DAILY PROGRAMME

Concurrent themes for Oral Presentations and Posters

Cellular Proteomics	**Disease & Clinical Proteomics**
Drug & Biopharmaceutical Proteomics	**Precision & Personalised Proteomics**
Methods, Systems & Bioinformatics	**Human Proteome Project**

Plenaries

All plenary speakers have been given one of the codes below followed by -01, -02 or -03 depending on the timeslot on the day they are speaking:

SP – Sunday Plenary
MP – Monday Plenary
TP – Tuesday Plenary
WP – Wednesday Plenary

Oral Sessions

All oral sessions have been given one code below. The first letter is the day of the week, the second letter is the theme letter, the number relates to whether the session take place in the morning (1) or afternoon (2):

Day:

M = Monday   T = Tuesday   W = Wednesday

Theme:

A = Cellular Proteomics   B = Drug & Pharmaceutical Proteomics
C =Methods, Systems & Bioinformatics   D = Disease & Clinical Proteomics
E = Precision & Personlised Proteomics   F = Human Proteome Project

Time:

1 = AM   2 = PM

Presentations have a secondary code related to the presentation type and position within the session:

K = Keynote Speaker
I = Invited Speaker
S = Short Oral

DAILY PROGRAMME

Sunday 17th September

15:45 – 17:45   **Liffey Hall 2**
HUPO Council Meeting

18:00 – 18:30   **Auditorium**
Opening Ceremony

OPENING PLENARY

18:30 – 20:00   **Auditorium**

SP-01
Systems medicine, big data and scientific wellness: transforming healthcare—a personal view
Leroy Hood, Institute for Systems Biology (ISB), USA

20:00 - 22:00   **The Forum**
Welcome Reception & Exhibition opens

Monday 18th September

07:45 – 08:15   **The Forum**
Meet the Experts Breakfast Session   **Bioinformatics Hub**
(Pre-registration required for this session)

Chair: Andrew Pitt, Aston University, UK
YPIC Co-Chair: Christine von Törne - Helmholtz Zentrum Munich GmbH, Germany

PLENARY SESSION

08:30 – 10:00   **Liffey B**
Chair: Steve Pennington, University College Dublin, Ireland

08:30 – 09:10   **MP-01**
Sugars and proteins: towards a synthetic biology
Ben Davis, University of Oxford, UK

MONDAY

09:10 – 09:50　　　　　　　　　　　**MP-02**

Deciphering the glycoproteome: a small step towards understanding the complexity of biological systems

Pauline Rudd, NIBRT, Ireland

09:50 – 10:00

Questions and Discussion

10:00 – 11:00　　　　　　　　　　　**The Forum**

Tea / Coffee Break Exhibition, Networking, Innovation Presentations and Poster Viewing

CELLULAR PROTEOMICS
MA1: CELLULAR DYNAMICS

11:00 – 12:30　　　　　　　　　　　**Liffey A**

Chair: Matthias Mann, Max-Planck Institute of Biochemistry, Germany

11:00 – 11:30　　　　　　　　　　　**MA1-01K**

Remodelling of proteome expression and turnover during cell transformation

Angus Lamond, University of Dundee, Scotland

11:30 – 11:50　　　　　　　　　　　**MA1-02I**

Proteomic exploration of the scope, dynamics, and stoichiometry of lysine acetylation

Chuna Choudary, University of Copenhagen, Denmark

11:50 – 12:00　　　　　　　　　　　**MA1-03S**

A pulsed SILAC-TMT multiplexing approach reveals protein synthesis and degradation differences on proteoform level

Jana Zecha, Technical University of Munich, Germany

12:00 – 12:10　　　　　　　　　　　**MA1-04S**

Proteomic analysis reveals strong secretion of IL-9 by group2 innate lymphoid cells upon IL-33/TL1A co-stimulation

Anne Gonzalez de Peredo, CNRS/IPBS, France

12:10 – 12:20　　　　　　　　　　　**MA1-05S**

Proteomic analysis of T cell activation-dependent changes in NF90 and bound histones

Timothy Wu, Stanford University, USA

12:20 – 12:30 **MA1-06S**

Role of adipocyte plasma membrane proteome in adipocyte differentiation and adipose function

Carmen Arasti, The University of Liverpool, UK

DRUG & BIOPHARMACEUTICAL PROTEOMICS
MB1: NEW METHODS FOR DRUG DISCOVERY

11:00 – 12:30 **Liffey B**

Chair: Rainer Cramer, University of Reading, UK

11:00 – 11:30 **MB1-01K**

Cell free methods for producing protein microarrays

Joshua LaBaer, Virginia G. Piper Center for Personalized Diagnostics, USA

11:30 – 11:50 **MB1-02I**

Instrumentation and methods for the identification and sequence analysis of intact proteins on a chromatographic timescale

Don Hunt, University of Virginia, USA

11:50 – 12:00 **MB1-03S**

New proteomics capabilities using super slim high resolution ion mobility-mass spectrometry

Richard Smith, Pacific Northwest National Laboratory, USA

12:00 – 12:10 **MB1-04S**

MAPPs (MHC-II associated peptides proteomics): an in-vitro, pre-clinical tool to compare candidate compounds' immunogenic liabilities

Axel Ducret, F. Hoffmann-la Roche Ltd, Switzerland

12:10 – 12:20 **MB1-05S**

Oncogenic protein network reconstruction using multi-omics Identifies the ELF3 tumor suppressor as a Wnt Antagonist

Rob Ewing, University of Southampton, UK

12:20 – 12:30 **MB1-06S**

Novel chemoproteomic characterization of covalent probe binding

Jarrod Marto, Dana-Farber Cancer Institute, USA

METHODS, SYSTEMS & BIOINFORMATICS
MC1: PROTEOMIC STRATEGIES

11:00 – 12:30   **Liffey Hall 1**
Chair: Christoph Borchers, University of Victoria, Canada

11:00 – 11:30   **MC1-01K**
Improved sensitivity and specificity of proximity-dependent biotinylation approaches for interactomics
Akilesh Pandey, Johns Hopkins University School of Medicine, USA

11:30 – 11:50   **MC1-02I**
Quantitative interaction proteomics: Insights into biological systems
Ben Collins, ETH Zurich, Switzerland

11:50 – 12:00   **MC1-03S**
Two-dimensional thermal proteome profiling in living cells, cell extracts and beyond
Thilo Werner, Cellzome GmbH a GSK Company, Germany

12:00 – 12:10   **MC1-04S**
Multi-omics approach to discover hidden coding regions in so-called non-coding RNA
Gerben Menschaert, Ghent University, Belgium

12:10 – 12:20   **MC1-05S**
Refining human proteome: integrated analysis of human tissues with a multi-omics approach
Dongxue Wang, Technical University of Munich, Germany

12:20 – 12:30   **MC1-06S**
Absolute venomics: absolute quantification of intact venom proteins through elemental mass spectrometry
Juan Calvete, CSIC, Spain

DISEASE & CLINICAL PROTEOMICS
MD1: CLINICAL PROTEOMICS

11:00 – 12:30   **Liffey Hall 2**
Chair: Tami Geiger, Tel Aviv University, Israel

11:00 – 11:30   **MD1-01K**
Clinical proteomics: my adventures in wonderland
Daniel Chan, Johns Hopkins University, USA

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11:30 – 11:50   **MD1-02I**

A glimpse of CNHPP: a proteomic landscape of diffuse-type gastric cancer

Jun Qin, National Center for Protein Sciences, China

11:50 – 12:00   **MD1-03S**

A clinical proteomics success story: from proteomics-based biomarker discovery to clinically actionable test

