

# DAILY PROGRAM

MONDAY, SEPTEMBER 19, 2016

<b>07:30-17:30</b>	<b>Registration (Lobby, 1F)</b>
<b>07:30-17:30</b>	<b>Speaker Ready Room (Room 103, 1F)</b>
<b>09:30-17:30</b>	<b>Exhibition &amp; Poster (Room 201, 2F and Banquet Hall, 3F)</b>
07:30-08:30	Neurodegenerative Disease Cluster Group (Room 102, 1F)
07:30-08:30	Membrane Proteome Cluster Group (Room 203, 2F)
08:30-09:15	Plenary Session 3 (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	[M01] Cancer & Translational Proteomics (Plenary Hall, 3F) [M02] Innovative MS Techniques for Global & Targeted Proteomics (Room 101 AB, 1F) [M03] Chemical Probes & Chemical Biology for Proteomics (Room 101 C, 1F) [M04] Metabolomics & Metabolic Disorders (Room 101 D, 1F) [M05] Brain & EyeOME: Connecting two images (Room 102, 1F)
12:30-13:30	Industry Seminar supported by SCIEX (Room 101 C, 1F) Industry Seminar supported by Waters Corporation (South Lounge, 3F) Industry Seminar supported by Thermo Fisher Scientific (North Lounge, 3F) Industry Seminar supported by Thermo Fisher Scientific (Joy Lounge, 4F) Industry Seminar supported by Agilent Technologies, Inc. (Elegance Lounge, 4F) Industry Seminar supported by Bruker Corporation (VIP Room, 4F)
13:45-15:30	[M06] Immunity, Inflammation & Infectious Diseases (Plenary Hall, 3F) [M07] Bioinformatics & Computational Proteomics (Room 101 AB, 1F) [M08] PTM Crosstalks I - Phosphoproteomics, Kinome & OGIcNAc (Room 101 C, 1F) [M09] New Technological Advancements (Room 101 D, 1F) [M10] Diabetes and Cardiovascular Diseases: Energy Balance in Disease Phenotypes (Room 102, 1F)
15:30-16:30	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
16:45-17:30	Plenary Session 4 (Plenary Hall, 3F)
17:30-18:15	Plenary Session 5 (Plenary Hall, 3F)
18:15-19:15	HUPO General Assembly (Room 101 AB, 1F)
19:30-21:30	Invited Speaker Dinner* (Room A, 33F, Taipei World Trade Center Club)

\* by Invitation Only

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

**07:30-08:30** **Room 102 (1F)**

Neurodegenerative Disease Cluster Group, JS Yoo, A Urbani

**07:30-08:30** **Room 203 (2F)**

Membrane Proteome Cluster Group, D Figeys, YJ Chen

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

**Bioinformatics Hub**

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

**Plenary Session 3**

**Chair:** **Robert Moritz, USA**

**8:30** **PL 03**

**The Proteome in Context**

*Ruedi Aebersold, ETH Zurich, Switzerland*

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

**09:30-10:30: Poster Session Even Number of Chromosome Teams**  
**(Chr 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, X, Y)** **Banquet Hall, (3F)**

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

**M01: Cancer & Translational Proteomics**

**Chairs:** **Christoph Borchers, Canada; Jau-Song Yu, Taiwan**

**10:30** **MK-01**

**iMALDI for Accurate Quantitation of the Expression and Phosphorylation Level of Akt in Tumour Biopsies**

*Christoph Borchers, University of Victoria- Genome BC Proteomics Centre, Canada*

**10:55** **MK-02**

**Verification of Oral Cancer Biomarkers and Their Translation to Clinical Settings**

*Jau-Song Yu, Chang Gung University, Taiwan*

**11:20** **MO01-001**

**Verification of Colorectal Cancer Biomarker Candidates in Plasma/Serum Extracellular Vesicles by Targeted Proteomics**

*Takeshi Tomonaga, National Institutes of Biomedical Innovation, Health and Nutrition, Japan*

