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<th>Time</th>
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<th>Speaker</th>
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<tr>
<td>13:30</td>
<td>121</td>
<td><strong>Equilibrium and flow of cluster-forming complex fluids</strong></td>
<td>Christos N. Likos, Faculty of Physics, University of Vienna, Boltzmannasse 5, AT-1090 Vienna</td>
<td>In this talk, I will present an overview of the unusual properties of a novel class of systems in soft matter physics, in which cluster formation takes place in the complete absence of attractions. After formulating a mathematical criterion as a necessary and sufficient condition for cluster formation, I will discuss the unusual structural, dynamical and phononic properties of cluster solids in equilibrium, showing, among others, that these are diffusive, that they provide for a realization of the Einstein model of solids and that at low temperatures cluster solids possess infinitely many isostructural critical points. Under shear flow, cluster solids organize in forms resembling the Abrikosov lattice of superconductors and they show a pressure flow behavior typical of colloidal glasses. Finally, I will demonstrate the construction of realistic microscopic models that allow for the formation of cluster crystals in the computer, opening the way to their experimental realization.</td>
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<td>14:00</td>
<td>122</td>
<td><strong>Optimized Fourier Monte Carlo Simulation of Solid and Hexatic Membranes</strong></td>
<td>Andreas Troester, Vienna University of Technology, Wiedner Hauptstrasse 8-10/136, AT-1040 Vienna</td>
<td>We present an exciting refinement of our Fourier Monte Carlo algorithm that is able to deal with long-range microscopic or effective interactions and in addition is free of critical slowing down [A.T, Phys. Rev. B 87, 104112 (2013)]. This allows to observe critical behavior with unprecedented statistical accuracy. The power of our approach is illustrated by simulations results for hexatic and solid membranes, whose elastic behavior has recently been re-investigated extensively in the context of graphene. A finite size scaling analysis gives numerical estimates for the critical exponent $\eta$, whose value and accuracy challenges those derived from other recent simulations and analytical approximations.</td>
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<td>14:15</td>
<td>123</td>
<td><strong>Biomimetic folding particle chains</strong></td>
<td>Peter Oostrum $^{1}$, Ivan Coluzza $^{2}$, Ronald Zirbs $^{1}$, Erik Reimhult $^{1}$</td>
<td>The sequence of the amino acids in proteins dictates their folded 3-D structure. We have recently by simulations shown that this principle can be applied to flexible strings of isotropically interacting particles with at least one attractive patchy interaction, allowing the design of new materials and structures [1-3]. Our goal is now to realize this directed self-folding on a colloidal size scale to study the folding in real time in real space [4]. We discuss our use of polymer brushes, depletion interactions and liquid-interface scaffold chemistry to realize the goal.</td>
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<td>14:30</td>
<td>701</td>
<td>Fluorescence and atomic force microscopy to visualize the interaction of HDL particles with lipid membranes</td>
<td>Gerhard J. Schütz, Vienna University of Technology, Institute of Applied Physics, Wiedner Hauptstraße 8-10, AT-1040 Vienna</td>
