their dysregulation in disease. However, the molecular mechanisms that drive these phase transitions, the biophysical properties of the resulting droplets, and the way their properties impact biological function, remain poorly understood. Here, we focus on LAF-1, an essential DEAD-box RNA helicase associated with P granules in the C. elegans germline. We find that purified LAF-1 can phase separate into liquid droplets at near physiological (low μM) concentrations. LAF-1 droplet formation is driven by its disordered N-terminal RGG domain, which is both necessary and sufficient for droplet formation. We combine microfluidic, FRAP, and single molecule imaging approaches to reveal the spatiotemporal properties and molecular dynamics inside the droplets. Our results provide mechanistic and structural insight into the phase transition-driven assembly of liquid-like organelles, and suggest that the biophysics of intracellular phase separation can sensitively control molecular dynamics and function.

**DNA Structure and Dynamics I**

### 1160-Pos Board B111

**Unfolding of Nanoconfined Circular DNA**
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Nanofluidic channels have become a versatile tool to manipulate single DNA molecules. They allow investigation of confined single DNA molecules from a fundamental polymer physics perspective as well as for example in DNA barcode techniques.

Circular DNA is of interest since it is found in many biologically relevant contexts, such as bacterial plasmids, viruses and eukaryotic mitochondrial DNA. Furthermore, the circular topology forces two strands in close proximity to each other in nanochannel, which changes the polymer physics compared to linear DNA. Circular DNA is difficult to study with traditional single molecule techniques because such techniques generally require the attachment of handles to the, but is readily accessed using nanofluidics.

Circular DNA has less entropy and higher conformational free energy than in its unfolded configuration. Therefore, as a double-strand break occurs and circular DNA opens up, it unfolds to its linear configuration inside the nanochannel. This study compares the static properties of confined linear and circular DNA as well as investigates the dynamics of the transition from circular to linear DNA as a double-strand break occurs.

We observe that the difference in extension between the circular and linear configurations depends on the degree of confinement, which we confirm with theoretical predictions. Our data for unfolding of the circular DNA to the linear configuration suggests that hydrodynamic friction between the DNA and the solvent is the main rate-determining factor but that DNA-DNA contacts are also important. Finally, by staining the DNA inhomogeneously, we can follow the local dynamics of the DNA as the folding occurs and conclude, for example, how the two different strands move relative to each other during the unfolding process. We are thus able to study the dynamics of confined DNA with unprecedented resolution and obtain completely new information about confined polymers.

### 1161-Pos Board B112

**Supercoil Diffusion along Stretched DNA by Brownian Dynamics**
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The dynamics of DNA supercoils are intimately connected to several fundamental cellular processes. Transcription is a prime example. While the rate of transcription is sensitive to the level of supercoiling, transcription produces positive (and negative) supercoils ahead of (and behind) RNA polymerase. Subject to thermal fluctuations and DNA-protein interactions, supercoils are dynamic structures which accumulate, rearrange, translocate, and dissipate. Recent single molecule studies have observed the dynamic formation, diffusion, hopping, and dissipation of supercoils. Here, we employ Brownian dynamics simulations of a discrete worm-like chain to build understanding beyond that provided by recent experimental efforts. Our computational model accounts for hydrodynamic interactions, thermal fluctuations, bending, torsion, extension, and electrodynamics in stretched DNA. We perform many simulations including trajectories representing 21 kilobasespairs of supercoiled DNA over the course of about 500 ms. We observe several metrics describing the dynamics of supercoils, including the average number of supercoils, their lifetime, first juxtaposition time, and diffusion constants. In addition, we explore the sensitivity of these quantities to DNA extension as well as sequence dependence (through the introduction of sites with elevated DNA flexibility).

### 1162-Pos Board B113

**Analysing Small DNA Constructs via a Chromophore Model within the Point Dipole Approximation**
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As all the genetic information contained within DNA is buried within the duplex helix, there must be a series of breathing fluctuations that expose the nucleic bases to aid roles like replication, transcription, and repair. The work presented here uses a classical chromophore model under the point dipole approximation to calculate the circular dichroism as well as the absorption spectra of oligonucleotides at individual conformational states. This analysis will aid in the evaluation of these breathing fluctuations by treating systems of dimers and small length oligonucleotides as local models of these fluctuations.