- 11:35 MO01-002**  
**Proteomic Multimarker Panel Complements CA19-9 Insufficiency in the Diagnosis of Pancreatic Ductal Adenocarcinoma**  
*Youngsoo Kim, Seoul National University, South Korea*
- 11:50 MO01-003**  
**Pathology-Driven Comprehensive Proteomic Profiling of the Prostate Cancer Tumor Microenvironment**  
*Stephen Pennington, UCD Conway Institute of Biomolecular and Biomedical Research, Ireland*
- 11:55 MO01-004**  
**Tissue Derived Neo-Antigens for T Cell-Based Cancer Immunotherapy**  
*Michal Bassani, UNIL/CHUV, Switzerland*
- 12:00 MO01-005**  
**LinkedOmics: Discovering Associations Between Genomic, Proteomic and Clinical Attributes in Human Cancer**  
*Jing Wang, Vanderbilt University Medical Center, USA*

**10:30-12:15****Room 101 AB (1F)****M02: Innovative MS Techniques for Global & Targeted Proteomics****Chairs:** Jesper Olsen, Denmark; Michael MacCoss, USA

- 10:30 MK-03**  
**Comprehensive Analysis of Human Proteomes with Similar Depth as RNA-Seq**  
*Jesper Olsen, University of Copenhagen, Denmark*
- 10:55 MK-04**  
**Comprehensive DIA with High Precursor Selectivity: How Can We Have Our Cake and Eat It Too?**  
*Michael MacCoss, University of Washington, USA*
- 11:20 MO02-001**  
**MS1 Based Quantification Optimization on DIA Methods on a Quadrupole-Orbitrap Mass Spectrometer**  
*Yue Xuan, Thermo Fisher Scientific, Germany*
- 11:35 MO02-002**  
**Digging Deeper into Large SWATH MS1 Windows Using Gas Phase Fractionation SWATH-MS**  
*Mark Molloy, Australian Proteome Analysis Facility, Australia*
- 11:50 MO02-003**  
**iST: Sample Preparation for High Throughput Clinical Proteomics- A Novel, Fast, Sensitive and Reproducible Sample Preparation for MS-based proteomics-**  
*Garwin Pichler, Preomics GmbH, Germany*

- 11:55 **MO02-004**  
**All MS/MS ions Monitoring Acquired by Data-Dependent Acquisition without Dynamic Exclusion: A New Concept for In-Depth Protein Quantification**  
*Fei Fang, Key Laboratory of Separation Science for Analytical Chemistry, China*
- 12:00 **MO02-005**  
**Analyses of Intact Proteins by LC-FT-ICR Mass Spectrometry at 21 Tesla**  
*Lissa C. Anderson, National High Magnetic Field Laboratory, USA*

10:30-12:15

Room 101 C (1F)

**M03: Chemical Probes & Chemical Biology for Proteomics****Chairs:** Alice Y. Ting, USA

- 10:30 **MK-05**  
**Spatially-Resolved Proteomic Mapping in Living Cells via Enzyme-Mediated Proximity Labeling**  
*Alice Ting, Stanford University, USA*
- 10:55 **MK-06**  
**Drug Resistance Assessed by Multi-Proteomics Approaches**  
*Simone Lemeer, Utrecht University, Netherlands*
- 11:20 **MO03-001**  
**Quantitative Activity-Based Profiling of Kinase Inhibitor Binding and Selectivity on Protein Microarrays Containing >300 Human Protein Kinases**  
*Jonathan Blackburn, University of Cape Town, South Africa*
- 11:35 **MO03-002**  
**Novel Hybrid Platform for Rapid, Highly Sensitive and Specific Quantification of Proteins and Their Post-Translational Modifications**  
*Liqi Xie, Fudan University, China*
- 11:45 **MO03-003**  
**A Highly Sensitive Probe for Fucosylated Glycans for Biomarker Discovery**  
*Naoyuki Taniguchi, RIKEN, Japan*
- 11:55 **MO03-004**  
**A Novel Set of Isobaric Peptide Labeling Reagent Enabled Proteomic Quantification over 10 Different Samples**  
*Yan Ren, BGI-Shenzhen, China*
- 12:00 **MO03-005**  
**TMTcalibrator™ Enhances Biomarker Discovery in Peripheral Fluids**  
*Hui-Chung Liang, Proteome Sciences Plc, United Kingdom*

10:30-12:15

Room 101 D (1F)