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<td>High density lipoprotein (HDL) plays a key role in cholesterol homeostasis: cholesterol-loaded HDL particles are transported from non-hepatic peripheral tissue to the liver, where they unload their cargo via receptor-mediated selective uptake. It is astonishing that – although blood levels of HDL are broadly used in diagnosis for the prognosis of developing cardiovascular disease – the cholesterol uptake mechanisms are still poorly understood. Particularly, it remains unclear how the amphipathic cholesterol crosses the aqueous phase between the HDL particle and the cell membrane. We applied state-of-the-art high-resolution and ultra-sensitive force and fluorescence microscopy techniques to image directly the interaction of HDL particles with the target membrane. Using high-speed atomic-force microscopy (AFM) we made a surprising discovery: when added to membranes, we observed HDL particles to integrate into the interleaflet core of the bilayer, generating “nano-blisters” with a size below 10 nm. Amphipathic cargo was able to leave such blisters, whereas hydrophobic cargo such as cholesteryl-ester remained associated with the particles. Using a combined fluorescence and force microscopy system we could directly visualize the transfer of single cargo molecules into supported lipid bilayers. Particularly, we compared the transfer of the fluorescently labelled amphiphilic DiI and Bodipy-labelled cholesterol with the hydrophobic Bodipy-labelled cholesteryl-ester. Our experiments revealed that i) cargo transfer requires contact; ii) only amphiphilic cargo is transferred. Interestingly, membrane elasticity was found to be crucial for the fusion: only highly elastic (and thus cholesterol-poor) membranes facilitate particle fusion, whereas inelastic cholesterol-rich membranes prevented the fusion. Live cell experiments show that the plasma membrane itself regulates a cell's cholesterol demand: high cholesterol levels act repulsive, low cholesterol levels fusogenic.</td>
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<td>15:00</td>
<td>702</td>
<td>Characterization of Curli A Production on Living Bacterial Surfaces by Scanning Probe Microscopy</td>
<td>Yoojin Oh 1, Yidan Cui 2, Hyunseok Kim 2, Yinhua Li 2, Peter Hinterdorfer 1, Sungsu Park 2</td>
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<td>1 Institute for Biophysics, Johannes Kepler University, Gruberstr. 40, AT-4020 Linz,</td>
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<td>2 Department of chemistry and nano science, Ewha Womans University, Daehyundong, Seodaemungu, KR-120-750 Seoul</td>
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<td>Atomic force microscopy was used to determine the effects of curli on topology and mechanical properties of live E. coli cells. Young’s moduli of both curli-deficient and curli-overproducing mutants were significantly lower than that of their wild-tupe strain, while decay lengths of the former strains were higher than that of the latter strain. Surprisingly, topological images showed that, unlike the WT and curli-overproducing mutant, the curli-deficient mutant produced a large number of flagella-like fibers, which may explain why the strain had a lower Young’s modulus than the WT. These results suggest that the mechanical properties of bacterial surfaces are greatly affected by the presence of filamentous structures.</td>
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<td>15:15</td>
<td>703</td>
<td>Innovating nanosensing technique to detect living bacteria and reveal resistance to antibiotics</td>
<td>Justin Notz, Sandor Kasas, Gianni Longo, Giovanni Dietler, EPFL, Laboratoire de Physique de la Matière Vivante, Institut de Physique des Systèmes Biologiques, BSP, CH-1015 Lausanne</td>
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<td>Bacterial pathogens are a major concern for health issues, it is crucial to detect and identify them with the shortest time delay as possible. Usually, once a bacterial infection is suspected, a time-consuming procedure dependent on the bacterial growth rate concludes to a diagnosis. In this study, we present a new technique that is capable of characterizing bacterial sensitivity to antibiotics in unmatched time scales (minutes). The experimental set-up is based on AFM technology. The device has already shown promising results with strains such as Escherichia coli, Staphylococcus aureus, Lactococcus lactis and many others are being tested.</td>
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<td>15:30</td>
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<td>Coffee Break</td>
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16:00 711 Cell mechanics measured with Atomic force microscopy

