BP 7: Poster I

Time: Monday 17:45–20:00 Location: P3

BP 7.1 Mon 17:45 P3

Self Assembled Asymmetric Lipid Bilayers in Microfluidic Channels — •Shashi Thutupalli[1], Ralf Seemann[1,2], and Stephan Herminghaus[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Experimental Physics, Saarland University, Saarbrücken, Germany

Biological lipid membranes are predominantly asymmetric. In the plasma membranes of eukaryotic cells, for example, there is an abundance of phosphatidylcholine and sphingomyelin in the outer leaflet while aminophospholipids are primarily in the cytosolic leaflet. The biological importance of asymmetric lipid bilayers has motivated many studies using model systems, such as planar bilayers, supported bilayers, and vesicles. However, there are numerous experimental difficulties regarding such model asymmetric bilayer systems, in particular studying membrane proteins and ion channels. Here we report a highly robust method to simultaneously form many asymmetric bilayers using gel emulsions generated in a microfluidic channel. Liposomes included inside a droplet of water in an external phase of oil reach the oil-water interface to form a lipid monolayer. Such droplets, comprising different lipid monolayers, are brought together to form asymmetric lipid bilayers at the droplet interfaces. Significant advantages in our system are the monodispersity of the membranes thus formed and the ability to simultaneously form symmetric and asymmetric membranes bounding the same droplet. Further, we present electrical characterization of these membranes and demonstrate ion conduction via the incorporation of the ion channel Gramicidin A into these membranes.

BP 7.2 Mon 17:45 P3

Scanning Fluorescence Correlation Spectroscopy on Membranes — •Jonas Ries, Salvatore Chiantia, Rachel Yu, and Petra Schwille — Biotec, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

When confocal fluorescence correlation spectroscopy (FCS) is applied on membranes, long measurement times are required and instabilities, photobleaching or poor knowledge of the detection area limit the accuracy. Here we present two implementations of scanning FCS (SFCS) to circumvent these problems. Scanning FCS with a scan path perpendicular to the membrane plane is robust against instabilities and allows for very long measurement times, which are required to study slow diffusion. It can be extended to measure calibration-free diffusion constants with scanning two focus FCS and to quantify binding on the membrane with scanning dual color FCS with alternating excitation. We applied this method to study the affinity of the Fgfr1(4) to its ligand Fgf8 in the membranes of living zebra fish embryos. Line-scan FCS with a scan path parallel to the membrane plane greatly increases the statistics by parallel acquisition. It allows for calibration-free diffusion and concentration measurements on membranes within seconds and is virtually not affected by photobleaching. Both approaches can be easily implemented with commercial laser scanning microscopes and allow for quantitative measurements in demanding systems previously not accessible by FCS.

BP 7.3 Mon 17:45 P3

Diffusion of single actin filaments bound to cationic lipid membranes — •Lydia Woiterski, Florian Rückerl, Josef A. Käs, and Carsten Selle — Institut für Exp. Physik I, Linnéstraße 5, 04103 Leipzig

Actin is one major component of the cytoskeleton in eukaryotic cells. The filaments form a quasi-two-dimensional network - the so-called actin cortex that plays an important role for cell motility. It is associated with the inner leaflet of the cell membrane via protein anchors. Recent studies show that there is a close interplay between the structure of the cytoskeleton and the membrane composition [1]. A model system which mimics the unspecific interactions of cytoskeleton and cellular membranes are actin filaments bound to inhomogeneous lipid membranes. First, the diffusion of single actin filaments adhered to cationic planar membranes will be studied using single polymer tracking. The membranes used are composed of DPPC, DOPC, cholesterol, and the cationic lipid DOTAP and the binding is driven by Manning condensation. Under certain conditions, these liquid membranes show coexistence of ordered and disordered phases. We propose that actin binding can be regulated by the phase state and that preferential binding to one of the coexistent phases occurs due to varied surface charge density. Our aim is a better understanding of how the polymer motion at the membrane can be modulated and the diffusion can be controlled by changing the energy landscape, e.g. by domain sizes and shapes.

1. Kwik, J.et al., PNAS, 2003, 100, p.13964.

BP 7.4 Mon 17:45 P3

Curvature-coupled protein diffusion in a fluctuating model membrane — •Stefan Leitenberger, Ellen Reister-Gottfried, and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart

The influence of an interaction between a protein and a fluctuating membrane on the dynamics of the system is analyzed. The energy is given by the Helfrich Hamiltonian in Monge-representation with a correction for the inserted protein. We derive coupled equations of motion for the membrane dynamics and the projected diffusion of the inclusion that are nummerically integrated in our simulation scheme.

In our model the influence of the protein-membrane interaction on the membrane dynamics modifies the height correlation function of the membrane. Two time regimes reflect the different time scale of membrane fluctuations and that of protein diffusion.

The effective lateral diffusion coefficient of the protein is also affected by the curvature-coupling. The resulting coefficient determined by our simulations is smaller than the free diffusion coefficient of the protein. This is in contrast to a previous result that neglects the influence of the particle on membrane fluctuations and shows enhanced diffusion. The analysis of the correlation functions contributing to the mean squared displacement of the protein reveals that the decrease is caused by a strong correlation between the stochastic force on the protein and the response of the membrane to the motion of the protein.

BP 7.5 Mon 17:45 P3

Elucidating structure and domain formation of biomimetic lipid bilayers — •Kristian Boye[1], Gernot Guigas[1], Eszter Molnar[2], Martin Holzer[3], Wolfgang Schamel[2], and Matthias Weiss[1] — [1]DKFZ - German Cancer Research Center, Heidelberg, Germany — [2]Max Planck Institute for Immunobiology, Freiburg, Germany — [3]Institute of Pharmaceutical Sciences, University of Freiburg, Germany

Membrane domains - also known as lipid rafts - are believed to be central to various functions of the cell, including signal transduction, lateral sorting, pathogen recognition and internalization processes. While the nature and stability of these domains in the living cell is still highly controversial, model membrane systems, such as giant unilamellar vesicles (GUVs), allow a direct observation of large, optically resolvable domains that result from the coexistence of two or more lipid phases.

We have used confocal fluorescence microscopy and fluorescence correlation spectroscopy to investigate the spatial and dynamic organization of lipids in artificially produced GUVs with lipid compositions mimicking that of the endoplasmic reticulum and that of the plasma membrane of T cells. In both cases, we observe domain formation and, in part, the formation of buds and tubules. We moreover have evidence that specific transmembrane protein complexes, like the one formed by the T cell receptor, partition into specific lipid subphases.

BP 7.6 Mon 17:45 P3

Influence of Tension on Coarse-Grained Model Membranes — •Jörg M. Neder[1], Beate West[2], Friederike Schmid[2], and Peter Nielaba[1] — [1]Department of Physics, University of Konstanz, 78457 Konstanz — [2]Department of Physics, University of Bielefeld, 33615 Bielefeld

Using a recently developed generic coarse-grained model for lipid bilayers [1] we investigate the effect of an applied tension on these systems at different temperatures. The recorded pressure profiles of the systems are consistent with the external tension. We observe a lowered extensibility of the bilayer in the gel phase compared to the fluid phase. In the region of the phase transition, where our system is in the ripple phase, both regimes of area compressibility are present: the fluid-like behavior for lower tensions and the gel-like decreased extensibility at higher tensions. The effect of laterally lowered pressure on properties of simple model proteins and the surrounding bilayer is examined. Further, the influence of tension on the effective interaction potential of

two cylindrical inclusions (cf. [2]) is analyzed via umbrella sampling. An extension of the elastic theory presented in [3] is used to fit fluctuation spectra of both height and thickness of stressed membranes.

[1] O. Lenz and F. Schmid, *Phys. Rev. Lett.* **98**, 058104 (2007)
[2] B. West et al., *Biophys. J.*, doi:10.1529/biophysj.108.138677 (2009)
[3] G. Brannigan and F. H. L. Brown, *Biophys. J.* **90**, 1501 (2006)

BP 7.7 Mon 17:45 P3

Dynamics of vesicle adhesion through a polymer cushion: role of layer thickness and tension — •Kheya Sengupta[1] and Laurent Limozin[2] — [1]CINAM/CNRS-UPR3118, Marseille, France — [2]INSERM UMR 600 - CNRS UMR 6212, Marseille, France

The adhesion of giant unilamellar phospholipid vesicles to planar substrates coated with extra-cellular matrix mimetic cushions of hyaluronan is studied using quantitative dual wavelength reflection interference contrast microscopy (DW-RICM). The thickness of the cushion is varied in the range of about 50 to 100 nm, by designing various coupling strategies. On bare protein coated substrates, the vesicles spread fast (0.5 sec) and form a uniform adhesion-disc, with the average membrane height about 4 nm. On thick hyaluronan cushions (>80 nm), the vesicle sits on the top of the cushion and spreading is totally prevented. On a thin and inhomogeneous cushion, the adhesion is modified but not totally impeded. The spreading is slow (˜20 sec) compared to the no-cushion case. We show that in addition to the quality of the cushion, the initial tension of the vesicles plays a crucial role in the spreading kinetics. We interpret our experimental results in the light of a theoretical framework which integrates the influence of polymers on the membrane-surface interaction potential on one hand and the role of this potential in the spreading kinetics on the other hand. We conclude that the slow kinetics arises partially from a reduction in the adhesion-strength but the main contribution comes from the increased viscosity in the presence of the polymer.

