

Monday March 30, 2009

- 13.30 **Closing of the Urine and Kidney Proteomics (EuroKUP) COST Action meeting**
(www.eurokup.org)
- 13.30-17.30 Trip to Mycenae (optional)
- 17.30-19.00 **Registration for the HPS meeting**

HPS meeting

HPS Opening Lectures (Chairs: A. Vlahou, I. Xenarios)

- 18.30-19.15 **T. Rabilloud**, CEA-Grenoble
What room for electrophoretic separations in modern proteomics?
- 19.15-20.00 **P.G. Righetti**, Polytechnic of Milano
The ProteoMiner and the FortyNiners: searching for gold nuggets in the proteomic arena
- 20.00-20.45 **B. Domon**, ETH Zurich
Paradigm shift in proteomic biomarker discovery and evaluation
- 21.00 **Welcome Dinner**

Tuesday March 31, 2009

Bringing –omics to the basic science and clinical service (Chairs: P.G. Righetti, G. Tsangaris)

- 9.00-9.20 **T. Luider**, ErasmusMC
Finding preeclampsia biomarkers in chorion villus biopsies by mass spectrometry
- 9.25-9.45 **H. Mischak**, Mosaiques-Diagnostics GmbH
CE-MS-based urinary proteomics as a powerful tool in clinical diagnosis, prognosis, and therapy evaluation
- 9.50-10.10 **V. Guryča**, F. Hoffmann-La Roche Ltd
Deeper exploration of proteome with a combination of multidimensional peptide separations with accurate mass and time tags (AMT) proteomics approach
- 10.15-10.35 **M. Baumann**, U Helsinki
MS-IMS (Maldi-Imaging) The use of Mass Spectrometry for tissue imaging
- 10.40-11.10 Industrial Workshop:
B. Fathollahi, Caliper Life Science
The application of high throughput microchip CE-SDS (LabChip®) in protein sciences

- 11.10-11.30 **Coffee Break** **Poster viewing**
(Chairs: **T.Rabilloud, S. Garbis**)
- 11.30-11.50 **H. Voshol**, Novartis Institutes for Biomedical Research
Pathway analysis using reverse protein arrays
- 11.55-12.15 **I. Xenarios**, Swiss Institute of Bioinformatics
Integration of biological knowledge: from avalanche of data to system modelling
- 12.20-12.40 **G. Thireos**, IMBB FORTH
Systems Biology: Just a slogan or a reality?
- 12.45-13.15 Industrial Workshop:
M. Macht, Bruker Daltonik GmbH
Pushing the limit in proteomic analyses: a novel mass spectrometer combining ultra-high mass resolution and accuracy for maximum protein sequence coverage
- 13.15-14.30 **Light Lunch** **Poster viewing**
- 14.30-15.00 Industrial Workshop: **Biorad**
A. Sacchi
How to improve a gold standard such as SDS-PAGE or 2D electrophoresis using the new Criterion Stain Free system
Scientific Session (Chairs: B. Domon, D. Sanoudou)
- 15.00-15.20 **E. Boschetti**
Isoelectric pre-fractionation of proteins and peptides with solid-state buffers prior to extensive proteomic analysis
- 15.20-15.35 **M.A. McDowall**
An integrated workflow solution for optimized discovery and targeted proteomics research
- 15.35-15.50 **H. Kovarova**
Monitoring of anti-cancer therapies and resultant chemoresistance
- 15.50-16.05 **C. Lane**
Moving protein candidates through the biomarker research pipeline: from discovery to validation using targeted mass spectrometry workflows
- 16.05-16.20 **S.J. Gadher**
Protein profiling of human follicular fluid: Quest for biomarkers of ovarian hyperstimulation syndrome
- 16.20-16.35 **M. Scigelova**
Advanced techniques for characterizing post-translational modifications on peptides and proteins using electron transfer dissociation
- 16.35-16.50 **S. Garbis**
Biomarker discovery in low-grade breast cancer tissue biopsies using a novel quantitative proteomic approach

- 16.50-17.00 **M. Aivaliotis**
Urine proteome analysis by two-dimensional gel-based protein separation coupled with nLC-ESI-MS/MS
- 17.00-17.10 **A. Anagnostopoulos**
Proteomic analysis of amniotic fluid in pregnancies with Klinefelter syndrome fetuses
- 17.10-17.30 **Coffee Break** **Poster viewing**

Scientific Session: Biomarker Validation
(Chairs: H. Voschol, E. Baumann)

- 17.30-17.50 **H. Mischak**
Mandatory requirements in biomarker identification
- 17.50-18.10 **J. Koehn**
FDA-requirements for biomarker validation
- 18.10-19.30 **Point- Counterpoint –Challenging the Expert Session:
Peptide/protein Quantification**
Righetti (ProteoMiner)
Rabilloud (2DE staining techniques)
Mischak (peptide profiling)
Domon(SRM)

Wednesday April 1, 2009

Scientific Session (Chairs: A. Charonis and H. Kovarova)

- 9.00-9.10 **T. Economou**
ProFI: The new proteomics facility at IMBB
- 9.10-9.20 **E. Balfoussia**
Proteomic analysis of a superathletes' plasma in a model of severe stress reveal as yet unknown mediator changes
- 9.20-9.30 **E. Fasoli**
Searching for allergens in maize cytoplasmic proteins: A proteomic study
- 9.30-9.40 **A. Farinazzo**
Exploring the chicken egg white and yolk proteomes with combinatorial peptide ligand libraries
- 9.40-9.50 **J. Zoidakis**
Development of a strategy for the analysis of metal-binding proteins in urine

- 9.50-10.00 **D. Glotsos**
Proteomic MS-spectra decomposition into intensity-regions for identifying potential biomarkers and improving discrimination accuracy between normal and cancerous spectra
- 10.00-10.10 **E. Giannopoulou**
An interactive tool for visualizing jointly properties of proteomic objects
- 10.10-10.20 **P. Tsakanikas**
An efficient 2-DE gel image analysis pipeline: Combining contourlets and active contours for reliable spot segmentation and quantification
- 10.20-10.45 General discussion
- 10.45-11.30 **Educational session**
H. Voschol
Tips and Tricks and Reproducibility of 2D PAGE
- 11.30-12.30 ***Light Lunch***

End of meeting

Sponsors

Bio-Rad Laboratories S.r.l, Life Science Group, Milano, Italy

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