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Elucidate Chromatin Folding at the Mesoscale XIANGYUN QIU, George Washington Univ — Knowledge of the three-dimensional structure of chromatin, an active participant of all gene-directed processes, is required to decode its (epi)genetics-structure-function relationships. Albeit often simplified as "beads-on-a-string", chromatin possesses daunting complexity in its intricate intra- and inter-nucleosome interactions, as well as the myriad types of molecules acting on it. On the other hand, the folding of chromatin from an extended chain of nucleosomes is highly constrained, e.g., by rather bulky nucleosomes and semi-rigid linker dsDNAs. Further given the well-defined nucleosome and dsDNA structures at the nanometer scale, this creates an opportunity for low-resolution structural methods such as small angle scattering to obtain mesoscale structures of chromatin, which can be further refined computationally to yield atomistic structures of chromatin. Here we present results from our recent studies of recombinant nucleosome arrays with solution small angle x-ray scattering (SAXS) and ensemble structure modeling.

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