BP 7.8 Mon 17:45 P3

Artificial Chloroplasts from Giant Unilamellar Vesicles — •Jakob Schweizer and Petra Schwille — Biotechnologisches Zentrum, TU Dresden, Tatzberg 47-51, 01307 Dresden

Giant unilamellar vesicles (GUVs) serve as a minimalistic model system for biological cell membranes. However, they are also an ideal tool to reconstitute membrane-associated sub-cellular structures, in order to mimick intracellular processes under defined conditions. Here we present a way to construct a rudimentary energy-producing active membrane from purely biological raw materials using three main components: lipids, bacteriorhodopsin and F0F1-ATP synthase. Powered by photon absorption, bacteriorhodopsin pumps protons into the vesicle, whereas the F0F1-ATP synthase utilizes the emerging proton gradient to produce ATP. The most crucial step is therefore the reconstitution of the functional proteins into the GUVs in the correct orientation for which the functionality of both proteins is tested individually. Establishing an artificial chloroplast can provide further insight into the evolution of biological chloroplasts. Moreover, these photo-sensitive systems will also serve as miniature power plants, providing the ATP essential for more complicated cellular model systems.

BP 7.9 Mon 17:45 P3

Fast algorithm for determinating the equilibrium configuration of a cable network model describing the actin cytoskeleton — •Karsten Schwarz and Heiko Rieger — Theoretical Physics, Saarland University, D-66041 Saarbrücken

The propagation of mechanical stress through the actin cytoskeleton is studied with a cable network model [1,2]. Cables represent actin filaments connecting two nodes of a network and exerting a specific force F on the two nodes, which depends only on the distance l between them: $F(l) = 0$ for $l \leq l_r$ and $F(l) = c \cdot (\frac{l}{l_r} - 1)$ for $l > lr$ (l_r is the rest-length of the cable). Some of the nodes are fixed, representing focal adhesions, the others arranging themselves according to the resulting force balances into an equlibrium configuration. Typical model networks comprise more than 10^5 nodes making the determination of their equilibrium configuration numerically hard. We map the force balance problem onto a convex optimization problem and present a method to solve this to arbitrary precision in polynomial time. We discuss applications of our method to modelling the migration of adhering cells. [1] Coughlin et al. Biophys.J. 84:1328-1336 (2003) [2] Paul et al. Biophys.J. 94:1470-1482 (2008)

BP 7.10 Mon 17:45 P3

Active chiral gels — •Sebastian Fürthauer, Stephan Grill, and Frank Jülicher — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Str. 38, 01187 Dresden, Germany

Many different physical systems display intriguing chiral phenomena, such as the handedness of biomolecules. Here we study consequences of chirality in the actomyosin cortical layer that underlies the membrane of eukaryotic cells. The theory we develop is an extension of the formalism of active polar gels to an active chiral material. We obtain the most general set of linear equations describing the large length and long time-scale dynamics of the gel, by using only conservation laws and symmetries of the system. Finally, we discuss chiral flow and polarity profiles that can emerge spontaneously in such systems.

BP 7.11 Mon 17:45 P3

Cytoskeletal filament length regulation by length-dependent depolymerisation rates — •Christoph Erlenkämper and Karsten Kruse — Theoretical Physics Department, Universität des Saarlandes, Saarbrücken, Germany

In living cells, the length distribution of cytoskeletal filaments often shows a sharp maximum at a finite value. This is in contrast to unregulated polymer growth, which typically leads to exponential distributions. We discuss a simple mechanism by which destabilizing proteins lead to effectively length-dependent disassembly rates. This mechanism produces sharply peaked steady-state distributions.

BP 7.12 Mon 17:45 P3

Dynamics of formin promoted actin polymerization — •Carsten Schuldt, Brian Gentry, Dan Strehle, and Josef A. Käs — Universität Leipzig, Germany

In vivo the semiflexible polymer actin is found as a single filament or is organized in networks and bundles. These structures contribute to the cytoskeleton, whose inherent properties determine the cell's morphology, both mechanically and functionally, and facilitate motility via protrusions and contractions. The assembly of some cytoskeletal actin bundles (contractile ring, filopodia) far from thermodynamic equilibrium is driven by a multi-domain protein called formin. This 'leaky capper' is known to remain bound to the growing ends of filaments and is capable of accelerating the polymerization rate.

We employ an optical tweezer setup in interaction with functionalized microbeads to measure formin's stall force and step size in vitro. Determinig the stall force will yield further insight into formin's ability to produce forces from biochemical energy. In particular, formin may be able to override the force limit of normal actin polymerization. The application of the sophisticated force clamp technique seems to be an apropriate technique to measure step size and examine the behavior of formin with and without external applied tension.

BP 7.13 Mon 17:45 P3

Self-organization of Dynein Motors Generates Meiotic Nuclear Oscillations — Sven Vogel[1], •Nenad Pavin[2,3], Nicola Maghelli[1], Frank Jülicher[2], and Iva Tolic-Norrelykke[1] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden 01307, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden 01187, Germany — [3]Department of Physics, Faculty of Science, University of Zagreb, Zagreb 10002, Croatia

Meiotic nuclear oscillations in the fission yeast Schizosaccharomyces pombe are crucial for proper chromosome pairing and recombination. We report a mechanism of these oscillations based on collective behavior of dynein motors linking the cell cortex and dynamic microtubules that extend from the spindle pole body in opposite directions. By combining quantitative live cell imaging and laser ablation with a theoretical description, we show that dynein dynamically redistributes in the cell in response to load forces, resulting in more dynein attached to the leading than to the trailing microtubules. The redistribution of motors introduces an asymmetry of motor forces pulling in opposite directions, leading to the generation of oscillations. Our work provides the first direct in vivo observation of self-organized dynamic dynein distributions, which, due to the intrinsic motor properties, generate regular large-scale movements in the cell.

BP 7.14 Mon 17:45 P3

Dependence of Eg5Kin force production on monastrol — •André Düselder, Stefan Lakämper, and Christoph Schmidt — 3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen

In the metaphase of mitosis, chromosomes are lined up in the midplane of the cell by the bipolar mitotic spindle. Tetrameric bipolar members

of the Kinesin-5 family of motor proteins play an important role in the establishment of this spindle. We have previously characterized the motile characteristics of Eg5, the Kinesin-5 from Xenopus laevis, using single-molecule fluorescence and optical-trapping experiments. Surprisingly, we observed a novel slip-clutch force sensing mechanism. It remains unclear whether this mechanism is an intrinsic property of the motor domains themselves or if it is due to regulatory domains residing in the stalk or tail domains.

In order to investigate the motile properties of the force-generating units of Eg5 alone, we constructed a stably dimeric chimera, termed Eg5Kin, consisting of the Eg5 motor domain fused to the stalk of D. melanogaster Kinesin-1. In the presence of increasing monastrol concentrations, we observed a reduction in processive run length, but not speed, of single motors.

To date, there has been no data on how monastrol affects Eg5- or Eg5Kin-motility (speed, stallforce, detaching force) under load. Here, we present results from experiments using single-bead optical-trapping interferometry of single Eg5Kin-motors in the presence of increasing monastrol concentrations.

BP 7.15 Mon 17:45 P3

How molecular crowding speeds up mechanotransduction — •Sebastian Sturm[1], Benedikt Obermayer[2], Andrea Kramer[1], and Klaus Kroy[1] — [1]ITP, Universität Leipzig — [2]ASC & CENS, LMU München

No higher forms of life could exist without the ability of biological cells to quickly sense and react to changes in their environment. In general, stimuli excite the cell membrane and have to be transmitted to the nucleus. Mechano-transduction through the cytoskeleton may arguably provide the fastest pathway for mechanical stimuli. Understanding the dynamics of tension propagation through biopolymer networks is thus an important task.

