









EU COST Workshop:

DGMS- Fachgruppe Affinity- Mass Spectrometry

"Biomolecular Recognition and Mass Spectrometry"

26th - 27th October 2015

Senatssaal Stadt Rüsselsheim

Senatssaal

Programme

Monday, 26th October 2015

09:00 – 10.00	Registration & Welcome Coffee
10:00	Welcome & Opening Addresses
	Michael Przybylski, Chairman
	Steinbeiszentrum Biopolymer Analysis & Biomedical Mass Spectrometry,
	Rüsselsheim
	Martin Schipper, Stadt Rüsselsheim
	Michael Glocker, DGMS- Fachgruppe Affinity- Mass Spectrometry;
	Head, Proteome Center, Universität Rostock
Session 1:	New Mass Spectrometry Tools in Proteomics and Affinity- Proteomics (Chair: Michael Glocker)
10:30	Frank Sobott, University of Antwerp, BE: "Protein higher-order structure characterization by native MS and ion mobility methods











11:00	Albert Lebedev, Moscow State University, Moscow, RU: Mass spectrometric determination of amphibian peptidome and its application for the differentiation of frogs' species and populations
11:30	Christian Bunse, Shimadzu GmbH, Duisburg, DE: LCMS- 8060 - A new level of sensitivity
12.00	Arno Graf, ERC GmbH, Riemerling, DE: Controlled reduction of disulphide bonds in protein therapeutics using an electrochemical reactor cell online with MS
12:30	Lunch
Session 2:	New Tools and Applications in Immunoaffinity- MS Chair: Katrin Marcus, Bochum
13:30	Michael Glocker, Medical University Rostock, DE Novel developments in mass spectrometric epitope mapping approaches and clinically relevant applications – towards 2 nd generation autoimmune disease diagnostics
14:00	Wolfgang Jabs, Bruker Daltonik, Bremen, DE Monoclonal antibody characterization using ultra-high resolution QTOF mass spectrometry
14:30	Frederik Weiss, NaturwissenschMedizin. Institute Reutlingen, DE: Quantifying the human cytochrome P450 system using affinity proteomics
15.00	Coffee Break











- Session 3: New Developments in Bioaffinity- Mass Spectrometry Chair: Petr Novak, Prague
 15.30 Friedrich Herberg, University of Kassel, DE: Analysis of protein kinase function using SPR and affinity tools
 16:00 Nico Dankbar, Xantec GmbH, Düsseldorf, DE The best of two worlds: Combining mass spectrometry with surface plasmon resonance
 16:30 Michael Przybylski, Steinbeis Centre for Biopolymer Analysis, Rüsselsheim, DE: Structure determination and affinity-quantification of biopolymer epitopes using online SPR-ESI-MS
- 17:00 Serge Muyldermans, Vrije Universiteit Brussels, BE: Nanobodies: Minimal sized, high-affintiy, high specificity reagents
- 17:30 **Ivana Jovceska**, University of Lubljana, SI Exploiting nanobodies in the search for protein markers of glioblastoma multiforms
- 18:30 Train to Mainz- Station Mainz-Römisches Theater and Historic Walk through Altstadt Mainz & Workshop Dinner Restaurant "Heiliggeist" Mainz
- 19.30 Workshop Dinner Restaurant "Heiliggeist"











Tuesday, 27th October 2015

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Session 4:	Development and Characterization of New Affinity Tools and Reagents Chair: Michael Przybylski, Rüsselsheim
09:00	Stefan Dübel, Technical University Braunschweig, DE: High throughput recombinant antibody generation for research: what has been achieved and what's still to do
09:30	Guillaume Bechade, Waters AG, Baden, CH A fully integrated hydrogen-deuterium exchange MS solution to support epitope mapping and ligand binding studies
10:00	Petr Pompach, Institute for Microbiology, Charles University Prague, CZ Direct immuno-affinity mass spectrometry for detection of haptoglobin phenotypes
10:30	Susanna Lundström, Karolinska Institutet, Stockholm, SE IgG-omics, a window into the human blood proteome with clinical implications
11:00	Coffee break











Session 5:	Immunoaffinity- mass Spectrometry: Instrumental Development and Clinical Applications Chair: Stefan Maeser, Rüsselsheim
11:30	Katrin Marcus, Ruhr-Universität Bochum, DE Enrichment of α-Synuclein as a potential biomarker for Parkinson's Disease through immunoprecipitation for characterization and quantification via Top Down Proteomics
12:00	Sibylle Heidelberger, Sciex Ltd., Warrington, UK: Direct analysis of plasma sphingolipids for research into lysosomal storage metabolism
12:30	Christopher Gerner , University of Vienna, AU: Assessment of the efficiency of antibody-based protein depletion for serum proteome profiling for the investigation of cancer-associated cachexia
13:00	Lunch
Session 6:	New Technologies of Mass spectrometry for Analysis of Biomolecular Interactions Chair: Serge Muyldermans, Petr Novak, Michael Przybylski
14:00	Eugene Nikolaev, Russian Academy of Sciences, Moscow, RU: Potentials of the ultra- high resolution FT-ICR-MS
14:30	Stefan Slamnoiu, Jeol GmbH, München, DE JEOL SpiralTOF - providing ultra-high mass resolution for MALDI-TOF applications











15:00	Natalia Starodubtseva, Research Center for Obstetrics, Gynecology and Perinatology, Russian Academy of Medical Sciences, Moscow, RU Proteomics in neonatology: Non-invasive diagnosis and prognosis of neonatal complications in neonates under intensive care
15:30	Coffee Break
16:00	Hartmut Schlüter, University of Hamburg, DE: Investigating protease-ligand interaction by the mass spectrometry assisted enzyme screening system (MES)
16:30	Kwabena Opuni, Medical University of Rostock, DE In-Silico epitope mapping: Experiences with the rheumatoid arthritis autoantigen glucose-6-phosphate isomerase (GPI)
17:00	Marius Iurascu, Steinbeis Centre Rüsselsheim & Univrsity of Konstanz, DE: Identification of an mixed-disulfide assembled epitope of an HLA-B27 antibody by affinity- mass spectrometry
17:20	Petr Novak, Czech Academy of Sciences, Prague, CZ: Planar functionalized surfaces for direct immunoaffinity desorption/ionization mas spectrometry
17:50	Concluding Discussion & Conclusion of Workshop
18:10	Visit and Guided Tour, City Museum Rüsselsheim
19:00 -	Dinner (individual)