

## BP 14: Posters: Protein Structure and dynamics

Time: Tuesday 9:30–12:30

Location: P1

BP 14.1 Tue 9:30 P1

**Langevin simulations of conformational changes in proteins under temperature gradients** — ●ANNE DOROTHEE MÜLLER and MARTIN E. GARCIA — Theoretische Physik, Universität Kassel, Fachbereich 10, Kassel, Germany

We developed a program to simulate conformational changes in small, globular proteins under temperature gradients by integrating the Langevin equations of motion. This program uses a potential based on the coarse-grained model developed by Nan-Yow Chen et al. [Phys-RevLett.96.078103(2006)]. Chen's force field does not need any a priori information about the native state of the protein and is known to be able to describe the folding of proteins to both alpha-helices and beta-sheets. Hence we investigated the protein 3ZNF which has part alpha-helix part beta-sheet as its native structures.

BP 14.2 Tue 9:30 P1

**A multiscale model for fibrinogen** — ●STEPHAN KÖHLER<sup>1,2</sup>, MARTIN MCCULLAGH<sup>3</sup>, FRIEDERIKE SCHMID<sup>1</sup>, and GIOVANNI SETTANNI<sup>1,4</sup> — <sup>1</sup>Institut für Physik, Johannes Gutenberg-Universität Mainz, Mainz, Germany — <sup>2</sup>Graduate School Materials Science in Mainz — <sup>3</sup>Department of Chemistry and Institute for Biophysical Dynamics, University of Chicago, Chicago, Illinois, United States — <sup>4</sup>Max Planck Graduate Center mit der Johannes Gutenberg-Universität Mainz

The blood protein fibrinogen (fg) plays an important role in the coagulation cascade and the immune response to injury. However, these functions may also be initiated by fg aggregation on extraneous bodies such as, e.g. medical implants. In our previous work, atomistic molecular dynamics simulations have been used to characterize fg flexibility in solution [1]. Due to the size of the protein complex, however, atomistic simulation of fg aggregates at surfaces are not possible with current computers. Lower resolution models are required to address these systems. Here we present a new coarse grained (CG) model for fg that systematically incorporates data from all atom molecular dynamics simulations. This model reduces the resolution from nearly 31000 interacting particles in an all atom model to 45 CG beads. A heterogeneous elastic network connecting the beads is able to capture the dynamics on large and intermediate scales while the charges assigned to the coarse grained beads elucidate the charge structure of fibrinogen.

[1] Fibrinogen flexibility and adsorption properties investigated using atomistic molecular dynamics simulations - S. Köhler, F. Schmid and G. Settanni, DPG meeting '14 abstract BP205

BP 14.3 Tue 9:30 P1

**Photoswitchable Dynamics of the Orange Carotenoid Protein (OCP) in Living Cells of Synechocystis sp. PCC6803** — ●FRANZ-JOSEF SCHMITT<sup>1</sup>, EVGENY MAKSIMOV<sup>2</sup>, VLADIMIR Z. PASCHENKO<sup>2</sup> und THOMAS FRIEDRICH<sup>1</sup> — <sup>1</sup>Institute of Chemistry, Biophysical Chemistry, TU Berlin, Straße des 17. Juni 135, D-10623 Berlin, Germany — <sup>2</sup>Department of Biophysics, Biology Faculty, Lomonosov Moscow State University, 119991 Moscow, Russia

The cyanobacterium *Synechocystis* sp. PCC6803 contains a photoswitchable protein, the orange carotenoid protein (OCP) which undergoes conformational changes under illumination in the blue spectral regime. After activation by light the OCP binds to the membrane extrinsic phycobilisome (PBS) complexes and leads to non-photochemical quenching (NPQ) of the PBS fluorescence reducing the flow of energy into the photosystems (PS) under high light conditions as protection mechanism. We investigated the energy migration in the PS II by time- and wavelength-resolved fluorescence spectroscopy in a wide temperature range between 4 K and 300 K. The decay associated spectra calculated from the time resolved spectra were simulated by rate equation systems to analyse the pathway of energy migration in the PBS of *Synechocystis* sp. WT and two mutants that exhibit PBS of reduced complexity. The simulations show that NPQ of PBS by OCP occurs in the PBS core with an apparent time constant of about 100 ps. At cryostatic temperatures the efficient NPQ by OCP is hampered showing that the protein flexibility and/or mobility is essential for NPQ.