Our approach combines two recent theoretical developments: (i) a systematic theory of tension propagation in single semiflexible polymers [1]; (ii) the glassy wormlike chain model accounting for the influence of a crowded and sticky environment. Extending our previous work, we present (asymptotic) analytical and numerical solutions to the theory and discuss a reinterpretation of the Glassy Wormlike Chain in terms of force transmission through the background medium.

[1] O. Hallatschek, E. Frey and K. Kroy, Phys. Rev. Lett. 94, 077804 (2005)
[2] K. Kroy and J. Glaser, The glassy wormlike chain. New Journal of Physics, 9(416), 2007.

BP 7.16 Mon 17:45 P3

In vitro assembly and characterization of keratin 8/18 intermediate filaments — •Anke Leitner[1], Norbert Mücke[3], Tatjana Wedig[2], Harald Herrmann[2], Michael Beil[4], and Othmar Marti[1] — [1]Department of Experimental Physics, Ulm University, Ulm, Germany — [2]Division of Molecular Genetics, German Cancer Research Center, Heidelberg, Germany — [3]Division Biophysics of Macromolecules, German Cancer Research Center, Heidelberg, Germany — [4]Department of Internal Medicine I, Ulm University, Ulm, Germany

In order to find out more about the mechanical properties of the keratin cytoskeleton it is usefull to have a look on in vitro assembled keratin filaments. In the work presented here we will show nanomechanical properties of the assembled keratin 8/18 filaments. The investigations are done by means of atomic force microscope (AFM). Two different substrates and ways of sample preparation are used. From the 2-dimensional AFM images we calculate the persistence length of the keratin 8/18 filaments with the worm-like-chain model.

BP 7.17 Mon 17:45 P3

Stiff-filament microrheology — Felix Zörgiebel[1], •Marcel Bremerich[1], Frederick C. MacKintosh[2], and Christoph F. Schmidt[1] — [1]3. Physikalisches Institut, Georg-August-Universität, 37077 Göttingen — [2]Department of Physics & Astronomy, Vrije Universiteit , 1081 HV Amsterdam

Active and passive microrheology techniques for probing viscoelastic properties of biological samples require the embedding of micron-sized particles. This can give rise to local perturbations and surface interactions. These effects have to be taken into account during data evaluation and form an obstacle for the investigation of living cells.

A way of circumventing these influences is the use of parts of the system itself, such as the microtubules as local probes by observing their thermal bending fluctuations in the surrounding medium. A detailed analysis of the spatial and temporal bending fluctuations can give information about local shear moduli and stress fluctuations in biopolymer networks in the absence of probe artifacts.

We have investigated a network of filamentous actin by attaching nanometer-sized gold particles to embedded microtubules and have measured thermal motions of the gold particles with an optical trap by laser interferometry with high bandwidth.

BP 7.18 Mon 17:45 P3

Hydrodynamic effects in diffusion-controlled reactions of semiflexible polymers — •Yann von Hansen, Michael Hinczewski, and Roland R. Netz — Physics Dept., Technical Univ. of Munich, Germany

We generalize a mean-field theoretical approach (MFT) for the dynamics of semiflexible polymers [1] that provides insight into the scaling regimes of end-monomer mean squared displacement $\langle r^2(t)\rangle$ examined in recent fluorescent miscroscopy experiments on DNA. It also has been shown to closely agree with Brownian hydrodynamics simulations. The resulting analytical Green's function $G(\vec{r},t)$ for individual monomer motion exhibits excellent agreement with simulations, and can be extended to treat the relative motion of freely diffusing particles and the polymer chain. An understanding of this motion is of fundamental importance for a wide spectrum of processes in biology and chemistry, ranging from protein-DNA interaction to polymerization. Using the MFT we analyze a variety of effects which influence the relative motion, including the hydrodynamic coupling of the internal polymer modes as well as the coupling between the polymer and particle. From these we can extract the overall dependence of the protein-DNA association rate as a function of the polymer contour length L and persistence length l_p. [1] M. Hinczewski, X. Schlagberger, M. Rubinstein, O. Krichevsky, R.R. Netz, arXiv:0809.0667, Macromolecules *in press* (2008).

BP 7.19 Mon 17:45 P3

Microtubules inside out — Jan Kleeblat, Christoph F. Schmidt, and •Iwan A. T. Schaap — 3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen, Germany

Microtubules are protein nano-tubes with a diameter of 25 nm which form a crucial part of the cytoskeleton. During the different states of the cell cycle, microtubules have to rapidly assemble and disassemble. To achieve this microtubules are non-equilibrium polymers with complex mechanical properties. We have here used Atomic Force Microscopy and molecular reconstructions to study the inside of microtubules, unfolded on a strongly adhesive substrate. We found evidence for a mechanical instabilty in the shells from the structure of the adhering sheets.

BP 7.20 Mon 17:45 P3

Imaging microtubule modulating proteins with atomic force microscopy — •Karen Hollenberg, Florian Hagene, Iwan A. T. Schaap, and Christoph F. Schmidt — 3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen

Microtubules have the most complex structure of the filaments forming the cytoskeleton and show alternating phases of growth and shrinkage. These microtubule dynamics are regulated by a variety of microtubule stabilizing and destabilizing proteins that allow the cytoskeleton to adapt to the needs of the cell.

We have set out to use atomic force microscopy in buffer to study how and where such stabilizing proteins bind to the microtubule lattice and compare this to the binding patterns of kinesin motor proteins at a single protein resolution.

BP 7.21 Mon 17:45 P3

Atomic force microscopy of collagen — •Nadine Drechsel, Stephanie Röper, Christian Dietz, and Robert Magerle — Chemische Physik, TU Chemnitz, D-09107 Chemnitz

Type I collagen is a protein material which is a basic constituent of all vertebrates. It can be found in various types of biological tissue, e.g., dermal tissue and bone tissue. We investigate purified collagen isolated from bovine hide which is adsorbed on a mica substrate in buffer solution (L-Glycin/KCl, pH 9,2). Collagen in a buffer solution, in moist air and in the dried state is studied with atomic force microscopy (AFM). For measurements in liquid, the sample is rinsed and imaged in buffer solution, for measurements in air collagen is transferred from the buffer solution to a cleaned mica substrate and subsequently either dried or imaged in moist air. In both cases we find the typical D-band with

a repeat distance of 67 nm. We also performed bimodal AFM measurements; the second flexural eigenmode of the cantilever was used for phase imaging while the amplitude of the first eigenmode was used as feedback signal. On a dried specimen we measured the dissipated energy between AFM tip and a collagen fibril. The results on the collagen fibril prepared from bovine hide are compared with measurements on native cortical human bone.

BP 7.22 Mon 17:45 P3

Optical Tweezer: A system for tracking several beads incorporated in the keratin cytoskeleton of pancreatic carcinoma cells — •Tobias Paust[1], Alexander Schmatulla[1], Ulla Nolte[1], Michael Beil[2], and Othmar Marti[1] — [1]Institute of Experimental Physics, University of Ulm, D-89069 Ulm, Germany — [2]Internal Medicine I, University of Ulm, D-89069 Ulm, Germany

The biophysical and viscoelastic properties of the keratin cytoskeleton have an effect on the ability of migration of the pancreatic carcinoma cells in the extracellular environment. Therefore this project handles about the investigation and characterization of these viscoelastic properties of the keratine networks. With the extraction of the cytoplasmatic elements out of the cell the keratin networks are isolated. This ensures that there are no biochemical interrupts of interactions between the network elements. The method of measurement implies the trapping of a polystyrene sphere and the subsequent movement by the laser light of an optical tweezer. In contact with the cytoskeleton it is possible to determine the mechanical properties of the cytoskeleton by analyzing auto- and crosscorrelation of the trapped bead. A high speed camera was incorporated to measure this spatial response by tracking many particles simultaneously with a time resolution better than 1ms. The first measurements depict the dependency of the response of multiple nanometric spheres on the time variable forces of the cytoskeleton.

BP 7.23 Mon 17:45 P3

Strain stiffening and soft glassy rheology in a generalized sliding filament model — •Philip Kollmannsberger, Claus Metzner, and Ben Fabry — Biophysics Group, Department of Physics, University of Erlangen-Nuremberg

Despite their enormous complexity and structural diversity, most biological materials show a remarkably similar viscoelastic phenomenology: nonlinear elasticity, power-law or logarithmic stress relaxation, and plastic length adaptation. We present a simple model based on Huxley's sliding filament model to demonstrate that such behavior can arise from generic structural properties, independent of the actual molecular constituents of the system. The material is represented by an uniaxial arrangement of parallel elastic elements that have a distribution of attachment angles. When the system is sheared or stretched, elements start to align, leading to strain stiffening due to a geometric recruitment of springs. The elastic elements have force-dependent average lifetimes described by energy traps with a broad distribution of energy trap depths. The elements can reattach at random positions and attachment angles after unbinding. Such nanoscale structural rearrangements lead to viscous flow and plastic length adaptation on a macroscopic scale. The model gives quantitative agreement for creep compliance, stress stiffening and plasticity in the case of cell microrheology. These results suggest that recruitment and dynamic unbinding of elastic elements are the common mechanism underlying the mechanical behavior of many complex biological materials from single cells to whole tissues.

