Softlithograpy is a low-cost strategy to produce micro- and nano devices. Here we demonstrate that the photoresist SU8, which is designed for thick and high aspect ratio application, can also be used to create 3D micro- and nanofluidic channels with dimensions <300 nm. In a multilayer lithography process, a sub 300 nm SU8 film is spincoated and processed, followed by a layer, which is several micron thick. The layers are aligned with a mask aligner allowing for a positioning precision better than 2 micron absolut.

The SU8 multilayers are replicated with Polydimethylsiloxane (PDMS), that is pretreated with an oxygen plasma before assembly to render the surfaces hydrophil. This combination of nano- and microfluidics allows new approaches to bioanalytical lab-on-a-chip devices, which will be discussed.

BP 7.48 Mon 17:45 P3

Deposition of engineered nanoparticles on human lung cells via the air liquid interface — •Andreas Comouth[1,2], Sonja Muelhopt[2], Harald Saathoff[1], Daniel Rzesanke[1], Alicja Panas[3], Carsten Weiss[3], Hanns-Rudolf Paur[2], Silvia Diabate[3], and Thomas Leisner[1] — [1]Institute for Meteorology and Climate Research, Forschungszentrum Karlsruhe, Germany — [2]Institute of Technical Chemistry, Thermal Waste Treatment Division, Forschungszentrum Karlsruhe, Germany — [3]Institute of Toxicology and Genetics, Forschungszentrum Karlsruhe, Germany

Epidemiological studies show a correlation between the concentration of ultrafine particles in the atmosphere and the rate of mortality and morbidity due to respiratory and cardiovascular disease. In order to get quantitative information about the lung toxicity of engineered airborne nanoparticles an in vitro exposure system has been build up and lung specific bioassays have been developed. Unlike submers exposure this set up is more realistic due to the deposition at the air liquid interface of lung cells as it happens in vivo. Further this method enables reproducible deposition conditions by in situ monitoring of particle size distribution and concentration via scanning mobility particle sizing (SMPS) as well as mass dose determination by a quartz crystal microbalance. After exposure at the air liquid interface the cells are analyzed to measure the biological responses such as viability, inflammatory or oxidative stress. In this way it is possible to study the influence of particle properties such as surface area, particle coatings as well as primary particle size and agglomerate size on lung toxicity.

BP 7.49 Mon 17:45 P3

The unwinding mechanism of the hexameric helicase Large Tumor Antigen — •Daniel Klaue and Ralf Seidel — Biotechnology Center, TU Dresden, Germany

Helicases are ATP-driven molecular motors that processively unwind dsDNA by shearing apart the individual strands . The mechanisms by which helicases accomplish strand separation are heavily debated. Two extreme possibilities are either a passive mechanism, in which reannealing of stochastically opened base pairs at the unwinding junction is sterically prevented , or an active mechanism in which the helicase actively ruptures base pairing. Whereas for the latter case the helicase velocity should be force independent, for the first case a strong force dependence is expected. Recently for hexameric helicases from bacteriophages, a largely passive DNA unwinding mechanism has been found. Here we investigate the eukaryotic hexameric helicase Large Tumor Antigen (T-antigen) from Simian Virus 40 on the level of a single molecule using magnetic tweezers, where unwinding of a DNA hairpin can be observed in real time. In contrast to its prokaryotic counter parts we find that within error DNA unwinding by T-antigen is force independent in agreement with an active unwinding mechanism. Interestingly, the refolding of the DNA, when T-Antigen passes the center of the hairpin and translocates on the single strand, occurs faster than unwinding. This suggests that the active unwinding occurs ahead of the unwinding junction which is shielded against applied force. In agreement with an active unwinding mechanism we also find that T-antigen is one of the most processive helicases known so far.

BP 7.50 Mon 17:45 P3

Single-Molecule Studies of DNA Translocating Restriction Enzymes — •Friedrich Schwarz[1], Kara van Aelst[2], Mark Szczelkun[2], and Ralf Seidel[1] — [1]BIOTEC TU-Dresden Germany — [2]University of Bristol, United Kingdom

Restriction enzymes (REs) are the central part of the bacterial defence system against invading viruses. These protein complexes recognize viral DNA by the methylation state of their target sequence and destroy it by cleaving it into pieces. For this, the majority of REs need to interact with two distant target sites. This long-range inter-site communication can be accomplished either by passive 3D diffusive looping or by 1D motion along the DNA contour. Among the different classes of REs, Type I and Type III play a special role due to their helicase domains, which are key to the inter-site communication.