BP 14.4 Tue 9:30 P1

**Glass-like transition in a dry protein: evidence from neutron scattering study** — ●A.V. FRONTZEK<sup>1</sup>, S.V. STROKOV<sup>1</sup>, J.P.

EMBS<sup>2</sup>, and S.G. LUSHNIKOV<sup>1</sup> — <sup>1</sup>Ioffe Physical Technical Institute, St.Petersburg, Russia — <sup>2</sup>Paul Scherrer Institut, Switzerland

The interest in proteins dynamics is stimulated by its close relation to the biological activity and mechanisms of functioning. Generally, biopolymers demonstrate the dynamical features typical for disordered systems. Such phenomena as the dynamical transition and a glass transition in hydrated proteins have been revealed and intensively investigated in past decades. However, it still remained an open question if a glass transition occurs in dry biopolymers. Our purpose was to study the vibrational and relaxational dynamics of two dry model proteins, bovine serum albumin and alpha-lactalbumin from bovine milk, at temperatures at which a glass or dynamical transition can occur (200-340K). The lyophilized powders of both proteins have been used for neutron scattering experiments at a neutron time-of-flight spectrometer FOCUS (SINQ). As a result, the inelastic incoherent dynamic structure factors and the density of states have been obtained and analyzed in broad temperature range. Anomalous temperature behaviour has been revealed for relaxational and low-frequency vibrational dynamics of investigated proteins in the vicinity of 250 K. The mean square atomic displacement has been demonstrated to exhibit a change in the slope of temperature dependence near the same temperature. The presented results point out that the glass-like transition occurs also in dry protein.

BP 14.5 Tue 9:30 P1

**Computational clarification of structural detail in polyglutamine aggregation** — ●MARKUS MIETTINEN — FU Berlin, Berlin, Germany

In many neurodegenerative diseases, such as Alzheimer's, Parkinson's and Huntington's, cell death is associated with protein misfolding and aggregation. We studied the events leading to aggregation of polyglutamine, the aggregation-prone part of the disease-associated protein in Huntington's and eight other diseases. It is believed that some structures in the initial stages of aggregation are highly toxic, but due to their fleeting nature it has been difficult to obtain direct experimental data on them. Combining a criterion based on available experimental data with extensive molecular simulations, we demonstrated the infeasibility of several structures, and could single out one motif as crucial for the initiation of aggregation. We suggest a pathway that could provide new insight into developing strategies to alleviate toxicity.

BP 14.6 Tue 9:30 P1

**Local averaging of single particle cryo-electron microscopy data** — ●AMUDHA KUMARI DURAISAMY<sup>1</sup> and GUNNAR F. SCHROEDER<sup>1,2</sup> — <sup>1</sup>Institute of Complex Systems, Forschungszentrum Juelich, 52425 Juelich, Germany — <sup>2</sup>Physics Department, Heinrich-Heine-Universität, Duesseldorf, Germany

Single particle cryo-EM is a powerful technique to study the structure of biomolecular assemblies that are often large, flexible and conformational heterogeneous. Most of the density maps obtained from cryo-EM experiments are limited in resolution by this conformational heterogeneity. Improving the resolution of the density maps, thus, requires to account for the structural heterogeneity. In principle, the resolution can be reached to the atomic level, if the images of the structures are aligned accurately [1]. In the biological macromolecules, the conformational motions leads to global structural changes, however there are often rather rigid domains. Those rigid domains could be used to align and average the density to reach higher resolution. This is analogous to NCS averaging used to improve the phase information in the field of X-Ray crystallography [2]. An algorithm is presented to average rigid domains and to improve the resolution of cryo-EM density maps.

References: [1] Henderson. R, Q. Rev. Biophys. 28 171-193 (1995). [2] Kleywegt. G and Read. R, Structure 5 1557-1569 (1997).

