PMF2020– 17th Proteomics Methods Forum

Hosted by MRC-Laboratory of Molecular Biology, Cambridge

PROGRAMME

Tuesday 15th September

13:00-13:05 Welcome

Session Chair – Clive D'Santos (CRUK)

13:05-13:25Technology I

Advantages of Implementing the Select Series Cyclic IMS for HDX MS Analysis

Malcolm Anderson (Waters UK)

µPillar Array Columns - Reproducibility and Robustness in nanoLC/MS and Beyond

Robert van Ling (Pharmafluidics)

13:25-14:10 Complementary approaches

Predicting PROTAC efficacy with native mass spectrometry

Rebecca Beveridge (University of Strathclyde, Glasgow)

Mass Spectrometry of oligonucleotides

Frank Sobott (University of Leeds/Astbury Centre for Structural Molecular Biology)

Peptidomics: bridging the space between large and small molecule mass spectrometry

Richard Kay (Cambridge University)

Discussion

14:15   Break

Session Chair – Kathryn Lilley (University of Cambridge)

14:30-1450   Technology II

ASMS 2020 unveiled : taking 4D-Proteomics™ to the next level

Daniel Tome (Bruker)

Protein Sample Prep at your pace: from individual tube up to 384 well plate, from tissue (fresh or fixed) down to single cell, single pot and robot friendly.

Nicolas Autret (Covaris)

Consumables update
Erik Verschuuren (MSWil)

14:50-15:45 Sub-Proteomes

Identifying proteins bound to native mitotic ESC chromosomes reveals chromatin repressors are important for compaction

Holger Kramer (MRC-London Institute of Medical Sciences)

Laser capture microdissection coupled mass spectrometry for fixed and stained tissues

Jeremy Herrara (University of Manchester)

SMALPs to isolate membrane complexes

Benedict Dirnberger (Cambridge University)

 Discussion

15:45   **Break**

16:00   **Plenary**

SARS-Cov2 RNA interacts with the host proteome

Alfredo Castello Palmores (Oxford University/MRC Centre for Virus Research

17:15-19:00Virtual Pub Night !

Wednesday 16th September

Session Chair-Ian Fearnley (MRC-Mitochondrial Biology Unit))

13:00-13:20Technology III

Going Quantitative: an update on quantitative strategies

Jenny Ho (ThermoScientific)

MALDI - get ready for the Digital Age

Tony Sullivan (Shimadzu)

13:20-14:20Protein modifications

Phosphopeptide enrichment: Insights on method selection (tips from the other side of the equator)

Stoyan Stoychev (Resyn Biosciences/CSIR)

Peptide location finger printing

Alex Eckersley (University of Manchester)

A refined targeted proteomic assay for absolute quantification of ubiquitin chain types

Tiaan Heunis (Newcastle University)

Discussion

14:20   **Break**

Session Chair-Robin Antrobus (Cambridge Institute for Medical Research)

14:30-14:50Technology IV

What's new from Sciex?

Nick Morrice (Sciex)

Exporting protein expression data for complex experiments using the Mascot Daemon Quantitation Summary.

Patrick Emery (Matrix Science)

14:50-15:35Quantitative Proteomics

Covid-19 or General blood proteomics TBC

Roman Fischer (Oxford University)

SWATH and it's application

Christoph Messner (The Francis Crick Institute)

15:35Discussion meeting roundup next steps David Knight

16:10Close Meeting