Bruce Wilcox, Applied Proteomics, USA

12:00 – 12:10   **MD1-04S**

Phosphoproteome networks identify focal adhesion kinase as new target in pancreatic ductal adenocarcinoma

Tessa Le Large, VU University Medical Center, Netherlands

12:10 – 12:20   **MD1-05S**

A two-step PRM strategy reveals a new biomarker signature of multiple sclerosis in cerebrospinal fluid

Philippe Marin, Institute of Functional Genomics, France

12:20 – 12:30   **MD1-06S**

Platelet proteomics: towards non-invasive cancer detection

Connie Jimenez, VU University Medical Center, Netherlands

PRECISION & PERSONALISED PROTEOMICS
ME1: PROTEOMICS OF SURVEILLANCE

11:00 – 12:30   **Liffey Meeting Room 2**

Chair: Albert Heck, Utrecht University, Netherlands

11:00 – 11:30   **ME1-01K**

Proteomics as diagnostic tool for platelet function

Albert Sickmann, ISAS, Germany

11:30 – 11:50   **ME1-02I**

Proteomics and immunoproteomics of gram-positive bacteria in host-pathogen interactions

Frank Schmidt, University Medicine Greifswald, Germany

11:50 – 12:00   **ME1-03S**

Discovery of inflammatory signaling adaptors regulated by autophagy

Erik Verschueren, Genentech, USA

12:00 – 12:10   **ME1-04S**

Systems biology of MHC class I antigen presentation studied in human cancer cell lines
Stefan Tenzer, Universitätsmedizin Mainz, Germany

12:10 – 12:20   **ME1-05S**

Insidious or ingenious: complexities of antigen presentation
Anthony Purcell, Monash, Australia

12:20 – 12:30   **ME1-06S**

MHC peptidomics provides a new outlook on its production & presentation pipeline
Arie Admon, Israel Institue of Technology, Israel

HUMAN PROTEOME PROJECT
MF1: LIVER & TOXICOPROTEOMICS

11:00 – 12:30   **Liffey Meeting Room 3**
Chair: Oliver Poetz, NMI, Germany

11:00 – 11:30   **MF1-01K**

Proteomics for study of liver diseases
Barbara Sitek, Ruhr University Bochum, Germany

11:30 – 11:50   **MF1-02I**

Variability in mass spectrometry-based quantification of clinically relevant drug transporters and drug metabolizing enzymes in the human liver
Per Artursson, Uppsala University, Sweden

11:50 – 12:00   **MF1-03S**

Serum extracellular vesicles contain protein biomarkers for primary sclerosing cholangitis and cholangiocarcinoma
Felix Elortza, CIC bioGUNE, Spain

12:00 – 12:10   **MF1-04S**

Prioritizing popular proteins in liver cancer. Remodelling of one carbon metabolism
Fernando Corrales, Centro Nacional de Biotecnologia (CSIC), Spain

12:10 – 12:20   **MF1-05S**

Targeted and panoramic views on the transcriptome and proteome of liver tissue and HepG2 cells
Elena Ponomarenko, Institute of Biomedical Chemistry, Moscow, Russia

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12:20 – 12:30   **MF1-06S**

Next-generation blood biomarkers for acute liver injury: in silico discovery and proteomics evaluation

Virginie Brun, The French Alternative Energies and Atomic Energy Commission (CEA) - "Exploring the Dynamics of Proteomes" Team, France

12:45 - 13:45   **(see below symposia for room allocations)**
Sponsored Symposia

Methods and instrumentation for a quantum leap in proteomics performance
Liffey A
Oliver Räther, Bruker Daltonik GmbH, R&D Manager, Germany
Prof. Matthias Mann, Max Planck Institute of Biochemistry, Germany

Biomarkers in ovarian cancer from SWATH maps of clinical samples
Liffey B
Robert Graham Ph.D., Sr Lecturer in Clinical Proteomics, Deputy Director Stoller Biomarker Discovery Centre, University of Manchester, UK

Applying waters DIA workflows in disease research
Liffey Hall 1
David Heywood, Senior Manager Omics Business Development
Prof. Daniel Martins-de-Souza, PhD, Institute of Biology, University of Campinas (UNICAMP), Brazil

Improved workflows for structural proteomics: studying protein interactions
Liffey Hall 2
Christoph Borchers, Ph.D., Director, UVic-Genome BC Proteomics Centre, Canada
Richard Scheltema, Ph.D., Junior Assistant Professor, Utrecht University, Netherlands

Introduction to CRISPR-Cas9 genome engineering and its potential application in proteomic research
Liffey Meeting Room 2
Laura Carleton, PhD

CELLULAR PROTEOMICS
MA2: CELLULAR PROTEOMICS IN HEALTH & DISEASE

14:00 – 15:30   **Liffey A**
Chair: Angus Lamond, University of Dundee, UK

14:00 – 14:30   **MA2-01K**
Studying protein structural changes on a proteome-wide scale in health and disease
Paola Picotti, University of Padua, Italy

14:30 – 14:50   **MA2-02I**
Microvesicle-based identification of cancer biomarkers for early detection of ovarian cancer
Tami Geiger, Tel Aviv University, Israel

14:50 – 15:00   **MA2-03S**
Identification of a novel translation machinery regulating NF1-associated tumors by affinity purification and SWATH (AP-SWATH)
Daiki Kobayashi, Kumamoto University, Japan

15:00 – 15:10   **MA2-04S**
Proteomic analysis of signaling specificity in breast cancer cells
Chiara Francavilla, The University of Manchester, UK

15:10 – 15:20   **MA2-05S**
Large-scale proteomic analysis of SIRT1- and tissue-dependent acetylproteome in mouse liver, testis and muscle
Marie Locard-Paulet, CNRS-IPBS, France

15:20 – 15:30   **MA2-06S**
Differential proteome and secretome analyses of iPS-derived neural differentiation to unravel schizophrenia features
Juliana Nascimento, University of Campinas, Brazil

DRUG & BIOPHARMACEUTICAL PROTEOMICS
MB2: NEW TECHNOLOGICAL ADVANCES

14:00 – 15:30   **Liffey B**
Chair: Aran Paulus, Thermo Scientific, USA

14:00 – 14:30   **MB2-01K**

Pulse Azidohomoalanine (AHA) labeling in mammals (PALM) analysis for global analysis of newly-synthesized proteins in animal models of disease

John Yates, The Scripps Research Institute, USA

14:30 – 14:50   **MB2-02I**

Comprehensive glycopeptide profiling in blood plasma for clinical applications

Hans Wessels, Radboud University Nijmegen Medical Centre, Netherlands

14:50 – 15:00   **MB2-03S**

Scanning the precursor range with OpenECHO: adding precursor specificity back to DIA analysis

Hannes Rost, Stanford University, USA

15:00 – 15:10   **MB2-04S**

Mass-spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation

Nikolai Slavov, Northeastern University, USA

15:10 – 15:20   **MB2-05S**

The SOMAscan® assay and SOMAmer® reagents: characterization and utility of novel biomarker discovery tools

Sheri Wilcox, Somalogic, Inc., USA

15:20 – 15:30   **MB2-06S**

Multiplexed activity profiling of cellular signaling pathways by data-dependent and targeted LCMS

Kimberly Lee, Cell Signaling Technology, Inc., USA

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METHODS, SYSTEMS & BIOINFORMATICS
MC2: LONGITUDINAL PROTEOMICS

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14:00 – 15:30   **Liffey Hall 1**

