



## PROGRAM

**Session Date/Time: Sunday, September 17, 2023 - 08:00 AM - 10:00 AM**

**PS01: The Non-canonical Proteome - A Novel Class of Clinically Targetable T Cell Antigens (Ticketed Session)**

- 08:00 PS01.01: Welcome Address  
*Juan Antonio Vizcaino, United Kingdom*
- 08:00 PS01.01: Welcome Address  
*Nicola Ternette, United Kingdom*
- 08:05 PS01.02: An Introduction to Riboseq  
*Jorge Ruiz-Orera, Germany*
- 08:15 PS01.03: An Introduction to Immunopeptidomics  
*Michal Bassani-sternberg, Switzerland*
- 08:30 PS01.04: Annotation of the Non-canonical Proteome - Current Requirements and Guidelines  
*Sandra Orchard, United Kingdom*
- 08:45 PS01.05: Short Talks: Advances, Challenges, and Validation Strategies in Riboseq Annotations  
*James Wright, United Kingdom*
- 09:15 PS01.06: Short Talks: Advances, Challenges, and Validation Strategies in HLA-associated Peptide Annotations  
*Wei Wu, Singapore*
- 09:15 PS01.06: Short Talks: Advances, Challenges, and Validation strategies in HLA-associated Peptide Annotations  
*Pouya Faridi, Australia*
- 09:15 PS01.06: Short talks: Advances, Challenges, and Validation Strategies in HLA-associated Peptide Annotations  
*Anthony Purcell, Australia*
- 09:15 PS01.06: Short Talks: Advances, Challenges, and Validation Strategies in HLA-associated Peptide Annotations  
*Susan Klaeger, United States*

**Session Date/Time: Sunday, September 17, 2023 - 09:00 AM - 12:00 PM**

**PCT01: Computational Proteomics/Bioinformatics (Ticketed Session)**

- Chair  
*Wout Bittremieux, Belgium*
- 09:00 PCT01.01: Introduction to Statistical Design and Analysis of MS-based Proteomics Experiments  
*Meena Choi, United States*
- 09:45 PCT01.02: An Overview of the MaxQuant Platform for Proteomics Data Analysis  
*Dmitry Alexeev, Germany*
- 10:30 PCT01.03: Demystifying Post-translational Modification Analyses: Best Practices and Pitfalls  
*Eunok Paek, Republic of Korea*
- 11:15 PCT01.04: An Overview of Machine Learning for Mass Spectrometry-based Proteomics  
*Wout Bittremieux, Belgium*



## PROGRAM

**Session Date/Time: Sunday, September 17, 2023 - 09:00 AM - 12:00 PM**

### **PCT02: Protein Interactions/Spatial Proteomics (Ticketed Session)**

- 09:00 PCT02.01: An Overview of Protein Interactions and their Location  
*Kathryn Lilley, United Kingdom*
- 09:45 PCT02.02: Spatial Proteomics for Exploring the Tissue Heterogeneity  
*Ruijun Tian, China*
- 10:30 PCT02.03: Mapping Functional Associations of Proteins  
*Christoph Messner, Switzerland*
- 11:15 PCT02.04: How to Catch your Protein's Friends: Practical Tips for Designing Pull-Down Experiments  
*Terence Chuen Wai Poon, Macao*

**Session Date/Time: Sunday, September 17, 2023 - 10:15 AM - 12:15 PM**

### **PS02: Advancing Biomedical Research and Healthcare: Proteomics and Multi-Omics Integration for Precision Medicine (Ticketed Session)**

- 10:17 PS02.01: Emerging Opportunities in Multi-omics Research towards Precision Medicine  
*Michael Snyder, United States*
- 10:37 PS02.02: Biology through a Multi-omics Prism: Challenges and Pathways for Synergistic Integration  
*Sara Ahadi, United States*
- 10:37 PS02.02: Biology through a Multi-omics Prism: Challenges and Pathways for Synergistic Integration  
*Daniel Hornburg, United States*
- 10:59 PS02.03: Bringing Multi-Omics to Clinics  
*Julia Wang, United States*
- 10:59 PS02.03: Bringing Multi-Omics to Clinics  
*Michael Roehrl, United States*
- 11:39 PS02.04: Moderator  
*Khatereh Motamedchaboki, United States*
- 11:39 PS02.04: Panelist  
*Michael Snyder, United States*
- 11:39 PS02.04: Panelist  
*Sara Ahadi, United States*
- 11:39 PS02.04: Panelist  
*Daniel Hornburg, United States*
- 11:39 PS02.04: Panelist  
*Julia Wang, United States*
- 11:39 PS02.04: Panelist  
*Michael Roehrl, United States*