### 1163-Pos Board B114

**CHARMM Drude Polarizable MD Simulations Reproduce Solution X-Ray Diffraction Patterns for B-DNA Sequences and Predict Differential Impact of the Li⁺, Na⁺, K⁺ and Rb⁺ Ions on DNA Conformational Properties**
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Recently we have presented the first generation CHARMM Drude polarizable force field for DNA, which is capable of reproducing the main conformational features of DNA in solution, such as A-to-B equilibrium and transitions between BII and BII substates. Our current efforts are directed towards further model improvement, by achieving a proper balance of the interactions among surrounding mobile ions, water and DNA. Compared to the additive (non-polarizable) models, explicit treatment of the electronic polarizability in the Drude model leads to a markedly improved description of the interplay between the ionic atmosphere and DNA conformational behavior. In particular, the Drude model is shown to more accurately reproduce counterion condensation theory predictions of DNA charge neutralization by condensed ions, as well as the experimental data on the competitive binding of Li⁺, Na⁺, K⁺ and Rb⁺ ions to DNA. The most intriguing results is that the model predicts a differential impact of these seemingly similar monovalent cations on DNA conformational properties - a phenomenon not observed in the state-of-the-art CHARMM36 and AMBER atomistic additive models. In addition, the Drude model reproduces the solution X-ray diffraction patterns for a number of B form DNA sequences at a level of accuracy similar to, or exceeding that of the above mentioned additive models. The obtained results indicate that CHARMM Drude polarizable MD simulations provide a more realistic model of the physical forces involved in the interactions of DNA with its ionic environment, offering the potential to yield new insights into salt-mediated biological processes involving DNA, such as protein-DNA recognition and chromatin folding.

### 1164-Pos Board B115

**Molecular Modeling and Simulations of DNA at Graphene-Water Interfaces towards Developing Biosensors and Drug Delivery Vehicles**
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The biocompatibility of Graphene oxide (GO) surfaces and their preferential affinity to single stranded DNA (ssDNA) over double stranded DNA (dsDNA) make GO-ssDNA complexes an attractive target for drug delivery applications. GO-ssDNA complexes also hold promise as biosensors: fluorescence can be achieved by desorption of fluorescently tagged ssDNA from GO surfaces by their complementary strands or DNA-binding proteins in solution. To tune nucleic acid sequences for targeting specific molecules, and to achieve high sensitivity abilities, it is important to quantify the interaction of individual nucleobases (A, T, G & C) and small oligonucleotides with GO or graphene surfaces, and understand the molecular mechanisms involved. Although experimental studies in the past (ITC, AFM) have focused on graphene-nucleobase interaction in water, a few theoretical studies have focused on the same interaction in vacuum, a quantitative understanding of graphene-nucleic acid interaction still remains elusive. To this end, we performed molecular dynamics simulations, guided by dispersion-corrected density functional theory (DFT) and ITC experiments, to accurately quantify and understand the molecular mechanism of nucleobases and nucleosides binding to graphene surfaces in water. As
part of this work, we modified the AMBER-99 all-atom molecular dynamics force-field parameters to accurately capture the van der Waals interaction between the atoms of the nucleobases and graphene. We rescaled the size of the graphene carbon and nucleobase atoms to match the graphene-nucleobase interaction energy profile in vacuum obtained using DFT calculations, and further rescaled the interaction energies to reproduce the binding free-energies in water obtained through ITC experiments. Our results provide a quantitative understanding of nucleobase-graphene interactions, and also build a platform to understand ssDNA binding to graphene surfaces, duplex formation at the graphene-water interface and their subsequent release to the bulk.

1165-Pos Board B116
Computational and Experimental Characterization of Ribosomal DNA and RNA G-Quadruplexes
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DNA G-quadruplexes in human telomeres and gene promoters are being extensively studied for their role in controlling the growth of cancer cells. They are also predicted to exist in the guanine (G)-rich genes encoding pre-ribosomal RNA (pre-rRNA), which are transcribed in the cell’s nucleus. Recent studies strongly suggest that these sequences are a potential anticancer target through the inhibition of RNA polymerase I (Pol I) in ribosome biogenesis. The structures of ribosomal G-quadruplexes at atomic resolution are unknown and very little biophysical characterization has been performed on them. In the present study, we have modeled two putative rDNA structures, NUC19P and NUC23P, which adopt a predominantly parallel topology (circular dichroism (CD) and nanosecond fluorescence experiments on pre-rRNA, reminiscent of the analogous telomeric quadruplex structures. One of the sequences, NUC19, showed a minor CD signature consistent with an antiparallel topology and was also modeled (NUC19A). To validate and refine the putative ribosomal G-quadruplex structures, we performed all-atom molecular dynamics (MD) simulations for 100 and 500 ns in the presence and absence of stabilizing K+ or Na+ ions, respectively. We introduce two novel metrics for quantifying the relative stability of the G-quadruplex tetrads: 1) the center of mass base-to-base distance between diagonal guanines, and 2) the torsional angle between four guanines. Our relative free energy profiles show that the rDNA G-quadruplex structures are more stable than RNA and NUC19P is more stable than NUC23P, which features extended loops. The antiparallel topology was determined to be a disordered configuration due to the lack of planarity after the simulation. Our study suggests that NUC19 and NUC23 form stable, predominantly parallel-topology G-quadruplexes. These well-defined structures are potential nucleolar targets for the design of novel chemotherapeutics.

