

Nucleosome Core and Compact Nucleosome Array Structures

Timothy J. Richmond, Curt Davey, Thomas Schalch, *ETH Zurich, Institute for Molecular Biology and Biophysics, Zürich, Switzerland.*
E-mail: richmond@mol.biol.ethz.ch

The fundamental building block of chromatin is the nucleosome comprising 157-240 bp of DNA, two each of the four core histone proteins, and a single linker histone H1/H5. The nucleosome core is the greater part of the nucleosome and contains 147 base pairs of DNA wrapped in 1.67 left-handed superhelical turns around the histone octamer. Arrays of nucleosome in their most compact form constitute the "30 nm" chromatin fiber.

The crystal structure of the nucleosome core particle refined to 1.9 Å resolution reveals the details of DNA conformation as well as all the direct and water-mediated histone-DNA contacts. The acute DNA bending induced by the histone proteins results in an alteration of the form of the double helix every five base pairs along its superhelical path. Sequence-dependent DNA conformations are apparent.

Two nucleosome core particle structures containing different 146 base pair DNA sequences contain distinct regions in which the DNA is relatively over-twisted and stretched. These regions represent trapped-intermediates relevant to the "twist-defect diffusion" mechanism for nucleosome sliding and provide a means of buffering DNA linker length variation in the chromatin fiber.

The crystal structure of a tetranucleosome determined at 9 Å resolution comprises two stacks of two nucleosomes with three segments of linker DNA running between them. This structure is compatible with a two-start helix, but not with a one-start helix. A continuous fiber model built by stacking tetranucleosomes results in a nucleosome higher structure that is nearly fully compact.

Keywords: DNA, nucleosome, chromatin fiber