
Thursday November 19th, 2015

- 9:00 – 9:15 Welcome; **Michael Bron**, Vice Principal Martin Luther University Halle-Wittenberg & Andrea Sinz, local organizer
9:15 – 10:00 **Michal Sharon** (Weizmann Institute, Rehovot), Discovering a new subunit for an old complex by native mass spectrometry
10:00 – 10:30 **Petr Novak** (Academy of Sciences, Prague), When X-ray crystallography fails: CD302 Antigen Structure via Mass Spectrometry and NMR spectroscopy
10:30 – 11:00 Coffee Break
11:00 – 11:15 **Charlotte Uetrecht** (Leibniz Inst. Exp. Virol., Hamburg), Studying viral assemblies with mass spectrometry
11:15 – 11:30 **Carla Schmidt** (University of Oxford), Dimeric 13-Subunit Cytochrome C Oxidase is Stabilised by Lipids and Regulated by Post-translational Modifications
11:30 – 11:45 **Janne Jänis** (University of Eastern Finland), Ligand Binding Preference of a Macrolide Specific Repressor Protein MphR(E)
11:45 – 12:00 **Nina Morgner** (Frankfurt University), LILBID-MS on membrane protein complexes
12:00 – 12:15 **Knut Kölbl** (University of Antwerp), Conformational Properties of Gas Phase Protein Molecular Ions from a Thermodynamic Perspective
12:15 – 12:30 **Marc Kipping** (Waters), Extensive Charge Reduction and Dissociation of Intact Protein Complexes Following Electron Transfer on a Quadrupole-Ion Mobility-Time-of-Flight MS
12:30 – 12:35 Poster Talk: **Dietmar Hammerschmid** (University of Antwerp), Structural characterization of the globin coupled sensor from *Geobacter sulfurreducens* (GsGCS) by using native mass spectrometry
12:35 – 12:40 Poster Talk: **Jingzhi Yang** (Proteome Center Rostock), From antibody structure - function correlation to multiplexed immuno-assays
12:40 – 12:45 Poster Talk: **Albert Konijnenberg** (University of Antwerp), Extending structural proteomics to integral membrane proteins
12:45 – 14:30 Lunch and Poster Session
14:30 – 15:10 **Franz Herzog** (LMU Munich), Cross-Linking and Mass Spectrometry: Architecture and Mechanism of Chromatin-Associated Complexes
15:10 – 15:40 **Olaf Jahn** (MPI Exp. Med. Göttingen), Structural characterization of synaptic calmodulin complexes by photoaffinity labeling and mass spectrometry: the (everlasting) Munc13 story
15:40 – 16:00 Coffee Break
16:00 – 16:15 **Nir Kalisman** (Hebrew University of Jerusalem), Two years later – The XL-MS model of the transcription pre-initiation complex revisited
16:15 – 16:30 **Alexander Leitner** (ETH Zurich), Monitoring large conformational changes in protein complexes with a dedicated quantitative cross-linking software pipeline
16:30 – 16:45 **Jens Meiler** (Vanderbilt University), De novo protein structure prediction from crosslinking data
16:45 – 16:50 Poster Talk: **Valentina D'Atri** (Univ. Bordeaux, INSERM), Structural characterisation of human telomeric G-quadruplexes by using Ion Mobility Mass Spectrometry (IM-MS) and Molecular Dynamics (MD) simulations
16:50 – 16:55 Poster Talk: **Pavel Reichmann** (IPB Halle), Description of an N-End Rule E3 Ligase Substrate Binding Site
16:55 – 17:00 Poster Talk: **Verena Tinnefeld** (ISAS Dortmund), Enrichment of cross-linked peptides from complex samples by charge-based fractional diagonal chromatography
17:45 – 18:45 City Night Tour through Halle (meet at Händel statue)
19:00 – Dinner Palais S (Address: Ankerstraße 3c, 06108 Halle) with Live Music