Chair: Andrew Pitt, Aston University, UK

14:00 – 14:30   **MC2-01K**

Quantitative proteomics in a wellness and disease setting

Rob Moritz, Institute for Systems Biology (ISB), USA

14:30 – 14:50   **MC2-02I**

Medical and biological insights derived from SOMAscan

Larry Gold, Somalogic, Inc., USA

14:50 – 15:00   **MC2-03S**

Profound aging-related changes of histone H3 tails in mouse tissues

Veit Schwämmle, University of Southern Denmark, Denmark

15:00 – 15:10   **MC2-04S**

Integrative omics profiling within the Swedish SCAPIS SciLifeLab (S3) wellness profiling program

Linn Fagerberg, Royal Institute of Technology, Sweden

15:10 – 15:20   **MC2-05S**

Identification of a damaging variant associated with idiopathic male infertility through degradation of TEX101 interactome

Andrei P. Drabovich, University of Toronto, Canada

15:20 – 15:30   **MC2-06S**

Longitudinal and network-based biomarker models for the prediction of ovarian cancer

Harry Whitwell, UCL, UK

DISEASE & CLINICAL PROTEOMICS
MD2: CANCER MOONSHOT

14:00 – 15:30   **Liffey Hall 2**

Chair: Henry Rodriguez, National Cancer Institute, USA

14:00 – 14:30   **MD2-01K**

Prospective from Taiwan cancer moonshot to address unmet clinical needs

Yu-Ju Chen, Institute of Chemistry, Academia Sinica, Taiwan

14:30 – 14:50   **MD2-02I**

Proteogenomic analysis of diffuse gastric cancers

Daehee Hwang, Daegu Gyeongbuk Institute of Science and Technology, South Korea

14:50 – 15:00   **MD2-03S**

Enhancing protein information by integrating genomics and proteomics in UniProt reference sets

Emanuel Alpi, EMBL-European Bioinformatics Institute, UK

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15:00 – 15:10   **MD2-04S**

Proteogenomic analysis of alternative splicing: protein isoforms as biomarkers for early detection of colorectal cancer

Malgorzata Komor, Netherlands Cancer Institute, Netherlands

15:10 – 15:20   **MD2-05S**

Integrated proteo-glyco-genomics identified the potential clinical target of cancer stem cells

Norie Araki, Kumamoto University, Japan

15:20 – 15:30   **MD2-06S**

Brain metastatic cancer cells mimicking neurons: a proteotranscriptomic analysis

Hubert Hondermarck, University of Newcastle, UK

PRECISION & PERSONALISED PROTEOMICS
ME2: BIOPSIES AND BODYFLUIDS

14:00 – 15:30   **Liffey Meeting Room 2**

Chair: Chris Sutton, University of Bradford, UK

14:00 – 14:30   **ME2-01K**

Towards a blood-based diagnostic biomarker panel for bipolar disorder

Sabine Bahn, University of Cambridge, UK

14:30 – 14:50   **ME2-02I**

Development of liquid-biopsies for personalized care in prostate cancer

John Semmes, Eastern Virginia Medical School, USA

14:50 – 15:00   **ME2-03S**

Plasma proteome profiling disentangles caloric restriction and bariatric surgery induced weight loss

Philipp Geyer, Max Planck Institute of Biochemistry, Germany

15:00 – 15:10   **ME2-04S**

Evaluation of plasma extracellular vesicles isolation protocols for proteome analysis

Keiko Kasahara, National Institutes of Biomedical Innovation, Health and Nutrition, Japan

15:10 – 15:20   **ME2-05S**

Accessing archival, formalin-fixed, paraffin-embedded tissue sample resources for proteomic analysis via PCT-SWATH

Tiannan Guo, Westlake Institute for Advanced Study, China

15:20 – 15:30   **ME2-06S**

High throughput, single shot plasma proteome profiling on a robust capillary flow setup of 1564 DiOGenes samples

Roland Bruderer, Biognosys AG, Switzerland

HUMAN PROTEOME PROJECT
MF2: DIABETES AND CARDIOVASCULAR

sponsored by

14:00 – 15:30   **Liffey Meeting Room 3**
Chair: Jennifer Van Eyk, Cedars Sinai Medical Center, USA

14:00 – 14:30   **MF2-01K**

Pattern of MAP kinase phosphatase, DUSP1, in human obesity, diabetes and cardiovascular diseases

Ali Tiss, Dasman Diabetes Institute, Kuwait

14:30 – 14:50   **MF2-02I**

The surfaceome of human cells: a sweet source of novel immunophentotyping and immunotherapy targets

Rebekah Gundry, Medical College of Wisconsin, USA

14:50 – 15:00   **MF2-03S**

Prognostic role of molecular forms of B-type natriuretic peptide in cardiovascular disease

Muhammad Zubair Israr, University of Leicester, UK

15:00 – 15:10   **MF2-04S**

MASP1, THBS1, GPLD1 and ApoA-IV are novel biomarkers associated with prediabetes: the KORA F4 study

Christine Von Toerne, Helmholtz Zentrum Munich GmbH, Germany

15:10 – 15:20   **MF2-05S**

Validation of novel plasma markers for venous thromboembolism using affinity proteomics combined with mass spectrometry

Laura Sanchez-Rivera, Science For Life Laboratory-Stockholm, Sweden

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15:20 – 15:30   **MF2-06S**

Proteomics of activated macrophages identifies novel innate immune signalling pathway promoting phenotypic switch in obesity

Matthias Trost, Newcastle University, UK

15:30 – 16:30   **The Forum**

**Tea / Coffee Break Exhibition, Networking,
Innovation Presentations and Poster Viewing**

PLENARY SESSION

16:30 – 17:30   **Liffey B**

Chair: Susan Weintraub, UT Health San Antonio, USA

16:30 – 17:10   **MP-03**

Probing biopharmaceutical proteins and protein assemblies by hybrid mass spectrometry approaches

Albert Heck, Utrecht University, The Netherlands

17:10 – 17:30

Questions and Discussion

17:30 – 18:30   **The Forum**

**Poster Reception
PhD Abstract Competition (Innovation Stage)**

Tuesday 19th September

07:45 – 08:15   **The Forum**

Meet the Experts Breakfast Session   **Bioinformatics Hub**

(Pre-registration required for this session)

Chair: Steve Pennington, University College Dublin, Ireland

YPIC Co-Chair: Dina Resetar - University of Rijeka, Croatia

PLENARY SESSION

08:30 – 10:00   **Liffey B**

Chair: Mark Baker, Macquarie University, Australia

TUESDAY

08:30 – 09:10   **TP-01**
The proteome in context
Ruedi Aebersold, Institute of Molecular Systems Biology and University of Zurich, Germany

09:10 – 09:50   **TP-02**
The human protein atlas - implications for human biology, drug development and precision medicine
Matthias Uhlen, Royal Institute of Technology (KTH), Sweden

09:50 – 10:00
Questions and Discussion

10:00 – 11:00   **The Forum**
Tea / Coffee Break Exhibition, Networking,
Innovation Presentations and Poster Viewing

CELLULAR PROTEOMICS
TA1: REGULATION OF SPATIAL PROTEOMES

11:00 – 12:30   **Liffey A**
Chair: Matthias Mann, Max-Planck Institute of Biochemistry, Germany

11:00 – 11:30   **TA1-01K**
What controls the three dimensional proteome?
Kathryn Lilley, University of Cambridge, UK

11:30 – 11:50   **TA1-02I**
TMT-based proteomic analysis identifies novel viral evasion pathways
Paul Lehner, University of Cambridge, UK