**Session Date/Time: Sunday, September 17, 2023 - 10:15 AM - 12:15 PM**

### **PS03: The $\pi$ -HuB Project: The Proteomic Navigator of the Human Body (Ticketed Session)**



## PROGRAM

- 10:15 PS03.01: Opening Introduction,  $\pi$ -HuB Progress  
*Fuchu He, China*
- 10:25 PS03.02: ProteomicsDB  
*Bernhard Küster, Germany*
- 10:35 PS03.03: Huiyan Progress, Application Guidelines  
*Ruijun Tian, China*
- 10:45 PS03.04: Progress in the Liver Project  
*Ying Jiang, China*
- 10:55 PS03.05 - ProtTalks  
*Tiannan Guo, China*
- 11:05 PS03.06: Panelist  
*Neil Kelleher, United States*
- 11:05 PS03.06: Panelist  
*Jennifer Van Eyk, United States*
- 11:05 PS03.06: Panelist  
*Juan Antonio Vizcaino, United Kingdom*

**Session Date/Time: Sunday, September 17, 2023 - 12:30 PM - 03:30 PM**

### **PCT03: Single Cell Proteomics (Ticketed Session)**

- 12:30 PCT03.01: Setting the Stage for this Interactive Training Course  
*Aleksandra Binek, United States*
- 12:35 PCT03.02: Single-cell Proteomics Creates Opportunities for Unique Research in Heart Disease  
*Aleksandra Binek, United States*
- 13:05 PCT03.03: Preparation Workflows for Single-cell Proteomics Analysis  
*Bogdan Budnik, United States*
- 13:35 PCT03.04: Separation methods in single-cell proteomics: Liquid chromatography (LC) or Capillary electrophoresis (CE)?  
*Si Wu, United States*
- 14:30 PCT03.05: From MS Acquisition to Biological Insights into Single-cell Heterogeneity  
*Florian A Rosenberger, Germany*

**Session Date/Time: Sunday, September 17, 2023 - 12:30 PM - 03:30 PM**

### **PCT04: Proteomics 101 (Ticketed Session)**

- Chair  
*Je Yoel Cho, Republic of Korea*
- Chair  
*Min-sik Kim, Republic of Korea*



## PROGRAM

- 12:30 PCT04.01 - Review of the History of How We Came to Use NanoLC-MS for Bottom-Up Proteomics  
*David Goodlett, Canada*
- 13:15 PCT04.02: Quantitative Proteomics: Measuring Protein Abundance by MS and How We Use It for Clinical Questions  
*Yeoun Jin Kim, United States*
- 14:00 PCT04.03: Enrichment Strategies for Sub-Cellular Proteomics and Post-Translational Modifications  
*Stuart Cordwell, Australia*
- 14:45 PCT04.04: Affinity and Interaction Proteomics to Understand Functional Biology  
*Wei Wu, Singapore*

**Session Date/Time: Sunday, September 17, 2023 - 01:15 PM - 03:15 PM**

### **PS04: Implementing Proteomics for Clinical Translation – Implementation and Future Promise (Ticketed Session)**

Chair

*Yu-Ju Chen, Taiwan*

- 13:17 PS04.01: Bridging Proteomics to the Clinic – A Multivariate Blood Test for Disease Activity in Multiple Sclerosis  
*Ferhan Qureshi, United States*
- 01:32 PS04.02: From Pre-Clinical Research to Clinical Settings: Development of a Biomarker Panel for Ovarian Cancer  
*Stefan Enroth, Sweden*
- 13:47 PS04.03: Proteomics-Based Diagnostics, How to Overcome Obstacles in the Development of Commercial Service  
*Myeong-Hee Yu, Republic of Korea*
- 14:02 PS04.04: Using the Immune Response to Detect Disease  
*Joshua Labaer, United States*
- 14:20 PS04.05: Panelist  
*Ferhan Qureshi, United States*
- 14:20 PS04.05: Panelist  
*Stefan Enroth, Sweden*
- 14:20 PS04.05: Panelist  
*Myeong-Hee Yu, Republic of Korea*
- 14:20 PS04.05: Panelist  
*Joshua Labaer, United States*
- 14:20 PS04.05: Panelist  
*Henry Rodriguez, United States*
- 14:20 PS04.05: Panelist  
*Yeoun Jin Kim, United States*
- 14:20 PS04.05: Panelist  
*Parag Mallick, United States*

**Session Date/Time: Sunday, September 17, 2023 - 01:15 PM - 03:15 PM**



## PROGRAM

### PS05: Science, Ethics, and Equity: Considering all Aspects of the Human Proteome (Ticketed Session)

- 13:15 PS05.01: Beyond the Genome: Ethical Issues in Large-Scale Proteomics Research  
*Kristien Hens, Belgium*
- 13:15 PS05.01: Beyond the Genome: Ethical Issues in Large-Scale Proteomics Research  
*Ina Devos, Belgium*
- 13:15 PS05.01: Beyond the Genome: Ethical Issues in Large-Scale Proteomics Research  
*Daan Kenis, Belgium*
- 13:15 PS05.02: Enhancing equity, diversity, and inclusion in STEM  
*Jennifer Geddes-McAlister, Canada*
- 14:15 PS05.03: Panelist  
*Jennifer Geddes-McAlister, Canada*
- 14:15 PS05.03: Panelist  
*Kristien Hens, Belgium*
- 14:15 PS05.03: Panelist  
*Daan Kenis, Belgium*
- 14:15 PS05.03: Panelist  
*Ina Devos, Belgium*