**M04: Metabolomics & Metabolic Disorders****Chairs:** Tsutomu Masujima, Japan; Frank Gonzalez, USA10:30 **MK-07****Single Cell Metabolomics and Applications***Tsutomu Masujima, RIKEN, Japan*10:55 **MK-08****The Role of Gut Microbiota, Bile Acids, Intestinal Farnesoid X Receptor Signaling, and Ceramides in Metabolic Disease***Frank Gonzalez, Center for Cancer Research, USA*11:20 **MO04-001****Global Data Standardization Algorithm for Applied Metabolomics***Petr Likhov, Institute of Biomedical Chemistry, Russia*11:35 **MO04-002****Systemic Proteomic and Metabolomic Analyses Identify Crucial Roles of the Polyol Pathway in Tumorigenesis***Anuli Uzozie, ETH Zurich, Switzerland*11:50 **MO04-003****Urine Proteomics for Evaluation of Taking Nano-Mist sauna Effects on the Health***Yoshitoshi Hirao, Niigata University, Japan*11:55 **MO04-004****Mass Spectrometry-Based Proteomic and Metabolic Analysis of Different Cell Lines after Perturbation of Cellular Cholesterol Regulation***Peter Blattmann, ETH Zurich, Switzerland*12:00 **MO04-005****imCorrect: New UHRMS Signal Handling Approach for More Accurate Elemental Composition Determination***Wei-Hung Chang, Academia Sinica, Taiwan*

10:30-12:15

Room 102 (1F)

**M05: Brain & EyeOME: Connecting Two Images****Chairs:** Peter Nilsson, Sweden; Richard Semba, USA10:30 **MK-09****Neuroproteomic Profiling of Proteins and Autoantibody Repertoires in Plasma and CSF***Peter Nilsson, SciLifeLab, KTH Royal Institute of Technology, Sweden*

- 10:55**      **MK-10**  
**Proteomic Approaches to Understanding Age-Related Macular Degeneration**  
*Richard Semba, Johns Hopkins University, USA*
- 11:20**      **MO05-001**  
**Proteomics Reveals Individual Patient Responses to Therapeutic Treatment for Dry Eye**  
*Roger Beuerman, Singapore Eye Research Institute, Duke-NUS, Singapore*
- 11:35**      **MO05-002**  
**A Comprehensive Inter-Grade Proteomic Analysis of Serum, CSF and Tissue in Glioma**  
*Manubhai Kp, Indian Institute of Technology Bombay, India*
- 11:50**      **MO05-003**  
**Building a Comprehensive Chick Retinal Proteome Dataset by Liquid Chromatography (LC) Fractionation for Tandem MS and SWATH Analysis**  
*Hu Xiao, Hong Kong Polytechnic University, China*
- 11:55**      **MO05-004**  
**Do Platelet-Derived Extracellular Vesicles Contain Specific Biomarkers Allowing for Early Diagnostics of Alzheimer's Disease?**  
*Helmut Meyer, Leibniz-Institut Für Analytische Wissenschaften - ISAS - e.V., Germany*
- 12:00**      **MO05-005**  
**Generating a Proteomic Profile of Neurogenesis, through a Quantitative Comparison of Neuroepithelial and Radial Glial Like Stem Cells**  
*Shaun Garnett, University of Cape Town, South Africa*

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

**M06: Immunity, Inflammation & Infectious Diseases**

**Chairs:**      **Ileana Cristea, USA; Donald Hunt, USA**

- 13:45**      **MK-11**  
**Proteomics in Viral Infectious Diseases: Global and Targeted Functional Insights into the Virus-Host Interface**  
*Ileana Cristea, Princeton University, USA*
- 14:10**      **MK-12**  
**Immunotherapy of Cancer; An Overview and Recent Results**  
*Donald Hunt, University of Virginia, USA*
- 14:35**      **MO06-001**  
**The Human Immunopeptidome: Can Big Data Improve the Precision of Immunotherapy?**  
*Anthony Purcell, Monash University, Australia*