11:50 – 12:00   **TA1-03S**
An image-based subcellular map of the human proteome
Emma Lundberg, Science For Life Laboratory (KTH), Sweden

12:00 – 12:10   **TA1-04S**
Determining network topology, distance restraints and activation markers from endogenous protein complexes
Marco Faini, ETH Zurich, Switzerland

12:10 – 12:20   **TA1-05S**
Quantifying and localizing the mitochondrial proteome using SWATH-MS
Yibo Wu, IMS, RIKEN, Japan

12:20 – 12:30 **TA1-06S**

ImportOmics: a new method for charting organellar proteomes by quantitative mass spectrometry

Christian Peikert, Albert Ludwigs University of Freiburg, Germany

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DRUG & BIOPHARMACEUTICAL PROTEOMICS
TB1: CELL SIGNALLING AND DRUG DISCOVERY

11:00 – 12:30 **Liffey B**

Chair: Ben Collins, Institute of Molecular Systems Biology, Switzerland

11:00 – 11:30 **TB1-01K**

Chemical proteomics reveals the target space of clinical kinase inhibitors

Bernhard Kuster, Technical University of Munich, Germany

11:30 – 11:50 **TB1-02I**

Systems biology of oncogenic kinase signalling

Pedro Cutillas, Barts Cancer Institute, QMUL, UK

11:50 – 12:00 **TB1-03S**

Comparative proteomics of dying & surviving cancer cells pinpoints drug targets & reveals essential proteins

Amirata Saei Dibavar, Karolinska Institutet, Sweden

12:00 – 12:10 **TB1-04S**

Selectivity determination of 1000 small molecule kinase inhibitors using chemical proteomics

Maria Reinecke, Technical University of Munich, Germany

12:10 – 12:20 **TB1-05S**

NSCLC cells use increased cell-cell contacts to resist early TKI treatment

Celine Mulder, Utrecht University, Netherlands

12:20 – 12:30 **TB1-06S**

Glucagon was identified as potential therapy target in colorectal cancer through label-free quantitative proteomic analysis

Min Li, Binzhou Medical University, China

TUESDAY

METHODS, SYSTEMS & BIOINFORMATICS
TC1: MULTIPLEX TECHNOLOGIES

11:00 – 12:30　　　　　　　　　　　　　　**Liffey Hall 1**

Chair: Roz Jenkins, University of Liverpool, UK

11:00 – 11:30　　　　　　　　　　　　　　**TC1-01K**

Immunoassays in multiplex for biomarker discovery and validation

Thomas Joos, NMI Naturwissenschaftliches und Medizinisches Institut, Germany

11:30 – 11:50　　　　　　　　　　　　　　**TC1-02I**

Standardising MS Omics for precise and accurate qualification/quantification

Andrew Percy, Cambridge Isotope Laboratories, Inc., USA

11:50 – 12:00　　　　　　　　　　　　　　**TC1-03S**

Functional protein networks and disease: an affinity based approach

Marius Ueffing, University Of Tübingen, Germany

12:00 – 12:10　　　　　　　　　　　　　　**TC1-04S**

Using cross-linking mass spectrometry and integrated modeling to study architecture and dynamics of signaling complexes

Florian Stengel, University of Konstanz, Germany

12:10 – 12:20　　　　　　　　　　　　　　**TC1-05S**

Open-glycomics: an open-access platform for automated glycan identification and quantitation

Christopher Ashwood, Macquarie University, Australia

12:20 – 12:30　　　　　　　　　　　　　　**TC1-06S**

Omics discovery index: supporting multi-omics analysis with public data

Yasset Perez-Riverol, The European Bioinformatics Institute (EMBL-EBI), UK

DISEASE & CLINICAL PROTEOMICS
TD1: PROTEOMICS APPLIED TO DISEASE

11:00 – 12:30　　　　　　　　　　　　　　**Liffey Hall 2**

Chair: Oliver FitzGerald, St Vincents University Hospital & Conway Institute UCD, Ireland

11:00 – 11:30　　　　　　　　　　　　　　**TD1-01K**

Psoriatic arthritis through the omics lens

Vinod Chandran, University of Toronto, University Health Network, Canada

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11:30 – 11:50   **TD1-02I**

Development of a large scale integrated platform for clinical proteomics and drug target discovery

Tony Whetton, The University of Manchester, UK

11:50 – 12:00   **TD1-03S**

Proteomics of differentiated cultures of human bronchial epithelial cells exposed to spores of Aspergillus fumigatus

Scott Tebbutt, University of British Columbia, Canada

12:00 – 12:10   **TD1-04S**

Urine angiotensin II signature proteins as biomarkers of fibrosis in patients with kidney transplant

Zahraa Mohammed-ali, University Health Network, Canada

12:10 – 12:20   **TD1-05S**

Detection of psoriatic arthritis at early onset: a multi-proteomic approach to developing a blood test

Angela Mc Ardle, University College Dublin, Ireland

12:20 – 12:30   **TD1-06S**

Antigen microarrays identify autoantibodies as potential predictors of response to anti-TNFα therapies in rheumatoid arthritis

Lucia Lourido, Science for Life Laboratory, Sweden

PRECISION & PERSONALISED PROTEOMICS
TE1: CANCER DIAGNOSTICS AND PROGNOSTICS

11:00 – 12:30   **Liffey Meeting Room 2**

Chair: Robert O'Conor, Irish Cancer Society, Ireland

11:00 – 11:30   **TE1-01K**

Bridging the gap in oncology diagnostics: converting omic data into clinically relevant assays

William Gallagher, University College Dublin, Ireland

11:30 – 11:50   **TE1-02I**

Tissue and plasma proteomics allows early stage colorectal cancer detection/ stratification that improves patient outcome

Mark Baker, Macquarie University, Australia

11:50 – 12:00   **TE1-03S**

Stroma liquid biopsy - the next wave of proteomic profiles for cancer biomarkers

Matthew Kuruc, Biotech Support Group Llc, USA

12:00 – 12:10   **TE1-04S**

Refining treatment recommendations for lymph-node-negative breast-cancer patients using novel protein-based prognostic signature: the OncoMasTR assay

Arman Rahman, University College Dublin, Ireland

12:10 – 12:20   **TE1-05S**

Possible causal link between insulin signaling deregulation and its etiology of aggressive prostate cancer

Spiros Garbis, University of Southampton, UK

12:20 – 12:30   **TE1-06S**

Discovery, verification and pre-validation of novel candidate urinary biomarkers of prostate cancer

Jonathan M Blackburn, University of Cape Town, South Africa

HUMAN PROTEOME PROJECT
TF1: PLASMA & IMMUNOPEPTIDOMICS

11:00 – 12:30   **Liffey Meeting Room 3**

Chairs: Jochen Schwenk, KTH Royal Institute of Technology, Sweden & Etienne Caron, ETH Zurich, Switzerland

11:00 – 11:30   **TF1-01K**

Developmental proteomics: the importance of age specific differences in the human plasma proteome

Vera Ignjatovic, Murdoch Children's Research Institute, Australia

11:30 – 11:50   **TF1-02I**

The human immunoepeptidome project – accelerating the development of personalized cancer immunotherapy

Michal Bassani, Lausanne University Hospital, Switzerland

11:50 – 12:00   **TF1-03S**

An optimised quantitative multidimensional protein identification technology for in-depth profiling of the human plasma proteome

Diana Baquero, University of Southampton, UK

12:00 – 12:10   **TF1-04S**

A comprehensive HLA peptidomic resource used to generate immunotherapeutics based on high affinity T-cell receptors
Alex Powlesland, Immunocore Ltd, UK