### Session Date/Time: Sunday, September 17, 2023 - 04:00 PM - 05:00 PM

#### MS01: Mentoring Session 1 - AI Tools in Grant Writing Applications, Research Articles, CVs (Academic, Journal Editor)

Chair

*Emily Hashimoto-Roth, Canada*

Chair

*Ruth Huttenhain, United States*

MS01.01: Panelist

*Laura Elo, Finland*

MS01.02: Panelist

*Min-sik Kim, Republic of Korea*

MS01.03: Panelist

*Jack Washington, United Kingdom*

### Session Date/Time: Sunday, September 17, 2023 - 05:45 PM - 07:30 PM

#### PL01: Opening Plenary: Jeremy Nicholson, Australia - Metabolic Systems Medicine and Phenomic Approaches to Understand the Natural History of COVID-19 and Long COVID

Chair

*Jennifer Van Eyk, United States*

- 18:00 PL01.01: Opening Remarks KHUPO  
*Jin Han, Republic of Korea*



## PROGRAM

- 18:00 PL01.01 Opening Remarks KHUPO  
*Je Yoel Cho, Republic of Korea*
- 18:10 PL01.02: Opening Remarks HUPO  
*Jennifer Van Eyk, United States*
- 18:15 PL01.03: Introduction to the Program  
*Jennifer Van Eyk, United States*
- 18:20 PL01.04: ECR Update  
*Ruth Huttenhain, United States*
- 18:20 PL01.04: ECR Update  
*Mathieu Lavallée-Adam, Canada*
- 18:32 PL01.05: Plenary Speaker - Metabolic Systems Medicine and Phenomic Approaches to Understand the Natural History of COVID-19 and Long COVID  
*Jeremy Nicholson, Australia*
- 19:20 PL01.06: Invite Delegates to Welcome Reception in Exhibit Hall  
*Jennifer Van Eyk, United States*

### Session Date/Time: Monday, September 18, 2023 - 08:00 AM - 09:00 AM

#### ISS02: New Generation of PEAKS: Deep Learning Enabled Software Solutions for Immunopeptidomics, Glycoproteomics, and Post-translational Modifications

- 08:00 The Non-canonical Immunopeptidome - What Contributes to Antigenic Diversity in Cancer and Autoimmune Disease  
*Anthony Purcell, Australia*
- 08:20 Mining Widespread Lactylation in the Human Proteome with Cyclic Immonium Ion  
*Hui Ye, China*
- 08:40 Glycan de Novo Sequencing and Label Free Quantification in PEAKS GlycanFinder  
*Kyle Hoffman, Canada*

### Session Date/Time: Monday, September 18, 2023 - 08:00 AM - 09:00 AM

#### ISS03: Confidence from Discovery to Clinical Research: Harnessing the Versatility of the ZenoTOF 7600

- 08:00 Multiple Applications of the ZenoTOF 7600  
*Peter Hoffmann, Australia*
- 08:30 TBD  
*Phil Robinson, Australia*

### Session Date/Time: Monday, September 18, 2023 - 09:15 AM - 10:00 AM

#### PL02: Plenary Session: Yu-Ju Chen, Taiwan - Evolution of Micro-to-nano Proteomics toward Precision Oncology

Chair

*Youngsoo Kim, Republic of Korea*



## PROGRAM

09:17 PL02.01: Plenary Speaker - Evolution of Micro-to-nano Proteomics toward Precision Oncology  
*Yu-Ju Chen, Taiwan*

**Session Date/Time: Monday, September 18, 2023 - 10:15 AM - 11:45 AM**

### CS01: Multi-omics

Chair

*Phil Robinson, Australia*

Chair

*Sun-young Kong, Republic of Korea*

10:16 CS01.01: Keynote Speaker - Transforming Health with Deep Data and Remote Profiling  
*Michael Snyder, United States*

10:41 CS01.02: Keynote Speaker: Population Proteomics: A Path to Precision Medicine  
*Chris Whelan, United States*

11:06 CS01.03: Molecular Responses During Bacterial Filamentation Reveal Inhibition Methods of Drug Resistant Bacteria  
*Dongxue Zhang, China*

11:19 CS01.04: Proteogenomic Analysis of Human Pancreatic Ductal Adenocarcinoma  
*Do Young Hyeon, Republic of Korea*