BP 7.24 Mon 17:45 P3

Imaging human bone with bimodal scanning force microscopy — •Stephanie Röper[1], Nadine Drechsel[1], Christian Dietz[1], Anke Bernstein[2], and Robert Magerle[1] — [1]Chemische Physik, TU Chemnitz, D-09107 Chemnitz — [2]Experimentelle Orthopädie, Martin-Luther-Universität Halle-Wittenberg, D-06097 Halle/Saale

Biological materials such as bone and teeth are nanocomposites of a soft organic matrix (type I collagen) that is reinforced by a stiff inorganic component (hydroxylapatite). Our study is focused on cortical human bone. The specimen surface was first mechanically grinded and polished, then 10 s etched with formic acid and finally flushed with methanol to stop the etching process. With optical microscopy and tapping mode scanning force microscopy (TM-SFM) a spot on the specimen was chosen for detailed investigation which displays a lamellar structure in the vicinity of a Haversian canal. TM-SFM images measured in air show collagen fibrils with typical D-bands with 67 nm periodicity. For bimodal TM-SFM the second flexural eigenmode of the cantilever was used for phase imaging while the amplitude of the first eigenmode was used as feedback signal. The second eigenmode phase image revealed an enhanced contrast compared to that of the first eigenmode. In addition we measured the energy dissipated between tip and specimen along a collagen fibril. The results obtained on native human bone were compared with measurements on collagen fibrils prepared from purified collagen isolated from bovine hide.

BP 7.25 Mon 17:45 P3

Surface properties relevant for the adhesion of marine microorganisms — •A. Rosenhahn[1], S. Schilp[1], X. Cao[1], F. Wode[1], M.P. Arpa Sancet[1], M. Heydt[1], M.E. Pettit[2], M.E. Callow[2], J.A. Callow[2], and M. Grunze[1] — [1]Applied Physical Chemistry, University of Heidelberg, 69120 Heidelberg, Germany — [2]School of Biosciences, University of Birmingham, Birmingham B15 2TT, UK

The prevention of biofouling is a major challenge for all manmade objects which are in long term contact with seawater. In order to systematically develop non toxic coatings, a fundamental understanding of basic surface properties relevant for adhesion of marine inhabitants is required. To determine the influence of selected surface properties we systematically vary wetting, hydration and charge by self assembly of oligo- and polymers. To obtain well defined morphologies, nanolithography and self assembled multilayers are used. The biological response is determined in settlement and adhesion strength assays using predominantly the green algae Ulva linza, but also barnacle cyprids and marine bacteria. It turned out that contact angles around the Berg limit, hydration of the coatings and micrometer sized structures render surfaces less attractive. Besides static assays we are interested in the time dependent dynamics of biofilm formation. To acquire and analyze the complex, 3D swimming and exploration patterns of algal zoospores, we apply digital in-line laser holography. The influence of surface properties on the motion patterns as well as specific recognition distances will be discussed.

BP 7.26 Mon 17:45 P3

Protein film formation on hydroxy apatite surfaces — •Christian Zeitz, Frank Müller, and Karin Jacobs — Saarland University, Experimental Physics, D-66041 Saarbruecken

The composition and the morphology of initial protein films play an important role in the formation of the so-called pellicle, the intraoral biofilm that builds up on tooth surfaces in contact with saliva. Recently, it has been shown on model surfaces that the chemical composition of the uppermost surface layer of a substrate as well as the subsurface composition determines the function of the pellicle and especially the development of the mature biofilm, including bacteria. The aim is to understand the pellicle formation under variable substrate conditions.

The focus of our study lies on the characterization of such protein films on two different kinds of enamel-like surfaces: fluoridated and unfluoridated hydroxyl apatite. It has been shown [1] that the application of acidic amine fluoride agents changes untreated surfaces not only in the uppermost layer but also affects the composition of the bulk material up to a depth of some hundred nanometers. Furthermore, the chemical composition of the (un-) fluoridated samples as a function of depth can be characterized by XPS-ESCA. Both types of surfaces are exposed to protein solutions. Within minutes, the proteins adsorb building up a biofilm, the morphology of which is characterized by AFM.

[1]: Müller et al., arXiv:0806.1425v1 ,2008

BP 7.27 Mon 17:45 P3

Probing the unfolding behavior of SNase mutants by SAXS — •Martin Schroer[1], Christina Krywka[2], Saskia Schmacke[1], Michael Paulus[1], Roland Winter[3], Catherine Royer[4], Bertrand Garcia-Moreno[5], and Metin Tolan[1] — [1]Fakultät Physik/DELTA, Technische Universität Dortmund, D-44221 Dortmund, Germany — [2]Institut für Experimentelle und Angewandte Physik, Christian-Albrechts-Universität zu Kiel, 24118 Kiel, Germany — [3]Physikalische Chemie I, Technische Universität Dortmund, D-44227 Dortmund, Germany — [4]3 CNRS, UMR5048, Centre de Biochimie Structurale, F-34090 Montpellier, France — [5]Department of Biophysics, Johns Hopkins University, 3400 North Charles Street, Baltimore, MD 21218, USA

Investigating the structure of proteins and their stability is of great interest as it is known that destabilization may lead to protein unfolding, misfolding and aggregation. These effects might be first steps for several diseases such as the Alzheimer disease and prion diseases. In

order to get a deeper insight into this process it is thus necessary to determine how the stability and conformation are changed when the protein's amino acid sequence is altered by point mutations.

In our recent SAXS (small angle x-ray scattering) studies we analyzed the unfolding behavior of different mutants of the model protein Staphylococcal Nuclease (SNase) as a function of temperature and pressure. Depending on the physicochemical properties of the particular amino acid exchanged, the stability of the mutants is altered significantly.

BP 7.28 Mon 17:45 P3

Improving protein structure prediction using sequence-derived structure profiles — •Katrin Wolff[1], Andrea Cavalli[2], Michele Vendruscolo[2], and Markus Porto[1] — [1]Institut für Festkörperphysik, TU Darmstadt, Germany — [2]Department of Chemistry, University of Cambridge, Cambridge, UK

A crucial step in the prediction of protein structures is the transition from low- to high-resolution models. There exist various tools that generate candidate sets that contain high-quality, yet coarse-grained, structures. In a subsequent refinement step these structures are improved to all-atom representations and minimized using a high-resolution energy functional. Due to limited computer time it is vital to restrict this refinement step to promising candidates and to identify the best structures. The energy functional used in the structure generation step, however, is only of limited use for the problem of selecting these 'good' structures. We discuss the use of structure profiles for this filtering step. As a proof of principle we show that the exact profile (derived from the native structure) is very reliable in choosing candidates with low RMSD to the native structure and clearly outperforms other filtering methods like filtering by energy or clustering the decoy set. Such structure profiles can be predicted to good accuracy from sequence [1,2]. We therefore explore the use of profiles as predicted from sequence and show that for sufficiently high accuracy this approach is also superior to the other methods of filtering.

[1] A. R. Kinjo *et al.*, BMC Bioinformatics **7**, 401 (2006).
[2] J. Minning, F. Teichert, U. Bastolla, M. Porto, in preparation.

BP 7.29 Mon 17:45 P3

Langevin-Dynamik-Simulation von Peptiden — Uwe Winter und •Tihamér Geyer — Zentrum für Bioinformatik, Universität des Saarlandes, Saarbrücken

Zwischen den Zeit- und Längenskalen, die jeweils mit Molekulardynamik (MD) und Brownscher Dynamik (BD) beschreibbar sind, klafft eine Lücke von etwa zwei Größenordnungen, in denen MD-Simulationen zu aufwändig sind und bei BD-Simulationen die nötige Auflösung nicht erreicht wird. Wir zeigen, wie durch eine explizite Berücksichtigung des Impulses der Gültigkeitsbereich der BD zu kleineren Zeitschritten hin erweitert werden kann und damit realistische ,,Langevin"-Simulationen kleiner flexibler ,,bead-spring"-Peptide möglich werden. Für eine korrekte und stabile Dynamik darf dabei die viskose hydrodynamische Dämpfung durch den Solvens nicht vernachlässigt werden. Wir vergleichen am Beispiel eines kurzen Peptids von 11 Aminosäuren, welches gegen eine MD-Trajektorie parametrisiert wurde, die jeweiligen Schwierigkeiten und Vorteile von BD- und Langevin-Beschreibung.