12:10 – 12:20   **TF1-05S**
Novel proteomic signatures of human blood vessel maturation revealed by SWATH analysis
Michael Taggart, Newcastle University, UK

12:20 – 12:30   **TF1-06S**
Deciphering HLA motifs across in-depth and large-scale immunopeptidomics datasets correctly predicts neo-antigens
Michal Bassani-Sternberg, Lausanne University Hospital, Switzerland

12:45 - 13:45   **(see below symposia for room allocations)**
Sponsored Symposia

Decyphering the proteome complexity
Liffey A
Hans Wessels, Ph.D., Radboud University, Medical Center, Netherlands
Andrew Webb, Ph.D., Walter and Eliza Hall Institute, Australia

The future of high-throughput human plasma proteomics
Liffey B
Prof. Manuel Mayr, King's College London
Dr. Roland Bruderer, Biognosys AG, Switzerland

Robust front-end solutions for clinical proteomics
Liffey Hall 1
Matthias Mann, Max Planck Institute of Biochemistry, Germany

Proteome profiling for the cancer moonshot program: from basic research to large scale analyses
Liffey Hall 2
Aaron Gajadhar, Ph.D.: Strategic Marketing Specialist, Thermo Fisher Scientific, USA
Gyorgy Marko-Varga, Ph.D.: Associate professor, Lund University Sweden

Agilent Technologies

Metabolomics analysis for confirmation of proteomics insights
Liffey Meeting Room 2
Christine Miller: Agilent Technologies, UK
Jennifer Van Eyk: PhD, Cedars-Sinai, USA

CELLULAR PROTEOMICS
TA2: CELLULAR PHOSPHOPROTEOMICS

14:00 – 15:30   **Liffey A**
Chair: Sara Zanivan, CRUK Beatson Institute - University of Glasgow, UK

14:00 – 14:30   **TA2-01K**
Probing the insulin network using phosphoproteomics
David James, University of Sydney, Australia

14:30 – 14:50   **TA2-02I**
Dissecting phosphotyrosine signaling networks by quantitative phosphoproteomics
Jesper Olsen, University of Copenhagen, Denmark

14:50 – 15:00   **TA2-03S**
Alternative proteins: the hidden world of potential biomarkers
Julien Franck, Prism Inserm U1192, France

15:00 – 15:10   **TA2-04S**
Quantitative phospho–proteomics in the mouse liver uncovers diurnal regulatory landscapes
Antonio Nunez-Galindo, Nestlé Institute of Health Sciences (NIHS), Switzerland

15:10 – 15:20   **TA2-05S**
In-depth analyses of protein abundance, phosphorylation, synthesis and degradation during neuronal development and synaptic plasticity
Maarten Altelaar, Utrecht University, Netherlands

15:20 – 15:30   **TA2-06S**
Profiling the phosphotyrosine interactome of receptor tyrosine kinases
Runsheng Zheng, Technical University of Munich, Germany

DRUG & BIOPHARMACEUTICAL PROTEOMICS
TB2: DRUG DISCOVERY

14:00 – 15:30   **Liffey B**

Chair: Pauline Rudd, National Institute for Bioprocessing Research and Training, Ireland

14:00 – 14:30   **TB2-01K**

How proteomics impacts projects in pharma
Hanno Langen, Roche, Switzerland

14:30 – 14:50   **TB2-02I**

Drug resistance assessed by mass spectrometry based omics technologies
Simone Lemeer, Utrecht University, Netherlands

14:50 – 15:00   **TB2-03S**

Physiological relevance of in vitro models of the liver for drug safety assessment
Rosalind Jenkins, University of Liverpool, UK

15:00 – 15:10   **TB2-04S**

Quantitative characterization of hepatic cytochrome P450 and UDP-glucuronosyltransferase enzymes: evaluation against catalytic activity
Brahim Achour, University of Manchester, UK

15:10 – 15:20   **TB2-05S**

Therapeutic target discovery by cancer proteomics in the era of large-scale genome-resequencing
Tesshi Yamada, National Cancer Center Research Institute, Japan

15:20 – 15:30   **TB2-06S**

Pharmacoproteomics of non-human primate cerebrospinal fluid upon BACE inhibition, a drug target for alzheimer's disease
Stephan Mueller, German Center for Neurodegenerative Diseases (DZNE), Germany

METHODS, SYSTEMS & BIOINFORMATICS
TC2: DATA QUANTIFICATION AND EXTRACTION

14:00 – 15:30   **Liffey Hall 1**

Chair: Rainer Cramer, University of Reading, UK

14:00 – 14:30   **TC2-01K**

False discovery rates in proteomics: a tale of two extremes
Lennart Martens, Ghent University, Belgium

14:30 – 14:50   **TC2-02I**

The ups and downs of protein expression regulation

Christine Vogel, New York University, USA

14:50 – 15:00   **TC2-03S**

Efficient and user friendly label-free quantification with the proline software suite

David Bouyssié, IPBS/CNRS, France

15:00 – 15:10   **TC2-04S**

iOmicsPASS: integrative-omics approach for predictive analysis with subnetwork signatures

Hiromi Koh, National University of Singapore, Singapore

15:10 – 15:20   **TC2-05S**

An unbiased protein association study on public human proteome reveals biological connections between co-occurring protein-pairs

Surya Gupta, VIB, Belgium

15:20 – 15:30   **TC2-06S**

Systematic analysis of drug-protein targets in native biological systems

Ilaria Piazza, ETH Zurich, Switzerland

DISEASE & CLINICAL PROTEOMICS
TD2: CLINICAL PROTEOMIC TUMOUR ANALYSIS CONSORTIUM

14:00 – 15:30   **Liffey Hall 2**

Chair: Chris Kinsinger, National Cancer Institute, USA

14:00 – 14:30   **TD2-01K**

Proteogenomic insights for cancer biology, prognosis and treatment

Karin Rodland, Pacific Northwest National Laboratory, USA

14:30 – 14:50   **TD2-02I**

Democratizing cancer proteogenomic data

Bing Zhang, Baylor College of Medicine, USA

14:50 – 15:00   **TD2-03S**

Strategic use of targeted proteomics for triage of biomarker candidates

Tao Liu, Pacific Northwest National Laboratory, USA

15:00 – 15:10   **TD2-04S**

Multiplexed mass spectrometric screening of EGFR mutation in non-small-cell lung cancer

Chi-Ting Lai, Academia Sinica, Taiwan

15:10 – 15:20   **TD2-05S**

Development of targeted mass spectrometry-based assays for ERCC1-202/XPF as potential biomarkers in lung cancer

Daniela Antonelli, Luxembourg Institute of Health (LIH), Luxembourg

15:20 – 15:30   **TD2-06S**

Deep phospho- and phosphotyrosine proteomics identified active kinases and phosphorylation network in Cetuximab-resistant colorectal cancer

Yuichi Abe, National Institute of Biomedical Innovation, Health and Nutrition, Japan

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PRECISION & PERSONALISED PROTEOMICS
TE2: GLOBAL PROTEOME AND MODIFICATIONS

14:00 – 15:30   **Liffey Meeting Room 2**

Chair: John Timms, University College London, UK

14:00 – 14:30   **TE2-01K**

The cell-based human proteome project: mapping human proteins and their complexes with complete molecular specificity

Neil Kelleher, Northwestern Univ., USA

14:30 – 14:50   **TE2-02I**

Perspectives of proteomics in laboratory medicine and total lab automation

Andrea Urbani, Catholic University of The "Sacred Heart", Italy

14:50 – 15:00   **TE2-03S**

Post-translational modification profiles on tau are distinct for alzheimer's disease and other tauopathies

