Monday 23rd October

09.00 – 17.00 Workshop A: Training school for cross-linking (IMBA lecture hall, Dr. Bohrgasse 3)

13.00 – 17.00 Workshop B Hydrogen-deuterium exchange. (GMI lecture hall -orange floor, Dr. Bohrgasse 3)

17.15-18.15 Key Note Lecture; Clemens Plaschka (MRC Laboratory of Molecular Biology, UK), Structural studies of pre-mRNA splicing. (IMP lecture hall, Vienna Bio-Center 1)

18.15 Welcome Mixer

Tuesday 24th October

08.30-09.00 Registration

09.00-09.15 Welcome

09.15-09.50 T1 Kasper Rand (University of Copenhagen, Denmark). Analysis of the conformation and interactions of complex proteins by HDX-MS – expanding the HDX-MS toolbox

09.50-10.10 T2 Riccardo Pellarin (Institute Pasteur, Paris, France). Title TBC.

10.10-10.30 T3 Alexander Leitner (IMSB ETH, Zurich, Switzerland), Structural insights into the architecture of the human importin-4 – histone H3/H4 – Asf1a complex using an integrative modeling strategy

10.30-10.50 T4 Franz Herzog (University of Munich, Germany). Title TBC.

10.50-10.55 PT1 Michal Rosulek (Charles University, Prague), Limited proteolysis on MALDI compatible biochip

10.55-11.00 PT2 Eleanor Dickinson (University of Copenhagen, Denmark), Thiol-ene microfluidic chip for sub-second timescale HDX-MS analyses and efficient
pepsin digestion of proteins.

11.00-11.30  **Coffee**

11.30-12.05  **T5 Andrea Sinz** (Martin-Luther University Halle-Wittenberg, Germany), Cross-Linking/Mass Spectrometry for Investigating Protein Complexes: Where Are We Now and Where Should We Go?

12.05-12.25  **T6 Terry Zhang** (Thermo), Electron Transfer Dissociation for Hydrogen/Deuterium Exchange Mass Spectrometry to the Study of Protein Conformation

12.25-12.45  **T7 Petr Novak** (Charles University, Czech Republic), Impact of Chemical Cross-Linking on Protein Structure and Function.

12.45-12.50  **PT3 Claudio Iacobucci** (Martin Luther University Halle-Wittenberg, Germany), Novel solution- and gas phase-chemistry of “old” protein cross-linkers

12.50-12.55  **PT4 Christian Stieger** (Institute for Molecular Pathology, Austria), Monitoring the structural rearrangement of Cas9 via multiplexed quantitative cross-linking MS

12.55-13.00  **PT5 Christoph Hage** (Martin Luther University Halle-Wittenberg, Germany), The First “Zero-Length” Mass Spectrometry-Cleavable Cross-Linker for Protein Structure Analysis.

13.00-13.05  **PT30 Elena L. Rudashevskaya** (ISAS, Dortmund, Germany), Revealing mitochondrial protein interactome by in organello chemical crosslinking and mass spectrometry

13.00-14.30  **Lunch and poster presentations**

14.30-15.05  **T8 Philip Andrews** (University of Michigan, USA), Protean proteins: Crosslinking and ion mobility MS provide complementary information on protein structural changes.

15.05-15.25  **T9 Nir Kalisman** (The Hebrew University of Jerusalem, Israel), Hybrid computational approach for cross-link identification at the proteome level.

15.25-15.30  **PT6 Carolin Sailer** (University of Konstanz, Germany), Using quantitative crosslinking mass spectrometry to study structural dynamics of the ubiquitin ligase E6AP

15.30-15.35  **PT7 Alexandra Stützer** (Max Planck Institute for Biophysical Chemistry, Göttingen, Germany), Analysis of protein-DNA cross-links in a chromatin model.

15.35-15.55  **Coffee**

15.55-16.35  **T10 Jim Bruce** (University of Washington, USA), In vivo cross-linking and mass spectrometry: new opportunities for systems structural biology.

16.35-16.40  **PT8 Steve Hessmann** (University of Strasbourg, France), Benchmarking mAb bioconjugation strategies using a combination of native MS and peptide mapping approaches

16.40-16.45  **PT9 Julia Lockhauserbäumer** (Leibniz Institute for Experimental Virology, Hamburg, Germany), Native MS demonstrates the supportive impact of carbohydrates on norovirus infection.