11:32 CS01.05: Integrative Proteogenomics Profiling Uncovers Non-histone Protein Methyltransferases as Novel Therapeutic Targets in Diffuse Midline Glioma  
*Arun Kumaran Anguraj Vadivel, Canada*

**Session Date/Time: Monday, September 18, 2023 - 10:15 AM - 11:45 AM**

### CS02: Precision Medicine

Chair

*Stefan Tenzer, Germany*

Chair

*Sang Hoon Song, Republic of Korea*

10:16 CS02.01: Keynote Speaker - Unlocking Food Composition Data and Cracking the Safe to Better Health  
*Jennifer Hall, United States*

10:41 CS02.02: Keynote Speaker - Unlocking the Potential of Precision Medicine (Genotype-To-Proteotype Analysis)  
*Henry Rodriguez, United States*

11:06 CS02.03: Ex Vivo Drug Response Heterogeneity Combined With Cell-Population-Specific Proteotyping Reveals Personalized Therapeutic Strategies for Patients With Multiple Myeloma  
*Sandra Goetze, Switzerland*

11:19 CS02.04: Precision Proteomic Landscape of Health-To-Disease Transitions of Rheumatic Musculoskeletal Disorders and Links to Cancer Associate irAEs  
*Allan Stensballe, Denmark*

11:32 CS02.05: Circulating Proteins in Breast Cancer Risk and Etiology  
*Jochen Schwenk, Sweden*



## PROGRAM

**Session Date/Time: Monday, September 18, 2023 - 10:15 AM - 11:45 AM**

### **CS03: Interactomes/Protein Networks**

Chair

*Christoph Messner, Switzerland*

Chair

*Mikhail Savitski, Germany*

- 10:16 CS03.01: Keynote Speaker - MitoAtlas, a Super-resolution Proteome Map of Mitochondria  
*Hyun-Woo Rhee, South Korea*
- 10:41 CS03.02: Keynote Speaker - Mapping the Diversity in Spatiotemporal Regulation of G Protein-Coupled Receptors  
*Ruth Huttenhain, United States*
- 11:06 CS03.03: Disease Representation in the Reactome Pathways Database  
*Henning Hermjakob, United Kingdom*
- 11:19 CS03.04: Mapping Evolutionarily Conserved Protein-Protein Interactions in the Vertebrate Brain  
*Vy Dang, United States*
- 11:32 CS03.05: The Social and Structural Architecture of an In-Depth Cellular Protein Interactome  
*André Michaelis, Germany*

**Session Date/Time: Monday, September 18, 2023 - 10:15 AM - 11:45 AM**

### **CS04: Proteomics of Brain Diseases**

Chair

*Chien-Yun Lee, Germany*

Chair

*Jong Bae Park, Republic of Korea*

- 10:16 CS04.01: Keynote Speaker - Antibody-based Neuroproteomics  
*Peter Nilsson, Sweden*
- 10:41 CS04.02: Keynote Speaker -Molecular Pathogenesis Based on Proteomic and Genomic Analysis in Alzheimer's Disease  
*Inhee Mook-Jung, Republic of Korea*
- 11:06 CS04.03: Draft Human Brain Proteome Atlas for Understanding the Molecular Basis of Brain Functions  
*Qi Xiao, China*
- 11:19 CS04.04: Paired CSF Proteins With Enhanced Potential to Monitor Neurodegeneration  
*Sara Mravinacova, Sweden*
- 11:32 CS04.05: Plasma-Multiprotein-Biomarker Models for Screening of Brain Amyloid Status and Early Diagnosis of Alzheimer's Dementia Using Multiple Reaction Monitoring-Mass Spectrometry  
*Youngsoo Kim, Republic of Korea*

**Session Date/Time: Monday, September 18, 2023 - 11:45 AM - 01:00 PM**

### **PP01: Odd Numbered Posters - Poster Viewing with Coffee Break**



## PROGRAM

PP01.01: Ecklonia Cava Extracellular Vesicles Mitigated UV-B Induced Skin Pigmentation and Basement Membrane by Modulating NRF2

*Kyung-A Byun, Republic of Korea*

PP01.03: OMICS Analysis for the Discovery and Verification of Novel Brain-specific Extracellular Vesicles for the Diagnosis of Brain Diseases

*Yuri Choi, Republic of Korea*

PP01.05: The Orbitrap Astral Mass Spectrometer Enables the Quantification of >5000 Proteins from a Plasma Extracellular Vesicle Sample

*Lilian Heil, United States*

PP01.07: Construction of Lipid Component Analysis Platform for Assessment of Extracellular Vesicles (Exosome) Therapy Products

*Eun Ji Jang, Republic of Korea*

PP01.09: Shotgun Proteomics Reveals Senomorphic Targets Based on SASP-mediated by Small Extracellular Vesicles

*Jesus Mateos, España*

PP01.11: Proteomic Profiling of Circulating Extracellular Vesicles from  $\beta$ -thalassemia/HbE Reveals Association of Immunoglobulin Inducing Membrane Vesiculation

