CPP 26 Biological systems II

Zeit: Dienstag 15:15–16:15 Raum: TU C230

CPP 26.1 Di 15:15 TU C230

Tracking of individual G-protein coupled receptors on living cells — •Michael Prummer, Bruno Meyer, Raphael Franzini, Jean-Manuel Segura, and Horst Vogel — Laboratory of Physical Chemistry of Polymers and Membranes, Institute of Chemical Sciences and Engineering, Swiss Federal Institute of Technology (EPFL), CH-1015 Lausanne, Switzerland

The neurokinin-1 receptor (Nk1R), a typical representative of the G-protein coupled receptor (GPCR) superfamily, is essential for nociception and is a central drug target for anti-depressants. The agonist Substance P induces intracellular calcium signaling and subsequent desensitization of the receptor by internalization. Here we report on the imaging of individual Nk1Rs on the plasma membrane of living HEK293 cells. Single-molecule wide-field microscopy was utilized to record trajectories of Nk1Rs, which were labeled enzymatically in situ at an N-terminal targeting sequence with Cy5. Single particle tracking analysis of the trajectories revealed immobile and mobile receptors with an experimental position accuracy of 35 nm. The trajectories are analyzed in terms of the microscopic diffusion coefficient of each molecule, as well as the probability distribution P(msd,dt) of the occurrence of the mean-square displacement msd after a time-lag dt, averaged over many molecules. Current investigations are focused on how the mobility of Nk1R is influenced by the initiation of the cellular signaling cascade upon ligand binding and the modulation of the G-protein activity. The ultimate goal is to monitor the fate of individual Nk1Rs from their resting state through ligand binding until internalization occurs.

CPP 26.2 Di 15:30 TU C230

Accessibility and intramolecular mobility of residues in native and non-native proteins as studied by time-resolved CIDNP — •Alexandra Yurkovskaya[1], Olga Morozova[1], Peter Hore[2], and Hans-Martin Vieth[3] — [1]International Tomography Center of SB RAS, 630090, Institutskaya 3a, Novosibirsk, Russia — [2]University of Oxford, South Parks Road, Oxford, OX1 3QH, UK — [3]Department of Physics, Free University of Berlin, D-14195 Berlin, Germany

Among the magnetic resonance methods used for investigating the structure and dynamics of proteins in their native and non-native states the Chemically Induced Dynamic Nuclear Polarization (CIDNP) technique allows the selective spectroscopy of specific amino acid residues located on the protein surface. Its use for exploring the solvent-exposure, reactivity and dynamic properties of tryptophan and tyrosine residues for the comparative study of the native, partly folded and denatured states of small monomeric proteins will be presented. As a novel application the kinetics of the dynamic nuclear polarization formed by electron transfer and detected by high-resolution NMR in the diamagnetic state of the proteins allows determination of the paramagnetic nuclear spin-lattice relaxation times (T_1) of short-lived radicals derived from the reactive residues. It will be shown how the analysis of the relaxation behavior opens the possibility of obtaining quantitative information about the correlation times of residue motion and characterizing the heterogeneity of the intramolecular dynamics of different residues in non-native states and the folding process.

CPP 26.3 Di 15:45 TU C230

Structural evolution of PYP and model compounds investigated by ultrafast polarization-resolved IR spectroscopy — •Karsten Heyne, Anwar Usman, Omar F. Mohammed, Jens Dreyer und Erik T.J. Nibbering — Max-Born-Institut, Max-Born Strasse 2A, D-12489 Berlin, Germany

Vibrational spectroscopy is capable of deducing structural properties of molecules. In particular, the fingerprint region is very sensitive to structural changes. Ultrafast nonlinear vibrational spectroscopy provides access to monitor the evolution of molecular structures resulting from conformational alterations or (photo-)chemical reactions such as isomerization, dissociation, proton transfer or hydrogen bond breaking. Here, we apply polarization-resolved femtosecond UV pump IR probe spectroscopy to determine the performance of p-coumaric acid (PCT) derivatives as model compounds emulating photoisomerization dynamics of photoactive yellow protein (PYP). From parallel and perpendicular polarized IR transients we derive the relative orientation between the UV excitation and the probed IR transition dipole moments. Complementary quantum chemical studies are performed to model the results. Combining experiment and theoretical calculations provides new insight into the structural evolution of PYP after photoexcitation.

CPP 26.4 Di 16:00 TU C230

Chromophore-matrix interaction in biological macromolecules — •J. Baier, M. Richter, C. Hofmann, S. Oellerich, and J. Köhler — Experimental Physics IV, University of Bayreuth

The spectral properties of multichromophoric systems are strongly affected by interactions between the individual chromophores as well as interactions between the chromophores and their host. An interesting macromolecular system for studying both types of interactions are photosynthetic pigment-protein complexes like the bacterial light-harvesting 2 (LH 2) complex of purple bacteria where Bacteriochlorophyll *a* (BChl *a*) pigments are embedded in a protein matrix. Both, intramolecular motions and fluctuations of the matrix lead to changes in the chromophore-protein interaction and influence the properties of the optical transitions.

We performed a statistical analysis of spectral diffusion and spectral jumps of absorptions from individual BChl *a* molecules based on long series of fluorescence-excitation spectra of single LH 2 complexes. The results provide a detailed picture about the dynamics of the coupling between the chromophore and the matrix, i.e. about changes in the local environment of an individual chromophore.