CPP 36: Biopolymers and Biological Systems

Time: Friday 10:30–12:45 Location: C 264

CPP 36.1 Fri 10:30 C 264

Spin Label EPR on Biological Systems — •Malte Drescher — Emmy-Noether-Gruppe am FB Chemie, Universität Konstanz, Fach M639, 78457 Konstanz

In spite of significant progress, the challenging areas for structure determination in biological systems are still ample: Membrane proteins, protein-protein interactions and membrane association are important for biological function, but because of the amphipathic nature of the first and the intrinsic disorder of the latter systems, conventional methods of structure determination usually do not work. By advanced EPR methods the interaction between spin labels can be measured from 5 Å to 5 nm. Paramagnetic labels can be attached to proteins, nucleic acids and lipids, and as native paramagnetic centres are scarce, the method is background free. Examples of applications to proteins and membranes will be discussed.

CPP 36.2 Fri 10:45 C 264

Digital in-line soft X-ray holography as microscopy technique for biological samples — •Axel Rosenhahn[1], Ruth Barth[1], Florian Staier[1], Todd Simpson[2], Silvia Mittler[2], Stefan Eisebitt[3], and Michael Grunze[1] — [1]Angewandte Physikalische Chemie, Universität Heidelberg, Germany — [2]Department of Physics and Astronomy, The University of Western Ontario, Canada — [3]BESSY m.b.H., 12489 Berlin, Germany

Digital in-line soft X-ray holography (DIXH) is a lenseless approach towards microscopy at short wavelength. We present measurements which successfully prove that the original Gabor geometry can be applied to X-rays and a lateral resolution of 400 nm can be achieved. Objects of different thickness and materials were used to determine the imaging properties of holographic microscopy in the VUV and soft X-ray wavelength range. By tuning the x-ray energy, element specific contrast can be obtained e.g. at the carbon K edge. These results are promising with respect to the possibility to exploit intrinsic contrast mechanisms for biological samples. Using fibroblasts and other cells, the sensitivity of the technique to resolve small structures inside these extended objects will be discussed. Although the spatial resolution still needs to be improved, these experiments are a starting point for future, lenseless holospectroscopy.

CPP 36.3 Fri 11:00 C 264

Reptation of individual F-Actin Filaments in 3D Networks — •Masashi Degawa, Norbert Kirchgessner, Bernd Hoffmann, Rudolf Merkel, and Margret Giesen — Institut für Bio- und Nanosysteme 4, Forschungszentrum Jülich, 52425 Jülich Germany

The mechanical properties of the cell are determined by a 3D network of polymerized protein filaments, the cytoskeleton. For deeper understanding of cell biomechanics, it is crucial to understand the physical properties of such polymer network. In the past, we have concentrated on the study of individual F-actin filaments within the network. Dynamics of the filaments were studied in the time scale of μsec to a sec where the transverse fluctuation from the filament contour is dominant and results were well described by the Glassy Worm-like chain Model [1]. Here we present dynamic studies of the same system, however, in the time scale of min to an hr where the motion along the filament contour is now dominant. F-Actin are labeled with TRITC and visualized with line-scan confocal scanning microscope. We measure the filament contour as a function of time. Specifically we focus on the curvature of the filaments, which in recent work indicate glass like properties, where the ergodic theorem breaks down [2]. [1] J. Glaser, et al. submitted to Eur. Phys. J. (2007) [2] M. Romanowska, et al. submitted to Phys. Rev. Lett. (2007)

CPP 36.4 Fri 11:15 C 264

Time-dependent Chain Rupture of Single Double-stranded DNA — •Hua Liang, Nikolai Severin, Igor m. Sokolov, and Jürgen P. Rabe — Department of Physics, Humboldt University, D-12489 Berlin, Germany

The rupture of single covalent bonds is a fundamental scientific issue. Under applied force this is a statistical process with a characteristic time scale depending on the force loading rate. This has been predicted theoretically and proven experimentally for fast force loading rates (1). In the established experimental methods such as dynamic force spectroscopy and dragging molecules with dynamic flow (2), information on the rupture of a single covalent bond is obtained from the breakage of a single polymer chain. However, these methods do not allow to investigate breakage of a covalent bond upon application of a static force. On the other hand, theory predicts that covalent bond rupture under static force is qualitatively different from rupture under dynamic force. Here we report a newly developed method (3) which allows placing a single polymer chain, e.g. a single double-stranded DNA molecule under a static force for an hour or more. The first results elucidate the difference between bond breaking under static force and dynamic force application. The data also allow us insight into the energy landscape of a covalent bond.