Jose Luis Toca-Herrera 1, Susana Moreno-Flores 1, Kathryn Melzak 1, Rafael Benitez 2, Maria Vivanco 3

1 Institute for Biophysics, Dept. Nanobiotechnology, BOKU - Vienna, Muthgasse 11, AT-1190 Vienna
2 Dept. Mathematics, UNEX, Spain, Avenida Virgen del Puerto 2, ES-10600 Plasencia
3 CIC Biogune, Parque tecnológico de Bizkaia, Ed. 801A, ES-48160 Derio

In this contribution, I would like to present recent results about cell mechanics obtained with atomic force microscopy and its relation with basic soft matter science. We will present a novel way to obtain viscoelastic properties (Young modulus, relaxation time and viscosity) of breast cancer cells based on stress relaxation and creep measurements. Additionally we will show the influence of applied stress on red blood cell shape [1-3]. The importance of such type of measurements on soft matter physics, cell biology, and biomedical science.


16:15 712 Measuring the stability of lipid membrane domains with nanometer resolution.

Georg Fantner, Blake Erickson, EPFL-STI-IBI-LBNI, Station 17, CH-1015 Lausanne

Lipid bilayers are a major component of cell membranes, as well as many intra cellular structures. They form a robust barrier to ions, proteins and other molecules, and act as an anchoring substrate for many membrane bound proteins. The stability and rigidity of lipid bilayers depends on the type of lipid and the temperature. Many naturally occurring lipids exhibit phase transition around room temperature, which drastically alters the membrane stability. In nature, lipid membranes consist of mixtures of many different types of lipids with proteins and other molecules, which also impact the stability of the membrane. The inhomogeneity of these membranes result in spatially distributed differences in stabilities. Here we present a method to measure this inhomogeneity in the stability of lipid membranes with nanometer resolution, by using atomic force microscopy induced phase transition. [Cancelled]

16:30 713 Protein partitioning in liquid-ordered (Lo) / liquid-disordered (Ld) domains

Benjamin Kollmitzer 1, Peter Heftberger 1, Michael Rappolt 2, George Khelashvili 3, Daniel Harries 4, Georg Pabst 1

1 Inst. of Molecular Biosciences, Biophysics Division, University of Graz, Schmiedstraße 6, AT-8042 Graz
2 School of Food Science and Nutrition, University of Leeds, Leeds LS2 9JT, UK
3 Department of Physiology and Biophysics, Weill Medical College of Cornell Univ., 1300 York Ave, New York 10065, USA
4 Institute of Chemistry and the Fritz Haber Research Center, The Hebrew Univ., Giv’at Ram, IL-Jerusalem 91904

The lack of transmembrane proteins partitioned in the current lipid-only models for membrane rafts calls for close scrutiny of raft mimetics. Using small angle X-ray scattering (SAXS) and molecular dynamic simulations (MD), we determined structural and elastic parameters (spontaneous curvature, bending rigidity, Gaussian curvature modulus) for coexisting Lo/Ld domains in ternary mixtures of dioleoylphosphatidylcholine/dipalmitoylphosphatidylcholine/cholesterol and dioleoylphosphatidylcholine/distearylophosphatidylcholine/cholesterol. Substituting these values into theoretical calculations, yields the energy penalty upon insertion of transmembrane proteins into Lo and Ld phases and consequently the preferred partitioning in one of these domains. We discuss our findings for different geometric protein shapes.
Conformational changes of the selectivity filter may block ion flow through K+-channels. Here we show that, after entering such an electrically silent conformation, K+ channels remain permeable to water. Using fluorescently labeled, constitutively open but either C-type inactivating or non-inactivating mutants of the bacterial K+ channel KcsA, we determined the number of reconstituted channels per vesicle and their unitary water permeability by fluorescence correlation spectroscopy and stopped-flow experiments, respectively. Water flux inhibition by K+ indicates a dissociation constant of ~300 mM for singly occupied channels. Thus, transport does not require electrostatic destabilization by entry of a second ion into the filter.

Characterization of augmented bone structures with μ-computed tomography and Raman spectroscopy

In the recent past bone graft substitutes are increasingly used in the medical field in order replace missing bone or promote new bone formation. Computed tomography methods provide density information of biomaterials, however, the question how far information on the chemical structure is accessible has not been intensively investigated yet. In the present study a bone sample consisting of autogenous bone derived cells and bovine bone mineral was investigated by computed microtomography imaging and by Raman spectroscopic imaging, and comparing the image data by means of regression analysis and digital image processing methods.

Raman spectroscopic investigation of urinary calculi and salivary stones

The capabilities and limitations of determining the composition of urinary calculi (34 patients) and salivary stones (27 patients) by Raman spectroscopy have been investigated by analysing Raman spectra obtained with 1064 nm laser excitation, and comparing them with Raman spectra both from specific reference substances and from a commercial Raman database. The composition results were also compared with those obtained by other analytical methods e.g. powder diffraction. Raman spectroscopy proves to be an analytical method which provides reliable results on the composition of urinary calculi and salivary stones quickly, non-destructively and without any need of sample preparation.

