

DAILY PROGRAM

TUESDAY, SEPTEMBER 20, 2016

08:00-17:30	Registration (Lobby, 1F)
08:00-17:30	Speaker Ready Room (Room 103, 1F)
09:30-17:30	Exhibition & Poster (Room 201, 2F and Banquet Hall, 3F)
08:30-09:15	Plenary Session 5 (Plenary Hall, 3F)
08:30-17:30	Bioinformatics Hub (Room 203, 2F)
09:30-10:30	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
10:30-12:15	[T01] Interactomics & Protein Network (Plenary Hall, 3F)
	[T02] Glycoproteomics - Technical Limitations & Prospects (Room 101 AB, 1F)
	[T03] PTM Crosstalks II - Lysine & other Modificomics (Room 101 C, 1F)
	[T04] Imaging Mass Spectrometry (Room 101 D, 1F)
	[T05] Liver & Toxicoproteomics: Metabolism, Drug Transformation & Toxicity (Room 102, 1F)
12:30-13:30	Industry Seminar supported by Bruker Corporation (South Lounge, 3F)
	Industry Seminar supported by SCIEX (North Lounge 3F)
	Industry Seminar supported by Meridigen Biotech Co., Ltd. (Joy Lounge, 4F)
	Industry Seminar supported by Merck Millipore and Sigma-Aldrich (Elegance Lounge, 4F)
	Industry Seminar supported by Thermo Fisher Scientific (VIP Room, 4F)
13:45-15:30	[T06] Antibodies & Protein Arrays (Plenary Hall, 3F)
	[T07] Integrative Glyco(proteo)mics for Glycobiology & Diseases (Room 101 AB, 1F)
	[T08] Proteome Dynamics: Stability, Turnover & Degradomics (Room 101 C, 1F)
	[T09] Spatial & Single Cell Proteomics (Room 101 D, 1F)
	[T10] Protein Standards and Model Organisms: Expanding our Horizons (Room 102, 1F)
15:30-16:30	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
	PhD Abstract Competition (Room 201, 2F)
16:45-17:30	Plenary Session 6 (Plenary Hall, 3F)
18:00-21:00	HUPO Congress Night* (Taipei New Horizon, 14F)

* Ticket Event

Registration Open 07:30-17:30 @Lobby, 1F
Speaker Ready Room Open 07:30-17:30 @103, 1F

08:30-17:30 Room 203 (2F)

Bioinformatics Hub

08:30-09:15 Plenary Hall (3F)

Plenary Session 6

Chair: Gerald Hart, USA

8:30 PL 06

Glycoproteomics – A genetic Approach to Deconstruction and Simplification of Protein Glycosylation

Henrik Clausen, University of Copenhagen, Denmark

09:30-10:30: Networking Break and Poster Viewing Room 201 (2F) and
(Even Poster Numbers) Banquet Hall (3F)

10:30-12:15 Plenary Hall (3F)

T01: Interactomics & Protein Network

Chairs: Jun Qin, China; Junmin Peng, USA

10:30 TK-01

Membrane Protein Complexes

Jun Qin, National Center for Protein Sciences, Beijing, China

10:55 TK-02

Multilayer Proteomics Approaches to Understanding Common Human Diseases

Junmin Peng, St. Jude Children's Research Hospital, USA

11:20 TO01-001

The Regulatory Role of Methylation and Methylation-Phosphorylation Crosstalk in Protein Interaction Networks

Marc Wilkins, University of New South Wales, Australia

11:35 TO01-002

Network Analysis Reveals a Dominant Role of Protein-Level Regulation in Coordinating Gene Functions

Bing Zhang, Vanderbilt University Medical Center, USA

11:50 TO01-003

Profiling the Phosphotyrosine Interactome of Receptor Tyrosine Kinases

Runsheng Zheng, Technische Universitaet Muenchen, Germany

- 11:55 **TO01-004**
Phylointeractomics Reconstructs Functional Evolution of Protein Binding
Dennis Kappei, Cancer Science Institute of Singapore, Singapore
- 12:00 **TO01-005**
Determining Network Topology, Distance Restraints and Activation Markers from Endogenous Protein Complexes
Marco Faini, ETH Zurich, Switzerland

10:30-12:15

Room 101 AB (1F)