BP 14.7 Tue 9:30 P1

**Ultrafast Side Chain Dynamics of Peptides at the Air-Water Interface** — ●MICHAEL DONOVAN, MISCHA BONN, and TOBIAS WEIDNER — Max Planck Institute for Polymer Research, Ackermannweg 10, 55128 Mainz, Germany

Proteins possess fluctuating structural forms, and very little is known about their dynamics at the interface between two bulk phases. Few tools are available to study dynamics at interfaces. For this reason we

chase to use a time resolved variant of the intrinsically surface specific vibrational spectroscopy Infrared-Visible Sum Frequency Generation. The rotational dynamics of side chains are followed by orthogonal infrared pump pulses and SFG probe pulses. The IR pulse bleaches specific side chain orientations. The recovery of the steady state signal, related to side chain rotational motion, is monitored in real time. Specifically, model amphiphilic LK peptides which consist of alternating leucines and lysines have been probed at the air water interface. Further experiments which utilize isotopically labeled side chains along the peptide backbone will allow us to resolve the rotational dynamics in further detail.

BP 14.8 Tue 9:30 P1

**Thermodynamic characterization of protein folding using Monte Carlo methods** — ●NANA HELLMANN, MORITZ WOLF, JULIA SETZLER, and WOLFGANG WENZEL — INT, Karlsruhe Institute of Technology, Eggenstein-Leopoldshafen, Germany

The study of protein folding has been a difficult challenge in molecular biology and simulation science. Up-to-date research showed reproducible folding of small protein using molecular dynamics simulations. These results can be only achieved by using time-consuming, specialized supercomputers [1]. In contrast to molecular dynamics simulations, Monte Carlo based simulations are not constrained solving Newton's equation of motion and therefore protein folding simulations can be compute on conventional computer architectures. In this study, we show reproducible all-atom folding transition of the villin headpiece 1VII, which was simulated by using SIMONA[2], a Monte Carlo based simulation package for nanoscale simulations including a variant of the Amber99SB\*-ILDN[3]. The results of these simulations demonstrate that Monte Carlo simulation techniques are generally applicable to the investigation of large-scale conformational changes of protein on conventional computer architectures. The thermodynamic characterization of simulated proteins can be compared with the experimental results while the computing time for observing folding/refolding events can be significantly reduced in comparison with molecular dynamics simulations. [1] Shaw et al. *Science* 330 (2010). [2] Wolf et al. *J Comput Chem* (2012). [3] Lindorff-Larsen et al. *Science* 334 (2011).

BP 14.9 Tue 9:30 P1

**Dynamics of the family of protein disulfide isomerases.** — ●JACK HEAL<sup>1</sup>, STEPHEN WELL<sup>2</sup>, EMILIO JIMENEZ-ROLDAN<sup>1</sup>, RUDOLF RÖMER<sup>1</sup>, and ROBERT FREEDMAN<sup>1</sup> — <sup>1</sup>University of Warwick, Coventry, England, CV4 7AL — <sup>2</sup>University of Bath, Bath, England, BA2 7AY

Protein disulfide isomerase (PDI) is a multifunctional enzyme that facilitates protein folding by disulfide bond formation and isomerisation. PDI consists of four thioredoxin-fold domains; the other members of the PDI family are formed of a small number of homologous domains. The function of some of the members is not well understood or characterised. Recently, the structure of human PDI has been determined for the first time through X-ray crystallography. These data add to a small number of previous X-ray crystal structures of the PDI family members that are available in the protein data bank. With these structures as input, we use rapid computational methods to simulate their overall flexibility and dynamics. We study quantitatively the relative domain orientations as well as the distance between functional sites, extending our recent study on yeast PDI. From this information, we construct a map of these motions and discuss the protein dynamics of the PDI family in the context of structure, sequence and function. We aim to use these techniques along with the experimental data available to fully characterise the whole family and use structure-derived information to inform discussion of protein function in general.