BP 7.30 Mon 17:45 P3

Oxygenation interactions of the metalloprotein hemocyanin in aqueous solution revealed by core-level spectroscopy — •Daniel Panzer[1], Christian Beck[2], Jochen Maul[1], Nora Bergmann[3], Gerhard Schönhense[1], Heinz Decker[2], and Emad Aziz[4] — [1]Institut für Physik, Staudinger Weg 7, Johannes Gutenberg-Universität, D-55099 Mainz — [2]Institut für Molekulare Biophysik, Welderweg 26, Johannes Gutenberg-Universität, D-55099 Mainz — [3]Max-Delbrück-Center for Molecular Medicine, D-13125 Berlin-Buch — [4]BESSY GmbH, Albert-Einstein-Strasse 15, D-12489 Berlin

Active metal sites play a key role in the biochemistry of oxygen and particularly in oxygen transport. Hemocyanin (Hc) is a widespread respiratory protein in arthropods and molluscs comprehending multiple copper active sites. Observing the binding, interaction and subsequent reactivity of dioxygen at these hemocyanin copper centres is thus essential for understanding its comprehensive chemical and biological functionality.

Here, we use core-level spectroscopy to measure the copper X-ray absorption structure of hemocyanin in aqueous solution and therewith very similar to physiological conditions. We identify the deoxygenated and the oxygenated state of the native Hc molecule by probing the local electronic structure of the oxygen-active metal centres. Our findings demonstrate an X-ray approach to observe the biochemical activity in an intact metalloprotein molecule and open perspectives for X-ray spectroscopy of complex biomolecules under in vivo conditions.

Funded by the DFG (DE 414/12-1 and SCHO 341/7).

BP 7.31 Mon 17:45 P3

Pebble-game rigidity analysis of protein crystal structures is highly sensitive to small structural variations — •Emilio Jimenez, Stephen Wells, and Rudolf Roemer — Department of Physics and Centre for Scientific Computing, University of Warwick, Coventry CV4 7AL, UK

Rigidity analysis using the "pebble game" can usefully be applied to protein crystal structures to obtain information on protein folding, assembly and the structure-function relationship. However, previous work using this technique has not made clear how sensitive rigidity analysis is to small structural variations. We present a comparative study in which pebble-game rigidity analysis is applied to multiple structures, derived from different organisms and different conditions of crystallisation, for each of several different proteins. It appears that the results are highly sensitive to relatively small structural variations.

We find that rigidity analysis is best used as a comparative tool to highlight the effects of structural variation. We advise caution when using pebble-game rigidity analysis as a coarse-graining method in biophysical modelling of proteins. Our comparative use of multiple protein structures brings out a previously unnoticed peculiarity in the rigidity of trypsin.

BP 7.32 Mon 17:45 P3

The mechanisms of lipid membrane-induced IAPP fibrillogenesis and its inhibition — •Sebastian Tiemeyer[1], Florian Evers[1], Christoph G. Jeworrek[2], Michael Paulus[1], Bernd Struth[3], Metin Tolan[1], and Roland Winter[2] — [1]Faculty of Physics / DELTA, TU Dortmund, 44221 Dortmund, Germany — [2]Faculty of Chemistry, TU Dortmund, 44221 Dortmund, Germany — [3]Deutsches Elektronen-Synchrotron, HASYLAB, Notkestr. 85, 22607 Hamburg, Germany

Protein misfolding plays an important role in many diseases like Alzheimer's, Parkinson's or type 2 diabetes mellitus. In the latter case, IAPP is thought to cause the death of insulin-producing beta-cells in the pancreatic islets of Langerhans. Previous experiments propose aggregation of IAPP to amyloid fibrils at beta-cell membranes followed by membrane disruption. X-ray reflectivity (XRR) experiments were performed at the beamline BW1 at HASYLAB in order to investigate the IAPP - lipid membrane interaction in the presence and absence of the red wine compound resveratrol. From the XRR data, we were able to identify the status of nucleation, aggregation and fibrillation of IAPP at the lipid membrane interface. Furthermore, the inhibition of the aggregation process by resveratrol was revealed.

BP 7.33 Mon 17:45 P3

Tip-enhanced single molecule fluorescence near-field microscopy for nanobiophysics — •Heinrich Gotthard Frey, Jan Paskarbeit, and Dario Anselmetti — Experimental Biophysics and Applied Nanoscience, Fakultät für Physik, Universität Bielefeld, Universitätsstraße 25, 33615 Bielefeld

For nanobiophysical applications, scanning near-field optical microscopy (SNOM) of single fluorescent dye molecules must combine high electrical field intensities in the sample near-field with high optical and topographical resolution [1] and the ability to image surface-immobilized biomolecules in aqueous solution. We show, that theses requirements can be satisfied using the electric field enhancement at the tip of far-field illuminated silicon AFM probes in aperture-less SNOM.

Single ATTO-740 dye molecules have been imaged at an optical resolution of 20-25nm (separation of two dye molecules) under ambient conditions and in aqueous solution with commercial silicon AFM probes and sophisticated phase-sensitive single photon counting technology in dynamic AFM mode of operation. Two illumination modes have been tested successfully: a) back-illumination via evanescent fields in a total-internal-reflection-microscopy setup using an oil-immersion objective lens and b) direct top-illumination side. Although both optical setups gave similar results, they differ considerably with respect of potential experimental applications that will be discussed [2].

[1] H.G. Frey et al., Nanotechnology 17, 3105-3110, 2006 [2] H.G. Frey et al., in preparation 2008

BP 7.34 Mon 17:45 P3

Dual-trap optical tweezer for single molecule studies of transcription — •Marcus Jahnel[1,2], Martin Behrndt[1,2], and Stephan W. Grill[1,2] — [1]Max Planck Institut for Molecular Cell Biology and Genetics, Dresden, Germany — [2]Max Planck Institut for the Physics of Complex Systems, Dresden, Germany

The ability to accurately monitor and manipulate individual macromolecules allows the study of key biological processes one molecule at the time. Here, we report the construction of a Brownian noise-limited dual-trap optical tweezer setup to investigate the dynamics of processive nucleic acid-dependent molecular motors. Splitting a 1064 nm solid-state laser beam by polarisation generates two optical traps, each independently manoeuvrable by either a piezo-driven mirror or an acousto-optical deflector. Each trap is capable of holding one end in a bead-molecular motor-nucleic acid-bead "dumbbell-type" experiment. Notably, a careful analysis and subsequent elimination of the cross-talk between the two polarisation states caused by the various optical elements allows the differential distance between the two traps to be determined with very high precision.

Encouraged by feasibility studies of the setup we now address the dynamics of RNA Polymerase during transcription of DNA into RNA, one of the most important cellular processes constituting the first step in transferring genetic information into functional proteins.

BP 7.35 Mon 17:45 P3

Three-bead assay for single molecule ncd study — •Christoph Pieper[1], Li Tao[2], Kerstin von Roden[1], Stefan Lakämper[1], Jonathan Scholey[2], and Christoph Schmidt[1] — [1]3. Physikalisches Institut, Georg-August-Universität, 37077 Göttingen — [2]Department of Molecular and Cell Biology, University of California at Davis, Davis, CA 95616

The ncd protein is a dimeric minus-end directed motor of the kinesin family. Previous experiments using optical tweezers and a three-bead, suspended-micotubule assay showed transient microtubule-binding events with a working stroke of about 9 nm at the end of the binding events. Binding events could be detected by the reduction in noise of the suspended microtubule. We have now developed an advanced assay, using a new FPGA board for the rapid online detection of these binding events. The FPGA further controls acousto-optical deflectors for beam steering and trap feedback. With this system feedback can activated on ncd binding to study the behavior of a single ncd motor under a defined load.

BP 7.36 Mon 17:45 P3

Monitoring single membrane proteins in an anti-Brownian electrokinetic (ABEL) trap — •Anastasiya Golovina-Leiker, Nawid Zarrabi, Monika Düser, Rolf Reuter, Jörg Wrachtrup, and Michael Börsch — 3.Physikalisches Institut, Universität Stuttgart, Germany

Brownian motion prevents the observation of one biomolecule for extended periods. Adam E. Cohen and W. E. Moerner have developed an anti-Brownian electrokinetic (ABEL) trap to trap individual protein molecules in free solution, under ambient conditions, without requiring any attachment to beads or surfaces [Cohen and Moerner, PNAS 2006). They also demonstrate trapping and manipulation of single lipid vesicles. We present an extension of their approach to trap membrane proteins reconstituted in lipid vesicles and to simultaneously monitor the conformational changes of the active enzyme by fluorescence resonance energy transfer.