Friday, November 20th, 2015

- 9:00 – 9:40 **Perdita Barran** (The University of Manchester), Adventures with Disorder and Charge
9:40 – 10:10 **Julia Chamot-Rouke** (Institut Pasteur, Paris), Application of top-down mass spectrometry to microbial proteomics
10:10 – 10:40 Coffee Break
10:40 – 10:55 **Philip Lössl** (University of Utrecht), Integrating native (ion mobility) MS, cross-linking/MS and top-down proteomics to decipher the interplay between phosphorylation and interactions of the mitotic regulators Aurora A, Bora, and Plk1
10:55 – 11:10 **Stéphanie Deroo** (University of Brussels), Towards the receptor-active conformation of apolipoprotein E: a combined XL/MS and molecular dynamics study
11:10 – 11:25 **Nadine Harrer** (LMU Munich), The structural architecture of the chromatin remodeler ISWI determined by cross-linking and mass spectrometry
11:25 – 11:40 **Giambattista Guaitoli** (DZNE Tübingen), Crosslinking-MS analysis combined with molecular modelling provides novel insight into the domain architecture of the PD-associated protein kinase LRRK2
11:40 – 11:55 **Gert von Helden** (Fritz Haber Institute Berlin), Unzipping of gas phase proteins - similar secondary structures at high charged states
11:55 – 12:10 **Tam Nguyen** (University of Copenhagen), A novel CE-MS interface for top-down MS analysis of proteins
12:10 – 12:15 Poster Talk: **Waldemar Hoffmann** (Fritz Haber Institute Berlin), Gas-Phase Infrared Spectroscopy of Ion Mobility-Selected Amyloid Intermediates
12:15 – 12:20 Poster Talk: **Melanie Göth** (Free University Berlin), Gas-Phase Microsolvation of Ubiquitin: Identification of Crown Ether Complexation Sites
12:20 – 12:25 Poster Talk: **Patrick Knight** (University of Leeds), Characterising the interaction of ataxin-3 and the poly-glutamine aggregation inhibitor QBP1
12:25 – 14:30 Lunch and Poster Session
14:30 – 15:00 **Kevin Pagel** (Free University Berlin), Separation of Oligosaccharide and Glycopeptide Isomers using Ion Mobility-Mass Spectrometry
15:00 – 15:15 **Mathias Müller** (Thermo Fisher Scientific), Analysis of Native Protein Complexes on a Benchtop Orbitrap Mass Spectrometer
15:15 – 15:30 **Dana Reichmann** (Hebrew University of Jerusalem), The nature and role of stress-regulated protein disorder in cellular proteostasis
15:30 – 15:45 **Pernille Foged Jensen** (University of Copenhagen), Dissecting the FcRn binding mode of antibodies with different pharmacokinetic profiles by hydrogen/deuterium exchange mass spectrometry

15:45 – 16:00	Ales Hnizda (Academy of Sciences, Prague), Integrative structural biology of relapsed-ALL specific cN-II mutants
16:00 – 16:05	Poster Talk: Rasmus Jakobsen (University of Copenhagen), Implementation of online electrochemical reduction of proteins into a Hydrogen/ Deuterium exchange Mass Spectrometry workflow
16:05 – 16:10	Poster Talk: Patrick Merkle (University of Copenhagen) Studying the Interaction between Affinity Enhanced T-Cell Receptors and Peptide-Bound Major Histocompatibility Complexes by Hydrogen/Deuterium Exchange Mass Spectrometry
16:10 – 16:15	Poster Talk: Marcus Nagel (UFZ Leipzig), First full-length Thyroid stimulating Hormone-Receptor structure elucidated by low resolution techniques
16:15 – 16:20	Poster Talk: Zsuzsanna Orban-Nemeth (IMP Vienna), Comprehensive XL-MS reveals parallel orientation and versatile conformations of plant HOP2/MND1
16:20 – 16:25	Poster Talk: Gabriel Mazzucchelli (University of Liege), De novo sequencing using MELD proteolysis coupled to "sequence assembly" algorithm
16:25 – 16:30	Poster Talk: Michal Rosulek (Charles University Prague), From monomer to tetramer: Mass spectrometric study of protein WrbA multimerization
16:30	Goodbye
16:35	Farewell Coffee
17:00	End of Symposium