For Type I REs it is established that the helicase domain acts as a dsDNA translocating motor. Cleavage is triggered after a pure 1D communication process, when two translocating motors from distant target sites collide. However details of the actual cleavage-collision process still remain unclear. In comparison, the communication mechanism for Type III REs has not been accurately defined and conflicting models including 3D diffusion and 1D translocation have been proposed. Our recent findings suggest that Type III REs move along DNA by diffusion. In order to explore the cleavage-collision process and to test the diffusion hypothesis we started to track the movement of Type I and III REs along DNA using a setup combining magnetic tweezers with single-molecule fluorescence.

BP 7.51 Mon 17:45 P3

Transport properties of G-quadruplex DNA measured with mechanically controllable break junction electrodes — •Shoupeng Liu[1], Samuel Weisbrod[2], Zhuo Tang[2], Andreas Marx[2], Elke Scheer[1], and Artur Erbe[1] — [1]Physics Department, University of Konstanz, D-78457 Konstanz, Germany — [2]Chemistry Department, University of Konstanz, D-78457 Konstanz, Germany

The conductance properties of G-quadruplex DNA are investigated while stretching the molecules mechanically. Electrodes which are fabricated using a mechanically controllable break junctions (MCBJ) setup enable us to measure the resistance of single or a small number of molecules in various stretching situations. The resistance as a function of the electrode distance, i.e. the so-called open-close curve, shows a plateau, which we associate with the folding and unfolding process of the molecule. From the measured current-voltage characteristics we deduce a semiconductor-like electronic band-structure. The results suggest a comparatively high conductance of the G-quadruplex structure which has promising usage in future nanoelectronics.

BP 7.52 Mon 17:45 P3

Transfer matrix modelling of DNA charge transport with a diagonal-ladder model — •Stephen Wells[1], Chi-Tin Shih[2,3], and Rudolf Roemer[1] — [1]Department of Physics and Centre for Scientific Computing, University of Warwick, Coventry CV4 7AL, UK — [2]Department of Physics, Tunghai University, 40704 Taichung, Taiwan — [3]Physics Division, National Center for Theoretical Sciences, Hsinchu, Taiwan

The structure of DNA, with its stacking of aromatic bases along the axis of the double helix, immediately suggests the possibility of significant charge transport along the molecule. There is increasing evidence that DNA can support a considerable degree of charge transport along the strand by hopping of holes from one base to another, and that this charge transport may be relevant to DNA regulation, damage detection and repair. A surprising amount of insight can be gained from the construction of simple tight-binding models of charge transport, which can be investigated using the transfer-matrix method. We review a set of ladder-like models for DNA charge transport and their extension to include more physically realistic diagonal-hopping terms. There appears to be a correlation between DNA charge-transport properties obtained from these models and the locations and frequency of disease-associated mutations in multiple genes. We present data on genes including p53 (the "guardian of the genome") and genes associated with retinoblastoma and cystic fibrosis.

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TmHU-DNA binding studied by atomic force microscopy — •Hergen Brutzer, Mathias Salomo, Friedrich Kremer, and Ulrich Keyser — Institute for Experimental Physics I, Leipzig University, Linnéstraße 5, D-04103 Leipzig, Germany

In contrast to the well-characterized processes of formation and destabilization of complexes from eukaryotic histones with DNA, little is known about interactions between histone-like proteins from prokaryotes and DNA. These proteins also kink and bend DNA leading to chromatin-like structures. The histone-like HU protein is nearly ubiquitous in all bacteria. Especially TmHU from Thermotoga maritima exhibits some extraordinary properties, such as the protection of DNA inside the bacterium against thermal denaturation. Experiments with optical tweezers suggest the existence of a threshold protein concentration for the formation of TmHU-DNA complexes. Here we use atomic