BP 7.37 Mon 17:45 P3

Single Molecule Force Spectroscopy to Study Receptor / Ligand Interactions — Mathias Salomo[1], •Marc Struhalla[2], and Friedrich Kremer[1] — [1]Universität Leipzig, Institut für Experimentelle Physik I, Linnèstraße 5, 04103 Leipig — [2]c-LEcta GmbH, Deutscher Platz 5b, 04103 Leipzig

Optical tweezers (OT) are ideally suited to study the interaction of single receptor-ligand bonds. Here we introduce a newly developed assay using optical tweezers to investigate the interactions between Protein A from Staphylococcus aureus, Protein G from Streptococcus spec. and different immunoglobulins. We demonstrate that the rupture forces depend on the loading rate and on the sodium chloride concentration. The measured loading rate effect is well known in the literature and the data we obtained and which were found to be in good agreement with an already published theoretical model can be used to directly determine interaction parameters like the dissociation rate. The dependence of the rupture forces on the salt concentration demonstrates the influence of hydrophobic interactions on the bond strength. Our experimental setup can probe the interaction between a single receptor and its specific ligand under changing conditions and hence offers manifold applications in single molecule biotechnology.

BP 7.38 Mon 17:45 P3

Monitoring the two rotary motors of a single FoF1-ATP synthase by triple-ALEX-FRET — •Torsten Rendler[1], Stefan Ernst[1], Monika G. Düser[1], Nawid Zarrabi[1], Anastasiya Golovina-Leiker[1], Rolf Reuter[1], Stanley D. Dunn[2], Jörg Wrachtrup[1], and Michael Börsch[1] — [1]3. Physikalisches Institut, Universität Stuttgart, Germany — [2]Department of Biochemistry, University of Western Ontary, London, Canada

Synthesis of ATP from ADP and phosphate is performed by a stepwise internal rotation of subunits of the enzyme FoF1-ATP synthase. The bacterial enzyme also catalyzes ATP hydrolysis. The opposite direction of rotation during ATP synthesis and hydrolysis was confirmed by single-molecule fluorescence resonance energy transfer, FRET, using specific labeling of the rotary subunits γ or ϵ in the F1 motor and the stator subunits. The step size in the F1 motor was 120°. In contrast the step size during proton-driven rotation of the c subunits in the Fo motor was 36° using single-molecule FRET. FRET artifacts could be minimized by 'duty cycle optimized alternating laser excitation'. As the two coupled motors of FoF1-ATP synthase showed apparently different step sizes, this mismatch has to be unraveled by mapping the contributions of rotor and stator subunits for transient energy storage. We present the simultaneous observations of F1 and Fo motor rotations using a single-molecule triple FRET approach, which indicate elastic deformations of the rotor between ϵ and c subunits during ATP hydrolysis as well as synthesis.

BP 7.39 Mon 17:45 P3

Fabrication of metallized solid state nanopores for single molecule experiments — •Ruoshan Wei, Daniel Pedone, Gerhard Abstreiter, and Ulrich Rant — Walter Schottky Institut, Technische Universität München, Deutschland

Nanopores in solid state membranes have emerged as powerful means to study single molecules. In translocation experiments, the trans-pore ionic current is monitored to detect the passage of individual molecules (nucleic acids or proteins). Engineered solid state pores hold considerable advantages over their biological counterparts with respect to stability and adjustability. With the aim of creating an electrically gateable pore which can be used to modulate the biomolecule translocation efficiency, we devised a novel concept where the nanopore is metallized on one side. Here we report on the device fabrication and electrical characterisation in aqueous electrolyte solution. Pores featuring diameters < 30 nm are fabricated in Si3N4 membranes by e-beam lithography. Subsequently, thin (< 20 nm) metal films of Pt or Au are evaporated on Ti adhesion layers. The surface roughness and film morphology are assessed for different deposition methods (e-beam vs. thermal evaporation). The trans-pore current as well as the device capacitances are studied using electrochemical impedance spectroscopy and FFT analysis of high-bandwidth current recordings. Within this framework, we investigate the reduction of current noise by surface passivation using silicone elastomers.

BP 7.40 Mon 17:45 P3

Comprehensive Acquisition and Analysis Software for Optical Tweezers — •Fabian Czerwinski and Lene B. Oddershede — Niels Bohr Institute, Blegdamsvej 17, Copenhagen

Optical tweezers have become a valuable tool in biophysics e.g. for precise detection and manipulation of individual (biological) molecules. We present a comprehensive Labview toolbox for optical tweezers with a photodiode-based detection system. Various incorporated methods allow for calibrating biological objects and optical handles directly [1,2]. Acquisition parameters can be precisely adjusted, leading to reliable feedback modes [3] and minimized noise [4]. Drift and noise are quantified on-the-fly by improved Allan-variance algorithms [5].

The main program is designed in a modular fashion to offer (optionally) independent as well as interconnected control of diode, stage and microfluidics. Further, it also contains support for data-streaming protocols. In order to assure minimal failure and negligible error rates, we utilize programming options such as multicore processing, cache-speed optimization and pipelined register control. The source code is available upon request and under Creative Common License. Future improvements will include an extended readout of image devices to facilitate parallel single-particle tracking and further possibilities for

calibration.

[1] Berg-Sorensen et al., Rev Sci Instr (17)594, 2004. [2] Tolic-Norrelykke et al., Rev Sci Instr (77)103101, 2006. [3] Greenleaf et al., PRL (95)208102, 2005. [4] Gibson et al., Opt Exp (16)5958, 2008. [5] Czerwinski, Matlab Central, 21727, 2008.

BP 7.41 Mon 17:45 P3

Design of a low-cost modular FCS, FRAP and Optical Tweezers setup for educational use — •Thorsten Bloem, Nadine Lang, Philip Kollmannsberger, and Ben Fabry — Biophysics, University of Erlangen, Germany

We demonstrate a flexible yet inexpensive optical setup for undergraduate education which alternately provides Fluorescence Correlation Sprectroscopy (FCS), Fluorescence Recovery after Photobleaching (FRAP) as well as Optical Tweezers (OT) reusing the same components. It is built around a 100x objective with 1,25 NA, two diode lasers (532 nm and 1064 nm) for fluorescence and trapping, a CCD camera and an avalanche photodiode (APD) as detectors, as well as standard optomechanics mounted on a 60x60 cm breadboard. The total price of less than 8 000,- EUR for the basic configuration makes modern imaging and manipulation techniques accessible for undergraduate institutions at a fraction of the cost of high-end research systems. Teaching modules for advanced lab courses are presented to demonstrate the use as an educational platform for modern optics, biological imaging and biophysics.

BP 7.42 Mon 17:45 P3

Phase contrast tomography of human brain using grating interferometry — •Georg Schulz[1], Marco Germann[1], Franz Pfeiffer[2], Timm Weitkamp[3], Christian David[2], and Bert Müller[1] — [1]Biomaterials Science Center, University Basel, Switzerland — [2]Paul Scherrer Institute Villigen, Switzerland — [3]ID19, ESRF Grenoble, France

In order to visualize the human thalamus, which is one of the most ambitious challenges in X-ray tomography, as it exhibits almost no absorption contrast, we use phase contrast tomography which is based on differences of the refraction index. No labelling of the tissue before the measurements is needed in order to segment the vessel tree from the surrounding tissue. In our study we use a grating interferometer consisting of a beam-splitter grating and an analyzer absorption grating. Here we can detect phase shifts in the range of several 10^{-8} *rad*. The presented results derive from measurements at ESRF Grenoble (beamline ID19) at an energy of 26 keV. The resulting voxel sizes range down to 7.5 μm. The examination of the reconstructed tomographic slices implies a measurement sensitivity for the real part of the refractive index of $0.7 \cdot 10^{-10}$, which corresponds to an electron density sensitivity of 0.04 e/nm^3 and a mass density sensitivity of approximately 0.1 mg/cm^3 for aqueous specimens. Blood vessels could be well identified and partially segmented using a simple intensity based segmentation tool. For a complete segmentation more sophisticated tools are needed.