*Kunwadee Phongpao, Thailand*

PP01.13: Standardized and Fully Automated Profiling of Plasma and Extracellular Vesicles Integrated with Evosep One Enables Large Scale Clinical Cohort Analysis

*Joel Vej-nielsen, Denmark*

PP01.15: Determining the Antigen Processing Requirements for Spliced Peptide Presentation

*Ritchlynn Aranha, Australia*

PP01.17: Identification and Validation the of HLA-I Proteasomal Spliced Epitopes by Immunopeptidomics

*Pouya Faridi, Australia*

PP01.19: A Comparison of Sputum Proteome Analysis in Asthma Patients Receiving Different Biologic Treatments

*Jeong-yeon Hong, Republic of Korea*

PP01.21: Correlation between CD4 T Cells and Lymphotoxin Beta Expression in Breast Cancer: A Comparative Medicine Approach.

*Haeju Lee, Republic of Korea*

PP01.23: MARS: a Novel Antigen Discovery Pipeline by Improved LCMS De-Novo Peptide Identification for Characterizing Non-Canonical Immunopeptidome

*Hanqing Liao, United Kingdom*

PP01.25: Exploring the Antigenic Landscape in Head and Neck Cancer

*Miriam Melake, United Kingdom*

PP01.27: Beyond Discovery: Streamlining Immunopeptidomics Methods for Drug Development.

*Arun Tailor, United States*

PP01.29: Enhanced Proteomic Coverage in Tissue Microenvironment by Immune Cell library-assisted DIA-MS

*Jhih-Ci Yang, Taiwan*

PP01.31: Boosting DIA Immunopeptidomics with Personalized Libraries Generated by a Deep Learning-based Workflow

*Wen-Feng Zeng, Germany*

## PROGRAM

PP01.33: Phosphoproteomics Reveals Alternative Roles of PknG in Mycobacterial Pathogenesis

*Seanantha Baros-Steyl, South Africa*

PP01.35: Towards a New Generation of Infectious Diseases Diagnosis Methods Using LC-MSMS and Artificial Intelligence

*Florence Roux-Dalvai, Canada*

PP01.37: Comparison of Olink and NULISAseq Proteomic Technologies Applied to a COVID-19 Case-control Cohort Showed High Similarity between The Two Technologies.

*Muhammad Umar Sohail, Qatar*

PP01.39: Auto-Immunoproteomics Analysis of COVID-19 ICU Patients Revealed Increased Levels of Autoantibodies Related to Male Reproductive System

*Muhammad Umar Sohail, Qatar*

PP01.41: Proteome Analysis of BP1092 – a Potential New Virulence Factor Regulator in Bordetella Pertussis

*Kristin Surmann, Germany*

PP01.43A: Multi-omics Approach Reveals Putative Serum Biomarkers for Congenital Zika Syndrome

*Fábio Nogueira, Brazil*

PP01.43: Landscape of the RBD-Specific Antibody Responses Triggered by the Inactivated Virus Vaccine Against the Omicron Variant Using Protein Microarray

*Junbiao Xue, China*

PP01.45: To Predict how Proteins Bind RNA: RBS-ID & pRBS-ID

*Jong Woo Bae, Republic of Korea*

PP01.47: FAX-RIC in peptide level enables robust mapping of RNA-binding regions of RNA interactome

*Seonmin Ju, Republic of Korea*

PP01.49: ARID3C Acts as a Regulator of Monocytic Differentiation Interacting with NPM1

*Hui-su Kim, Republic of Korea*

PP01.51: Comprehensive Profiling of Human Brain Protein Complexes Using Co-fractionation Mass Spectrometry

*DongGeun Lee, United States*

PP01.55: Systematic Proteomic Analysis of MUDENG Interactome Using TurboID Proximity Labeling

*Jung Soo Hyun, Republic of Korea*

PP01.57: The First Profile of Steroid Hormones in Human Aqueous Humor is Generated from the LC MS/MS Approach

*Hongkai Xu, China*

PP01.59: Defining Novel AMPK Substrates by Lysosome-enriched Phosphoproteomics

*Ashfaql Hoque, Australia*

PP01.61: The Expectation and Reality of the HepG2 Core Metabolic Portrait

*Olga Kiseleva, Russian Federation*

PP01.63: MSMP: an Integrated Mass Spectrometry Database of Medicinal Plants for Natural Products Identification

*Ziyi Li,*

PP01.65: The Role of AC9 in Glucagon Secretion in Islet  $\alpha$  Cell Specific AC9 Knockout Mice

*Yanping Zhu, China*

PP01.67: Adaptive Focused Acoustics(R) Technology for Confident, Robust, and Reliable Sample Preparation in Protein Analysis

