of DNB on kinesin-MT detachment. DNB was found to bind within the interface between kinesin and the tubulin dimer. SMD simulations of kinesin detachment from the kinesin-MT complex in the presence of DNB binding are presented and discussed.

1704-Pos Board B596
Evaluation of Modeling the Influence by Monovalent Cations in DNA Structure on Very Cation Sensible Structures 'G-Quadruplex DNA' using Molecular Dynamics with Charmm Force Field
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The structure of bio-molecules such as DNA and RNA depends strongly on the cation binding sites. Epigenetic regulation mechanism may depend in part on the structure of DNA and its ability to interact with regulatory proteins. Understanding of the dynamic role of cations on DNA structure and how they get affected by several modifications involved in chromatin remodeling will give light on how exactly these mechanisms control such complicated scenarios. Nevertheless, even the location and effect of the cations on DNA or RNA structure on simple systems (protein free) is not clearly understood or predictable, or how well we can model such systems with the current available modeling methods. We choose a model system of G-quadruplex DNA, molecules well known to depend for its structures strongly on the cations present, to study the effect of the cation location and number in the modeling of these structures in order to evaluate how well molecular dynamics (CHARMM) performs.

1705-Pos Board B597
Self-Assemble of Interlocked G-Quadruplex through the Structural Characterization by Molecular Dynamics in Order to Predict Non Canonical DNA Folding
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The structure and dynamics of G-quadruplex DNA is relevant to the understanding of their role in the cell. Sequences that fold into G-quadruplex structures have been identified into sequences such from telomeres and regulatory elements both related with aging and cancer. In this article we report the detailed characterization at atomic level of G-quadruplex units to obtain a better comprehension on how these units can self-assemble into interlocked G-quadruplexes (more than a single unit assembled). Previously we reported the construction of interlocked G-quadruplexes by a thermal cyclic procedure (similar in implementation as the ones used in the cycling steps in a PCR protocol) parting from the sequence 5'-TGGG-3'. Based on our experimental data reported previously, models were built for the structures, and minimization and analyses via molecular mechanics was carried out in order to understand the factors that determine the more stable structures. This has been supplemented with molecular dynamics simulations. It was found that the identity of the 5'and 3' ends of the oligonucleotides is of the uppermost importance in the stability of the DNA assemblies in this study.
Furthermore, the presence of cations in the regions of the molecule where the degree of steric hindrance allows more room for the cations could play a significant role in the dynamics of conformation of the interlocked G-quadruplexes at those sites. In summary, the results allow a better comprehension of these sequences with the finality to be able to predict other sequences that could fold in a similar fashion as well as the suitability to analyze their dynamics by *in silico* methods.

1706-Pos Board B598
DNA Assembly of Nanofibers from Duplex - Quadruplex DNA
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Non canonical DNA structures are becoming a point of attention, because repetitive sequences have shown to adopt other alternative conformations to B-DNA. Here we show the analysis by electrophoresis and spectroscopic methods of sequences that form what has been named as synapsable DNA. These DNA is assembled from two different DNA strands that have a mismatched region that it is believe contains bases stacked rather than regular hydrogen bonding pairing, this stabilization pattern is referred as zipper-like. We used a zipper-like motif of eight G's mismatch base pairs bracked by B-form geometry at its sides. Subsequently, two strands of DNA were added in a preformed buffer with K+ ions which allowed the formation of a quadruplex "synapsable" via Hoogsteen hydrogen bonding. With Atomic Force Microscopy we found fibers assembled from these sequences. We hypothesize that the stability and assemble mechanism of the structures formed is the result of the guanine quartet that gives greater rigidity compared to DNA double. This type of DNA could be important for matrices and nanotechnology applications.

1707-Pos Board B599
Translation in the RNA World: Insight from the Proto-Ribosome Model
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To quote Carl Woese ''Translation not only defines gene expression, but it is the sine qua non without which modern (protein-based) cells would not have come into existence.'' Yet to understand how this universal process might have developed requires an evolutionary RNA-World-centered concept of translation. A theory of the primitive RNA-based translation mechanism is developed starting from segments of the ribosome that comprise the symmetric A- and P-cores of the peptidyl-transferase center (PTC). We have computationally engineered RNA structural motifs, such as the frequently occurring tetra-loops and A-minor interactions, into the PTC to construct the model of a prebiotic proto-ribosome. The stability of the model, and thus the probability of its primordial existence, increases as we build up the complexity of the RNA molecule. We found that a minimal size of about 190 nucleotides (95 for each symmetric monomer) is required for the proto-ribosome to reach microsecond stability under physiological conditions. Moreover, this stable model is able to hold the charged tRNA CCA-end in both the A- and P-sites long enough, so that the substrates can be reoriented into a transition state favorable for peptide bond formation. To support our computational model of the proto-ribosome, native polyacrylamide gel electrophoresis was performed on separate A- and P-cores to confirm their unique native folding conformations; and isothermal titration calorimetry (ITC) was used to measure the binding rate of the two components with and without substrates. Our results demonstrate that a functional RNA molecule could have existed as the primitive translation apparatus capable of making short statistical peptide chains, and therefore, enable the transition of the ancient RNA world into the world of the modern cells.

1708-Pos Board B600
Urea Induced Denaturation of Pre-Q1 Riboswitch
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To decipher the molecular underpinnings of urea-induced RNA denaturation in detail, we performed all-atom molecular dynamics (MD) simulations of PreQ1-riboswitch (RS) in aqueous urea solution. Urea displays its denaturing power in diverse molecular environments of the RS structure. Our simulations reveal that hydrogen bonds and stacking interaction of urea with nucleobases lead to the denaturation of RNA structures by stabilizing isolated bases as well as destabilizing interbase hydrogen bonds. Detailed studies of simulation trajectories show that, together with water, urea-base interaction is highly dynamic; the lifetimes of individual geminate pairs between urea and bases due to hydrogen bondings and stacks are only ~ (0.1-1) ns. As a consequence of the highly dynamic motions of urea, water, and nucleobases, the early stage of base pair disruption is triggered by water molecules permeating into the hydrophobic domain between RNA bases. The permeation of water is critical to increase the accessibility of ureas to transiently disrupted bases since it facilitates ureas to displace interbase hydrogen bonds. Urea's unique ability to interact with both water and polar, nonpolar components of nucleotides makes urea a powerful chemical denaturant for nucleic acids.

1709-Pos Board B601
Investigating the Role of an Extended Hydrogen Bonding Network within the Hairpin Ribozyme Active Site
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From previous studies involving molecular dynamics (MD) simulations and X-ray crystal structures, a chain of five to seven long-residing, ordered water molecules was discovered within the otherwise solvent-protected active site of the hairpin ribozyme (1,2). This water chain is part of an extended hydrogen bonding network within the active site. This network was proposed to be involved both in proton transfer reactions and in mediating long-range communication between the RNA residues in the active site, features important for ribozyme catalytic activity. Until now, however, the functional relevance of this hydrogen bonding network has not been explored. In order to gain insight into the relationship between the hydrogen bonding network and catalytic activity, we are first using MD simulations to computationally scan for ribozyme variants with disrupted hydrogen bonding networks. Specifically, we are studying the behaviour of the hydrogen bonding network in simulations incorporating single-atom modifications in core residues A38, A10, A9 and U42. The use