- 14:50 MO06-002**  
**Quantitative Host-Pathogen Protein Network Analysis Using Data-Independent Acquisition Mass Spectrometry Analysis**  
*Johan Malmström, Lund University, Sweden*
- 15:00 MO06-003**  
**Proteomic of Host-Microbiome Interactions in a Pediatric Inflammatory Bowel Disease Inception Cohort to Identify Protein Biomarkers**  
*Daniel Figeys, University of Ottawa, Canada*
- 15:10 MO06-004**  
**Challenges of Biomarker Discovery in Developing Countries: A Proteomics Investigation to Identify Unique Disease Signatures in Infectious Diseases**  
*Sanjeeva Srivastava, Indian Institute of Technology Bombay, India*
- 15:15 MO06-005**  
**Robust Temporal Profiling of GRB2 Protein Complexes in Primary T Lymphocytes Using SWATH Mass Spectrometry**  
*Etienne Caron, ETH Zurich, Switzerland*

13:45-15:30

Room 101 AB (1F)

**M07: Bioinformatics & Computational Proteomics****Chairs:** Lennart Martens, Belgium; Nuno Bandeira, USA

- 13:45 MK-13**  
**More Power and More Depth: New Tools for Proteomics Data Processing**  
*Lennart Martens, VIB UGhent, Belgium*
- 14:10 MK-14**  
**Exploring the Diversity in the Human Proteome**  
*Nuno Bandeira, University of California, San Diego, USA*
- 14:35 MO07-001**  
**Investigating the Basic Assumptions in Protein Abundance Estimation Using SWATH-MS Data**  
*Wenguang Shao, ETH Zurich, Switzerland*
- 14:50 MO07-002**  
**Reactome - Interactive Pathway Analysis for Proteomics**  
*Henning Hermjakob, EMBL-EBI, United Kingdom*
- 15:05 MO07-003**  
**MSCypher: A High-Throughput Peptide Identification Strategy for Complex Mixtures**  
*Andrew Webb, The Walter and Eliza Hall Institute, Australia*
- 15:10 MO07-004**  
**neXtProt in the Context of Human Proteomics Projects**

*Lydie Lane, Swiss Institute of Bioinformatics, Switzerland*

15:15

**MO07-005**

**A Genetic Algorithm to Locate Responsive Subpathways for Time-Course Proteomic Data**

*Eu-Yu Lai, Academia Sinica, Taiwan*

13:45-15:30

Room 101 C (1F)

**M08: PTM Crosstalks I - Phosphoproteomics, Kinome & O-GlcNAc**

**Chairs:** **Martin Larsen**, Denmark; **Gerald Hart**, USA

13:45

**MK-15**

**Modulation of Multiple PTMs Upon Brief Cellular Stimulation**

*Martin Larsen, University of Southern Denmark, Denmark*

14:10

**MK-16**

**Nutrient Regulation of Cellular Physiology by Extensive Crosstalk between O-GlcNAcylation & Phosphorylation**

*Gerald Hart, Johns Hopkins University, USA*

14:35

**MO08-004**

**Profiling Kinome Activities Using Kinase-Specific Substrate Peptides**

*Naoyuki Sugiyama, Kyoto University, Japan*

14:50

**MO08-002**

**Proteome Dynamics Reveal Temporal Regulation of O-GlcNAcylation/ Phosphorylation in Determining Apoptosis of Activated B Cells**

*Hsin-Yi Wu, Academia Sinica, Taiwan*

15:05

**MO08-003**

**Subtilisin for Large Scale (Phospho)Proteomics – the Beginning of a Wonderful Love Story?**

*Humberto Gonczarowska-Jorge, Leibniz-institut Für Analytische Wissenschaften - ISAS, e.V., Germany*

15:10

**MO08-005**

**Tyrosine Phosphorylation Changes due to Calcium Signaling Cascade Post-Sampling Prevented by Enzyme Heat Inactivation**

*Mats Borén, Denator, Sweden*



13:45-15:30

Room 101 D (1F)