Saving Joint with Aerosolphysics

Using electrospray method to analyze wear debris from artificial joints. Well known aerosol techniques have been applied to determine the size distribution and concentration of wear particles found in joint fluids. The organic fraction (cells and large molecules) are removed by digestion. Knowing these data the risk of clogging of blood vessels can be medicinally reduced.
Probing metabolism in vivo in real time via hyperpolarized NMR

Arnaud Comment, Institute of Physics of Biological Systems, EPFL, CH-1015 Lausanne

The tremendous gain in signal-to-noise ratio resulting from hyperpolarization techniques and in particular dissolution dynamic nuclear polarization (DNP) opened new perspectives in biomedical magnetic resonance (MR) research. Hyperpolarization increases MR sensitivity by several orders of magnitude offering the opportunity to perform real-time in vivo MR spectroscopy experiments. It is thus possible to probe fast biochemical transformations from labeled precursors to metabolic products in vivo.

A DNP polarizer operating at 5 T and 1 K was used to hyperpolarize $^{13}$C-labeled biomolecules for metabolic studies in rodents at 9.4 T. An automated protocol based on a custom-designed separator/infusion pump was developed to keep the delay between dissolution and injection as short as 3 s. It will be shown that even molecules with rather short relaxation times could be detected in vivo. Real-time metabolic studies in skeletal muscles, heart and brain will be presented.

Photomodification and Nanopatterning of Polystyrene for Bioapplications

R. A. Barb $^1$, B. Magnus $^2$, M. Fahrner $^3$, T. Greunz $^4$, D. Stifter $^4$, R. Marksteiner $^2$, C. Romanin $^3$, J. Heitz $^1$

$^1$ Institute of Applied Physics, Johannes Kepler University Linz, Altenberger Straße 69, AT-4040 Linz

$^2$ Innovacell Biotechnologie AG, Mitterweg 24, AT-6020 Innsbruck

$^3$ Institute of Biophysics, Johannes Kepler University Linz, Gruber Straße 40, AT-4020 Linz

$^4$ Center for Surface and Nanoanalytics, Johannes Kepler University Linz, Altenberger Straße 69, AT-4040 Linz

Surface chemistry, wettability and nanotopography are important features for materials used in bioapplications as they strongly influence cell-substrate interactions. We investigated the influence of two types of photomodification on polystyrene (PS) foils and Petri dishes, for bioapplications. Photomodification was done with a UV Xe$_2^+$ excimer lamp (172 nm) and with KrF laser (248 nm) for periodic surface structures (LIPSS). Contact angle and XPS measurements shown an improvement in wettability and a significant change in surface chemistry in both cases. Cell seeding experiments indicate that photomodified PS strongly influence cell adhesion, proliferation and orientation.

The work was funded by FFG, project CellStretch, BMWFJ and National Foundation for Research, Technology and Development.

Fractal characterization of tissue with the new Pyramid Method

Michael Mayrhofer-Reinhartshuber, Philipp Kainz, Helmut Ahammer

Institute of Biophysics, Medical University of Graz, Harrachgasse 21/IV, AT-8010 Graz

The characterization of tissue by in-silico analysis is an active field of research in digital pathology. Successively improved imaging techniques in medicine reveal ever finer morphological details in the gained images, which enhance the outcome of different image-processing algorithms. Nevertheless, since the majority of real word objects exhibit similar structures at different scales [1], the application of fractal methods is obligatory if significant and comparable results should be obtained [2]. By using this approach our group was able to characterize different types of samples, e.g. to distinguish between different grades of neoplasia [3]. Currently we developed a new method for the calculation of the fractal dimension based on the well established Box Counting Method (BCM). The astounding results showed that in case of binary images this new method is able to obtain results with the same quality as with BCM but within significantly faster computational times [4]. Ongoing developments towards an implementation for real histological (grey value/color) images confirm this trend. Therewith high resolution images can be processed in a few seconds, which is a prerequisite for the aim of real-time analysis in digital pathology.