Hanno Steen, Boston Children's Hospital, USA

15:00 – 15:10   **TE2-04S**

Combining heavy-methyl SILAC labelling with targeted MS to profile the dynamic histone methyl-proteome

Alessandro Cuomo, European Institute of Oncology, Italy

15:10 – 15:20   **TE2-05S**
Pervasive co-expression of spatially proximal genes is buffered at the protein level
Georg Kustatscher, Wellcome Trust Centre for Cell Biology, UK'

15:20 – 15:30   **TE2-06S**
The citrullinome in tissue and biofluids for disease phenotyping & personlized medicine
Allan Stensballe, Aalborg University, Denmark

HUMAN PROTEOME PROJECT
TF2: CANCER & GLYCOPROTEOMICS

14:00 – 15:30   **Liffey Meeting Room 3**
Chairs: Nicki Packer, Macquarie University, Australia

14:00 – 14:30   **TF2-01K**
Targeted glycoproteomics for novel bladder cancer biomarkers: a step towards precision oncology
José Alexandre Ferreira, Portuguese Institute of Oncology of Porto, Portugal

14:30 – 14:50   **TF2-02I**
Glycoproteins: candidate urinary biomarkers in prostate cancer
Giuseppe Palmisano, University of Sao Paulo, Brazil

14:50 – 15:00   **TF2-03S**
Fucosylated glycoproteins associated with advanced prostate cancer
Hui Zhang, Johns Hopkins University, USA

15:00 – 15:10   **TF2-04S**
A site-specific O-GlcNAc of tumor suppressor FoxO3a serves as a molecular signature of pancreatic cancer
Young-Ki Paik, Yonsei University, South Korea

15:10 – 15:20   **TF2-05S**
pTyr-phosphoproteomics of serial tumor biopsies from patients with advanced cancer treated with protein kinase inhibitors
Mariette Labots, VU Medical Center, Netherlands

DAILY PROGRAMME

15:20 – 15:30   **TF2-06S**

Phosphoproteomics in metastatic colorectal cancer for predicting response to anti-EGFR therapy

Robin Beekhof, VU Medical Center, Netherlands

15:30 – 16:30   **The Forum**

**Tea / Coffee Break Exhibition, Networking,
Innovation Presentations and Poster Viewing**

15:45 – 16:15   **Liffey Hall 2**

British Society for Proteome Research AGM

PLENARY SESSION

16:30 – 17:30   **Liffey B**

Chair: Emma Lundberg, Science for Life Laboratory (kth), Sweden

16:30 – 17:10   **TP-03**

Proteomics for signaling and clinical studies

Matthias Mann, Max-Planck Institute of Biochemistry, Germany

17:10 – 17:30

Questions and Discussion

17:30 – 19:00   **Liffey Hall 1**

HUPO2017 General Assembly

19:30 – 00:00   **The Guinness Storehouse**

HUPO2017 Gala Evening

(transport provided from congress venue to CCD)

Wednesday 20th September

07:45 – 08:15   **The Forum**

Meet the Experts Breakfast Session   **Bioinformatics Hub**

Chair: Andrea Urbani, Catholic University of The "Sacred Heart", Italy

YPIC Co-Chair: Maarten Dhaenens - Ghent University, Belgium

WEDNESDAY

PLENARY SESSION

08:30 – 10:00   **Liffey B**
Chair: Mike Snyder, Stanford University, USA

08:30 – 09:10   **WP-01**
Changing the course and impact of chronic disease: personalizing medicine
Jenny van Eyk, Cedars Sinai Medical Center, USA

09:10 – 09:50   **WP-02**
Omics convergence in cancer research: advances in precision medicine
Henry Rodriguez, National Cancer Institute, USA

09:50 – 10:00
Questions and Discussion

10:00 – 11:00   **The Forum**
Tea / Coffee Break Exhibition, Networking,
Innovation Presentations and Poster Viewing

10:10 – 10:50   **Liffey Meeting Room 3**
ECR Manuscript Competition

CELLULAR PROTEOMICS
WA1: CELLULAR STRESS RESPONSES

11:00 – 12:30   **Liffey A**
Chair: Kathryn Lilley, University of Cambridge, UK

11:00 – 11:30   **WA1-01K**
Remodeling of the SUMO proteome in response to proteotoxic stress
Ron Hay, University of Dundee, UK

11:30 – 11:50   **WA1-02I**
Novel roles of PRMT1-mediated protein-methylation in DNA damage response and miRNA biogenesis revealed by MS-proteomics
Tiziana Bonaldi, European Institute of Oncology (IEO) Italy

11:50 – 12:00   **WA1-03S**
Identifying oxidation-specific post-translational modifications during diet-induced liver inflammation
Juliane Weisser, CeMM Research Center for Molecular Medicine, Austria

12:00 – 12:10　　　　　　　　　　**WA1-04S**

Characterising the role of protein kinase CK2 in regulating aluminium toxicity in yeast

Filip Veljanoski, Western Sydney University, Australia

12:10 – 12:20　　　　　　　　　　**WA1-05S**

Defining the dynamic pro-inflammatory response of human monocyte-derived macrophages using the hyperLOPIT spatial proteomics approach

Claire Mulvey, University of Cambridge, UK

12:20 – 12:30　　　　　　　　　　**WA1-06S**

Links between cell wall remodelling and metabolism in E. coli, a proteomic view

Thibault Chaze, Institut Pasteur, France

DRUG & BIOPHARMACEUTICAL PROTEOMICS
WB1: BIOPHARMACEUTICALS AND BIOMARKERS

11:00 – 12:30　　　　　　　　　　**Liffey B**

Chair: Hanno Langen, Roche, Switzerland

11:00 – 11:30　　　　　　　　　　**WB1-01K**

Bioprocess monitoring using quantitative proteomics, glycomics and glycoproteomics

Jonathan Bones, National Institute for Bioprocessing Research and Training, Ireland

11:30 – 11:50　　　　　　　　　　**WB1-02I**

Serum N-glycome – a biomarker for ovarian cancer diagnosis

Veronique Blanchard, Charité Medical University, Germany

11:50 – 12:00　　　　　　　　　　**WB1-03S**

Improved top/middle-down antibody characterization using multiple ion activations on an Orbitrap Tribrid mass spectrometer

Kristina Srzentić, Northwestern University, USA

12:00 – 12:10　　　　　　　　　　**WB1-04S**

Better access to intact proteoforms by cold vaporization of tissues with picosecond infrared laser ablation

Marcel Kwiatkowski, University of Groningen, Netherlands

12:10 – 12:20　　　　　　　　　　**WB1-05S**

Identification and quantification of host cell proteins (HCPs) in human plasma derived biotherapeutics

K. Ilker Sen, Protein Metrics Inc., USA

12:20 – 12:30 **WB1-06S**

Characterization and quantification of CHO host cell proteins during monoclonal antibody purification by SWATH-MS

Chia-Yi Lillian Liu, Bioprocessing Technology Institute, Singapore

METHODS, SYSTEMS & BIOINFORMATICS
WC1: BIG DATA

11:00 – 12:30 **Liffey Hall 1**

Chair: Mark Baker, Macquarie University, Australia

11:00 – 11:30 **WC1-01K**

Knowledge mining from -omics datasets in the era of big data
FuChu He, National Center for Protein Sciences, China

11:30 – 11:50 **WC1-02I**

Proteomics, embracing the chaos
Juri Rappsilber, Institute of Technology, Berlin, Germany & University of Edinburgh, Scotland