*Debadeep Bhattacharyya, United States*

## PROGRAM

PP01.69: Broad-scale Multiomics Reveals Protein Signature Suggestive of Microbiome Dysbiosis and Inflammatory Bowel Disease Risk

*Ray Chen, United States*

PP01.71: Exploring the Synergy of A-to-I RNA Editing and Splicing: Unveiling a Promising Target for Cancer Therapeutics

*Anton Goncharov, Russian Federation*

PP01.73: Integrated Omics Analysis of the HEPG2 Cell Line: Unraveling Molecular Insights through Transcriptomics, Translatomics, and Proteomics

*Ekaterina Ilgisonis, Russian Federation*

PP01.75: Proteomic Profiles Associated with Early Life Exposome in Asthma and Atopic Dermatitis : ECHO-COCOA Study.

*Yeonwoo Jo, Republic of Korea*

PP01.77: Multi-omics Analysis for Characterization of Extracellular Vesicle

*Hye-Jung Kim, Republic of Korea*

PP01.79: The Combination of Quantitative Proteomics And Systems Genetics Analysis Reveals TNR is Associated With Novelty Seeking

*Hui Li, China*

PP01.81: Unexpectedly Large Plasma Proteome Variation and its Genetic Determinants in Children and Adolescents

*Lili Niu, Denmark*

PP01.83: The Combination of Quantitative Proteomics And Systems Genetics Analysis Reveals PTN is Associated With Sleep Loss Induced Cognitive Impairment

*Shuijing Pan, China*

PP01.85: Multi-Omics Integration of Thousands of Plasma Proteins: Unveiling Type 2 Diabetes Signatures and Clinical Associations in Large-Scale Study

*Willy Pena Buttner, United States*

PP01.87: Splicing Inhibitors Sensitise Cancer Cells to DNA Damage

*Victoria Shender, Russian Federation*

PP01.89: Higher and Higher N: SimpliFi Data Analysis for the Masses Now Takes Masses of Samples

*John Wilson, United States*

PP01.91: GlyPAQ Kit: Easy, Fast, and Standardized Sample Preparation for Simultaneous Processing of Deglycosylated Peptides and N-glycans for Structural Analysis.

*Melinda Wojtkiewicz, United States*

PP01.93: De Novo Assembly of RNA-sequencing Reads Defines Non-canonical Viral-human Fusion Transcripts as a Source for Antigen Presentation in Cervical Cancer

*Qian Yang, United Kingdom*

PP01.95: Data-independent Acquisition (DIA) Performance on Proteomic Samples using a Zeno Trap

*Ihor Batruch, Canada*

PP01.97: A Comprehensive Spectral Library of Chicken RPE Proteome by Novel Ion Mobility Fractionation Coupled to dia-PASEF Technology

*Jingfang Bian, Hong Kong*

PP01.99: Functionalized Nanoparticles Provide Quantitative Large-Scale, Unbiased, and Deep Plasma Proteomics

*Lee Cantrell, United States*

## PROGRAM

- PP01.101: A Pioneering Deep Proteomics Data Analytics Pipeline: Illuminating a New Functional Breast Cancer Subtype  
*Senuri De Silva, Singapore*
- PP01.103: An EasyPep Magnetic Solution for Automated Proteomics Sample Preparation  
*Maowei Dou, United States*
- PP01.105: Optimizing Protein Precipitation of Human Cell Lines for Profiling Proteomics via LC-MS  
*Jaehee Ha, Republic of Korea*
- PP01.107: High-throughput Proteomics on a Novel High-resolution Accurate Mass (HRAM) Platform  
*Daniel Hermanson, United States*
- PP01.109: Protein Array Analyses Identify STAT5-GLDC as Potential Mediators of Lactation Stimulation of Breast Tumorigenesis via Metabolic Remodeling  
*Shixia Huang, United States*
- PP01.111: Highly Multiplexed APEX2 Proximity Labeling for Spatiotemporal-Resolved Profiling of Submitochondrial Proteome  
*Donggi Jang, Republic of Korea*
- PP01.113: Evaluation of the Relative Quantitative Performance Using Tandem Mass Tags on a New High-resolution Accurate Mass Platform  
*Julia Kraegenbring, Germany*
- PP01.115: High Throughput and High Coverage Workflow for Plasma Proteome Analysis with Automation and Multi-proteases Strategy  
*Qingrun Li, China*
- PP01.119: New Set of Isobaric Labeling Reagents for Quantitative 16Plex Proteomics  
*Xiaolian Ning, China*
- PP01.121: A Benchmarking Workflow for High-Throughput DIA Label-Free Quantification Using a Novel High Resolution Accurate Mass Platform  
*Anna Pashkova, Germany*
- PP01.125: Chimerys Server: Deploying the Power of the Cloud in your Basement  
*Tobias Schmidt, Germany*
- PP01.127: Automated Sample Preparation for Human Plasma Proteomics by SP3  
*Malte Sielaff, Germany*
- PP01.129: An Automated High-throughput Sample Preparation platform utilizing S-Trap Digestion  
*Haneul Song, Republic of Korea*
- PP01.131: GeLC-FAIMS-MS: Multidimensional Sample Prefractionation for In-Depth Middle-Down Proteomics  
*Nobuaki Takemori, Japan*
- PP01.133: Ultrahigh-throughput Quantification of Acute Phase Plasma Proteins Using Acoustic Ejection Mass Spectrometry (AEMS) and Peptide Enrichment  
*Jennifer Van Eyk, United States*
- PP01.135: Evaluation of Two Sample Preparation Kits for Analyzing Chick Choroid Proteome Using Microflow LC Zeno-SWATH Mass Spectrometry  
*FENGJUAN JESSICA YU, Hong Kong*
- PP01.137: Target Identification of Natural Products and Chinese Medicine Using Mass Spectrometry  
*Yuling Chen, China*