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<td>723</td>
<td>The open pore of SecYEG does not show physiologically relevant ion selectivity</td>
<td>Denis Knyazev, Lukas Winter, Nicole Ollinger, Christine Siligan, Peter Pohl</td>
<td>Institut für Biophysik, Johannes Kepler Universität Linz, Gruberstr. 40, AT-4020 Linz</td>
<td>The bacterial translocon SecYEG resides in the cytoplasmic membrane and translocates secretory proteins from the cytoplasm to the periplasm. In its open and unoccupied state, it is a large ionic channel with ~0.5 nS conductivity under physiological conditions. Unhindered proton flow through this channel would be lethal due to collapse of the transmembrane proton gradient. We showed that SecYEG has a very modest preference for anions over cations (the permeability ratio is 4.1±1.6). We thus conclude that opened SecY by itself cannot sustain the proton motif force across the cytoplasmic membrane.</td>
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<td>724</td>
<td>Advancing high resolution structural analysis of lipid membranes using a generic algorithm</td>
<td>Peter Heftberger 1, Benjamin Kollmitzer 1, Fred Heberle 2, Jianjun Pan 2, John Katsaras 2, Norbert Kucerka 3, Georg Pabst 1</td>
<td>Institute of Molecular Biosciences, Biophysics Division, University of Graz, Schmiedlstrasse 6, AT-8042 Graz</td>
<td>We adapted a high resolution method for jointly refining small-angle x-ray and neutron scattering data of unilamellar vesicles to the more general case of multimamellar vesicles. By using a generic algorithm, the new method is capable of retrieving component volume distributions of a phospholipid bilayer from x-ray data only. The analysis was tested on several phospholipids, and binary mixtures with cholesterol. Our results are in good agreement with previous reports using a simultaneous analysis of neutron and x-ray data. Finally, we showed that the structural information of hydrophobic hydrocarbon chains can be further improved upon the additional analysis of neutron scattering data.</td>
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<td>725</td>
<td>Studies on the Cherenkov effect for improved TOF-PET</td>
<td>Stefan Brunner 1, Lukas Gruber 1, Albert Hirtl 2, Johann Marton 1, Ken Suzuki 1</td>
<td>Stefan Meyer Inst. for Subatomic Physics, Austrian Academy of Sciences, Boltzmannstrasse 3, AT-1090 Wien</td>
<td>In inorganic scintillators, as they are used in PET, photons are emitted after a cascade of energy relaxation processes, each process introducing a time spread to the photon emission. For the emission of Cherenkov photons, these processes are bypassed, resulting in a high time precision and therefore improved resolution of TOF-PET systems. Results of measurements using Cherenkov radiators in PET -like coincidence setups with a 22Na source will be presented. Furthermore, we will present results of Geant4 simulation studies on the impact of the Cherenkov effect on the photon yield, the photon arrival times and coincidence time resolution of TOF-PET systems.</td>
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<td>726</td>
<td>Progress in the Structure-based Simulation of Plant Light-Harvesting Complexes</td>
<td>Frank Müh, Dominik Lindorfer, Marcel Schmidt am Busch, Thomas Renger</td>
<td>Institute for Theoretical Physics, Johannes Kepler University Linz, Altenberger Strasse 69, AT-4040 Linz</td>
<td>Water-oxidation in plants occurs in supercomplexes that contain a catalytic core and various light-harvesting complexes (LHCl, CP24, CP26 and CP29). We applied our combined quantum chemical / electrostatic approach to calculate the exciton Hamiltonian of LHCl and CP29 on the basis of the known crystal structures in order to gain a molecular understanding of light-harvesting. Simulations of linear optical spectra allow us to assess the validity of the computed quantities. The two homologous complexes LHCl and CP29 are compared with respect to the location of the terminal emitter domain and the pigment-protein interactions that lead to specific transition energy shifts.</td>
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<td>727</td>
<td>The density and distribution of sacrificial bonds in polymer chains determines the amount of dissipated energy</td>
<td>S. Soran Nabavi, Markus A. Hartmann</td>
<td>Institut für Physik, Montanuniversität Leoben, Franz-Josef Strasse 18, AT-8700 Leoben</td>
<td>A common strategy for natural materials to increase their toughness while retaining a considerable stiffness is the use of sacrificial bonds (SBs). This study investigates the influence of the density and arrangement of SBs on the mechanical properties, especially the amount of dissipated energy of a single polymer chain using Monte Carlo simulation methods. The results show that: first, molecular chain fluctuations reduce the efficacy of sacrificial bonds. Second, increasing SB density increases the amount of dissipated energy per loading cycle. Third, a regular spatial arrangement of SBs is highly desirable for efficient energy dissipation.</td>
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The ability to place individual proteins onto nano-confined spaces plays a constantly growing role in bioscience. One of the possibilities to generate sub-micrometer sized structures is direct laser writing (DLW) lithography. The resolution of DLW can be enhanced by stimulated emission depletion (STED) for assembly of polymeric structures down to several tens of nanometers. Using a pulsed 780 nm laser for two-photon DLW and a 532 nm laser for STED, we are able to obtain structure sizes of down to 55 nm and manufacture two clearly separated lines with 120 nm distance. The structures show good biocompatibility and allow an easy biofunctionalization with proteins down to the single protein level.