11:50 – 12:00 **WC1-03S**

A leap over the hurdle in label-free quantitative proteomics: uniting spectral counting and peak-intensity-based methods
Ludger Goeminne, VIB/Ghent University, Belgium

12:00 – 12:10 **WC1-04S**

Controlling false discovery rates on large-scale proteome datasets in jPOST
Yasushi Ishihama, Kyoto University, Japan

12:10 – 12:20 **WC1-05S**

PECAsuite: a comprehensive software package for time-specific, multi-layered analysis of gene expression regulation
Hyungwon Choi, National University of Singapore, Singapore

12:20 – 12:30 **WC1-06S**

Direct detection of stop codon read-through events using proteomics in Drosophila melanogaster
Simon Hubbard, The University of Manchester, UK

DAILY PROGRAMME

DISEASE & CLINICAL PROTEOMICS
WD1: CANCER PROTEOMICS

11:00 – 12:30   **Liffey Hall 2**

Chair: Juri Rappsilber, Institute of Technology, Berlin, Germany & University of Edinburgh, Scotland

11:00 – 11:30   **WD1-01K**

Subcellular proteomics and friends; finding lipid raft-dependent RNA-binding proteins that regulate exosome microRNA cargo selection

Michelle Hill, QIMR Berghofer Medical Research Institute, Australia

11:30 – 11:50   **WD1-02I**

Using proteomics to explore the pro-invasive crosstalk between stromal and cancer cells

Sara Zanivan, CRUK Beatson Institute, UK

11:50 – 12:00   **WD1-03S**

Time-resolved proteome & phosphoproteome analysis to dissect pemetrexed induced signaling cascade in non-small-cell lung cancer

Denise Putri, Taipei Medical University, Taiwan

12:00 – 12:10   **WD1-04S**

Mass spectrometry imaging (MSI) and laser micro dissection for cancer diagnostics on tumour tissue

Peter Hoffmann, University of South Australia, Australia

12:10 – 12:20   **WD1-05S**

The integration of proteomic, imaging and clinical features into a classifier that risk-stratifies lung nodules

Paul Kearney, Integrated Diagnostics, US

12:20 – 12:30   **WD1-06S**

Spatial tissue proteomics quantifies inter- and intra-tumoral heterogeneity in hepatocellular carcinoma

Alessandro Ori, Leibniz Institute On Aging, Germany

PRECISION & PERSONALISED PROTEOMICS
WE1: FROM BENCH TO THE CLINICS

11:00 – 12:30   **Liffey Meeting Room 2**

Chair: Thomas Joos, NMI Naturwissenschaftliches und Medizinisches Institut, Germany

11:00 – 11:30 **WE1-01K**

Integrated 'omics and their role in personalized healthcare now and in the future

Alain Van Gool, Radboud University Medical Center, Netherlands

11:30 – 11:50 **WE1-02I**

Integrated omics for tissue-based mapping of the human proteome

Cecilia Lindskog, Uppsala University, Sweden

11:50 – 12:00 **WE1-03S**

Proteomes of paired plasma and cerebrospinal fluid and their association with biomarkers of Alzheimer disease

Loïc Dayon, Nestlé Institute of Health Sciences, Switzerland

12:00 – 12:10 **WE1-04S**

Exploratory affinity assays for personalized plasma profiling

Jochen Schwenk, Science for Life Laboratory (KTH), Sweden

12:10 – 12:20 **WE1-05S**

Platelet extracellular vesicles in human plasma contain biomarkers suited for early diagnostics of alzheimer's disease

Helmut Meyer, ISAS - e.V. – Dortmund, Germany

12:20 – 12:30 **WE1-06S**

Applying proteomics to build a precise, predictive test for diabetic kidney disease

Richard Lipscombe, Proteomics International, Australia

HUMAN PROTEOME PROJECT
WF1: INFECTIOUS DISEASE & FOOD AND NUTRITION

11:00 – 12:30 **Liffey Meeting Room 3**

Chair: Concha Gil, Complutense University of Madrid, Spain & Paola Roncada, Instituto Spallanzani, Italy

11:00 – 11:30 **WF1-01K**

Viral infection-driven dynamics of proteome organization

Ileana Cristea, Princeton University, USA

11:30 – 11:50 **WF1-02I**

Metaproteomic tools to study individual human gut microbiota

Daniel Figeys, University of Ottawa, Canada

11:50 – 12:00   **WF1-03S**

Identification of potential biomarkers for vivax malaria using clinical isolates: a proteomics intervention

Sanjeeva Srivastava, Indian Institute of Technology Bombay, India

12:00 – 12:10   **WF1-04S**

Studying the effect of food systems on gut epithelium cells analyzed by LC-MS proteomics

Steffen Bak, Dupont Nutrition Biosciences ApS, Denmark

12:10 – 12:20   **WF1-05S**

Host macrophage modulation of cell death and related pathways during early MSSA and MRSA infection

Alessio Soggiu, University of Milan, Italy

12:20 – 12:30   **WF1-06S**

A personalized model of cholesterol homeostasis mechanisms based on trans-omics data integration

Peter Blattmann, ETH Zurich, Switzerland

12:45 - 13:45   **(see below symposia for room allocations)**
Sponsored Symposia

Advances in accurate, high-throughput quantitative proteomics
Liffey Hall 1
James Duncan, Ph.D.:Assistant Professor Fox Chase Cancer Center
Kathryn Lilley, Ph.D.:Cambridge Centre for Proteomics, Department of Biochemistry, University of Cambridge

Quantitative analysis of two cancer signaling pathways using multiplex-immunoprecipitation and targeted mass spectrometry
Liffey Hall 2
John Rogers, Senior R&D Manager, Thermo Fisher Scientific

Improving high-throughput proteomics research
Liffey Meeting Room 2
Rudi Grimm: Agilent Technologies
Prof Manuel Mayr: MD, PhD, King's College London

CELLULAR PROTEOMICS
WA2: REGULATORY NETWORKS

14:00 – 15:30   **Liffey A**

Chair: Matthias Mann, Max Planck Institute of Biochemistry, Germany

14:00 – 14:30   **WA2-01K**

The proteomics of protein kinase signaling

Michael Yaffe, Massachusetts Institute of Technology, USA

14:30 – 14:50   **WA2-02I**

Integrated analyses of epigenetic complexes and networks

Michael Washburn, Stowers Institute for Medical Research, USA

14:50 – 15:00   **WA2-03S**

Composition and dynamics of the myddosome during the innate immune response

Aleksandra Nita-Lazar, NIH: National Institute of Allergy and Infectious Diseases, USA

15:00 – 15:10   **WA2-04S**

A human lectin microarray for sperm surface glycosylation analysis

Sheng-ce Tao, Shanghai Jiao Tong University, China

15:10 – 15:20   **WA2-05S**

Library and de novo sequencing hybridization: a method for identification of cis-spliced MHC peptides

Pouya Faridi, Monash University, Australia

15:20 – 15:30   **WA2-06S**

Quantitative mass spectrometry to identify oviductal fluid proteins related to reproduction

Hans Yu, University of Veterinary Medicine Vienna, Austria

DRUG & BIOPHARMACEUTICAL PROTEOMICS
WB2: LATE BREAKING

14:00 – 15:30   **Liffey B**

Chair: Fernando J. Corrales, Centro Nacional de Biotecnología (CSIC), Spain

14:00 – 14:30   **WB2-01K**

Proteomic dissection of the tumour microenvironment in prostate cancer

Steve Pennington, University College Dublin, Ireland

14:30 – 14:50   **WB2-02I**

Translating MS protein assays into the clinic: potential of post-translationally modified proteins for clinical MS protein tests