1. M. Grandbois et al, Science 283 (1999) 1727-1730;
2. D. Bensimon et al, Physical Review Letters 74 (1995) 4754-4757;
3. N. Severin et al, Nano Letters 6 (2006) 2561-2566.

CPP 36.5 Fri 11:30 C 264

Cyclization of short DNA fragments: the effects of electrostatic interactions — •A. G. Cherstvy[1] and R. Everaers[2] — [1]Theorie-II, IFF, FZ Juelich, D-52425 Juelich, Germany — [2]Ecole Normale Superieure de Lyon, 46 Allee d'Italie, 69364 Lyon Cedex 07, France

Cyclization of short DNA fragments is known to be a reliable method for measuring the elastic response of DNA molecules to twisting and bending [1]. Although the DNA is one of the most highly charged biopolymers known in nature, the standard theories developed for calculation of the ring formation probabilities by semiflexible polymers [2] neglect completely the electrostatic interactions along DNA chain. We show how the Shimada-Yamakawa theory for DNA cyclization factors [2] is modified due to the presence of charges on DNA. We also study [3] to which extent the phenomenon of Manning's conterion condensation on a straight highly charged cylinder [4] will differ for a DNA ring. We are interested also how the Odijk-Skolnick-Fixman theory of electrostatic persistence of weakly bent rod-like polyelectrolytes [5] will be modified for small circles of DNA.

[1] K. Rippe, et al., Trends Biochem. Sci., 20, 500 (1995). [2] J. Shimada and H. Yamakawa, Macromol., 17 689 (1984). [3] A. G. Cherstvy and R. Everaers, work in preparation. [4] G. S. Manning, J. Phys. Chem. B, 111 8554 (2007). [5] T. Odijk, J. Pol. Sci., 15 477 (1977).

CPP 36.6 Fri 11:45 C 264

Reversible photothermal dehybridization of DNA attached to gold nanoparticles — •Maximilian Reismann[1], Jan Bretschneider[2], Ulrich Simon[2], and Gero von Plessen[1] — [1]I. Inst. of Physics (IA), RWTH Aachen University, Germany — [2]Inst. for Inorganic Chemistry, RWTH Aachen University, Germany

Heat released from laser-irradiated metal nanoparticles can be applied to control biomolecules attached to the nanoparticles. Several studies have investigated destructive processes caused by nanoparticle-assisted photothermal heating, such as hyperthermia of malignant cells. In contrast, the photothermal control of non-destructive, *i.e.* reversible, biomolecular reaction processes has rarely been studied. Here we investigate the reversible photothermal control of the DNA dehybridization process. For this purpose, gold nanoparticle networks are synthesized using complementary single-stranded DNA as linker molecules. The well-known color change of such nanoparticle networks that occurs upon disassembly or assembly is applied to continuously monitor the state of the networks using optical spectroscopy. The DNA-nanoparticle network suspensions are heated by irradiation with focused c.w. laser light. This heating causes a disassembly of the networks, indicating the dehybridization ('melting') of the DNA double strands. After laser irradiation, the networks reassemble, thus indicating the reversibility of the dehybridization process. It is shown that the DNA melting occurs predominantly within the 100 μm wide laser focus, where the intensity is highest, thus enabling a highly local control of the reaction.

