

Thursday 29 March 2012			
Lecture room	Bioinformatics / Identification Lecture hall 1	Quantitation Lecture hall 2	Current applications Lecture hall 3
<i>Chairperson</i>	<i>Rob Vreeken</i>	<i>Maarten Altelaar</i>	<i>Filip Cuyckens</i>
14:30 – 14:55	Joachim Thiemann (AGILENT TECHNOLOGIES) Software for pathway informed metabolomics	Rainer Bischoff Studying the MMP-9 Proteolytic System by Tandem Mass Spectrometry in the SRM Mode	Johann Far The usefulness of Ion Mobility-Mass Spectrometry for Small Molecules Analysis
14:55 – 15:20	Dirk Valkenburg An elegant algorithm to calculate the aggregated isotopic distribution and exact center-masses	Ana Guerreiro Proteome signatures of the cyanobacterium <i>Synechococcus elongatus</i> PCC7942 circadian rhythm	Erik Emke Determination of functionalized engineered carbon nanoparticles in environmental samples by HPLC-UV/LTQ-ORBITRAP MS
15:20 – 15:45	Fatemeh Zamanzad Ghavidel The empirical assessment of the quality of the SEQUEST XCorr scores	Pieter Colin A fast and reliable quantification of 13 β -lactam antibiotics in human plasma by SPE-UPLC-MS/MS	Rob van der Heijden (BRUKER) amaZon Speed: unmatched ion trap performance through innovation
<i>Break</i>			
16:15 – 16:40	Ferry Heus Venom profiling for ion channel drug discovery by hyphenating nano-LC/MS and post-column biochemical detection	Gideon Oudgenoeg Label free Selected Reaction Monitoring for biomarker validation; assay development in biological matrix or using synthetic peptides	Arjen Gerssen The use of NanoUPLC and Triziac NanoTile UPLC Quadrupole Time-of-Flight Mass Spectrometry in the field of small molecules
16:40 – 17:05	Peter Verhaert Natural Peptides to Drugs: What can we learn from frogs?	Stephen Lock (AB SCIEX) Increasing selectivity in LC/MS/MS analysis using techniques such as MRM3, SelexION™ and high resolution LC/MS/MS	Elena Chernetsova ID-CUBE DART high resolution mass spectrometry and its capabilities in phytomedicine analysis
17:05 – 17:30	Ioana Barbu Characterization of protein complexes by ion mobility and computational modeling	Catherine Bresseur Measurement of Trace Level Dechlorane Flame Retardants in Human Blood by GCXGC-NCI-HRTOFMS	Maurien Olsthoorn Mass spectrometric protein and metabolite analysis for the production of bio-based chemicals

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	Identification Lecture hall 1	Non-mainstream Lecture hall 2	Current applications Lecture hall 3
<i>Chairperson</i>	<i>Henk Dekker</i>	<i>Valérie Gabelica</i>	<i>Bernard Leyh</i>
11:15 – 11:40	Magda Claeys Characterization of biogenic secondary organic aerosol: current state of knowledge and recent applications	Liam McDonnell Imaging Mass Spectrometry Based Molecular Histology Differentiates Microscopically Identical and Heterogeneous Tumors	Léon Coulier LC-MS analysis of organic acids: a continuous struggle for sensitivity
11:40 – 12:05	Pierre-Hugues Stefanuto Forensic Study of Volatile Organic Compounds Released from Decaying Bodies	Julia Jungmann A New Molecular Imaging Approach: Mass Spectrometry Imaging of Bimolecular Ions Using an In-Vacuum Pixel Detector	Michael Giera Targeted and untargeted lipidomics analysis of human synovial fluid
12:05 – 12:30	Kai Scheffler (THERMO FISHER SCIENTIFIC) Targeted Protein Quantitation Workflow for Biomarker Discovery	Donald Smith C ₆₀ Secondary Ion FT-ICR MS	Nick Dekker Glucosylsphingosine as a novel plasma biomarker for Gaucher disease
<i>Lunch / Poster session</i>			
14:00 – 14:25	Albert Heck Tackling the Complexity of the Phosphoproteome by using a variety of Enrichment and Separation technologies	Marcus Mreyen (SHIMADZU) Closing a gap in the analytical field - Fastest triple quadrupole MS technology for ultra fast HPLC separation	Linda Switzar Identification of drug-protein adducts in biological samples
14:25 – 14:50	Hansuk Buncherd Selective enrichment and identification of cross-linked peptides to study 3-D structures of protein complexes by mass spectrometry	Julien De Winter Size dependence of the folding of multiply charged sodium cationized polylactides revealed by ion mobility mass spectrometry and molecular modelling	Ruben t'Kindt Profiling and characterizing skin ceramides using LC-QTOF-MS
14:50 – 15:15	Filip Cuyckens Product ion mobility as a promising tool for assignment of positional isomers of drug metabolites	Jos Oomens Molecular structure in MS by ion spectroscopy: non-equilibrium distributions from ESI	Keith Worrall (WATERS) Utilising the Increased Peak Capacity of UPLC Ion Mobility ToF MS and MSE to Overcome Sample Complexity