

28th Faltertage on "Protein Folding, Dynamics and Stability", October 20-22, 2017

Friday, October 20, 2017

09:00 Opening Remarks

Fundamentals of protein folding and stability (*Chairman: Thomas Kiefhaber*)

09:05 George Rose (Johns Hopkins University, Baltimore, USA)

Protein folding: non-specific interactions promote highly specific chain organization

09:50 Dominik Horinek (Universität Regensburg)

Molecular insights into protein thermodynamics in solution

10:20 Coffee break

Protein interactions and assembly (*Chairman: Reinhard Sterner*)

10:50 Maximilian Sauer (Glockshuber lab, Universität Zürich, Switzerland)

How bacteria invade the bladder and what protects us from urinary tract infections

11:20 Alexander Christiansen (Reinstein lab, MPI for Medical Research, Heidelberg)

Stability of Marvirus Capsid Proteins at different assembly stages

11:50 Tanja Thalhammer (Seckler lab, Universität Potsdam)

Impact of hexamer dissociation kinetics on the efficiency of rapid-acting insulins

12:20 Tamilarasan Selvaraj (Behrens/Golbik lab, MLU Halle-Wittenberg)

Biophysical and biochemical characterization of the viral suppressor protein p38 (turnip crinkle virus)

12:50 Lunch break

In vivo folding and crowding (*Chairman: Jochen Reinstein*)

14:30 Iwo König (Schuler lab, Universität Zürich, Switzerland)

Single molecule spectroscopy of protein folding and dynamics in living cells

15:00 Maria Camilles (Saalwächter lab, MLU Halle-Wittenberg)

Investigating molecular dynamics of concentrated solution of crystallin protein using NMR spectroscopy

15:30 David Gnuttt (Ebbinghaus lab, Ruhr-Universität Bochum)

The macromolecular crowding effect in the living cell and its implications for superoxide dismutase 1 folding

16:00 Susanne Link (Balbach/Weininger lab, MLU Halle-Wittenberg)

UV-B induced modifications of eye lense crystallins

16:30 Coffee break and poster session

18:30 Evening lecture

Roland Winter (TU Dortmund)

Exploring the conformational space and dynamics of biomolecular systems using pressure perturbation

Saturday, October 21, 2017

Amyloid formation (Chairman: Jochen Balbach)

09:00 Aphrodite Karpurniotu (TU München)

Key residues controlling a cross-amyloid interaction versus amyloid self-assembly

09:30 Michael Schleegeer (Kiefhaber lab, MLU Halle-Wittenberg)

Dynamic and structural properties of monomeric polyQ chains as the basis to understand its high propensity to form fibrils

10:00 Werner Kremer (Universität Regensburg)

High hydrostatic pressure (HHP), xenon as probe and spin labeling of the N-terminal domain reveal a whole variety of structural transitions in full length human prion protein

10:30 Coffee break

Enzyme dynamics and chaperones (Chairwoman: Elisabeth Schwarz)

11:00 Ralf Seidel (Universität Leipzig)

Dynamics of target recognition by CRISPR-Cas enzymes

11:45 Sandra Schlee (Sterner lab, Universität Regensburg)

Relationship between active site loop dynamics and catalysis in indole-3-glycerol phosphate synthase

12:15 Gabriel Zoldak (Rief lab, TU München)

A folding nucleus and minimal ATP binding domain of Hsp 70 identified by single molecule force spectroscopy

12:45 Phillipp Schmid (Buchner lab, TU München)

On substrate binding and the oligomeric structure of the molecular chaperone alphaB crystallin

13:15 Lunch break

14:45 Students Awards of the Rainer Rudolph Foundation

Maximilian Plach (Universität Regensburg)

Evolution of substrate specificity and protein interactions in three enzyme superfamilies

Rebecca Ebenhoch (Boehringer Ingelheim)

Structural studies on ketohexokinase

16:00 Poster Session II and Coffee

18:00 Evening lecture

Daniel Herschlag (Stanford University, USA)

The structure, dynamics and energetics of hydrogen bonds inside proteins

Sunday, October 22, 2017

Protein and peptide dynamics (Chairman: Ulrich Weininger)

09:00 Tim A. Keiderling (University of Illinois at Chicago, USA)

Modeling protein folding with peptides. Site-specific equilibria and dynamics with vibrational spectra using isotope labeling

09:45 David Scheerer (Hauser lab, Universität Konstanz)

Impact of aromatic interactions on the folding of β -sheet peptides probed by laser-excited T-Jump IR spectroscopy

10:15 Coffee Break, Removal of Posters

Protein design (Chairman: Rudi Glockshuber)

10:45 Laura Itzhaki (University of Cambridge, UK)

Tandem-repeat proteins: dissect and redesign of folding and function

11:30 Patrick Ernst (Plückthun lab, Universität Zürich, Switzerland)

Preventing a peptide from sliding with computational redesign and structural biology

12:00 Christina Martina (Matagne lab, Université de Liège, Belgium)

De novo protein design: the Octarellin story so far

12:30 Closing Remarks

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