detailed structure of B threaded into a short DNA sequence [d(CGCGAATTCGCG)]; at 25 °C. To obtain further insights into this unusual binding mode, the structural characterization is supplemented by kinetic and thermodynamic studies.

3226-Pos Board B87
Sequence and Structure Dependent DNA-DNA Interactions
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Molecular forces between dsDNA strands are largely dominated by electrostatics and have been extensively studied both experimentally and theoretically. Quantitative knowledge has been accumulated on how DNA-DNA interactions are modulated by varied biological constituents such as ions, cationic ligands, and proteins. Despite its central role in biology, the sequence of DNA has not received substantial attention and “random” DNA sequences are typically used in biophysical studies. However, ~50% of human genome is composed of non-random-sequence DNAs, particularly repetitive sequences. Furthermore, the prevalent monovalent cations such as monovalent ions play key roles in gene functions. Such DNAs with specific sequences or modifications often take on structures other than the canonical B-form. Here we report series of quantitative measurements of the DNA-DNA forces with the osmotic stress method on different DNA sequences and modifications, from short repeats (e.g., poly(dA-dT) and poly(dG-dC)) to the most frequent varieties of solvent and molecular factors such as ions, post-translational modifications, and histone variants. Here we combine small angle x-ray scattering and molecular mechanics calculation. The results of research are convenient to interpret in terms of Seatchard coordinates. On the basis of osmotic stress spectrum the binding curves of DNA-cis-DDP and DNA-cis-DDPd dependant on ligands concentrations, pH etc [2]. We have used the method of UV-spectrophotometry and molecular mechanics calculation. The results and major groove widths).

3227-Pos Board B88
Elucidating the Role of Ions in DNA Condensation: Measurements of the Ion Atmosphere Surrounding Condensed DNA Pellets using Inductively-Couple Plasma Atomic Emission Spectroscopy
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Nucleosome aggregation and the related process of chromatin condensation are known to be greatly influenced by ion concentration, ion valence, and the presence and charged state of the positively charged histone tails. In particular, previous studies have shown the importance of the H3 and H4 tails to nucleosome aggregation; however, the exact role of these tails in nucleosome-nucleosome attraction has yet to be determined. Using small-angle x-ray scattering, we report on a low-resolution structural study of a variety of nucleosome core particle constructs (wild type as well as H3 and H4 mutants), the response of these constructs to changes in ion concentrations and the implications of these results for current theories of nucleosome packing.

3228-Pos Board B89
Quantify Cation-Dependent Forces Between Nucleosomes
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Nucleosome-nucleosome interactions play fundamental roles in chromatin assembly and chromosome conformation, and consequently regulate gene expression. The interaction between nucleosomes is in turn modulated by wide varieties of solvent and molecular factors such as ions, post-translational modifications, and histone variants. Here we combine small angle x-ray scattering and theoretical modeling to quantify the inter-nucleosome force in solution as a function of mono- and di-valent cation concentrations. Both natural-source and recombinant mononucleosomes are studied, as well as tail-deletion mutants of interest. Inter-nucleosome forces are found to be much smaller than predicted from the bare or effective charges. Tail-deletion mutations show trends as expected from the total charges carried by each histone tail. We discuss our results on the basis of theories of polyelectrolytes, and attribute the quantitative differences to the non-uniform charge patterns and conformational plasticities of nucleosomes.