T02: Glycoproteomics - Technical Limitations & Prospects

Chairs: **Katalin Medzihradzsky, Hungary; Hui Zhang, USA**

- 10:30 **TK-03**
Extracellular Glycosylation: How to See the Forest Despite All the Trees
Katalin Medzihradzsky, Biological Research Centre, Szeged, Hungary
- 10:55 **TK-04**
Comprehensive Analysis of N-Linked Protein Glycosylation Using NGAG and Mass Spectrometry
Hui Zhang, Johns Hopkins University, USA
- 11:20 **TO02-001**
In-Depth Analysis of Human Plasma Glycoproteins by a Combination of High-Resolution Native Mass Spectrometry and Middle-Down Proteomics
Vojtech Franc, University of Utrecht, Netherlands
- 11:35 **TO02-002**
Confident, Automated N-Glycoproteomics Profiling in Enriched and Unenriched Cell Samples
Scott Peterman, Thermo Fisher Scientific, USA
- 11:50 **TO02-003**
Identification of Intact Glycopeptides with In-Silico Deglycosylation Strategy for O-Glycoproteomics Analysis
Hongqiang Qin, Chinese Academy of Sciences, China
- 11:55 **TO02-004**
Glycoproteomic Analysis of Human Plasma Using SWATH-MS
Chi-Hung Lin, Macquarie University, Australia
- 12:00 **TO02-005**
A Suite of SWATH Glycoproteomic Approaches for Easy Global Glycoprotein Analysis
Ben Schulz, The University of Queensland, Australia

10:30-12:15

Room 101 C (1F)

T03: PTM Crosstalks II - Lysine & Other Modifications**Chairs:** **Chunaram Choudhary**, Denmark; **Yingming Zhao**, USA**10:30** **TK-05****Systems-Wide Analysis of Properties and Functions of Lysine Acetylation and Ubiquitylation***Chunaram Choudhary, University of Copenhagen, Denmark***10:55** **TK-06****Discovery and Initial Characterization of a Family of Lysine Acylation Pathways***Yingming Zhao, The University of Chicago, USA***11:20** **TO03-001****Unravelling Crosstalks between SUMOylation and Other Protein Modifications in Human Cells Using Dynamic Proteomics***Frederic Lamoliatte, Universite de Montreal, Canada***11:35** **TO03-002****Towards Comprehensive Analysis of Protein ADP-Ribosylation***Yonghao Yu, UT Southwestern Medical Center, USA***11:50** **TO03-003****Acetylome Analysis Reveals Carbon Metabolism as a Key Factor Enhancing Thermogenesis in White Adipocytes***Hsin-Yi Chang, Kyoto University, Japan***11:55** **TO03-004****Effects of Co-/Post-Translational Modifications on Protein Function***Hisashi Hirano, Yokohama City University, Japan***12:00** **TO03-005****Efficient Enrichment of SUMOylated Peptides from Alpha-Lytic Protease Digest Using K- ϵ -GG Remnant Immuno-Affinity Purification***Hongbo Gu, Cell Signaling Technology, USA*

10:30-12:15

Room 101 D (1F)

T04: Imaging Mass Spectrometry**Chairs:** **Peter Hoffmann**, Australia; **Per Andrén**, Sweden**10:30** **TK-07****Peptide and Glycan Mass Spectrometry Imaging as Diagnostic Tool in Cancer Research***Peter Hoffmann, University of Adelaide, Australia***10:55** **TK-08****Molecular Imaging of the Brain by Mass Spectrometry***Per Andrén, Uppsala University, Sweden*

- 11:20 TO04-001**
Molecular Imaging of Protein in Tissues Using Ambient Ionization Top-Down Mass Spectrometry
Cheng-Chih Hsu, National Taiwan University, Taiwan
- 11:35 TO04-002**
3D MALDI Imaging Mass Spectrometry Using Next Generation Technologies - Reconstruction of a Molecular Imaged Epididymis
Charles Pineau, Protim - Inserm U1085, France
- 11:45 TO04-003**
Localization and Identification of Peptides from Tissue Using High-Speed MALDI TOF/TOF Mass Spectrometry
Sabu Sahadevan, Bruker Daltonics, France
- 11:55 TO04-004**
Monitoring ErbB1 and ErbB2 Interaction and Activation Using Engineered Cell Lines and Duolink Proximity Ligation Assay by High-Content Imaging
Tracy Adair-Kirk, MilliporeSigma, USA
- 12:00 TO04-005**
Molecular Profile Discrimination and Mapping of Skeletal Muscle Regeneration in Rat Crush Model Using MALDI Imaging
Anne Denys, Université Paris 13, UMR CNRS 7244, France

10:30-12:15

Room 102 (1F)