BP 7.43 Mon 17:45 P3

Einfluss der Eigenschaften dielektrischer Schichten auf das Verhalten von Metallelektroden-Zellkultur-Grenzflächen — •Mathias Müller, Christian Warnke, Alexander Franke, Michael Charpentier, Antje Reiher, Kay-Michael Günther, Hartmut Witte, Jürgen Christen und Alois Krost — Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg

Für das elektrische Anregen und Auslesen von Zellkulturen haben sich planare Elektrodenanordnungen (MEAs) etabliert. Bei der Adaption der MEAs an das jeweilige biologische System spielen die elektrischen Übertragungsmechanismen der anregenden Pulse eine wichtige Rolle. Diese Transfervorgänge werden insbesondere durch die Verwendung dielektrischer Schichten auf den Elektroden beeinflusst. Aus diesem Grund haben wir den Einfluss von TaO_x- und SiO_x-Schichten sowie von Photolacken und Polymid auf die elektrischen Übertragungseigenschaften von Au/Ti-Fingerelektroden-Anordnungen untersucht. Die Oberflächen der Elektroden und der dielektrischen Schichten wurden durch Nomarski-Mikroskop und AFM und die elektrischen Eigenschaften mit DC-und AC-Messungen charakterisiert. Mittels Impedanzspektroskopie wurden die Eigenschaften des Überganges Elektrode/Isolatorschicht/Elektrolyt bei verschieden leitfähigen Elektrolytlösungen untersucht. Die Anordnungen wurden schließlich hinsichtlich ihrer Anwendung als Anregungs- sowie Ausleseelektroden für Neuronen- und Hefezellen, charakterisiert. Zusätzlich konnte die elektrolytische Produktion von Gasen in Abhängigkeit von den Schichtparametern der Strukturen nachgewiesen werden.

BP 7.44 Mon 17:45 P3

Competitive Homogeneous Hapten Immunoassay Based on Fluorescence Quenching by Gold Nanoparticles — Benjamin Ehlers[1], Sergiy Mayilo[1], •Meike Koster[1], Michael Wunderlich[1], Thomas A. Klar[1,2], Hans-Peter Josel[3], Dieter Heindl[3], Alfons Nichtl[3], Konrad Kürzinger[3], and Jochen Feldmann[1] — [1]Photonics and Optoelectronics Group, Department of Physics and CeNS, Ludwig-Maximilians-Universität München, Munich, Germany — [2]Institute of Physics and Institute of Micro- and Nanotechnologies, Technical University of Ilmenau, Ilmenau, Germany — [3]Roche Diagnostics GmbH, Penzberg, Germany

We report on a competitive, homogeneous immunoassay for the detection of the hapten digoxigenin, a drug used to cure atrial fibrillation. The assay consists of gold nanoparticles functionalized with anti-digoxigenin antibodies and fluorescently labelled digoxigenin. Initially, the labelled digoxigenin is bound to the gold nanoparticles and the fluorescence is effectively quenched. Upon the addition of digoxigenin, a competition takes place for the antibodies on the gold nanoparticles leading to labelled digoxigenin free in solution and therefore an increase of fluorescence. By using time-resolved spectroscopy, it is found that the quenching is due to energy transfer from the dye to the gold nanoparticle. The assay is sensitive in the therapeutically relevant concentration range of 0.5 to 3 ng/mL. The method can be applied both in buffer solution and in serum. The same principle of competitive fluorescence quenching can be applied to detect other haptens.

BP 7.45 Mon 17:45 P3

NIR SERS hybrid probes for in vitro and in vivo bioanalytics — •Andrea Matschulat[1,2], Ilona Dörfel[1], Franziska Emmerling[1], and Janina Kneipp[1,2] — [1]Federal Institute of Materialsresearch and Testing (BAM) — [2]Department of Chemistry, Humboldt University, 12489 Berlin, Germany

Raman Spectroscopy, a method with many applications ranging from condensed matter physics to bioanalytical chemistry, offers several advantages such as the rapid and non-destructive study of vibrational fingerprints of chemical and biological compounds. With SERS, scattering efficiencies can be enlarged by a factor of $\sim 10^6$ in bulk samples. This versatile and selective technique provides more sensitive detection, accompanied by high spatial resolution due to local optical near-fields generated by noble metal nanostructures. Our work is concerned with the construction and characterization of Au and Ag nanoparticles whose unique plasmonic properties are tuned for the sensitive NIR-SERS probing of complex biosamples. In our studies, we were successful in detecting spectral fingerprints of various Raman reporter species (DTNB, NT, MBA and PATP) that contrast strongly with commonly used reporter fluorophores due to their larger SERS cross sections. Further, their utilization in multiplex approaches under physiological conditions enables the identification of different types of labelled SERS probes. In first *in vitro* experiments, we have introduced SERS hybrid probes, with which intrinsic information of pollen extracts can be obtained. The role of BSA as a stabilizing agent for nanoparticles and linker for multiple analytes in both will also be discussed.

BP 7.46 Mon 17:45 P3

Biological application of atomic scale magnetometry using single defects in diamond — •Thomas Wolf, Gopalakrishnan Balasubramanian, Roman Kolesov, Fedor Jelezko, and Jörg Wrachtrup — 3. Physikalisches Institut, Universität Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart

Diamonds contain natural defect centres in their lattice structure known as colour centres. Electron spin states in these colour centres can be changed and measured with optical techniques at room temperature. The potential of locating one of these centres spatially on the nanometer scale with potential for sub-nm precision by using magnetic resonance techniques has been recently shown by our group and collaborators. Using small nanocrystals containing a NV-centre (nitrogen-vacancy) we intend to implement diamond as non-toxic biological marker having potential to overcome the classical resolution limit of light microscopy under physiological conditions.

BP 7.47 Mon 17:45 P3

Sub 300 nm Softlithography with SU8 — •Jörg Käsewieter, Jan Regtmeier, and Darius Anselmetti — Experimental Biophysics & Applied Nanoscience, Faculty of Physics, Bielefeld University, Germany

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]1Institute for Meteorology and Climate Research, Forschungszentrum Karlsruhe, Germany — [2]2Institute 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

force microscopy to study the concentration dependence by alternative means and minimize influence by external forces. The end-to-end distance and the height of the complexes were measured in dependence of protein concentration (50-5000 nM). With increasing protein concentration the end-to-end distance decreases from 70 to 38 nm while the height increases from 0.7 to 2.2 nm for 250 bp dsDNA, indicative of the formation of a globular structure of the TmHU-DNA complex. Most likely this originates from a secondary organizational level during TmHU-DNA binding observed in optical tweezers experiments.

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Buckling Transition during DNA Supercoiling studied by Magnetic Tweezers — •Hergen Brutzer, Daniel Klaue, and Ralf Seidel — DNA motors group, BIOTECnology Center, University of Technology Dresden, D-01062 Dresden

In contrast to its well-characterized stretching and bending behavior, the response of DNA upon twisting is less understood. Initially, under the action of an external force, the molecule extension remains almost constant upon twisting. Once a critical buckling torque is reached a linear decrease in extension with added twist is observed, due to the formation of a superhelical structure. Recent experiments, however, revealed the existence of an abrupt extension change at the buckling transition, i.e. upon superhelix formation. Here we studied this abrupt buckling using magnetic tweezers, in order to elucidate its origin. We recorded the population of the pre and post-buckling states as function of the applied twist with high resolution. Depending on the applied force, the superhelix in the post buckling state comprises considerably more than one turn. Applying a two-state model in which the energy for the first turn of superhelix formation is larger than for the subsequent turns, the observed buckling transition can be explained nearly quantitatively. The model suggests a plectonemic structure with one initial loop of high curvature and a subsequent superhelix with lower DNA curvature. With decreasing salt concentration the appearance of the buckling transition is less pronounced, which is also supported by the model.

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Two dimensional semiflexible polymer rings — •Fabian Drube, Karen Alim, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstrasse 37, D-80333 München, Germany

The shape of DNA plays a crucial role in many biological processes like protein-DNA interaction. Especially circular DNA shows interesting shape characteristics due to its geometrical constraint. While measuring the three dimensional structure of DNA is not feasible at the moment, recently, circular DNA on a mica surface has been studied experimentally [1]. Comparing these data with the wormlike chain model reveals that topological self-avoidance effects are substantial. We introduce a novel tube-like model of semiflexible polymers to account for excluded volume effects. With extensive Monte-Carlo simulations we quantify the ensuing conformations of circular DNA and compare those with available experimental data.

[1] G. Witz, K. Rechendorff, J. Adamcik, and G. Dietler, Conformation of circular DNA in two dimensions, Phys. Rev. Lett. **101**, 148103 (2008)

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A coarse-grained model for RNA tertiary structure formation — •Thomas Schötz and Ulrich Gerland — Arnold Sommerfeld Center for Theoretical Physics and CeNS, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München

RNA folding is relatively well understood on the secondary structure level, i.e. structure formation in the abstract space of base pairing patterns. However, on the level of the three-dimensional structure in real space, there are hardly any modeling approaches short of full-fletched molecular dynamics simulations, which are challenging even for small RNA molecules. Towards the ultimate goal of filling this gap, we construct a coarse-grained bead-spring type polymer model for RNA, which behaves like a freely jointed rouse chain as long as the bases are unpaired. However, when the short-range sequence-dependent interactions between the bases set in, more complex interactions between adjacent base pairs act to spontaneously create double-helical segments with a non-vanishing bending rigidity and torsion stiffness. We study the rich behavior of this model, including the sequence-dependent folding dynamics as well as static and dynamic properties of the folded tertiary structure, by the use of Brownian dynamics simulation techniques. This approach allows us to examine the dynamic formation and destruction of typical tertiary structure elements, including small pseudo-knotted structures, which play an important role in molecular biology.

