

Joint BSPR/EBI Conference 2011
From the Visible to the Hidden Proteome
Wellcome Trust Conference Centre, Cambridge UK, 12th – 14th July 2011

Programme

Tuesday 12th July 2011

08:30-10:00 Registration / Poster Setup / Coffee

10:00-10:15 Welcome on behalf of BSPR (David O'Connor, President, BSPR)
Welcome on behalf of EBI (Henning Hermjakob, EMBL-EBI)

Keynote Lecture 1
Chaired by David O'Connor

10:15-11:00 Mike Taussig, Babraham Institute, Cambridge
Affinity Reagents and Protein Arrays for Proteome Analysis

11:00-11:30 Tea / Trade Exhibition

Session 1: The Dynamic Proteome
Chaired by David O'Connor

11:30-12:00 Anthony Whetton, University of Manchester, Manchester
A proteomic approach to study the biology of normal and leukaemic stem cells

12:00-12:15 Amy Claydon, University of Liverpool, Liverpool*
Proteome dynamics in ejaculate composition

12:15-12:30 Cliff Rowe, University of Manchester, Manchester
Defining and quantifying the proteomes of in vitro liver models

12:30-14:30 Buffet Lunch / Trade Exhibition

Poster Session I

12:30-14:30 Authors of even-numbered posters in attendance
Poster judges: Peter Jungblut, Stephen Pennington, Paola Picotti, Robert Tonge, Anthony Whetton

BSPR AGM

13.30-14:00 BSPR Annual General Meeting

Session 2: Quantitative proteomics: To label or not to label

Chaired by Rob Beynon

- 14:30-15:00 Paola Picotti, ETH, Zürich, Switzerland
Targeted proteomics from proteins to proteome maps: potential and bottlenecks
- 15:00-15:30 Claus Jorgensen, Institute of Cancer Research, London
Quantitative analysis of cell-specific signaling from co-cultured cells
- 15:30-15:45 Richard Kay, Quotient Bioresearch Ltd, Fordham
Challenges of validating LC-MS/MS methods for quantifying proteins in biological matrices
- 15:45-16:00 Simon Hubbard, University of Manchester, Manchester
Comparing quantitative proteomics approaches for yeast chaperones
- 16:00-16:30 Tea / Trade Exhibition

Session 3: The Deep Proteome: Discovery and Quantification

Chaired by Chris Sutton

- 16:30-17:00 Jesús Vázquez, CBMSO, Madrid, Spain
A general statistical framework for the analysis and integration of quantitative proteomics data obtained by stable isotope labeling
- 17:00-17:30 Eric Schirmer, Wellcome Trust Centre for Cell Biology, Edinburgh
Extensive Tissue Variation in the Nuclear Envelope Proteome
- 17:30-17:45 Sara Zanivan, Beatson Institute for Cancer Research, Glasgow
In vivo SILAC-based quantitative proteomics and phosphoproteomics of skin cancer development
- 17:45-18:00 Ritesh Krishna, University of Liverpool, Liverpool
Automated integration of Mass Spectrometry based Proteomics evidence for improvement of gene annotations

Plenary Lecture

Chaired by Steve Pennington

- 18:00-18:45 Tim Hunt, CRUK, London
Switches and Latches in the Control of Cell Division
- 18:45-20:15 Drinks Reception / Trade Exhibition
(Sponsored by BSPR)
- 20:15 Dinner (Residential delegates only)

Wednesday 13th July 2011

Keynote Lecture 2
Chaired by John Timms

09:00-09:45 Tommy Nilsson, McGill University Health Centre, Montreal, Canada
TBA

Session 4: Tackling the Serum/Plasma Proteome
Chaired by John Timms

09:45-10:15 Gil Omenn, University of Michigan, USA
Tackling the serum/plasma proteome: The human plasma peptide atlas and the relationship to the HUPO Human Proteome Project

10:15-10:30 Martin Soste, ETH, Zürich, Switzerland
A mass spectrometric map of cancer-associated proteins and its applications to human plasma and urine

10:30-10:45 Stephane Camuzeaux, UCL, London*
Biliary tract cancer serum profiling using magnetic bead-based peptide extraction and MALDI-TOF mass spectrometry

10:45-11:30 Coffee / Trade Exhibition

Session 5: Plant, Fungal and Microbial Proteomics
Chaired by Kathryn Lilley

11:30-12:00 Peter Jungblut, MPI for Infection Biology, Berlin, Germany
The Protein species concept: Consequences for peptide and protein-centric investigations

12:00-12:30 Laurence Bindschedler, University of Reading, Reading
Delving into the *in planta* proteome of the barley powdery mildew reveals novel key players in infection

12:30-12:45 Myriam Ferro, CEA, Grenoble, France
AT_CHLORO, a comprehensive chloroplast proteome database with subplastidial localization

12:45-13:00 Annemarie Matthes, MPI of Molecular Plant Physiology, Potsdam-Golm, Germany*
SIPSEC nucleoproteomics: a method for the contamination-free identification of DNA-associated proteomes in plants

