

Rolduc2019 | 4th NVMS-BSMS Conference on Mass Spectrometry | Program

Sunday			
14:30-16:30	Registration		
16:30-17:15	Aula Major	K1 Developing Mass Spectrometry to examine Dynamic Proteins - Perdita Barran	Chair: Jef Rozenski
17:15-18:00	Aula Major	K2 A deeper view of localized lipid biochemistry using advanced mass spectrometry imaging approaches - Shane Ellis	Chair: Manfred Wührer
18:15-22:00	Buffet dinner & Welcome party		
Monday			
9:00- 9:10	Aula Major	Opening	
9:10- 9:55	Aula Major	K3 Mass spectrometry in verification of use of chemical weapons - Paula Vanninen	Chair: Annemieke Kolkman
9:55-11:10	Aula Major	Poster presentations (PhD students)	Chair: Eva de Rijke / Jef Rozenski
11:10-11:45	Coffee break		
	Hall 1	Hall 2	Hall 3
Topic	Large molecules	Small molecules	Non-mainstream
Chair	Manfred Wührer	Eva de Rijke	Annemieke Kolkman
11:45-12:05	O1 Automated enrichment of secreted and newly synthesized proteins - David Vargas-Diaz	O2 Adduct Ion Structures & Stability in Travelling Wave & Trapped IMS; a view - Maarten Honing	O3 Tissue physiology and venom toxin distribution in the envenomed mouse - Erika Amstalden van Hove
12:05-12:25	O4 Extending Native Top-Down Mass Spectrometry mass range by UVPD - JeanFrançois Greisch	O5 Metabolism of orally administered medium-chain triglyceride - Dewi van Harskamp	O6 IMMS and Molecular Dynamics Provide Insights on ESI Mechanisms - Quentin Duez
12:25-14:00	Lunch and poster session		
Topic	Large molecules	Small molecules	Non-mainstream
Chair	Richard Scheltema	Isabelle Kohler	Pascal Gerbaux
14:00-14:20	O7 MIND: A double-linear model to accurately determine monoisotopic precursor mass in high-resolution top-down proteomics - Dirk Valkenborg	O8 Combined LC-HRMS and effect-based monitoring of chemical water quality - Andrea M Brunner	O9 The structures of ETD-Product Ions Revealed by IR Ion Spectroscopy - Lisanne Kempkes
14:20-14:40	O10 Reproducible LC/MS in Biopharma: a new paradigm - Guillaume Béchade (Waters)	O11 A New Lipidomics Workflow Applied to Plasma and Cellular Extracts - Christian Klein (Agilent)	O12 sponsor Bruker
14:40-15:00	O13 Benchmarking IM-MS gas-phase data based on cross-linking strategies - Emeline Hanozin	O14 Fast profiling and classification of wines and wine quality via SAWN-MS - Alina Astefanei	O15 Estimation of proportions of molecules by optimal transport - Michał A. Ciach
15:00-15:30	Coffee break		
Topic	Identification - large molecules	Identification	Quantification
Chair	Arjen Gerssen	Ann van Eeckhaut	Jan van Bocxlaer
15:30-15:50	O16 High-resolution model of Fibrin clots by crosslinking mass spectrometry - Oleg Klykov	O17 Challenges in the MS-based analysis of therapeutic peptides - Thomas de Vijlder	O18 BPA, BADGE and analogues: a new sensitive LCESI-MS/MS method - Stefan van Leeuwen
15:50-16:10	O19 Comprehensive glycosylation analysis of pancreatic cell lines - Tao Zhang	O20 sponsor Thermo	O21 Challenges & Applications for Quantitation of ASOs and siRNAs in plasma and tissues with LCMS/MS and HPLC-fluorescence assays - Benno Ingelse
16:15-17:00	Aula Major	K4 From Fundamental Mass Spectrometry to analytical methods - Edwin de Pauw	Chair: Jef Rozenski
17:00-18:00	Aula Major	Arthur Brandt	
18:10-18:30	Aula Major	Annual assembly NVMS/BSMS	
18:30	Conference dinner		
20:30	Conference party		

Tuesday			
9:00-10:00	Aula Major	Poster presentations (PhD students)	Chair: Isabelle Kohler / Jef Rozenski
10:00-10:45	Aula Major	K5 Making non-targeted LC/HRMS screening quantitative - Anneli Krueve	Chair: Filip Cuyckens
10:45-11:15	Coffee break		
	Hall 1	Hall 2	Hall 3
Topic	Large molecules	New developments	Large molecules
Chair	Loïc Quinton	Edwin de Pauw	Filip Cuyckens
11:15-11:35	O22 Site-specific glycosylation mapping of human Fc gamma receptor IIIb - David Falck	O23 Gas-phase structure of peptoid ions: impact of structural factors - Emilie Halin	O24 pacMASS2 – de novo prediction of the aminoacid sequence of peptides and proteins - Jürgen Claesen
11:35-11:55	O25 Turning Synapts into versatile platforms for structural analysis of large biomolecules - Jan Commandeur (MS Vision)	O26 sponsor Perkin Elmer	O27 Proteomics gone fast - and what to do with it - Markus Ralser (Sciex)
12:00-13:30	Lunch and poster session		
Topic	Large molecules	New developments	Identification
Chair	Manfred Wührer	Jan Commandeur	Willy Janssens
13:30-13:50	O28 Sweet and sour: analysis of intact proteins by HILIC-MS - Andrea F.G. Gargano	O29 Combining MSI and top-down proteomics to predict immunotherapy response in NSCLC patients - Eline Berghmans	O30 Lipid profiling of carotid atherosclerotic by MALDI-MSI - Astrid M. Moerman
13:50-14:10	O31 IMS prevents misinterpretation of MS data after glycan rearrangement - Javier Sastre Toraño	O32 Ambient H/D Exchange LAESI-MS for Imaging and Structure Elucidation - Fred van Geenen	O33 Selection of peptide markers for MS-based detection of hazelnut in food - Kaatje van Vlierberghe
14:20-15:05	Aula Major	K6 Cellular cartography at molecular detail: in situ crosslinking mass spectrometry - Juri Rappsilber	Chair: Maarten Altelaar
15:05-15:50	Aula Major	K7 New horizons of Orbitrap mass spectrometry Alexander Makarov	Chair: Maarten Altelaar
15:50	Aula Major	Poster award ceremony & goodbye	
16:00	Busses depart to Heerlen train station		