



Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome

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Chromosomal Mapping

The conformation of the genome in the nucleus and contacts between both proximal and distal loci influence gene expression. In order to map genomic contacts, **Lieberman-Aiden *et al.*** (p. 289, see the cover) developed a technique to allow the detection of all interactions between genomic loci in the eukaryotic nucleus followed by deep sequencing. This technology was used to map the organization of the human genome and to examine the spatial proximity of chromosomal loci at one megabase resolution. The map suggests that the genome is partitioned into two spatial compartments that are related to local chromatin state and whose remodeling correlates with changes in the chromatin state.

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