CPP 36.7 Fri 12:00 C 264

Structural Changes of Casein Micelles in a Calcium and an Enzym (Rennet) Gradient Film — •Ronald Gebhardt[1], Manfred Burghammer[1], Christian Riekel[1], Stephan Volkher

Roth[2], and Peter Müller-Buschbaum[3] — [1]European Synchrotron Radiation Facility, BP 220, F-38043 Grenoble Cedex 09, France — [2]HASYLAB at DESY, Notkestr. 85, 22603 Hamburg, Germany — [3]TU München, Physik-Department, LS E13, James-Franck-Str.1, 85747 Garching, Germany

Caseins are phosphoproteins consisting of blocks with high amounts of hydrophobic and hydrophilic amino acids. Due to their amphiphilic nature they are able to built up casein micelles which are broadly distributed in size. The stability of the casein micelles is ensured by an outer kappa-casein layer. Concentration gradients of calcium and rennet were choosen to destabilize the association structures in casein films. While rennet cuts off the hairs of the layer, calcium leads to a compactation of the micelles and a decrease of the layer thickness by satturating the negative charged caseins. This first step of milc conversion, followed normally by aggregation and flocculation and finaly gel formation, can be well investigated in casein gradient films using grazing incident small angle scattering with a micrometer sized beam (microGISAXS). Differnt structural conformations along the reaction pathway are frozen inside the film and can be detected with high statistical relevance in a nondestructive way.

R. Gebhardt , M. Burghammer , C. Riekel, S. V. Roth , and P. Müller-Buschbaum (2007) Macromol. Biosci. accepted

CPP 36.8 Fri 12:15 C 264

Protein dynamics-induced modulation of excitation energy transfer — •Marc Brecht, Volker Radics, Jana Berit Nieder, Hauke Studier, and Robert Bittl — Fachbereich Physik, Freie Universität Berlin, Arnimalle 14, 14195 Berlin, Germany

Electron and energy transfer in proteins are key processes in bioenergetics. Their understanding on a molecular level can serve as important guideline for the design of nanoscale assemblies. Energy transfer between pigment molecules requires a match between their transition energies for energy emission and absorption. The tuning of these pigment energies in proteins is achieved by pigment-protein interactions. In general, these interactions are regarded as static properties determined by the three-dimensional structure of pigment-protein complexes. Employing single-molecule fluorescence spectroscopy on photosystem I [1] we demonstrate that protein dynamics, even at cryogenic temperatures, significantly influences the transition energy of pigments and, as a consequence, modulates energy transfer pathways. Our finding shows that the energy transfer pathway in photosystem I is not uniquely defined by the three-dimensional structure of the complex. This variability of energy transfer pathways introduced by protein dynamics might be important for the extreme robustness of photosystems [2].

[1] Brecht, M., Studier, H., Elli, A. F., Jelezko, F., and Bittl, R. (2007) Biochemistry, 46(3):799-806. [2] Brecht M., Radics V., Nieder J. B., Studier H., Jelezko F., Bittl R. submitted

CPP 36.9 Fri 12:30 C 264

Thermodynamics of proteins: pressure and temperature denaturation curves — •Johannes Wiedersich[1,2], Simone Köhler[1], Josef Friedrich[1], and Arne Skerra[3] — [1]Lehrstuhl für Physik Weihenstephan, TU München — [2]Physikdepartment E13, TU München — [3]Lehrstuhl für Biologische Chemie, TU München

The folding and unfolding of proteins shows a complex scenario, the details of which are not yet fully understood. One important aspect concerns the stability of proteins. By means of fluorescence spectroscopy we obtain the equillibrium constant for the denaturation of the engineered fluorescein-binding protein FluA as a function of both pressure and temperature. From the full thermodynamic analysis of the transition curves all of the involved global thermodynamic parameters of protein folding are determined, in particular the changes in entropy and volume, compressibility, thermal expansion and specific heat.

We demonstrate that the phase diagram of protein folding is closed and assumes an elliptic shape. The thermodynamic condition for such an elliptic phase diagram is related to the degree of correlation between fluctuations of the changes in volume and enthalpy at the phase boundary. This correlation is moderately low, on the order of 0.05 in our case. Our study suggests that the elliptic phase diagram is a consequence of the inherent conformational disorder of proteins and that it may be viewed as the thermodynamic manifestation of the high degeneracy of conformational energies that is characteristic for this class of macromolecules.