BP 14.10 Tue 9:30 P1

**Influence of surface and subsurface properties on the structure and activity of adsorbed bactericidal proteins** — ●CHRISTIAN SPENGLER<sup>1</sup>, CHRISTIAN KREIS<sup>1</sup>, STÉPHANE MESNAGE<sup>2</sup>, HENDRIK HÄHL<sup>1</sup>, and SIMON FOSTER<sup>2</sup> — <sup>1</sup>Saarland University, Experimental Physics, D-66041 Saarbrücken — <sup>2</sup>University of Sheffield, Krebs Institute, Department of Molecular Biology and Biotechnology, Sheffield S10 2TN, United Kingdom

Protein adsorption is the first step in biofilm formation: Protein films serve as a conditioning layer that enables and affects the attachment of bacteria and other organisms. Hence, the understanding and control of protein layers is an important task that is relevant to life sciences and engineering. Previous studies revealed that the structure and density of adsorbed proteins and the adhesion force of bacteria depend on

both the surface properties and the subsurface composition of the adsorbent material [1,2]. These findings raise the question whether or not the activity of adsorbed proteins is also influenced by the properties of the underlying material. In this study, we investigate how the activity – the bactericidal effect – of adsorbed lysozyme and lysostaphin is affected by surface properties. The activity is thereby characterized by measuring the turbidity of a very sensitive protein assay containing purified peptidoglycan.

[1] Hähl et al., *Langmuir* **28** (2012) 7747-7756

[2] Loskill et al., *Langmuir* **28** (2012) 7242-7248

BP 14.11 Tue 9:30 P1

**Resolving conformational switching of AAA+ protease FtsH in real time using single-molecule FRET** — ●MARTINE RUER, PHILIP GRÖGER, NADINE BÖLKE, and MICHAEL SCHLIERF — B CUBE - Center for Molecular Bioengineering, TU Dresden, 01307 Dresden

FtsH is a highly conserved, homo-hexameric AAA+ protease embedded in the bacterial membrane, where it recognizes, unfolds, translocates and degrades protein substrates to be degraded. Previous crystal structure data of *Thermotoga maritima* FtsH in an ADP and an ATP-bound state show an ATPase and a protease domain linked by a flexible hinge, facilitating a large conformational change event upon ADP/ATP binding. Based on these structural data, a model was presented where the unfolding and proteolytic mechanism are tightly coupled. However, in protease assays FtsH shows an ATP independent mechanism. How is the chemical energy converted into mechanical work for protein unfolding and translocation? We are using single-molecule Förster Resonance Energy Transfer (smFRET) experiments to resolve the conformational changes of FtsH upon ATPase and protease activities. Therefore, we have developed an in vitro assay with vesicle encapsulated, self-assembled FtsH hexamers in absence or presence of degradation substrates. In absence of a degradation substrate, the labeled FtsH protease shows 2 or 3 conformational states and the conformational switching is strongly dependent on the ATP concentration. In further experiments, we study the ATP dependent kinetics of the different conformational states in dependence of various protein substrates.

BP 14.12 Tue 9:30 P1

**Friction between hydrogen bonding peptides** — ●JULIAN KAPPLER and ROLAND NETZ — Institut für Theoretische Physik, Freie Universität Berlin, 14195 Berlin, Germany

Understanding how friction arises from microscopic interactions is not only important for improving the efficiency of machines, but also for a detailed understanding of biologically relevant systems. We use all-atom MD simulations to study the friction between pairs of various kinds of stretched homo-polypeptide strands in water: While fixing one peptide strand, we pull the second one with constant velocity along its axis, thereby simulating a non-equilibrium steady state. In our analysis we particularly focus on the roles of i) the hydrogen bonds (and cooperative effects thereof) between the pairs and ii) the interaction of the pulled peptide with the surrounding water.

BP 14.13 Tue 9:30 P1

**Fluorescence Lifetime Spectroscopy of Free and Enzyme-bound NADH** — ●ANDRÉ WEBER<sup>1,2</sup>, WERNER ZUSCHRATTER<sup>2</sup>, and MARCUS HAUSER<sup>1</sup> — <sup>1</sup>Abteilung Biophysik, Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg, Universitätsplatz 2, 39106 Magdeburg, Germany — <sup>2</sup>Leibniz-Institut für Neurobiologie, Speziallabor Elektronen- und Laserscanmikroskopie, Brenneckestr. 6, 39118 Magdeburg, Germany

NADH plays a keyrole in energy metabolism of cells and its autofluorescence acts as an indicator for metabolic states of a cell. Certain enzymes, so called dehydrogenases, build up products from substrates by a transport of hydrogen to NAD<sup>+</sup>.

