping. The nucleosome unwrapping model can explain also the variable DNA accessibility and the nucleosome-induced cooperativity, which were observed experimentally.

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