1166-Pos Board B117
Nanoviscosity Effect of G-Quadruplex and Single Strand DNA
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G-quadruplex is of interest due to its appearance in the telomere sequence, the oncogene promoter region, etc. Its diffusion and change of structure, especially under high viscosity, are important for understanding its dynamics. We present the difference in the diffusion dynamics of the G-rich DNA sequence between single-strand DNA (ssDNA) and G-quadruplex in polyethylene glycol (PEG) solutions. The nanoviscosity effect is observed according to PEG’s molecular weight. In the PEG 200 solution, both the ssDNA and the G-quadruplex have macroviscosity; in the PEG 10000 solution, the G-quadruplex has nanoviscosity and the ssDNA has macroviscosity; and in the PEG 35000 solution, both the ssDNA and the G-quadruplex have nanoviscosity. The experimental results are consistent with the theoretical prediction.

1167-Pos Board B118
Interaction Mode of DNA and Polycarbazole-Titanium Dioxide Nanocomposite: Molecular Docking Simulation and In-Vitro Antimicrobial Study
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Polycarbazole-titanium dioxide (PCz/TiO2-8) nanocomposite was synthesized for the first time by in-situ oxidative polymerization with ammonium per sulphate as an oxidizing agent in the presence of TiO2 nanoparticles and characterized by SEM, TEM, XRD, DTA and TGA techniques. The results of above analysis confirmed that the incorporation of TiO2 nanoparticles in PCz indicating the formation of the nanocomposite due to strong interaction between TiO2 and PCz matrix responsible for enhancing the properties as compared to pristine PCz. The PCz/TiO2-8 nanocomposite was tested for antimicrobial activity and was found to exhibit the activity against gram negative as well as gram positive strains at micromolar concentrations. SEM and TEM results show that PCz has polymerized on the surface of the TiO2. The four types of 3D molecular field descriptors or field points as extrema of electrostatic, steric, and hydrophobic fields are explained. These field points are used to define the properties necessary for a molecule to bind to a characteristic way into a specified active site. A molecular docking simulation was used to predict the modes of interactions of the drugs (PCz and PCz/TiO2-8) with DNA. The molecular docking conclusion indicated that the modes of interactions between the two (PCz and PCz/TiO2-8) and DNA helix can be regarded as groove binding. Keywords: Titanium dioxide, SEM, nanocomposite, antimicrobial study.

1168-Pos Board B119
Lattice-Free 3D Structure-Prediction of Programmed DNA Assemblies
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DNA is a highly programmable, self-assembling nanoscale material in which reliable Watson-Crick basepairing enables the rational design of nearly arbitrary molecular architectures for use as chromophore, nanoparticle, and RNA scaffold, cellular delivery vehicles, and fluorescent reporters and probes. Because the cost of synthesis per DNA object is high and structural validation is time consuming and limited, we previously introduced a computational framework to enable the in-silico prediction of 3D structure from programmed secondary sequence. However, that approach assumed that neighboring DNA helices would pack together to assemble into either square or honeycomb parallel lattices, greatly limiting the diversity of DNA objects that could be designed. To overcome this limitation, here we introduce a generalized computational framework that reads as input programmed secondary structural elements including duplexes and four-way junctions to predict 3D solution structure and mechanical properties of folded DNA assemblies, free of any lattice-constraints on the final folded structure. We demonstrate utility of the procedure by applying it to planar and hemispherical concentric rings, curved tile-based ribbons, and a 3D crystal of tensegrity triangles. Results are compared quantitatively with experimental AFM, TEM, and X-ray diffraction data when possible. The present approach enables 3D structure prediction of programmed DNA assemblies that have an increasing number of applications in biomolecular science and technology.

1169-Pos Board B120
Brownian Dynamics of Folded DNA and Protein Assemblies
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Molecular simulation of long time-scale dynamical motions of proteins and DNA/RNA assemblies is currently impossible using all-atom approaches. In order to partly overcome this limitation, Normal Mode Analysis (NMA) is commonly applied in vacuum to molecular assemblies to enable the calculation of large length-scale molecular motions, albeit with no feedback on their functionally crucial relaxation time-scales in solvent. Moreover, vacuum Normal Modes may differ substantially from Brownian Modes because linearized molecular motions in solvent are typically over-damped, whereas vacuum NMA assumes purely harmonic, inertia-dominated motion. To overcome the limitations associated with vacuum NMA, we introduce here a linearized Brownian Dynamics framework that enables the simulation of the over-damped motion of high molecular weight protein, DNA, and RNA assemblies based on the finite element method. We apply the procedure to simulate microsecond over-damped dynamics of T4 polymerase and programmed DNA nanostructures, and compare quantitatively Brownian Mode shapes with corresponding vacuum Normal Mode shapes, as well as analyze their respective relaxation time-scales. The present computational framework enables the simulation of long time-scale conformational dynamics of high molecular protein, DNA, and RNA assemblies in solvent that are inaccessible to all-atom approaches even on super-computers.

1170-Pos Board B121
Combined Magneto-Optical Tweezers and Supersolution Fluorescence Imaging for Probing Dynamic Single-Molecule Topology of DNA, and Protein Machines that Manipulate DNA Topology
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Magnetic tweezers are a force and torque transduction tool ideal for probing single biological molecules whose function depends upon topological twisting,