**M09: New Technological Advancements****Chairs:** Neil Kelleher, USA; Kathryn Lilley, United Kingdom13:45 **MK-17****Proteomics 2.0: Recent Advances in Top Down Proteomics***Neil Kelleher, Northwestern University, USA*14:10 **MK-18****Capturing the Dynamic Spatial Proteome***Kathryn Lilley, University of Cambridge, United Kingdom*14:35 **MO09-001****Structural Characterization of Protein Phosphorylation and Antibody Complexes by Top/Middle-Down Mass Spectrometry***Jingxi Pan, University of Victoria-Genome BC Proteomics Centre, Canada*14:50 **MO09-002****Trapped Ion Mobility Spectrometry: An Additional Dimension of Separation for Proteomics Applications***Melvin Park, Bruker Daltonics, USA*15:05 **MO09-003****Qualitative and Quantitative Characterization of a Novel Scanning Quadrupole DIA Method for Omics Analysis***Johannes Pc Vissers, Waters Corporation, United Kingdom*15:10 **MO09-004****ProteusQC™: the Versatile Standard for Bottom-Up Proteomics***Andrew Percy, Cambridge Isotope Laboratories, USA*15:15 **MO09-005****Sampling of Tissues for Proteomics by Soft Laser Ablation***Hartmut Schlueter, University Medical Center Hamburg-Eppendorf, Germany*

13:45-15:30

Room 102 (1F)

**M10: Diabetes and Cardiovascular Diseases: Energy Balance in Disease Phenotypes****Chairs:** Loïc Dayon, Switzerland; Maggie Lam, USA13:45 **MK-19****Proteomic and Metabolic Health Phenotypes in Dietary Clinical Interventions***Loïc Dayon, Nestlé Institute of Health Sciences, Switzerland*14:00 **MK-20****Proteome Homeostasis and Remodeling in the Stressed Myocardium***Maggie Lam, University of California, Los Angeles, USA*

- 14:15**      **MO10-001**  
**Changes in Protein Expression Patterns in Islets of Langerhans: Implications for Treatment of Children with Obesity and Type 2 Diabetes**  
*Peter Bergsten, Uppsala University, Sweden*
- 14:30**      **MO10-002**  
**Proteomic Phenotyping of Human Arterial Samples Identifies Novel Markers of Early Atherosclerosis**  
*David Herrington, Wake Forest School of Medicine, USA*
- 14:45**      **MO10-003**  
**Proteomic Analysis of Membranes in Mouse and Human Cardiovascular Tissues**  
*Anthony Gramolini, University of Toronto, Canada*
- 15:00**      **MO10-004**  
**Glycoproteomics of the Aortic Extracellular Matrix: An Approach for Studying Diabetes and Cardiovascular Risk**  
*Ferheen Baig, King's College London, United Kingdom*
- 15:05**      **MO10-005**  
**Phosphoproteomics Identifies CK2 as a Negative Regulator of Beige Adipocyte Thermogenesis and Energy Expenditure**  
*Kosaku Shinoda, University of California, San Francisco, USA*
- 15:10**      **MO10-006**  
**Protective Effects of GLP-1 Analogues Against Cellular Stress: An *in Vitro* Proteomic Study**  
*Ali Tiss, Dasman Diabetes Institute, Kuwait*
- 15:15**      **MO10-007**  
**Poorly Controlled Diabetes Mellitus is Associated with Decreased Aspirin-Mediated Acetylation of Platelet Cyclooxygenase 1 (COX-1) at Serine 529**  
*Jean-Charles Sanchez, Geneva University, Switzerland*

**15:30-16:30: Networking Break and Poster Viewing (Odd Poster Numbers)** Room 201 (2F) and Banquet Hall (3F)

**15:30-16:30: Poster Session Odd Number of Chromosome Teams (Chr 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, Mito and Related Technologies (Pillas: MS, Ab, Bioinformatics))** Banquet Hall (3F)

**16:45-17:30** Plenary Hall (3F)

**Plenary Session 4**

**Chair: Yu-Ju Chen, Taiwan**

**16:45 PL 04**  
**Proteogenomic Analysis of Cancer: New Opportunities in Cancer Biology and Precision Medicine**  
*Henry Rodriguez, National Cancer Institute, National Institutes of Health, USA*

**17:30-18:15** Plenary Hall (3F)

**Plenary Session 5**

**Chair: Daniel W. Chan, USA**

**17:30 PL 05**  
**The Phoenix Center and CNHPP**  
*Fuchu He, Beijing Proteome Research Center, China*

**18:15-19:15** Room 101 AB (1F)

**HUPO General Assembly**