T05: Liver & Toxicoproteomics: Metabolism, Drug Transformation & Toxicity

Chairs: **Fernando J. Corrales**, Spain; **Oliver Poetz**, Germany

- 10:30 TK-09**
Systematic Analysis of One Carbon Metabolism by SRM. Implications in the Progression of Chronic Liver Disorders
Fernando Corrales, University of Navarra, Spain
- 10:55 TK-10**
Drug-Drug Interaction – Analyses of CYP450 Enzymes and Transporters in Mice and Men
Oliver Poetz, University of Tübingen, Germany
- 11:20 TO05-001**
Personalized Proteomic Characterization of Hepatitis B Virus-Associated Hepatocellular Carcinomas
Ying Jiang, National Center for Protein Science, Beijing, China
- 11:35 TO05-002**
In Vitro Investigation Of An Adverse Outcome Pathway Of Cholestatic Liver Injury Using Quantitative Phosphoproteomics
René Zahedi, Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany

- 11:50 TO05-003**
Differential Proteomic Analysis of Cholangiocarcinoma Cells and Cell-Derived Extracellular Vesicles by Label Free Mass Spectrometry
Felix Elortza, CIC bioGUNE, CIBERehd, ProteoRed-ISCIII, Spain
- 12:00 TO05-004**
Proteome Analysis of Microdissected Tumor Cells Reveals Annexin A10 as Biomarker Candidate for Differentiation of ICC And Liver Metastases of PDAC
Thilo Bracht, Ruhr Universität Bochum, Germany

13:45-15:30 **Plenary Hall (3F)**

T06: Antibodies & Protein Arrays

Chairs: **Heng Zhu, USA; Mathias Uhlén, Sweden**

- 13:45 TK-11**
Application of Protein Microarrays in Epigenetics and Biomarker Discovery
Heng Zhu, Johns Hopkins University, USA
- 14:10 TK-12**
Validation of Antibodies to Study the Human Proteome
Mathias Uhlén, KTH Royal Institute of Technology, Sweden
- 14:35 TO06-001**
Status of the Affinity Binder Knockdown Initiative
Tove Alm, Scilifelab, KTH Royal Institute of Technology, Sweden
- 14:50 TO06-002**
Heterogeneous Ribonucleoprotein K (hnRNP K) Binds the 5' Terminal Sequence of the Hepatitis C Virus RNA and Mature miR-122
Chien-Sheng Chen, National Central University, Taiwan
- 15:05 TO06-003**
A High-Content Functional Mycobacterium Tuberculosis Proteome Microarray and Its Applications
Yang Li, Shanghai Jiao Tong University, China
- 15:10 TO06-004**
Utilizing Protein Microarray to Monitor Blood-Brain Barrier Disruption and Active Inflammation in Plasma Samples from Multiple Sclerosis Patients
Malene Moeller Joergensen, Aalborg University Hospital, Denmark
- 15:15 TO06-005**
Mapping Transcription Factor Interactome Networks Using HaloTag Protein Arrays
Junshi Yazaki, Riken, Japan

T07: Integrative Glyco(proteo)mics for Glycobiology & Diseases**Chairs:** **Nicolle Packer**, Australia; **Hisashi Narimatsu**, Japan**13:45** **TK-13****Advances in Glycoproteomics Facilitate the Discovery of a New Class of Functionally Important Cancer and Inflammation-Centric Human Glycoproteins***Morten Thaysen-Andersen, Macquarie University, Australia***14:10** **TK-14****Accurate Mass- and Glycan Composition-Based Assignment of Glycosylation Site-Specific Glycomes of Complex Glycoprotein Mixture***Hiroyuki Kaji, National Institute of Advanced Industrial Science & Technology (AIST), Japan***14:35** **TO07-001****Identification of Intact Glycopeptides at a Proteome Scale***Mingqi Liu, Fudan University, China***14:50** **TO07-002****Integrated Glycoproteomics Demonstrates Fucosylated Serum Paraoxonase 1 Alterations and functions in Lung Cancer***Je Yoel Cho, Seoul National University, South Korea***15:05** **TO07-003****Decoding Site-Specific Alteration of Sialo-Glycoproteome in EGFR-Subtype of Non-Small Cell Lung Cancer***Yi-Ju Chen, Academia Sinica, Taiwan***15:10** **TO07-004****Identifying Antibody and Lectin Recognition to HIV N-Glycans Through Native Mass Spectrometry and Glycoproteomic Analysis of Viral Envelope Spikes***Weston Struwe, University of Oxford, United Kingdom***15:15** **TO07-005****Dynamic Mapping of Human Frontal Cortex According to the Developmental Stage via Neuroglycomic Approach***Jua Lee, Chungnam National University, South Korea*

T08: Proteome Dynamics: Stability, Turnover & Degradomics**Chairs:** Christopher Overall, Canada; Donald Kirkpatrick, USA**13:45** **TK-15**

Positional Proteomics Technologies to Functionally Annotate Tissue Proteomes in Pathology: Mechanistic Analysis Linear Ubiquitination by LUBAC in Immunodeficiency Disease by TAILS