13:00-14:30 Buffet Lunch / Trade Exhibition

Poster Session II

13:00-14:30 Authors of odd-numbered posters in attendance

Poster judges: Peter Jungblut, Stephen Pennington, Paola Picotti, Robert Tonge, Anthony Whetton

Session 6: Advances in Bioinformatics
Chaired by Rolf Apweiler

- 14:30-15:00 Jürgen Cox, MPI for Biochemistry, Martinsried, Germany
TBA
- 15:00-15:30 Christian von Mering, University of Zürich, Switzerland
Optimality and evolution of protein abundance levels in eukaryotes
- 15:30-15:45 Maria Martin, EBI, Cambridge
UniProt complete proteomes for IPI species: a reference database for proteomics
- 15:45-16:00 Rui Wang, EBI, Cambridge
PRIDE Inspector: a tool to visualize and validate MS proteomics data
- 16:00-16:15 Rafael Jimenez, EBI, Cambridge
Clustering and scoring molecular interactions relying on community standards
- 16:15-16:30 Chenggong Zong, University of California, Los Angeles, USA
A modular spectral library for cardiovascular proteomics and synergy
- 16:30-17:00 Tea / Trade Exhibition

Session 7: Exploring the Post-Translational Space
Chaired by Stephen Pennington

- 17:00-17:30 Martin Larsen, University of Southern Denmark, Denmark
New selective strategies for phosphopeptide and glycopeptide enrichment applied to neuronal signaling and development
- 17:30-17:45 Vincent Geoghegan, University of Oxford, Oxford
Global analysis of arginine methylation
- 17:45-18:00 Agnieszka Kraj, Antec, Zouterwoude, The Netherlands
Protein cleavage, disulfide bonds reduction, covalent DNA adduct formation and more using electrochemistry/MS

Panel Discussion

The next steps in Proteomics – What is needed and what can be achieved?
Chaired/Moderated by David O'Connor

- 18:00-18:45 Mike Taussig, Sam Hanash, Gil Omenn, David O'Connor
- 18:45-20:15 Drinks Reception / Trade Exhibition
(Sponsored by Matrix Science)
- 20:15 Conference Dinner (By ticket only)

Thursday 14th July 2011

Keynote Lecture 3
Chaired by Rainer Cramer

08:45-09:30 Sam Hanash, Fred Hutchinson Cancer Research Center, Seattle, USA
Mouse to Human Search for Epithelial Tumor Markers

Session 8: Novel Methodologies and Techniques
Chaired by Rainer Cramer

09:30-10:00 Karl Mechtler, Institute of Molecular Pathology, Vienna, Austria
Accurate Quantification of 14,500 Arabidopsis thaliana phosphorylated peptides sites in response to DNA damage

10:00-10:15 Martin Barrios-Llerena, University of Edinburgh, Edinburgh*
The use of a novel quantitation strategy based on Reductive Isotopic Di-Ethylation (RIDE) to evaluate the Effect of Glufosinate on the unicellular algae *Ostreococcus tauri*

10:15-10:30 Claire Evers, University of Manchester, Manchester
A QconCAT Standard for Calibration of Ion Mobility Mass Spectrometry

10:30-10:45 Anthonius Heemskerk, Leiden University Medical Center, Leiden, The Netherlands
Potential of Ultra-Low Flow CE-ESI-MS for Proteomic Studies

10:45-11:00 Andrew Dowsey, Imperial College London, London
A novel isotope distribution model, integrated chemical noise estimation and sparse restoration significantly improves deconvolution of raw mass spectra

11:00-11:30 Coffee / Trade Exhibition

Session 9: Clinical Proteomics
Chaired by Steve Pennington

11:30-12:00 Kai Stühler, Medical Proteome-Center, Bochum, Germany
Tissue-proteomics - A tool for the discovery of novel biomarkers

12:00-12:30 Marius Ueffing, University of Tübingen, Germany
Structural and functional protein network analysis predicts novel systemic functions for the G-protein coupled receptor rhodopsin

12:30-12:45 Johannes Griss, EMBL/EBI, Hinxton*
Building a proteome atlas of primary human cells for clinical proteomics research

12:45-13:00 Diane Munday, University of Leeds, Leeds
Quantitative proteomic analysis and validation of human respiratory syncytial virus-host cell interactions

13:00-14:30 Buffet Lunch / Trade Exhibition

Closing Session
Chaired by David O'Connor

14:30-14:45 **Prize Awards**

Presentation of Poster Prize

(Sponsored by Royal Society of Chemistry)

Presentation of Early Stage Investigator Award

(Sponsored by CRB Discovery)

Announcement of MJ Dunn Fellows and BSPR Fellowships

(Sponsored by BSPR)

14:45-15:00 Closing remarks: David O'Connor

15:30 Buses depart to Stansted / Cambridge

Note: ** Indicates oral communications entered for the Early Stage Career Investigator Award*