

# Programme

## 25<sup>th</sup> Rhine-Knee Regional Meeting on Crystallography of Biomacromolecules

### Day 1: Wednesday, September 28<sup>th</sup>, 2011

15:30 - 17:00	Registration ( <i>Reception and Foyer</i> )
17:00 - 18:00	Welcome apero and general information from Campus Sursee ( <i>Foyer</i> )
18:00 - 19:30	Dinner ( <i>Restaurant Il Mercato</i> )
19:40 - 19:50	Welcome address ( <i>Seminar room 408</i> ) - Guido Capitani & Vincent Olieric
19:50 - 21:10	<b>Session 1 - Methods in Crystallization and Crystallography - Chair: Guido Capitani</b>
	<b>Jérôme Basquin</b> , <i>MPI Munich</i> Crystallization of macromolecular complexes : use of limited proteolysis as a rational tool in construct design
	<b>Armin Ruf</b> , <i>Roche</i> Evaluation of protein binders as crystallization facilitators
	<b>Mareike Kurz</b> , <i>University of Zurich</i> The CrystalHarp™, an advanced high throughput capillary plate for protein crystallization
	<b>Florence Pojer</b> , <i>EPFL</i> Protein crystallography core facility of EPFL
	<b>Sandro Waltersperger</b> , <i>SLS PSI</i> The versatile MX-beamlines at the Swiss Light Source, recent developments and their benefits on data quality
21:10 - 21:20	Pause
21:20 - 22:10	<b>Keynote Lecture - Kay Diederichs, University of Constance - Making the most of your data</b>
22:10 - 24:00	Networking ( <i>Bistro La Piazza</i> )

### Day 2: Thursday, September 29<sup>th</sup>, 2011

07:00 - 08:30	Breakfast ( <i>Restaurant Il Mercato</i> )
08:40 - 10:00	<b>Session 2 - New structures - Chair: Günter Fritz</b>
	<b>Michael Buch</b> , <i>University of Tübingen</i> Structural and functional analysis of the major capsid protein of murine polyomavirus, VP1
	<b>Justine Maillot</b> , <i>IGBMC Strasbourg</i> Methylation by CARM1: A structure based approach to design inhibitors and peptide mimics
	<b>Volker Niemann</b> , <i>University of Tübingen</i> Structural analysis of NreA of <i>Staphylococcus carnosus</i>
	<b>Karin Betz</b> , <i>University of Constance</i> Structural studies on the incorporation of an artificial base pair by KlenTaq DNA polymerase
	<b>Kerstin Reiss</b> , <i>University of Tübingen</i> Interaction between the T1L reovirus attachment protein and its carbohydrate receptor
10:00 - 10:30	Znüni Break ( <i>Bistro La Piazza</i> )
10:40 - 12:00	<b>Session 3 - Challenging structures - Chair: Meitian Wang</b>
	<b>Bernhard Spingler</b> , <i>University of Zurich</i> Metal complexes in macromolecular X-ray structures: Which challenges can you expect ?
	<b>Lada Sycheva</b> , <i>EPFL</i> Crystal structure of the product of gene 131 of the <i>Pseudomonas aeruginosa</i> bacteriophage $\phi$ KZ
	<b>Günter Fritz</b> , <i>University of Freiburg</i> Structure determination of NQR, a redox-driven sodium pump from <i>Vibrio cholerae</i>
	<b>Julius Rabi</b> , <i>ETHZ</i> Crystal structure of the eukaryotic 40S ribosomal subunit in complex with initiation factor 1
	<b>Nikolaus Schmitz</b> , <i>ETHZ</i> The crystal structure of the signal recognition particle in complex with its receptor
12:00 - 13:20	Lunch ( <i>Restaurant Il Mercato</i> )
13:30 - 17:30	<b>Excursion - Guided tour of Lucerne and of the Swiss Museum of Transport</b>
	13:30 : Departure by bus to Lucerne 14:15 : Start of the city tour 15:00 : Walk towards the Swiss Museum of Transport 15:30 : Arrival at the Swiss Museum of Transport 16:45 : Departure by bus to Campus Sursee 17:30 : Arrival at Campus Sursee

18:00 - 19:20	<b>Session 4 - Complementary techniques - Chair : David Sargent</b>
	<b>Philippe Dumas, IBMC Strasbourg</b> Using Mathematica, a software with symbolic capabilities, for doing crystallography
	<b>Kaisa Kisko, BMR PSI</b> Combining low-resolution small-angle X-ray scattering with high resolution crystallographic information for understanding vascular endothelial growth factor receptor activation
	<b>Eric Ennifar, IBMC Strasbourg</b> The use of Isothermal Titration Calorimetry to increase success in crystallization of macromolecular complexes
	<b>Sasa Bjelic, BMR PSI</b> Towards quantifying protein-protein interactions using synchrotron-based oxidative footprinting
	<b>Florian Dworkowski, SLS PSI</b> Complementing macromolecular crystallography with <i>in-situ</i> spectroscopy at the SLS
19:20 - 20:50	Dinner ( <i>Restaurant Il Mercato</i> )
21:00 - 22:20	<b>Session 5 - New Structures and Imaging - Chair: Eric Ennifar</b>
	<b>Dominik Frei, BMR PSI</b> Structural Basis of Haptocorrin Ligand Binding
	<b>Arnaud Goepfert, University of Basel</b> FIC proteins: these potent AMPylators are regulated by intra- or intermolecular active site obstruction
	<b>Bärbel Blaum, University of Tübingen</b> Structural studies of polyomavirus capsid proteins with sialylated receptors
	<b>Tatiana Latychevskaia, University of Zurich</b> Imaging individual biological molecules with coherent low-energy electrons
	<b>Mirna Saliba, University of Zurich</b> Micro-lens assisted fourier transform holography
22:20 - 24:00	Networking ( <i>Bistro La Piazza</i> )

### Day 3: Friday, September 30<sup>th</sup>, 2011

07:00 - 08:30	Breakfast ( <i>Restaurant Il Mercato</i> ) and check-out ( <i>Reception</i> )
08:40 - 10:20	<b>Session 6 - Macromolecular crystallography in industry - Chair: Vincent Olieric</b>
	<b>Santina Russo, eXpose</b> Enhancing the cycle, data collection service at the SLS
	<b>Vernon Smith, Bruker</b> The new D8 systems for macromolecular crystallography
	<b>Daniel Frey, Esbatech</b> Crystallization and structural analysis of scFv-target complexes
	<b>Sascha Gutmann, Novartis</b> Structural biology in drug discovery, a case study
	<b>Lars Prade, Actelion</b> Structural biology in pharma
10:20 - 10:50	Znüni Break ( <i>Bistro La Piazza</i> ) and group picture
11:00 - 11:50	<b>Keynote Lecture - Clemens Schulze-Briese, Dectris - Better data from real crystals</b>
11:50 - 12:00	Concluding remarks and 26 <sup>th</sup> Regio meeting announcement
12:00 - 14:00	Lunch ( <i>Restaurant Il Mercato</i> ) and departure