Christopher Overall, University of British Columbia, Canada

14:10 **TK-16**

Ubiquitin Proteomics – Revelations of a Master Manipulator

Donald Kirkpatrick, Genentech, USA

14:35 **TO08-001**

Copy Number Alteration Programmed Protein Turnover Quantified by pSILAC and SWATH Mass Spectrometry

Yansheng Liu, ETH Zurich, Zurich, Switzerland

14:50 **TO08-002**

High Resolution Mass Spectrometry Cellular Thermal Shift Assay (HR-MS-CETSA) - Post-Translational Modifications Impact on Protein Stability

*Radoslaw Sobota, Agency for Science, Technology and Research (A*STAR), Singapore*

15:05 **TO08-003**

A Dynamic Picture of the Proteome and Ibiquitinome Upon Proteasome Inactivation

Jeroen Demmers, Erasmus University Medical Center Rotterdam, Netherlands

15:10 **TO08-004**

Proteome Turnover Analysis Reveals Substrates and Physiological Role of Membrane Proteases

Ansgar Poetsch, IIB-CONICET-UNMDP Mar del Plata, Argentina

15:15 **TO08-005**

A Novel Function of CRL2 Ubiquitin Ligase in Protein Quality Control

Hsiu-Chuan Lin, Academia Sinica, Taiwan

13:45-15:30

Room 101 D (1F)

T09: Spatial & Single Cell Proteomics

Chairs: Emma Lundberg, Sweden; Bernd Bodenmiller, Switzerland

13:45 TK-17

The Human Cell Atlas

Emma Lundberg, Scilifelab, KTH Royal Institute of Technology, Sweden

14:10 TK-18

Analysis of Tumor Heterogeneity in Three Dimensions by Imaging Mass Cytometry

Bernd Bodenmiller, University of Zurich, Switzerland

14:35 TO09-001

Quantitative Proteome-Wide Profiling of the Retromer Cargo Landscape

Christina Bell, Harvard Medical School, USA

14:50 TO09-002

Refining the Details in the Tissue-Based Map of the Human Proteome

Cecilia Lindskog, Uppsala University, Sweden

15:05 TO09-003

Membrane Localization of Metabolic Enzymes and Metabolic Modulation in a Cell Division Mutant of *Escherichia Coli* Identified by Omics Approaches

Yu-Ling Shih, Academia Sinica, Taiwan

15:10 TO09-004

Determining Post-Translational Modifications of Nuclear Proteins

Ryotaro Ban, Yokohama City University, Japan

15:15 TO09-005

Single-Cell Proteome Profiling: Innovations in Sample Preparation

Masaki Wakabayashi, Kyoto University, Japan

13:45-15:30

Room 102 (1F)

T10: Protein Standards and Model Organisms: Expanding Our Horizons

Chairs: Eric Deutsch, USA; Joshua Heazlewood, Australia

13:45 TK-19

Recent Progress and New Projects for the HUPO Proteomics Standards Initiative

Eric Deutsch, Institute for Systems Biology, USA

14:10 TO10-001

The ProteomeXchange Consortium: 2016 Update

Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, United Kingdom

- 14:25 TO10-002**
proBAMconvert: Organizing MS Identifications in a Genome-Centric Fashion Enables Proteogenomics and Proteomics Integration
Gerben Menschaert, University of Ghent, Belgium
- 14:30 TO10-003**
The HUPO-PSI Quality Control Working Group: Making QC More Accessible for Biological Mass Spectrometry
Mathias Walzer, University of Tuebingen, Germany
- 14:35 TK-20**
The Golgi Localized UDP-GlcNAc Transporter is Required for the Maturation of Complex N-Glycans in Plants
Joshua Heazlewood, The University of Melbourne, Australia
- 14:50 TO10-004**
Adipose Tissue Pathways in Obesity: Iberian Pig as Large Animal Model of Metabolic Disorders
Cristian Piras, University of Milan, Milan, Italy
- 15:05 TO10-005**
Proteomics in Food Safety: Monitoring Competition between *Listeria Monocytogenes* and *Lactococcus Lactis* by Imaging Mass Spectrometry
Isabella Alloggio, Università degli studi di Milano, Italy
- 15:20 TO10-006**
Proteome Alterations in the Porcine Endometrium during Embryo Implantation
Thomas Fröhlich, LMU-Munich, Germany

15:30-16:30: Networking Break and Poster Viewing
(Odd Poster Numbers)

**Room 201 (2F) and
 Banquet Hall (3F)**

16:45-17:30

Plenary Hall (3F)

Plenary Session 7

Chair: Catherine E. Costello, USA

- 16:45 PL 07**
Complementary Methods for Probing Protein Assemblies and Interactions
Albert Heck, Utrecht University, The Netherlands