These IgGs are made for walkin':
Random antibody movement on bacterial and viral surfaces
Johannes Preiner, CBL Linz, Gruberstrasse 40, AT-4020 Linz

Immunoglobulins are key for the immune system. Via their Fab arms IgGs can bind two neighboring epitopes resulting in higher avidity and slower dissociation as compared to monovalent Fabs. By using the high speed atomic force microscope we demonstrate that IgG molecules do not remain stationary on surfaces of regularly spaced epitopes but exhibit “bipedal” random walking. Their mobility depends on symmetry and spacing of the antigens; monovalent Fabs do not move. We identified steric strain as the main reason for short-lived bivalent binding. Upon collision, the randomly walking antibodies form transient clusters. Such aggregates might serve as docking sites for the complement system and/or phagocytes.

Chemically tagged DNA tetrahedra as linker for single molecule force spectroscopy
Michael Leitner 1, Julian Brummeir 2, Johannes Preiner 1, Tibor Hianik 3, Maja Snejdarkova 4, Peter Hinterdorfer 2, Alexandra Poturnayova 4, Hermann Gruber 2, Andreas Ebner 1
1 Center for Advanced Bioanalysis, Gruberstrasse 40-42, AT-4020 Linz
2 Institute of Biophysics, Department for Applied Experimental Biophys Bioanalysis, Gruberstr. 40, AT-4020 Linz
3 Faculty of Mathematics, Physics and Computer Sciences, Comenius University, Safarikovo namestie 6, SK-81806 Bratislava
4 Institute of Biochemistry and Animal Genetics, Slovak Academy of Sciences, Moyzesova 61, SK-90028 Ivanka pri Dunaji

Atomic force microscope (AFM) has developed to one of the key techniques in nanoscience. The enhancement of the cantilever to a molecular biosensor yielded to techniques that allow for the detection of forces between single receptor ligand complexes in the pico newton range down to a single chemical bond (MRFS). Furthermore, the combination of recognition and topographical measurements, simultaneous topography and recognition imaging (TREC), is capable of determining receptor distributions on surfaces at the nano scale. Nevertheless there are still limitations for a wide use of these techniques as standard tool in applied life science and in the clinical field. The main limitation is the complex chemical tip functionalization of the AFM cantilever, which restricts these techniques to experts in basic science. In this work we present an alternative way of functionalizing the AFM tip for MRFS and TREC by the use of DNA building blocks. For this, tetrahedra shaped DNA building blocks were bonded to gold coated cantilevers via three disulfide vertices. For a test system the forth vertex carried a biotin tag. Alternatively, it was equipped with a short single strand DNA and used in combination with DNA aptamers containing the corresponding counter sequence. Compared to commonly used complex standard tip functionalization, the here described procedure can be done with basic chemical knowledge via a simple incubation or pick up procedure. It could thus be one important step to enable the use of functionalized cantilevers to many research labs.