Dobrin Nekelov, Isoformix, USA

14:50 – 15:00   **WB2-03S**

Development of a novel LC concept for clinical proteomics

Nicolai Bache, Evosep Biosystems, Denmark

15:00 – 15:10   **WB2-04S**

Bioorthogonal labeling of human prostate cancer tissue slice cultures for glycoproteomics

David Spiciarich, University of California, US

15:10 – 15:20   **WB2-05S**

Omics investigation of FDG-PET based heterogeneity in solid tumors

Mohamed Jarboui, WSIC, Department of Preclinical Imaging and Radiopharmacy, Germany

15:20 – 15:30   **WB2-06S**

Metabolites imaging and shotgun proteomics to decipher the role of epididymis in sperm maturation

Charles Pineau, Protim, France

METHODS, SYSTEMS & BIOINFORMATICS
WC2: ONE HEALTH

14:00 – 15:30   **Liffey Hall 1**
Chair: Subhra Chakraborty, National Institute of Plant Genome Research, India

14:00 – 14:30   **WC2-01K**

We are not alone: the roles of farm animal proteomes for human health

Emøke Bendixen, AARHUS - Department of Molecular Biology and Genetics, Denmark

14:30 – 14:50   **WC2-02I**

Immunoproteomic approaches to host-pathogen interactions

David Goodlet, University of Maryland, USA

14:50 – 15:00   **WC2-03S**

Proteomic and functional analysis of NBDHEX in Giardia duodenalis

Marialuisa Casella, Istituto Superiore di Sanità, Italy

15:00 – 15:10   **WC2-04S**

High-resolution quantitative proteomics applied to the discovery of biomarkers of innate immune response in tuberculosis

Jesús Mateos, Spanish Research Council-CSIC, Spain

15:10 – 15:20   **WC2-05S**

A system approach to identify genetic and environmental regulators of virulence in Mycobacterium tuberculosis

Amir Banaei-Esfahani, ETH Zurich, Switzerland

15:20 – 15:30   **WC2-06S**

Towards a quantitative map of the human proteome: monitoring of tissue specific proteins during meningitis

Johan Malmstršm, Lund University, Sweden

DISEASE & CLINICAL PROTEOMICS
WD2: PROTEIN STRUCTURES AND MODIFICATIONS

14:00 – 15:30   **Liffey Hall 2**
Chair: Juri Rappsilber, Institute of Technology, Berlin, Germany & University of Edinburgh, Scotland

14:00 – 14:30   **WD2-01K**

A dream: from a protein's sequence to its structure - modern structural proteomics techniques

Christoph Borchers, University of Victoria, Canada

14:30 – 14:50   **WD2-02I**

Unbiased enrichment of the phosphoproteome gives unprecedented insight into novel human signalling mechanisms through pHis, pAsp, pLys, pArg

Claire Eyers, University of Liverpool, UK

14:50 – 15:00   **WD2-03S**

Phosphoproteomics of an AML cell line panel pinpoints hyperactive tyrosine kinases as targets for treatment.

Carolien Van Alphen, VU Medical Centre, Netherlands

15:00 – 15:10   **WD2-04S**

LC-SRM targeted quantification of 20S proteasome complexes stoichiometry & dynamics using absolute SILAC

Thomas Menneteau, IPBS - CNRS UMR, France

15:10 – 15:20   **WD2-05S**

Phosphoproteomics dissection of the cross-talk between MAPK & PI3K-mTOR pathways in different cancer models

Maruan Hijazi, Queen Mary University of London, UK

15:20 – 15:30   **WD2-06S**

Comprehensive analysis of human protein N-termini enables assessment of various protein forms

Cheolju Lee, Korea Institute of Science and Technology, Republic of Korea

PRECISION & PERSONALISED PROTEOMICS
WE2: HEALTH AND DISEASE

14:00 – 15:30   **Liffey Meeting Room 2**

Chair: Alex Ebhardt, University College Dublin / Systems Biology Ireland, Ireland

14:00 – 14:30   **WE2-01K**

Managing health and disease using big data

Mike Snyder, Stanford University, USA

14:30 – 14:50   **WE2-02I**

Proteome landscape of hepatocellular carcinoma

Ying Jiang, National Center For Protein Science, China

14:50 – 15:00   **WE3-03S**

Establishment of a fully synthetic, mirror-image biological system

Jörg Hoheisel, German Cancer Research Center, DKFZ, Germany

15:00 – 15:10   **WE2-04S**

Mass spectrometry histochemistry unveils hidden treasures in formalin fixed paraffin embedded biobanked tissue

Peter Verhaert, ProteoFormiX, Belgium

15:10 – 15:20   **WE2-05S**

Stratification biomarkers in personalised medicine for osteoarthritis: results from the MOVES study

Valentina Calamia, Inibic, Spain

15:20 – 15:30   **WE2-06S**

Analysis of proteomic variation in the human population: a comprehensive iPS cell proteome

Dalila Bensaddek, University of Dundee, UK

HUMAN PROTEOME PROJECT
WF2: PSI AND KIDNEY/URINE

14:00 – 15:30   **Liffey Meeting Room 3**

Chair: Henning Hermakob, EMBL-European Bioinformatics Institute, UK

14:00 – 14:30   **WF2-01K**

Enabling the dissemination and reuse of proteomics data: status and new projects of the HUPO proteomics standards initiative

Eric Deutsch, Institute for Systems Biology, USA

14:30 – 14:50   **WF2-02I**

Towards standardization of urine proteomics and peptidomics

Tadashi Yamamoto, Niigata University, Japan

14:50 – 15:00   **WF2-03S**

The draft human proteome as of 2017: metrics from the HUPO human proteome project

Gilbert Omenn, University of Michigan, USA

15:00 – 15:10   **WF2-04S**

The ProteomeXchange consortium: 2017 update

Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, UK

15:10 – 15:20   **WF2-05S**

Large scale quantitative urine proteomics of Japanese healthy volunteers

Bo Xu, Niigata University, Japan

15:20 – 15:30   **WF2-06S**

All that's listed does not code

Michael Tress, Spanish National Cancer Research Centre (CNIO), Spain

15:30 – 16:00   **Liffey Foyer Area**
Tea / Coffee Break

DAILY PROGRAMME

CLOSING PLENARY SESSION

16:00 – 18:00   **Liffey B**
Chair: Rob Moritz, Institute for Systems Biology. USA

16:00 -16:45   **WP-03**
Translating a trillion points of data into therapies, diagnostics and new insights into disease
Atul Butte, Institute for Computational Health Sciences, University of California, USA

16:45 – 18:00
HUPO/EuPA/BSPR/MCP Awards Ceremony and Lectures

18:00
Congress Close

EMBL-WELLCOME GENOME CAMPUS CELLULAR PROTEOMICS TRACK AT HUPO2017

HUPO2017 are delighted to have partnered with EMBL-Wellcome Genome Campus in the Cellular Proteomics track at this year's HUPO Congress. We would like to thank them for their support. See the full programme listing for the sessions and speakers in the Cellular Proteomics track.

THE BIOINFORMATICS HUB

The Bioinformatics Hub is a place where bioinformaticians gather together with three aims: (i) to provide their advice, knowledge, and support to anyone with a relevant question; (ii) to discuss current issues and challenges in proteomics informatics with the entire community; and (iii) to work on interesting, synergistic projects and to freely exchange tools, algorithms and know-how with each other, across all labs, seniorities and levels of experience.

The Bio-Inormatics Hub will be open daily from 09:30 – 17:30

The BioInformatics Hub is proudly sponsored by