BP 18: Posters - DNA, RNA and Related Enzymes

Time: Monday 17:30–19:30 Location: Poster C

BP 18.1 Mon 17:30 Poster C

Molecular Dynamics simulations for the detection of unfolding pathways and stable conformations of DNA structures — •Ewa Anna Oprzeska-Zingrebe and Jens Smiatek — Institute for Computational Physics, University of Stuttgart, Stuttgart, Germany

The formation of specific DNA secondary and tertiary structures has been reported to play a key role in various range of biological processes, such as transcription termination or intermolecular binding. Among them, a pivotal role has been ascribed to DNA i-Motif and G-Quadruplex structures, which due to their biological appearance in telomeric and centromeric DNA are considered as potential targets for various diseases. Recent studies on high-temperature unfolding simulations of the DNA i-Motifs have revealed the existence of stable hairpin configurations as an intermediate step in the unfolding pathway of DNA higher-order structures. In our study, we investigate a simple 7-nucleotide DNA hairpin structure with the sequence d(GCGAAGC) to achieve detailed insight into the stability of DNA hairpin structures and their interaction with the osmolyte urea.

BP 18.2 Mon 17:30 Poster C

Single DNA Molecules and Colloids in a Thermophoretic Trap — •Tobias Thalheim, Marco Braun, Andreas Bregulla, and Frank Cichos — Molecular Nanophotonics Group, Institute of Experimental Physics I, University of Leipzig, Germany

We report on the trapping of single and multiple colloids as well as single DNA molecules in solution. We show, that the actual fuel of Brownian motion - temperature - is also capable of confining Brownian motion. A thermophoretic trap has been developed which employs temperature gradients, which are dynamically generated by the optical heating of a plasmonic structure. An optical feedback mechanism allows to control the number of colloids or molecules in the trap. The study of the motion of two colloids in the trap reveals not only the compression of the mean distance of the two particles in the trap but also a correlation of the spatial distribution of the particles inside the trapping region. The compression of the mean distance of the two colloidal particles suggests that also the macromolecular conformation of a single semiflexible polymer can be compressed by the action of the temperature gradients. First results of experiments on single lambda-DNA molecules provide evidence, that an inhomogeneous temperature profile is able to distort the conformation of the DNA, which paves the way for compression and free expansion experiments of single DNA molecules.

BP 18.3 Mon 17:30 Poster C

The maximum number of independently hybridizing DNA strands — •Mina Mohammadi-Kambs[1], Kathrin Hölz[2], Mark Somoza[2], and Albrecht Ott[1] — [1]Universität des Saarlandes, Department of Experimental Physics — [2]University of Vienna, Institute of Inorganic Chemistry, Faculty of Chemistry

In the cell molecular information processing is based on molecular recognition and binding. Although DNA hybridization is sometimes understood as lock and key interaction, it is not completely clear how the two molecules can identify each other. Even with a few mismatched bases, hybridization still occurs and this makes it difficult to predict hybridization in crowded and competitive environments. Here we study how different strands need to be to avoid competition for the same molecule. In this work we first numerically derive the maximal number of possible sequences, which can coexist without competing to bind to each other's perfect match. Experimentally we determine the appropriate minimum number of mismatched bases and investigate the behavior of DNA in a scenario where many sequences bind to their surface bound complements so that competition is minimized.

BP 18.4 Mon 17:30 Poster C

Subnuclear Microarchitecture is Established when Transcription is Activated in Zebrafish Embryos — •Lennart Hilbert[1,2,3], Yuko Sato[4], Hiroshi Kimura[4], Alf Honigmann[3], Vasily Zaburdaev[2], and Nadine Vastenhouw[3] — [1]Center for Systems Biology Dresden — [2]MPI for Physics of Complex Systems — [3]MPI of Molecular Cell Biology and Genetics — [4]Tokyo Institute of Technology

DNA transcription is a fundamental process of cellular function. Still, the driving forces of spatial organization of the transcription machinery in the nucleus remain poorly understood. Here, we used the onset of transcription in zebrafish embryos as a model system to investigate the contribution of transcription to spatial organization. To enable super-resolution microscopy of subnuclear organization, we dissociated embryos into individual cells. Clones of these cells exhibited transcription onset as seen in embryos. We imaged DNA and active RNA polymerase II (Pol II) in fixed clones by widefield and 3D STED super-resolution microscopy. DNA was first homogeneously distributed but segregated into spatially confined domains after transcription onset. Pol II foci with a granular sub-micron structure were seen. Focus frequency and structural complexity increased with intensifying transcription. After transcription onset, a nucleus-wide, interconnected network of Pol II-compartments formed. Live cell Pol II detection with fluorescence-tagged antibody fragments reproduced the fixed cell results. The techniques enabled by embryo dissociation will support comprehensive assessment of transcription as a driver of subnuclear organization.

BP 18.5 Mon 17:30 Poster C

Measuring DNA translocation forces through MoS2 nanopores — •Dennis Kreft, Sebastian Knust, and Dario Anselmetti — Bielefeld University

We measured the forces acting on a single strand of dsDNA during translocation through nanopores in molybdenum disulfide (MoS2) mono- and bilayer membranes by Optical Tweezers. The system includes a video-based force detection and analysis system allowing for virtually interference-free axial force measurements [1].

Preliminary measurements of the translocation of a λ-DNA dimer through a 40 nm Helium-ion drilled nanopore in a MoS2 bilayer resulted in a force of (4.5 ± 1.5) pN @ 50 mV. We will show further measurements performed with an overall force resolution of 0.5 pN at a sample rate of 2042 Hz.

[1] S. Knust et. al., Rev. Sci. Instrum. **83**, 103704 (2012)

BP 18.6 Mon 17:30 Poster C

Thermally driven length selection increases RNA self-replication rates — •Juan M. Iglesias Artola and Moritz Kreysing — MPI-CBG, Dresden, Germany

It is widely believed that modern life on Earth was preceded by RNA molecules able to store information and to catalyze their own replication. In recent years a vast amount of effort has been dedicated to the understanding of how RNA molecules manage to replicate, and indeed a cross-catalytic replication cycle has been demonstrated experimentally[1]. However, it remains unclear how such multi-component reaction networks[2] could have self-assembled under prebiotic conditions. Particularly problematic seems the strongly non-linear concentration dependence of ligation rates, which necessitates high substrate concentrations in order to guarantee temporal persistence of the replication cycle. Using the R3C ligase as a model system, we show how a recently described thermally imbalanced micro-environment[3] is suitable to increase ligation rates by orders of magnitude through a) active accumulation of RNA strands in a small compartment, b) selection of successfully ligated products, and c) separation from inhibitory hydrolysis products. For the origin of life, we consider environmentally altered reaction kinetics key to reach reproduction rates in excess of significant decay rates; a pre-requisite not only to sustain reaction of a dilute model replicator, but also a requirement for replication networks to arise spontaneously. Refs.: [1] Lincoln et al. Science 323 (2009), [2] Higgs et al, N. Nat. Rev. Genet. 16 (2015), [3] Kreysing, et al. Nat. Chem. 15 (2015),