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Stretching of a DNA/HU-protein complexes in SMD simulations — •Carsten Olbrich and Ulrich Kleinekathöfer — Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany

The protein HU is a member of a family of prokaryotic proteins that interacts with the DNA in a non-specific way [1]. Its major function is the binding, compaction and stabilization of DNA. Steered molecular dynamic (SMD) simulations are applied to DNA which is either bound to the HU protein of the bacteria Anabaena (AHU) or of the Thermotoga maritima (TmHU). Using these all-atom simulations including explicit water and about 80,000 atoms in total, we are able to gain insight into the discrete disruptions events which occur when the DNA releases from the protein body. These disruptions were first observed in experiments performed with optical tweezers [2]. By comparing the unbinding pathways of the complexes, different binding strengths of AHU and TmHU to DNA can be found.

[1] R. Dame and N. Goosen, FEBS Lett. **529**, 151 (2006).
[2] M. Salomo, F. Kremer et al., J. Mol. Biol. **359**, 769 (2006).

BP 7.58 Mon 17:45 P3

Optical tweezers measurements of threading DNA and DNA-ligand-complexes through solid-state nanopores — •Andy Sischka[1], Christoph Kleimann[1], Wiebke Hachmann[2], Marcus M. Schäfer[3], Ina Seuffert[4], Katja Tönsing[1], and Dario Anselmetti[1] — [1]Experimental Biophysics and Applied Nanosciences, Bielefeld University, Germany — [2]Molecular and Surface Physics, Bielefeld University, Germany — [3]Center for Nanotechnology (CeNTech), Münster, Germany — [4]Fachbereich Physik, Fach M621, University of Konstanz, Germany

We developed a versatile and high precision 3D optical tweezers setup, capable for force measurements completely based on detection of backscattered light with minimal optical interference to measure forces in the sub-pN regime and to manipulate single molecules. With this novel setup, single dsDNA-molecules were threaded into a solid-state nanopore by applying electrical voltage across the membrane, as the electrostatic force and the ionic current through the pore were measured. Here, individual force steps could be observed for each DNA-molecule entering the nanopore. Active pulling of a single Lambda-DNA-molecule out of the nanopore by linearly increasing the bead-membrane distance induced a force signal with only very weak force oscillations of about 2 pN, until the DNA was completely pulled out of the nanopore. Binding of dedicated protein ligands (peroxiredoxin, and E.coli RNA-polymerase) to dsDNA caused a significant change in the apparent electrostatic forces that are required for threading and unthreading the DNA-ligand-complex through the nanopore.

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Force-induced unfolding of G-quadruplex — •Hui Li[1], En-hua Cao[2], and Thomas Gisler[1] — [1]Universität Konstanz, Fachbereich Physik, 78457 Konstanz, Germany — [2]Institute of Biophysics, Chinese Academy of Sciences, Beijing 100101, China

Telomeric DNA sequences can form four-stranded (quadruplex) structures both in vivo and in vitro in presence of cations. However, the folding process of quadruplex is still a mystery and has so far not been accessible with conventional molecular dynamics (MD) simulation. In this publication we study the unfolding of a parallel G-quadruplex from human telomeric DNA by mechanical stretching using steered molecular dynamics (MD) simulation. We find that the force curves and unfolding processes are strongly dependent on the pulling sites. If the stretching springs are connected to the sugar backbone, the force curve shows a single peak and the unfolding can be regarded as a two-state transition. When the stretching springs are connected to the terminal nucleobases, the force curve shows two peaks indicating that unfolding proceeds through an intermediate state. The free energy profile for the base-pulling scenario computed from the force-extension curves using the Jarzinsky equation shows a shoulder which corresponds to the intermediate state. After releasing the force constraint, equilibrium simulations for 8 ns show that the molecule does not refold back to its original structure once it was stretched to the intermediate state. Folding pathways of parallel G-quadruplex are proposed according to the simulated structures.

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Probing DNA Tetrahedra — •Alexander Benkstein[1], Iwan A. T. Schaap[1], Christoph M. Erben[2], Andrew J. Turberfield[2], and Christoph F. Schmidt[1] — [1]3. Physikalisches Institut, Fakultät für Physik, Georg-August Universität, 37077 Göttingen — [2]Clarendon Laboratory, Department of Physics, University of Oxford, Parks Road, Oxford OX1 3PU, UK

Well established synthesis procedures and the "programmability" of DNA binding via base pairing makes DNA ideal for the design of nanostructures.

We here investigate the mechanical characteristics of self assembled tetrahedra from DNA oligomers with dimensions smaller than 10nm. For this purpose, the tetrahedra are modified to bind to gold surfaces and are studied by atomic force microscopy in combination with fluorescence microscopy.

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AlGaN/GaN-Biosensoren - stabile DNA-Sensoren — •Stefanie Linkohr, Christoph Nebel, Vadim Lebedev, Volker Cimalla und Oliver Ambacher — Fraunhofer Institut für Angewandte Festkörperphysik IAF, Tullastraße 72, 79108 Freiburg

AlGaN/GaN-Sensoren sind hoch sensitive und chemisch stabile Biosensoren, die sowohl für die Detektion von Ionen und Biomolekühlen sowie für die Untersuchungen von biologischen Aktivitäten von Zellen in Flüssigkeiten und Gasen geeignet sind. Weiterhin ermöglichen diese Sensoren durch geeignete Funktionalisierung der GaN-Oberfläche die Untersuchung von DNA-Molekülen. Bei den untersuchten Sensoren handelt es sich um AlGaN/GaN-Heterostrukturen, die mit einer SiO-SiN-PMMA-Multilayer-Passivierung gegen den Kontakt mit Flüssigkeit isoliert sind. Dabei handelt es sich um pH-sensitive-ISFETs dessen Empfindlichkeit bei 59 mV/pH liegt und die in einem pH-Bereich von 4 - 9 eine gute Langzeitstabilität aufweisen. Zur Biofunktionalisierung mit DNA wird das geöffnete Gate mit 10-amino-dec-1-ene Molekülen, funktionalisiert. Unter Benutzung einer hochdruck Halogen UV-Lichtquelle (200 nm) wird die GaN-Oberfläche über 2 bis 8 h beleuchtet. Die Funktionalisierung der GaN-Oberfläche wird mit Hilfe von Rasterkraftmikroskopie, Rastertunnelmikroskopie und röntgeninduzierte Photoelektronenspektroskopie charakterisiert und zeigt das inselartige Wachstum der Olefin-Moleküle. Nach der Funktionalisierung verringert sich die Empfindlichkeit des Transistors, so dass DNA [Ck 20] Hybridisierung und Denaturierung beobachtet werden kann.

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Investigating the chemo-mechanical properties of two-dimensional actin networks — •Kai Uhrig[1,2], Rainer Kurre[1,2], Martin Streichfuss[1,2], Friedrich Erbs[1,2], Simon Schulz[1,2], Anabel Clemen[1,2], Tamas Haraszti[1,2], Christian Böhm[1,2], and Joachim Spatz[1,2] — [1]MPI for Metals Research, Dept. Spatz, Heisenbergstr. 3, 70569 Stuttgart — [2]Univ. of Heidelberg, Biophys. Chem. Dept., INF 253, 69120 Heidelberg

The actin cortex, a quasi two-dimensional network of actin, plays an important role in cell stability, motility and viscoelasticity. In vivo, its characteristic properties are controlled by various crosslinkers, such as actin binding proteins or ions. To investigate the influence of a specific crosslinker on the network's behaviour exclusively we create and probe biomimetic models of the actin cortex. This is realized using microbeads trapped by holographic optical tweezers (HOTs) as scaffold for the actin filaments. With this technique we are able to create actin networks in arbitrary geometry and determine the forces exerted by different crosslinkers. Using a special microfluidic flowcell we have full control over the chemical environment in our experiments. The acting forces are measured by highspeed imaging, whereas simultaneous fluorescence microscopy yields information about the structure and density of the actin network. In another approach we use micropillars as framework and measure unzipping forces of crosslinked actin filaments.