## PROGRAM

PP01.139: Drug Target Identification of a Multi-Pass Transmembrane G Protein Coupled Receptor Antagonist Using Limited-Proteolysis Coupled Mass Spectrometry (LiP-MS)

*Yuehan Feng, Switzerland*

PP01.141: Identification of Target Proteins of Natural Compound in NAFLD Using DARTS-LC-MS/MS Proteomic Analysis and Mode of Action Study

*Yunyeong Jang, Republic of Korea*

PP01.143: Harnessing the Power of Limited Proteolysis and Ultra-Deep Mass Spectrometry Proteomics for Small Molecule Drug Target Identification and MOA Deconvolution

*amaury lachaud, Switzerland*

PP01.145: Discovery of Pan-IAP Degradors via a CRBN Recruiting Mechanism

*Gaseul Lee, Republic of Korea*

PP01.147: Revealing Protein-Protein Association Networks Through Proteome Thermal Stability Changes

*Daniel Martinez Molina, Sweden*

PP01.149: Integrated Glycomics and Proteomics in Cell Therapy to Uncover Cell-Specific Glycan Signatures and Protein Networks

*Myung Jin Oh, Republic of Korea*

PP01.151: Identification of Proteomic Landscape of Drug-binding Proteins in Living Cells by Proximity-dependent Target Identification

*Cheolhun Park, Republic of Korea*

PP01.153: Anti-cancer Compound Target Identification via Chemical Proteomics

*Sein Park, Republic of Korea*

PP01.155: Comparative Proteomic Analysis of Drug Shikonin Addition to Liver Cancer

*Zening Wang, China*

PP01.157: Formalin-Fixed Paraffin-Embedded Thyroid Nodule Proteomics and Machine Learning Analysis to Distinguish Carcinoma and Benign

*Hee-Sung Ahn, Republic of Korea*

PP01.159: Novel EGFR-Specific Peptides Identified Using Ribosome Display

*Kiattawee Choowongkamon, Thailand*

PP01.161: Craspase Specificity and Substrate Repertoire in Native and Model Proteomes

*Konstantinos Kalogeropoulos, Denmark*

PP01.163: Deep Phenotyping of Serum Proteome in Search for Early-stage Biomarker of Diabetes Neuropathy Using Micro-flow LC-MS/MS

*Gurjeet Kaur, Denmark*

PP01.165: nanoCSC Reveals Novel Insight into the Surfaceome of Primary Human Cardiomyocytes in Heart Failure.

*Mane Polite Roneldine Mesidor, United States*

PP01.167: Neoantigen Identification in Renal Cell Carcinoma Tissue by Mass Spectrometry

*Poorichaya Somparn, Thailand*

PP01.169: Unleashing Rapid Kinase Activity Analysis Using FRET-based Biosensor for Drug Screening Platform