Long and short lipid molecules experience the same interleaflet drag in lipid bilayers
Andreas Horner 1, Sergey Akimov 2, Peter Pohl 1
1 Institut für Biophysik, Johannes Kepler Universität Linz, Gruberstraße 40, AT-4020 Linz
2 Frumkin Institute of Physical Chemistry and Electrochemistry, RAS, Leninskiy pr. 31/4, RU-119071 Moscow

Membrane interleaflet viscosity $\eta$ affects tether formation, phase separation into domains, cell shape changes, and budding. Contrary to the expected contribution to interleaflet coupling from interdigitation, the slide of lipid patches in opposing monolayers conferred the same value $\eta \approx 3 \times 10^8$ Js m$^{-4}$ for the friction experienced by the ends of both short and long chain fluorescent lipid analogues. Consistent with the weak dependence of the translational diffusion coefficient on lipid length, the in-layer viscosity was, albeit length-dependent, much smaller than $\eta$. 

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The target of this project is the construction of an imaging microscope setup which uses two-photon excitation for automated measuring. The setup includes a Zeiss M1.m Imaging Microscope within a mechanical xyz movable stage for scanning different samples. The excitation beam is delivered by an ultrafast fiber laser which generates 780 nm wavelength. One-, two- and three-dimensional measurements are performed by the setup. The resulting fluorescence is measured by a spectrometer. Every spectrum will be safe and analyzed for building an image of the sample. There were different kinds of samples used. Especially some calibration samples, FISH (fluorescent in situ hybridization) and some fluorescence microspheres with different sizes and colors. After finishing the microscope setup, measurements of different samples has been started to characterize the properties of the system and to show how hyper spectral imaging works.

The great stability of several avidin proteins over a wide pH range, particularly when combined with biotin, has been studied qualitatively in the last fifty years. In the present study, a more detailed investigation is made by performing molecular recognition studies, using AFM force spectroscopy. The applied measuring principle enables the investigation of forces and dynamics of the interaction between the proteins and a corresponding ligand, during a pH treatment and with different loading rates. Therefore, the ligand (biotin) is coupled via a bifunctional PEG-crosslinker on the outer AFM tip apex, whereas the receptor is immobilized on the probe surface. By repeatedly approaching and withdrawing of the tip in z-direction, receptor-ligand complexes are formed and released. If this experiment is repeated at different pulling speeds (loading rates) and pH values, the energy landscape and the pH stability of the receptors can be examined. The measurements have been clearly shown that the three examined proteins are stable over a wide pH range. Moreover chimericavidin does not offer the pH stability on single molecule level as expected. All in all, the three proteins open the possibility for more applications, like for e.g. surface sensors, which are exposed extremes of pHs.

We present PDMS and glass based microfluidic devices for trapping individual fluorescent particles in solution phase using electrokinetic forces. Trapping single wall carbon nano tubes will enable the characterization and manipulation of non-fluorescent proteins in their native environments.

We present a theory of optical spectra of pigment-protein complexes that allows to include both the excitonic and the exciton-vibrational coupling on an equal footing. The theory is applied to two different types of the water soluble chlorophyll binding protein (WSCP) containing chlorophyll dimers. First, it is tested in simulation of optical spectra of class Iib WSCP with known crystal structure, and then it is applied to class Ila WSCP with unknown structure, in order to check whether a similar arrangement of chlorophylls as in type Iib WSCP can be assumed. Using a homology modeling of the unknown structure in combination with quantum chemical/ electrostatic calculations we propose an explanation of the 10 nm redshift observed of its optical bands with respect to class Iib WSCP.