
Thursday November 27th

08:00 Registration open

08:45-09:00 Opening

09:00-10:30 Session 1 - Native mass spectrometry and ion mobility

Keynote lecture:

Albert Heck	Mass Spectrometry and its role in studying intact proteins, proteoforms and protein complex structure, dynamics and assembly
Charlotte Uetrecht	Studying viral assemblies with mass spectrometry and XFELs
Neil Oldham	Ion mobility-mass spectrometry and covalent modification in studying the structure and interactions of a structurally dynamic enzyme
Sarah Cianféroni	Combining native MS approaches to decipher archaeal box H/ACA ribonucleoprotein particle structure and activity
Michal Sharon	Unraveling the modular structure of protein complexes using native mass spectrometry: The case of the Arp2/3 complex

10:30-11:00 Coffee break

11:00-12:30 Session 2 - Intact protein characterization

Julia Chamot-Rooke	Analysis of Histidine-rich proteins involved in Helicobacter pylori virulence by Top-Down Proteomics
Peter O'Connor	Does deamidation cause protein misfolding?
Edwin de Pauw	Probing the conformational changes during desolvation of ions using orthogonal mobility methods
Bob Galvin	Complimentary solutions for the characterization of biopharmaceuticals
Jonathan Williams	The analysis of some structural human hemoglobin variants using ETD and AP-ECD

12:30-13:40 Lunch break and posters

13:40-14:00 Vendor session 1

Waters - Guillaume Béchade	Waters HDX high resolution-ion mobility MS solution for epitope mapping and higher order structural analysis
MS Vision - Jan Commandeur	Analysis of intact antibodies by native MS on Q-TOF instruments

14:00-15:30 Session 3 - Protein aggregation and Amyloid

Alison Ashcroft	Examination of ataxin-3 aggregation by structural mass spectrometry techniques: A rationale for expedited aggregation upon polyglutamine expansion
Michal Dadlez	Ion Mobility separation coupled with MS reveals alternative structural forms of Alzheimer's disease A β peptide
Natalia Carulla	Hydrogen/deuterium exchange protected oligomers populated during A β fibril formation correlate with neuronal cell death
Stéphanie Deroo	Key molecular interactions between the amyloid β peptide and apolipoprotein E isoforms revealed by chemical crosslinking/mass spectrometry
Michael Przybylski	Fragmentation and aggregation of physiological and Parkinson-synucleins revealed by ion mobility and affinity-mass spectrometry

15:30-16:00 Coffee break

16:00-17:00 Session 4 - Protein conformational studies

Kris Gevaert	The kinase switch mechanism studied using limited proteolysis combined with stable isotope labelling
Kevin Pagel	UV photodissociation of conformer-selected protein ions
Tassos Economou	Deciphering bacterial protein secretion using a multi-pronged approach: from proteins to proteomics

17:00-18:00 Drinks & posters

19:00 Conference dinner with harbour cruise on "Jan Plezier II" boat

Start 19:00, latest departure 19:30 from Londenbrug (by MAS museum, old port)

Friday November 28th

08:30-10:00 Session 5 - H/D exchange

Keynote lecture:

Ganesh Anand	Transmembrane signalling in membrane receptor kinases by amide H/D exchange mass spectrometry
Kasper Rand	Measuring the hydrogen/deuterium exchange of proteins by mass spectrometry: applications and developments
Christoph Borchers	Top-down HDX to structurally characterize protein therapeutics and biosimilars
Kai Scheffler	High resolution protein characterization on the orbitrap platform
Thorleif Lavold	A novel high-throughput site-specific binding screening platform

10:00-10:30 Coffee break

10:30-12:30 Session 6 - Native mass spectrometry and ion mobility

Petr Novak	Mass spectrometric mapping of bacterial stress-response protein WrbA molecular self-assembly
Basri Gülbakan	Soft ionization mass spectrometry studies of aptamer-ligand interactions
Carla Schmidt	Post-translational modifications and their effect on protein complex formation and stability
Rita Grandori	Studying intrinsically disordered proteins by mass spectrometry
Massimiliano Porrini	Do dodecameric DNA duplexes retain their solution helical features in gas phase?
Elisabetta Boeri Erba	When mass spectrometry meets structural biology: new answers to old questions
Nina Morgner	LILBID-MS reveals structural insights into a hybrid FOV0 ATPase

12:30-14:00 Lunch break and posters

14:00-14:30 Vendor session 2

Advion - Andrew Creese	LESA and FAIMS: An ideal partnership?
Agilent - Joachim Thiemann	The 6560 - a gentle CCS calculation machine for native MS applications
Shimadzu - Helen	ISDn: in-source decay and MSn of proteins with post-translational modifications using MALDI-Quadrupole Ion-Trap

Montgomery

TOF Mass Spectrometer

14:30-16:00 Session 7 - Crosslinking approaches

Knut Kölbl

Folding and complex assembly of micro-proteins followed by nanoHPLC/nanoESI-MS/MS: Details of an induced fit folding mechanism

Alex Leitner

Recent advances in cross-linking/mass spectrometry of large protein complexes

Akram Alian

Trapping protein-nucleic acid complexes by covalent cross-linking

Christian Arlt

3D-structural characterization of the N- and C-terminal regions of p53 by combining cross-linking/MS and native MS

Henning Urlaub

Elucidation of molecular contact sites in protein-nucleic acid complexes using mass spectrometry

16:00-16:30 Coffee break

16:30-17:55 Session 8 - Protein structure and conformational space

Argyris Politis

A hybrid structural biology method for modelling transient protein complexes

Michael Glocker

Mass spectrometric characterization of limited proteolysis activity in human plasma samples

Virginie Redeker

A novel bio-orthogonal cross-linker for improved protein/protein interaction analysis

Matteo Degiacomi

Mass Spectrometry-driven modeling of protein assemblies

Esther Martin

Characterisation of nucleosomes and their binding partners using mass spectrometry and ion mobility

Stephan Rauschenbach

Controlling protein conformation on surfaces by soft-landing ion beam deposition

17:55-18:00 Poster prizes and farewell

18:00-19:00 Drinks



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