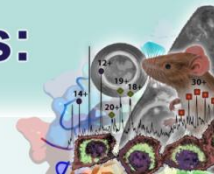




# Functional Proteomics:

*from Proteins to Organisms*

3-4 December 2013, Nottingham



## Tuesday 3 December 2013

08:00 - 09:30 Registration

09:30 - 09:45 Welcome

### Session 1: Protein structure

09:45 - 10:15 Conformational changes of multi-protein complexes determined by mass spectrometry  
*Juri Rappsilber (Edinburgh)*

10:15 - 10:30 ProteomeXchange data curation and delivery via PRIDE  
*Attila Csordas (Hinxton)*

10:30 - 11:00 A mass spectrometry based framework to determine protein structure  
*Perdita Barran (Manchester)*

11:00 - 11:30 **Coffee, Posters and Trade Exhibition**

### Session 2: Vendors

11:30 - 11:45 Data-independent acquisition (DIA) analysis on the Q Exactive mass spectrometer  
*Madalina Oppermann (Thermo Fisher Scientific)*

11:45 - 12:00 Pushing the limits of protein research with SWATH™ acquisition  
*Tom Knapman (AB Sciex)*

12:00 - 12:15 Automating disulphide bond reduction for characterisation of biopharmaceuticals – a simple approach that can be coupled to MS, for enhanced sequence coverage and improved HDX experiments  
*Simon Lambert (ARC Sciences Ltd)*

12:15 - 12:30 Heat stabilization retains phosphorylation states by permanent enzyme inactivation  
*Beatrice Orback (Denator)*

12:30 - 12:45 The Simple Western: a fully automated tool for protein characterisation, quantification and cell signalling analysis  
*Neil Vincent (ProteinSimple)*

12:45 **Lunch, Posters and Trade Exhibition**

13:45 **BSPR Annual General Meeting**

14:00 - 15:45 **Dedicated Poster Session and Trade Exhibition with Coffee**

15:45 - 16:30 **Early Career Investigator Presentations**

Sensitive and robust differential analysis of label-free LC-MS by direct statistical analysis of the raw data  
*Hanqing Liao (Manchester)*

Quantitative phosphoproteomics unveils temporal dynamics of thrombin signaling in endothelial cells  
*Maartje van den Biggelaar (Amsterdam)*

Proteomics of a fuzzy organelle: interphase chromatin  
*Georg Kustatscher (Edinburgh)*

**Session 3: Post-translational modifications**

- 16:30 - 17:00 Struggling towards a comprehensive characterization of phosphoproteomes  
*Shabaz Mohammed (Oxford)*
- 17:00 – 17:15 Quantitative mass spectrometric analysis reveals the target acetylome of epigenetic inhibitor UVI5008  
*Vikram Sharma (Plymouth)*
- 17:15 - 17:30 Dissection of specificity in protein deubiquitination by novel activity-based probes  
*Holger Kramer (Oxford)*
- 17:30 - 18:00 Mechanisms of signalling plasticity and heterogeneity that contribute to cancer drug resistance  
*Pedro Cutillas (London)*
- 18:00 **Wine Reception (sponsored by Matrix Science UK), Posters and Trade Exhibition followed by Conference Buffet Dinner and networking in Conference venue bar (open until 23:30)**

**Wednesday 4 December 2013**

08:00 - 09:00 Registration

**Session 4: Protein function in tissues and organisms**

- 09:00 - 09:30 Mass spectrometry tissue imaging and profiling: finding the right roles within pharmaceutical R&D  
*Richard Goodwin (Manchester)*
- 09:30 - 09:45 Cardiac proteomic profiling identifies novel plasma membrane proteins that regulate cardiac function  
*Parveen Sharma (Toronto)*
- 09:45 - 10:00 PROTEOSUITE – an open source framework for the analysis of quantitative proteomics based around psi standards  
*Faviel Gonzalez (Liverpool)*
- 10:00 - 10:30 Direct mass spectrometric profiling of biological tissues - from histological sections to endoscopy  
*Zoltan Takats (London)*
- 10:30 - 11:00 **Coffee, Posters and Trade Exhibition**

**Session 5: Protein function in time and space (1)**

- 11:00 - 11:30 Labeling and enrichment strategies for the analysis of protein synthesis and secretion  
*Jeroen Krijgsveld (Heidelberg)*
- 11:30 - 11:45 Cell-specific proteomic analysis of contact-initiated tumourendothelial signalling identifies novel regulators of transendothelial migration  
*Marie Locard-Paulet (London)*
- 11:45 - 12:30 **Keynote Lecture:** Identifying sites where post-translational modifications regulate the interactome from proteomics and structural data  
*Rob Russell (Heidelberg)*
- 12:30 - 12:45 **Awards**
- 12:45 - 13:45 **Lunch, Posters and Trade Exhibition**

**Session 6: Protein function in time and space (2)**

13:45 - 14:15 Quantitative analysis of protein complexes over space and time  
*Marius Ueffing (Tubingen)*

14:15 - 14:45 Quantitative interaction proteomics for epigenetics  
*Michiel Vermeulen (Utrecht)*

14:45 - 15:00 Proteomics informed by transcriptomics: techniques, tools and results  
*Conrad Bessant (London)*

15:00 - 15:30 Challenges in the analysis of dynamic signaling complexes  
*Matthias Gstaiger (Zurich)*

15:30 - 16:00 **Close of Meeting**