Through comparison of FTIR and NMR spectra, respectively, one can qualitatively and quantitatively observe the effects of methylation and fluorination on DNA structure and dynamics. Preliminary results demonstrate that these different covalent modifications of the cytosine base affect the structure and dynamics in different ways. Both modifications alter the BI/BII ratio but fluorination does not appear to affect the dynamics as significantly as methylation. We attribute the enhanced quenching of backbone dynamics by methylation to the formation of a strong dipolar interaction between the negatively charged backbone oxygen with the hydrogens of the methyl group whose proximity to the backbone is closer in BII than BI. Comparisons of fluorination and methylation effects on sequences containing both the EcoRI and Cre binding sites, as well as their modulation due to sequence context, will be presented.

1778-Pos Board B622
Enthalpy-Entropy Contribution to Carcinogen-induced DNA Conformational Heterogeneity
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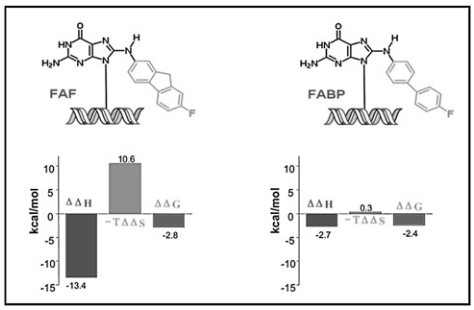
Aromatic amines are among the most notorious chemicals in the environment. The formation of DNA adducts is thought to be a hallmark for the initiation of chemical carcinogenesis. Aromatic amine-DNA adducts are known to exist in a sequence-dependent equilibrium of the major groove B-type (B) and base-displaced stacked (S) conformations. We have conducted extensive calorimetry/NMR studies on the model lesions FAF and FABP in order to understand how thermodynamics influence the nature of S/B-conformational heterogeneity and subsequent molecular interactions with polymerases and repair proteins. Results indicated large differences in enthalpy-entropy compensations for FABP and FAF. The small and flexible FABP exclusively adopts the less perturbed B-conformer, thus resulting in small enthalpy/entropy change. This is in contrast to FAF, which stacks better and exists as a mixture of B- and S-conformers, thus contributing to large enthalpy/entropy compensation. The results indicate that it is not just the stacking argument, but also the favorable entropy of the S-conformer over B-conformer that determines the S/B-conformational heterogeneity at an ambient temperature.



1779-Pos Board B623
Scaling Behavior of Single Stranded DNA Measured by Small Angle X-ray Scattering
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Polyelectrolytes, or charged polymers, are prevalent in biological systems, yet their physical properties are far less well understood than those of neutral polymers. We report on measurements using small angle x-ray scattering to study bulk ensemble-averaged properties of small (up to 100 bases) poly-deoxythymine (poly-dT) and poly-deoxyadenine (poly-dA) molecules. By studying homomeric single stranded DNA (ssDNA), we can observe their polymeric properties without interference from secondary structure formation. This gives us insight to the conformational space explored by single stranded nucleic acids in folding processes, and the nucleotide dependence of loop flexibility of DNA and RNA junctions. We observe, as is consistent with base-stacking of purines, that poly-dA is stiffer than poly-dT. For poly-dT, the radius of gyration (R_g) scales with the number of monomers with a Flory exponent (ν) which decreases slowly with increasing salt, but drops sharply below that expected for a self-avoiding random walk (SAW) polymer ($\nu \sim 0.588$) with more than 500 mM of added sodium acetate. This is perhaps due to the condensation of charges around the DNA and/or the change in solvent quality with added salt. The ratio (r) of the square of the maximum pair-wise distance (D_{max}) to R_g fluctuates around 10, suggesting that ssDNA compacts locally. Assuming that D_{max} is a fair estimate of the end-to-end distance of the polymer, a value of 12 is expected for r in the case of a rod, and about 6.3 for a SAW polymer. This localized clustering is consistent with the electrostatic blob model of de Gennes *et al.* The persistence length of poly-dT - determined by fitting the data to a worm-like chain model - increases in a sublinear fashion with increasing Debye screening length, unlike the behaviors predicted by polyelectrolyte theories.