The fluorescence lifetimes of NADH allow for differentiation between free diffusing and protein-bound NADH and are sensitive to pH, temperature and ionic strength.

We investigate the concentration dependent reaction dynamics of dehydrogenases while binding to NADH and substrates in solution with various pH values via fluorescence lifetime spectroscopy of NADH fluorescence. Through time and space correlated single photon counting we analyse the wavelength dependence of the fluorescence decays.

BP 14.14 Tue 9:30 P1

**Adsorption kinetics and structure of hydrophobins at interfaces** — ●JONAS RAPHAEL HEPPE<sup>1</sup>, HENDRIK HÄHL<sup>1</sup>, PHILIPP

HUDALLA<sup>2</sup>, LUDGER SANTEN<sup>2</sup>, and KARIN JACOBS<sup>1</sup> — <sup>1</sup>Saarland University, Experimental Physics, D-66041 Saarbrücken — <sup>2</sup>Saarland University, Theoretical Physics, D-66041 Saarbrücken

Protein adsorption to interfaces is a common, but complex process with many applications. Besides the attachment to the solid/liquid interface, the adsorption to the interface between water and other liquids or air is of major technological interest. Amphiphilic proteins stabilize this interface and hence serve as emulsifying or foaming agent. To control the processes, a deeper understanding of the competitive processes and interactions leading to the final adsorbate is necessary.

Hydrophobins (HFB) are a class of proteins that may serve as ideal model candidates. Produced by filamentous fungi, they are conformationally stable, highly surface active, and form ordered monolayers at the water surface [1]. We studied the adsorption of HFB wild types and specifically designed mutants featuring different geometry or charge.

To access the adsorption kinetics, we used ellipsometry to record *in situ* the adsorbed amount at the air/water interface and on solid substrates varying the conditions of surface and solution. Moreover, we analyzed the resulting structure of the adsorbates by applying XRR.

Our results reveal differences in the adsorption kinetics depending on the electrical and steric properties of the proteins as well as the ambient parameters. The experiments are accompanied by theoretical modeling. [1] S. Varjonen et al., *Soft Matter* 7 (2011) 2402

BP 14.15 Tue 9:30 P1

**Sorting cryo-EM images into classes of similar molecular conformations** — ●MICHAELA SPIEGEL<sup>1</sup> and GUNNAR SCHRÖDER<sup>1,2</sup> — <sup>1</sup>ICS-6 Computational Structural Biology, Forschungszentrum Jülich, Germany — <sup>2</sup>Physics Department, Heinrich-Heine-Universität Düsseldorf, Germany

The resolutions of density maps which are reconstructed from single-particle cryoelectron microscopy (cryo-EM) images are often limited by the conformational heterogeneity of the biological macromolecules. To increase the resolution, the images have to be sorted into groups of similar conformations. The common approaches of sorting images typically compare densities (either in 2D or 3D). However, a large difference in conformation does not necessarily lead to a large difference in density. We are developing a new sorting method that is based on comparing conformations. For this we are using a bootstrapping approach and refine pseudo-atomic models against an ensemble of bootstrapped density maps. These models capture the conformational variance and can be used for sorting the images. This procedure also reveals the conformational heterogeneity and is able to determine global conformational motions of large macromolecular structures and assemblies.

BP 14.16 Tue 9:30 P1

**Optical activity of chiral molecules and its analog on a macroscopic scale** — ●CARINA HÄUSLER, HENDRIK BETTERMANN, and MATHIAS GETZLAFF — Institute of Applied Physics, University of Duesseldorf

Optical activity of chiral molecules like proteins in nm-range is barely understood due to its complex behavior but it may provide a new non-invasive blood sugar measurement for diabetes patients. It is the goal to develop an experimental setup for students which demonstrates the analogy between nm-sized molecules and cm-sized helices. The latter creates a simple approach for this optical phenomenon without the use of chemical processes. The measurement setup consists of a source for linearly polarized light and an analyzer to determine the degree of rotation of the electric field vector after transmission. Biologically relevant substances like glucose, fructose, and camphor are studied by visible light whereas chiral copper helices with dimensions in the cm-regime are studied by radiation in the GHz range. The specific amount of rotation is identified in both scales in the same way which is not known for molecules in cm-range yet. The data also shows a direct comparison of enantiomeric excess in both scales. Furthermore, the experiment demonstrates the mutarotation of glucose and a wavelength depending amount of rotation in the nm-range.

