

Thursday, September 23, 2010		
13:00 - 16:00		Registration
15:30 - 16:00		Coffee break
16:00 - 16:15	<i>Norbert Sträter Christian Roth</i>	Welcome words and organizational remarks
Introduction of new HEC groups, Mariusz Jaskolski		
16:20 - 16:30	<i>Markus Wahl</i>	Cooperation of RNA and proteins in the spliceosome
Session 1, Chair: Udo Heinemann		
16:30 - 16:50	<i>Karine dos Santos Free University of Berlin</i>	Structural studies of spliceosome catalytic activation
16:50 - 17:10	<i>Gert Weber Free University of Berlin</i>	Structural studies of snRNP assembly
17:10 - 17:30	<i>Matthias Zebisch University of Leipzig</i>	High resolution snapshots along the reaction pathway of a bacterial nucleotide diphosphohydrolase
17:30 - 17:50	<i>Ulrike Krug University of Leipzig</i>	Microbial NTPDases: structure and function
18:00 - 19:00		Dinner
Session 2, Chair: Norbert Sträter		
19:00 - 19:15	<i>Marianna Biadene Bruker-AXS</i>	Liquid metal jet micro-focus X-ray source: Highest brilliance for home lab instrumentation
19:15 - 19:30	<i>Jürgen Graf Incoatec</i>	High-brilliance Microfocus X-ray Sources for Protein Crystallography
19:30 - 19:45	<i>Mark Benson Rigaku</i>	Latest developments for the home source from Rigaku
HEC Lecture, Chair: Manfred Weiss		
19:45 - 20:45	<i>Alexander Popov ESRF Grenoble</i>	Radiation damage and practical aspects of data collection

Program

Friday, September 24, 2010		
8:00 - 9:00		Breakfast
Session 3 , Chair: <i>Matthias Bochtler</i>		
9:00 - 9:20	Sven Dahms Leibniz Institute Jena	Structure and Biochemistry of the APP E2-domain
9:20 - 9:40	Miriam Küster Leibniz Institute Jena	Structure of an APP-interacting protein
9:40 - 10:00	Eirini A. Gkougkoulia University of Vienna	Structural studies on ancestral α -actinin from <i>Entamoeba histolytica</i>
10:00 - 10:20	Chengcheng Wang MDC Berlin	Structural and Functional Studies of Yeast TRAPP-associated Protein Tca17
10:20 - 10:40	Jennifer Hanna MDC Berlin	Self-association of Quality Control Components in the ER
10:40 - 11:10		Coffee break
Session 4 , Chair: <i>Kristina Djinovic Carugo</i>		
11:10 - 11:30	Monika Sokołowska IIMCB Warsaw	Crystal structure of a GIY-YIG nuclease in complex with DNA
11:30 - 11:50	Grzegorz Chojnowski IIMCB Warsaw	DIBER: protein, DNA or both?
11:50 - 12:10	Piotr Neumann University of Göttingen	Crystal structure of a homodimeric 4-thiouridine synthetase - RNA complex
12:10 - 12:30	Tomas Koval IMC Prague	Crystallization of a fully glycosylated plant nuclease and its structure determination
12:30 - 12:50	Nick Quade HZI Braunschweig	Structural investigation of virulence factor regulation by RovA from <i>Yersinia pseudotuberculosis</i>
13:00 - 14:00		Lunch
14:00 - 18:00		Excursions
18:00 - 19:00		Dinner
Session 5 , Chair: <i>Manuel Than</i>		
19:00 - 19:20	Bernd Gardill University of Erlangen	Don't behave like a rat: Corticosteroid-binding globulin and the serpin S --> R transition
19:20 - 19:40	Anja Drescher GE Healthcare	Unravel the quality of your protein preparation by label-free interaction analysis and find components that have impact on co-crystallization
19:40 - 20:00	Astrid Rau Jena Bioscience	From gene to crystallization within two days. Convenient protein production by in vitro LEXSY.
20:00 - 20:20	Karthik Paithankar BESSY Berlin	Application of in situ crystal screening at BESSY-MX beamline 14.1
20:20 - 20:40	Michael Krug BESSY Berlin	XDSi - A GUI for processing multiple datasets using XDS

Saturday, September 25, 2010		
8:00 - 9:00		Breakfast
Session 6 , Chair: <i>Winfried Hinrichs</i>		
9:00 - 9:20	Maryna Lahoda University Nove Hrady	Structural analysis of mutated DhaA protein from <i>Rhodococcus rhodochrous</i>
9:20 - 9:40	Navdeep Sidhu University of Göttingen	Crystal Structure of a Krebs Cycle Holoenzyme
9:40 - 10:00	Mirek Tarnawski IBC Poznan	Crystallography of RuBisCO chaperone RbcX from a thermophilic organism
10:00 - 10:20	Julius Kostan University of Vienna	Structural and functional characterisation of a chlorite dismutase
10:20 - 10:40	Hubert Mayerhofer EMBL Hamburg	Active and inactive form of a Raf-like signal transduction kinase
10:40 - 11:10		Coffee break
Session 7 , Chair: <i>Yves Muller</i>		
11:10 - 11:30	Mikio Tanabe Halomem Halle	Structure of pathogenic bacterial outer membrane proteins and a strategy of membrane protein structure determination
11:30 - 11:50	Anja Menzel HZI Braunschweig	Towards the structure of full-length ABCB6, a human porphyrin-transporter
11:50 - 12:10	Ulrike Bräuer University of Halle	Structural studies of the aminotransferase LivB
12:10 - 12:30	Claudio Shah MDC Berlin	Combining EPR, electron microscopy and crystal structure analysis to understand membrane remodelling for EHD2
12:30 - 12:40		Closing remarks
13:00 - 14:00		Lunch
14:00		Departure