16.45-16.50  **PT10 Bright D. Danquah** (University Medicine Rostock, Germany), Intact Transition Epitope Mapping - Thermodynamic Weak-force Observation
**Wednesday 25th October**

09.00-09.35  **T11** Lan Huang (UC Irvine, California, USA), Uncovering the molecular details underlying the regulation of the Human 26S Proteasome by cross-linking mass spectrometry

09.35-09.55  **T12** Carla Schmidt (Martin Luther University Halle-Wittenberg, Germany), The synaptic vesicle cycle is governed by heterogeneous and macromolecular protein microdomains.

09.55-10.00  **PT13** Yi Shi (University of Pittsburgh School of Medicine, Pittsburgh, PA), Integrative Structural Proteomics of an Organelle Sized Assembly

10.00-10.05  **PT14** Lukas Slavata (Institute of Microbiology CAS, Prague, Czech Republic), Transcription factor-DNA interaction studied by structural mass spectrometry

10.05-10.10  **PT15** Antonio Calabrese (University of Leeds, UK), Insights into outer membrane protein biogenesis from structural mass spectrometry

10.10-10.15  **PT16** Julian Bender (Martin Luther University Halle-Wittenberg, Germany), Structural dynamics and flexibility of the neuronal calcium-sensor Synaptotagmin-1

10.15-10.20  **PT17** Kai-Michael Kammer (University of Konstanz, Germany), Using cross-linking mass spectrometry and integrated modelling to study the architecture of macromolecular complexes

10.20-10.25  **PT18** Cecilia Emanuelsson (Lund University, Sweden), Structural model of the oligomeric human molecular chaperone DNAJB6 comprised of dimers and a site for interaction with aggregation-prone peptides at the dimer interface

10.25-10.30  **PT19** Gianluca Degliesposti (University of Cambridge, UK), Structural, biochemical and XL-MS investigation of Timeless-Tipin interactions

10.30-11.00  **Coffee**

11.00-11.35  **T13** Kostantinos Thalassinoss (University College London, UK), Combining native, ion mobility and crosslinking mass spectrometry to study protein structure and dynamics.

11.35-11.55  **T14** Fan Liu (FMP, Berlin, Germany), Developing structural interactomics and its application in cell biology.

11.55-12.15  **T15** Charlotte Uetrecht (Heinrich Pette Institute, Hamburg, Germany), Hitting proteins with a sledgehammer - structural characterization in XFELs.

12.15-12.20  **PT20** Manuel Matzinger (University of Vienna, Austria), Enrichment strategy for cleavable cross-linking technology in living cells

12.20-12.25  **PT21** Andreas Linden (Max Planck Institute for Biophysical Chemistry, Göttingen, Germany), Elucidating the Interactome of B-cell signaling proteins SYK and SLP65 of Homo sapiens and Gallus gallus by Cross-Linking Mass
The use of LC-SDA for cross-linking and mass-spectrometry (XL-MS)  

Covalent Protein Painting Evaluates Protein Surface Accessibilities in vivo  

reveals a common binding surface for endogenous peptide- and protein ligands to the Sortilin receptor  

Analysis of Escherichia coli ProQ RNA binding by HDX-MS  

Study of structural changes of Reptin in dependence on ATP and Liddean (ATP-mimetic) by hydrogen deuterium exchange coupled to mass spectrometry.  

New Insights into Secondary Active Transporters by Hydrogen/Deuterium - Mass Spectrometry  

Structural effects of glycan binding to norovirus capsid proteins studied by HDX MS  

Structural basis of quiescence and activation of the translocase motor SecA: A paradigm for the regulation of molecular motors.

Dynamic protein structure: from protein disorder to membrane pores.  

Insights into (un)structure-function relationships of intrinsically disordered chaperones.  

Identification and quantification of cross-linked peptides in the MaxQuant software.  

Dual Cleavable Crosslinking Technology (DUCCT): A High Confidence Approach for Identifying Protein Crosslinking by Differential Tandem Mass Spectrometry  

Using cross-linking mass spectrometry to structurally probe protein complexes involved in signaling.

Concluding remarks
Poster Presentations

**P1 Joanna Zamel** (The Hebrew University of Jerusalem, Israel) Cross-Linking and Mass Spectrometry in Living Yeast Cells

**P2 Antonia Vogel** (IMP, Vienna), Structural and functional studies of the UNC45-myosin complex

**P3 Ronja Pogan** (Heinrich Pette Institute, Hamburg, Germany), Indications for strain dependent stability profiles in norovirus virus-like particles

**P4 Anne Rehkamp** (Martin Luther University Halle-Wittenberg, Germany) Structural Insights into Retinal Guanylyl Cyclase/GCAP-2 Interaction Obtained by Cross-linking/Mass Spectrometry

