

Kiel Mass Spectrometry Forum 2019

Oct., 07./08., 2019, University Kiel, Germany

Program

Monday, Oct. 07th, 2019

Time	Name/Institution	Title
11.00		Registration open & coffee
12.45	Andreas Tholey & Tobias Demetrowitsch, Univ. Kiel, D	Welcome & Presentation of the “Kiel Network of Analytical Spectroscopy and Mass Spectrometry”
Session: Metabolomics & Lipidomics I – Chair: Joachim Thiery		
13.00	Karsten Hiller Univ. Braunschweig, D	Keynote Lecture: Profiling metabolism - but where to look at?
13:45	Karin Schwarz Univ. Kiel, D	Multi-databases assisted exploration for metabolite identification
14:15	Christer S. Ejsing Odense University, DK; and EMBL, Heidelberg, D	Shotgun lipidomics: Harnessing the power of high resolution mass spectrometry for the analysis of complex lipid samples
15.15	Waters: Gunnar Weibchen	Targeted Omics Method Library for Biomedical Research – Expand What’s Possible
15:40		Group Photo
15:45		Coffee Break
Session: Proteomics I - Sample preparation and structural Biology Chair: Ole Jensen		
16:25	Andreas Tholey Univ. Kiel, D	Small droplets for large numbers - approaches for digital microfluidics supported LC-MS based microproteomics and multi-omics
16:55	Julia Kehr Univ. Hamburg, D	Characterization of mobile, RNA-binding plant proteins
17:25	Boris Krichel Heinrich Pette Institute - Leibniz Institute for Experimental Biology, Hamburg, D	Structural mass spectrometry goes viral
17:55	Sciex, <i>represented by guest speaker:</i> Vadim Demichev Crick Institut, Univ. Cambridge, UK	Ultra-fast proteomics with scanning SWATH
18:20		Short Break
18.30	Ben Krause-Kyora Univ. Kiel, D	Talk beyond mass spec: Live and let die – medical ancient DNA research
19:15		Poster Session & Buffet, Wine & Beer
23.00		End day 1

Tuesday, Oct. 08th, 2019

Time	Name/Institution	Title
Session: Proteomics II – Top-down and Applications Chair: Isabelle Fournier		
08:30	Ole N. Jensen Odense University, DK	Keynote Lecture: Enhancing protein characterization and PTM mapping by middle-down and top-down mass spectrometry and new computational tools
09:15	Robert Blick / represented by Stefanie Haugg Univ. Hamburg, D	Mass spectrometry of high mass proteins
09:45	Maria Riedner Univ. Hamburg, D	Systematic search for urotensin-II and urotensin-II related peptide generating proteases
10:15	Thermo Fisher Scientific: Moritz Janda	"Genius made simpler: Improving everyday protein profiling to quantitative analysis"
10:40		Coffee Break
Session: Metabolomics II – Lipidomics & Clinical Metabolomics Chair: Christer Ejsing		
11:15	Christoph Krisp Univ. Hamburg, D	The virtual center for mass spectrometry Hamburg/Schleswig-Holstein
11:20	Dominik Schwudke Research Center Borstel, D	Mycobacterial phospholipids as diagnostic marker in translational tuberculosis research
11:50	Joachim Thiery Univ. Leipzig / Univ. Kiel, D	Quantitative mass spectrometry in clinical research and patient care
12:20	Ute Ceglarek, Univ. Leipzig, D	Clinical metabolomics from research to diagnosis
12:50		Lunch (Mensa II)
Session: Imaging MS & Technology Chair: Andreas Tholey		
14:15	Hartmut Schlüter Univ. Hamburg, Univ. Clinics Eppendorf, D	Laser assisted metabolomics and proteomics
14:45	Christoph Röcken Univ. Kiel, and UKSH, Kiel, D	MALDI imaging MS in amyloidosis research
15:15	Deniz Tasdemir Geomar Kiel, D	Comparative metabolomics and mass spectrometry imaging for understanding surface-based host-microbe interactions in marine realm
15:45	Bruker: Lucy Woods	Introducing timsTOF fleX for MALDI guided SpatialOMx
16:10	Isabelle Fournier Lille University, F	Keynote Lecture: MS Imaging from ex vivo to in vivo: From bench to bedside
16:55	Andreas Tholey Univ. Kiel, D	Conclusions and End of Conference