BP 14.17 Tue 9:30 P1

**Competing paradigms of protein dimerization tested by solution SAXS** — ●STEFANO DA VELA<sup>1</sup>, FAJUN ZHANG<sup>1</sup>, VASYL HARAMUS<sup>2</sup>, and FRANK SCHREIBER<sup>1</sup> — <sup>1</sup>Institut für Angewandte Physik - Universität Tübingen, Tübingen, Germany — <sup>2</sup>Helmholtz-Zentrum Geesthacht: Zentrum für Material- und Küstenforschung GmbH, Geesthacht, Germany

Small Angle X-Ray Scattering (SAXS) is a versatile and popular tool for the characterization of proteins in solution. In this contribution we use the capabilities of SAXS, Size Exclusion Chromatography and complementary Dynamic and Static Light Scattering techniques to investigate the association and interactions of Ovalbumin, Bovine Serum Albumin and Immunoglobulin G. These proteins are chosen as different paradigms for protein dimerization. We explore the architecture, the effective dimensions and hydration state of monomers and dimers in relation to the solution parameters. Furthermore, we assess the influence of the dimerization on the quality of the information which can be obtained from SAXS data and the effect of the resulting shape polydispersity on the overall protein-protein interaction parameters. A deeper insight into the dimerization process can serve as basis for further studies on its influence on protein phase behaviour and on protein dynamics in concentrated solutions.

BP 14.18 Tue 9:30 P1

**Diffusion of peripheral membrane proteins on intracellular membranes** — ●JULIA HOFFMANN and MATTHIAS WEISS — University of Bayreuth, Bayreuth, Germany

Biological processes, such as secretion and signaling in living cells, depend crucially on the diffusive properties of the involved proteins. The mobility of proteins is determined by their environment as well as by their size and thus by their ability to form oligomers. Fluorescence correlation spectroscopy (FCS) is a common and sensitive technique to characterize the diffusive processes of proteins *in vivo*. We used this technique to investigate different peripheral membrane protein types, including membrane anchored Ras proteins and proteins involved in the cell's secretion machinery. FCS measurements of membrane anchored N-Ras mutants for example, show predominantly anomalous diffusion on intracellular membranes. In contrast, FCS experiments on Sec16, a regulating protein of the COPII machinery in the early secretory pathway, show slowed diffusion on membranes of endoplasmic reticulum due to oligomerization. These insights into the diffusion and oligomerization of peripheral membrane proteins yield valuable information about physico-chemical mechanisms that support, for example, secretion events.

BP 14.19 Tue 9:30 P1

**Using Molecular Dynamics Simulation to Obtain Protein Pigment Interaction in Photosynthetic Pigment Protein Complex** — ●XIAOQING WANG, SEBASTIAN WUESTER, and ALEXANDER EISFELD — Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Strasse 38, 01187 Dresden, Germany

Protein pigment interaction is very important on the electronic excitation energy transfer and spectral properties in photosynthetic pigment-protein complex. However, investigating the interaction from full quantum mechanics is out of reach because of the large number of protein atoms and the complicated arrangement of pigment molecules. In our work classical molecular dynamics simulation is used to simulate the dynamics of pigment-protein complex on the ground state. The local excitation energies and transition dipole-dipole couplings which used to build the Hamiltonian of the complex are extracted from the structure information of the molecular dynamics trajectories. In order to investigate the protein pigment coupling interaction the spectral density is calculated. Since the excitation energy is calculated by electrostatic energy shift caused by the atomic charge of protein environment we can investigate the influence of various parts of the protein. The method also might help to understand the effects on the molecular dynamics parameters.