**P5 C. Arlt** (Martin Luther University Halle-Wittenberg, Germany) An Integrated Mass Spectrometry Based Approach to Probe the Structure of the Full-Length Wild-Type Tetrameric p53 Tumor Suppressor

**P6 Marie Barth** (Martin Luther University Halle-Wittenberg, Germany) Covalent labelling of proteins for structure elucidation

**P7 Christian H. Ihling** (Martin Luther University Halle-Wittenberg, Germany), Evaluation of a Deuterated (D12) Version of the MS/MS-Cleavable Cross-Linker Disuccinimidyldibutyric Urea (DSBU)

**P8 Petra Darebná** (Czech academy of sciences) In-situ enrichment and detection of biotinylated molecules using functionalized MALDI chips

**P9 Gizem Dinler-Doganay** (Istanbul Technical University, Turkey) Bag-1 isoforms interact differentially with cell survival pathway regulators and ERAD mechanism players to modulate cancer progression in breast cancer cells

**P10 Marie V. Lukassen** (Aarhus University, Denmark), Employing Liquid Chromatography, NH2-Terminal Sequencing and Mass Spectrometry to Solve a Disulfide Bond Pattern

**P11 František Filandr** (Czech academy of sciences) How Cellobiose Dehydrogenase and Lytic Polysaccharide Monooxygenase Orchestrate Cellulose Degradation

**P12 Petr Halada** (Czech academy of sciences) Deciphering the influence of cellobiose dehydrogenase glycosylation pattern on its structure and function.

**P13 Caroline Haupt** (Martin Luther University Halle-Wittenberg, Germany), Proteoliposomes as a tool for structural analyses of membrane protein complexes

**P14 Tommy Hofmann** (Martin Luther University Halle-Wittenberg, Germany), Quantification of lipids in protein-lipid complexes

**P15 Janine Kopicki** (Heinrich Pette Institute, Hamburg, Germany), Investigating assembly of Ebola virus nucleoprotein and accessory proteins with native mass spectrometry

**P16 Ruzena Liskova** (Czech academy of sciences), Comparison of interactions of TEAD transcription factor with its DNA response elements from C-MYC exon and enhancer

**P17 Jana Lorenz** (Martin Luther University Halle-Wittenberg, Germany), Mass Spectrometry-Based Interaction Studies of FocA from Escherichia coli to Study its Influence for Formate Transport

**P18 Petr Man** (Czech academy of sciences), The utility of aspartic proteases in protein phosphorylation mapping
**P19 Eugen Netz** (MPI for developmental biology, Tübingen, Germany) OpenProXL: a fast and versatile XL-MS identification tool

**P21 Zsuzsanna Orbán-Németh** (IMP, Vienna) Structural prediction of protein models using distance restraints derived from chemical cross-linking mass spectrometry data

**P24 Pavla Vankova** (Czech academy of sciences), The role of hydrophobic interactions in the regulation of Hsp70 conformational transition

**P25 Dale Cooper-Shepherd** (Waters Corporation, UK), Native Ion Mobility Mass Spectrometry for the Characterization of Biotherapeutics

**P26 Malcolm Anderson** (Waters Corporation, UK), Implementation of hydrogen-deuterium exchange mass spectrometry for characterisation of peptide-receptive Major Histocompatibility Complex class I molecules

**P27 Şule Yilmaz** (MPI for Biochemistry, Munich, Germany), Development of software packages to MaxQuant for mass spectrometry-based chemical cross-linking studies

**P28 Federica Marini** (Catholic University, Rome) The Human Mitochondria Proteome: state of art and new challenges for Mass Spectrometry

**P29 Jaroslav Srp** (AS CR Prague) Potato Kunitz inhibitors evolved a novel non-canonical binding mode for serine proteases

**P30 Zhuo Chen** (TU Berlin) What more can cross-linking/Mass spectrometry tell us

**P31 F. O’Reilly** (TU Berlin) High-resolution protein structures by mass spectrometry and computational biology – science fiction or science reality?

**P32 Yulia Pivovarova** (Medical University of Vienna, Austria), Structural studies of a dimeric SET domain lysine methyltransferase from Toxoplasma gondii

**P33 Christine Piotrowski** (Martin Luther University Halle-Wittenberg, Germany), Cross-Linking and Mass Spectrometry Shed New Light on the bMunc13-2/Calmodulin Interaction

**P34 Iwan Parfentev** (MPI for biophysical chemistry, Goettingen, Germany), Characterization of protein-protein interactions in the synapse by chemical cross-linking mass spectrometry

**P35 Emma Stepanic** (MFPL, Vienna), Structural studies of centriole assembly in Drosophila