Posters

D. Hammerschmid	Structural characterization of the globin coupled sensor from <i>Geobacter sulfurreducens</i> (GsGCS) by using native mass spectrometry
Jingzhi Yang	From antibody structure - function correlation to multiplexed immuno-assays
Albert Konijnenberg	Extending structural proteomics to integral membrane proteins
Valentina D'Atri	Structural characterisation of human telomeric G-quadruplexes by using Ion Mobility Mass Spectrometry (IM-MS) and Molecular Dynamics (MD) simulations
Pavel Reichman	Description of an N-End Rule E3 Ligase Substrate Binding Site
Verena Tinnfeld	Enrichment of cross-linked peptides from complex samples by charge-based fractional diagonal chromatography
Waldemar Hoffmann	Gas-Phase Infrared Spectroscopy of Ion Mobility-Selected Amyloid Intermediates
Melanie Göth	Gas-Phase Microsolvation of Ubiquitin: Identification of Crown Ether Complexation Sites
Patrick Knight	Characterising the interaction of ataxin-3 and the poly-glutamine aggregation inhibitor QBP1
Rasmus U. Jakobsen	Implementation of online electrochemical reduction of proteins into a Hydrogen/ Deuterium exchange Mass Spectrometry workflow
Merkle P.S.	Studying the Interaction between Affinity Enhanced T-Cell Receptors and Peptide-Bound Major Histocompatibility Complexes by Hydrogen/Deuterium Exchange Mass Spectrometry
M. B. M. Nagel	First full-length Thyroid stimulating Hormone-Receptor structure elucidated by low resolution techniques
Z. Orban-Nemeth	Comprehensive XL-MS reveals parallel orientation and versatile conformations of plant HOP2/MND1
Gabriel Mazzucchelli	De novo sequencing using MELD proteolysis coupled to "sequence assembly" algorithm
M. Rosulek	From monomer to tetramer: Mass spectrometric study of protein WrbA multimerization
J. Lockhauserbäumer	Norovirus infection pathway: glycan binding triggers structural changes
Johannes Heidemann	Structural investigation of co-assembled clathrin adaptor protein complexes by native mass spectrometry
Boris Krichel	Quaternary structure of endolysin reveals how its activity is regulated by a secondary translation product
Gili Ben-Nissan	Native mass spectrometry as a tool to discover structural impairment of Parkinson's disease related proteins
Jan Commandeur	Improving desolvation on q-tof instruments for native applications
Elisabetta Boeri Erba	Characterisation of Rip-2 kinase autophosphorylation and oligomeric state by mass spectrometry and crystallography
S. Chatterjee	IM-MS characterisation of protein therapeutics
Josephine Abi-Ghanem	Effect of the non-canonical G•U wobble base pair on the binding mechanism of RNA kissing complexes
Natália Carulla	SDS-PAGE analysis of Aβ oligomers is disserving research into Alzheimer's disease: appealing for ESI-IM-MS
E.Grifnée, G.Mazzucchelli	Structural characterisation of protein by using enzymatic reactor
Tomas Jecmen	Expression of photo-reactive cytochrome b5 reductase for mapping its interaction surface with redox partner cytochrome b5
R. Ptackova	Photo cross-linking via L-Photo-Met and MS to study the interaction of 14-3-3 with phosphorylated Raf peptide
Miroslav Šulc	The photo-initiated cross-linking via pMet and MS: the tool to study the protein-protein interactions
Moritz Fischer	Synthesis of less hydrophobic Derivatives of MS/MS-Cleavable Cross-Linkers: Synthesis and Evaluation of Reactivity for effective Protein Structure Analysis
Christoph Hage	Dissociation behavior of bifunctional TEMPO-benzyl active ester for peptide structure analysis by free radical initiated peptide sequencing (FRIPS) mass spectrometry in negative ion mode
Rico Schwarz	Monitoring Conformational Changes in Peroxisome Proliferator-Activated Receptor β/δ by Cross-Linking/Mass Spectrometry
Christine Piotrowski	Structural Analysis of the bMunc13-2/Calmodulin Interaction by Cross-Linking and Mass Spectrometry
Fan Liu	Proteome-wide profiling of the structure and interaction of protein assemblies by cross-linking mass spectrometry
Björn Häupl	Characterization of protein kinase D2 complexes by chemical cross-linking and mass spectrometry
Konstanze Bosse	SILAC-Based Secretome Analysis of Non-Small Cell Lung Cancer Cell Lines
C. U. Schröder	A comprehensive look at the cross-linking pattern of human, bovine and frog elastin
J. Wang	Production and characterization of elastin-like biomaterial in vitro cross-linked by lysyl oxidase like 2 protein
A.C. Mora Huertas	Insights into the age-related changes in elastic fibers from skin
G. Rutsdottir, K. Bernfur	Characterization of V181A, a dimeric Hsp21 mutant by SAXS and CXMS
Michael Götze	Efficient Identification of Cross-Linked Peptides with StavroX and MeroX in Structural Proteomics
Lutz Fischer	False Discovery Rate Estimation in Cross-Linking/Mass Spectrometry and application in Protein Structure Determination
Möller, I.R.	Applying Hydrogen-Deuterium Exchange Mass Spectrometry to Analyze the Dynamics and Drug Binding of the Human Serotonin Transporter
Petr Halada	Expanding the acid protease toolbox for H/D exchange
Michael O. Glocker	Ion Mobility and Surface Topology Mapping Reveals the Cause of the Protein G' e - IgG Affinity Switch
Peter Højrup	An Integrated Approach for Probing Protein Structure by Mass Spectrometry
Petr Man	Transcription factor – DNA interaction studied by structural mass spectrometry

Alan Kadek
Maxime Bourguet
Nicholas J. Bond
Sandra Richter

Electrostatics-driven conformational dynamics of cellobiose dehydrogenase probed by structural mass spectrometry
Structural MS for the characterization of yeast U3 snoRNP assembly
Structural and molecular studies of IL-33 disulphide isoforms
Proteomic identification of reinforcement- polarity dependently regulated synaptic proteins in an auditory learning paradigm in mice

Edwin De Pauw
Leonhard H. Urner
Gerard Comamala
Sabrina Pfennig
Christian Arlt
Jiří Hausner

Bottom-up and top-down high-throughput sequencing of toxins with pharmacological interest
Photoswitchable Nanocarriers for Gas Phase Membrane Protein Analysis
Studying Back-exchange Effects on Protein Analysis by Hydrogen/Deuterium exchange Mass Spectrometry
Regulation of the Chromatin Remodeler ISWI by its N-terminal domain
3D-Structural Characterization of the N- and C-terminal Regions of p53 by Combining Cross-Linking/MS and Native MS
Dynamics of chloride channel from E. coli studied by hydrogen/deuterium exchange



Creative Molecules Inc.



Waters
THE SCIENCE OF WHAT'S POSSIBLE™



Thermo
SCIENTIFIC

