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Folding of Nucleosome Arrays STEVEN HOWELL, George Washington University, ISABEL JIMENEZ-USECHE, Purdue University, KURT ANDRESEN, Gettysburg College, CHONGLI YUAN, Purdue University, XIANGYUN QIU, George Washington University — Chromatin conformation and dynamics is central to gene functions including packaging, regulation, and repair. At the molecular level, the basic building block of chromatin is a nucleosome core particle (NCP) made of 147 base pairs (bp) of dsDNA wrapped around an octamer of histone proteins. These NCPs are connected by short 10-90 bps of linker DNA as beads on a string. Key factors determining the packaging of NCP arrays to form chromatin include ionic condition, linker DNA length, and epigenetic modifications, especially of the histone tails. We have investigated how the conformations of model tetra-NCP arrays are modulated by these factors using small angle x-ray scattering (SAXS). Here we present recent studies of the effects of ion (KCl and MgCl2), linker length, and histone modification (tail deletions) on NCP arrays. Our SAXS measurement makes it possible to learn about both the global compaction of NCP arrays and local inter-NCP spatial correlations within the same array.

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