1780-Pos Board B624
Macrosolute Effects on Nucleic Acid Interactions
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The intracellular environment contains a variety of solutes that cumulatively occupy a significant volume of the cell (20-30%). The high volume occupancy generates a system which is macromolecularly crowded. This crowding, also known as the excluded volume effect, can lead to an increase in the chemical activity of solutes and influence thermodynamic and kinetic values as compared to a dilute system. Using synthetic, inert cosolutes to provide a simplified mimic of the crowding in the intracellular environment, DNA structures were studied. We demonstrate that crowding can lead to the differential stabilization of a complementary DNA duplex over duplexes containing a single mismatched base pair, effectively increasing the specificity of the hybridization reaction. In systems with molecularities ranging from one to four we demonstrate that as the molecularity of a system increases the crowding effects also increase. An increase in Tm of up to 12°C was noted for a multi-branch DNA structure with four arms. Crowding mediated enhancement of the rate of hybridization was found to be independent of sequence but dependent upon structure.

1781-Pos Board B625
The Interaction of Monovalent Cations with a Model DNA Hairpin
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Capillary electrophoresis was used to study the interactions of monovalent cations with DNA hairpins, using as a model the 16 residue oligonucleotide ATCCTATTTTAGGAT, which is known to form a stable hairpin with a 6 base pair stem and a 4 base loop. The unstructured 14 base oligonucleotide ACCTGATCACGTTA served as a reference analyte. All measurements were performed in the absence of Mg^{2+} at pH 7.3 using diethylmalonate as the buffering anion. Increasing the concentration of Na^+ in the buffer increased the melting temperature of the hairpin, as predicted by the mFOLD algorithm. Isothermal measurements at 20° indicate that Na^+ forms a saturable complex with the hairpin, with a K_D of about 100 mM, but does not form a complex with the unstructured reference oligonucleotide. These measurements suggest that the increase in the melting temperature of the hairpin with increasing Na^+ is due to the preferential binding of Na^+ ions to the hairpin conformation. The cations Li^+, K^+, $Tris^+$ and tetramethylammonium$^+$ (TMA^+) bind equally well to the model hairpin and affect its melting temperature similarly. The tetraethylammonium$^+$ (TEA^+) ion also binds equally well to the hairpin, but only to the extent of ~50% saturation. The tetrapropylammonium$^+$ (TPA^+) and tetrabultylammonium$^+$ (TBA^+) ions bind to the hairpin very weakly if at all. Surprisingly, the melting temperature of the hairpin is systematically diminished as TMA^+ is replaced in turn by TEA^+, TPA^+ or TBA^+, suggesting that the larger tetraalkylammonium ions may destabilize the hairpin conformation by a through-solvent mechanism.

1782-Pos Board B626
Observation of Oligonucleotide Dynamics by means of Fluorescent Nucleoside analog 6MI
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To improve current understanding of the structural recognition mechanism of architectural DNA binding proteins such as HU and IHF, we are investigating the structure and dynamics of different DNA substrates. We are able to make these observations on both global and local levels by incorporating the fluorescent guanosine nucleoside analog 6-methylisoxanthopterin (6-MI), with H-bonds with cytosine similar to guanosine. We have previously shown this probe does not significantly perturb the global structures of duplex DNA molecules. 6-MI was systematically incorporated into a 34 base oligonucleotide. Initial characterization of local DNA environment included time resolved fluorescence and rotational correlation measurements of the duplex oligomers relative to 6-MI monomer and single stranded DNA. Analysis of time-resolved fluorescence decay yields 3 lifetime components of 0.4 ns, 4 ns and 6.5 ns. The largest