SFB 1078

Protonation Dynamics in Protein Function

Colloquium

Mon, **December 16,** 2013

14:30 – 16:30

Freie Universität Berlin
Physics Department
Lecture Hall A

(Arnimallee 14, 14195 Berlin-Dahlem)

Invited speakers

Prof. Karin Hauser – University of Konstanz – Germany

Protein folding dynamics studied with IR-spectroscopy and residue-specific resolution

Understanding the molecular mechanism of protein folding is of fundamental interest since misfolded proteins can lose their function or even cause diseases. Much of our knowledge has been derived from in vitro studies showing that the time-scales of protein folding events range over many orders of magnitude. We develop time-resolved infrared spectroscopic approaches to study protein folding, misfolding and aggregation. A laser-induced temperature-jump technique combined with tunable quantum cascade lasers has been established to analyze ns-to-µs dynamics. Isotopic editing is used as non-perturbing spectroscopic probe providing residue-specific resolution. In my talk I will focus on our peptide studies. Peptides may be regarded as smallest folding units of proteins and are ideal model systems to gain insight into structure formation as well as fibrillogenesis.

Prof. Juri Rappsilber – Technical University Berlin – Germany

Protein conformation changes monitored by mass spectrometry

Life is a marvellous and complex network of dynamic processes. Structural biology currently provides wonderful insights on highly purified proteins (often trimmed to remove flexible domains) yielding snapshots that reveal much about how protein domains interact and how ligands are bound. However, I cannot help but imagine how much more we could learn if we were to study intact proteins in their native environments as parts of dynamic processes possibly within huge macromolecular assemblies. I think with quantitative cross-linking/mass spectrometry (CLMS) we start holding a tool in our hands that will make important contributions to this. We have shown recently that cross-linking analysis is compatible with quantitation by stable isotope labelling (Fischer et al. 2013). Quantitative CLMS shows its full power as part of an integrated structural biology approach that includes tools that outline the shape of protein complexes (cryoEM and SAXS) and tools that reveal high-resolution structures of subunits (X-ray crystallography, NMR). I will present here how quantitative CLMS as part of integrated structural biology can provide structural and biological insights into key proteins.

Coffee and tea are ready at 14:15 and during the break.

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