*Lueacha Tabtimmai, Thailand*

PP01.171: Accounting for Common Genetic Variation in Proteomics

*Marc Vaudel, Norway*

## PROGRAM

- PP01.173: Improved Prediction of Response to Immune Checkpoint Blockade Therapy Across Multiple Cancer Types  
*Seonjeong Woo, Republic of Korea*
- PP01.175: Investigating the Molecular Neighbourhood of a Key Target in Alzheimer's Disease  
*Weronika Buczek, United Kingdom*
- PP01.177: Investigation of Proteomics Changes in Schizophrenic hiPSC-derived Brain Organoids Using Mass Spectrometry and Imaging  
*Lucrezia Criscuolo, Denmark*
- PP01.179: Thermal Proteome Profiling of Astrocytes with Variants in Alzheimer's Disease Risk Gene APOE  
*Jungsu Kim, United States*
- PP01.181: Weighted Protein Co-expression Network Analysis of Plasma Proteomes in Affective Disorders Using Multiple Reaction Monitoring-Mass Spectrometry  
*Yeongshin Kim, Republic of Korea*
- PP01.183: Multi-proteomic Analysis of 5xFAD Mice Reveals New Molecular Signatures for Early-stage Alzheimer's Disease  
*Seulah Lee, Republic of Korea*
- PP01.185: Regulation of Neuroinflammation in Alzheimer's Disease via the Immune Checkpoint Molecule Discovered by Proteomic Data Science Approach  
*Hagyeong Lee, Republic of Korea*
- PP01.187: Galectin 3 Binding Protein as Potential Biomarker for Early Detection of Glioma  
*Rashmi Rana, India*
- PP01.189: Gender- and Brain Region-Specific Alterations in Protein N-glycosylation in an Animal Model of Depression Induced by Chronic Adolescent Stress  
*InWoong Song, Republic of Korea*
- PP01.191: Proteomic Analysis of Tau-BiFC Mouse Model Exposed to Particulate Matter  
*Ji Hyun Back, Republic of Korea*
- PP01.193: Integrating MALDI-MSI with LCM-MS: Advancing Spatial Multi-omics Analysis in Brain Tissue  
*Byoung-Kyu Cho, United States*
- PP01.195: Lipidomics Strategies via MALDI-MSI Based on HR-MS for Molecular Signature in Tissues from Pancreatic  $\beta$ -cells BAG3 KO Mouse Models  
*Federica Di Marco, Italy*
- PP01.197: Spatial Proteome Mapping of Annotated Tumour Regions in Pancreatic Ductal Adenocarcinoma Tissues Reveals Eight Distinct Tumour Subpopulations  
*Lay Cheng Lim, Malaysia*
- PP01.199: Exploring the Potential of Transplanted Colon Organoids to Mimic Human Physiology in Mice Using Deep Visual Proteomics  
*Frederik Post, Denmark*
- PP01.201: Mapping the Spatial Proteome: Exploring Tissue Heterogeneity Through TMT Labeling and Multiplexed Mass Spectrometry Analysis  
*Yuanwei Xu, United States*

**Session Date/Time: Monday, September 18, 2023 - 01:15 PM - 02:15 PM**

**ISS04: Deep Exploration into Proteome Universe Combining Proteograph XT Workflow with Orbitrap Astral MS**



## PROGRAM

13:15 Speaker

*Daniel Hornburg, United States*

**Session Date/Time: Monday, September 18, 2023 - 01:15 PM - 02:15 PM**

### ISS05: Bruker Seminar

13:15 Sub-minute Gradient Capillary LC/MS/MS for High-speed, High-sensitivity and In-depth Proteomics

*Yasushi Ishihama, Japan*

13:40 High-sensitive Spatial and Cell-type Proteomics

*Ruijun Tian, China*

**Session Date/Time: Monday, September 18, 2023 - 01:15 PM - 02:15 PM**

### ISS06: Olink Seminar

13:15 Going Deep – Complementing Mass Spectrometry-based Methods with Affinity Probing to Enrich Plasma Proteome Coverage

*Stefanie Hauck, Germany*

13:45 Multiplex Techniques in Clinical Proteomics: A Complementary Tool for Biomarker Discovery

*Frank Schmidt, Qatar*

**Session Date/Time: Monday, September 18, 2023 - 02:30 PM - 03:35 PM**

### CS05: New Technologies for Large Scale Proteomics

Chair

*Sheri Wilcox, United States*

Chair

*Alexey Chernobrovkin, Sweden*

14:31 CS05.01: Keynote Speaker - Deep Plasma Proteomics at Scale: 8,000+ Protein Groups Across a 3,000 Subject Biomarker Study

*Bruce Wilcox, United States*

14:56 CS05.02: An In-Depth Investigation Into the Performance of Affinity and Mass Spectrometry Platforms on Large-Scale Plasma Proteomics Studies

*Sara Ahadi, United States*

15:09 CS05.03: Broad Target Scanning (BTS) - A Pragmatic LC-MS Acquisition Method for Collecting Population-Scale Real-World Proteomics Data

*Dmitry Avtonomov, United States*

15:22 CS05.04: Multiplexed Deep Plasma Profiling Using a Novel High-Resolution Accurate Mass Spectrometer

*Vincent Albrecht, Germany*

**Session Date/Time: Monday, September 18, 2023 - 02:30 PM - 03:35 PM**

### CS06: 3 Minute Thesis Competition



## PROGRAM

- 14:30 3MT01.01: 3 Minute Thesis Finalist  
*Mane Polite Roneldine Mesidor, United States*
- 14:35 3MT01.02: 3 Minute Thesis Finalist  
*Alireza Nameni, Belgium*
- 14:40 3MT01.03: 3 Minute Thesis Finalist  
*Dina Schuster, Switzerland*
- 14:45 3MT01.04: 3 Minute Thesis Finalist  
*Janaina Silva, Brazil*
- 14:50 3MT01.05: 3 Minute Thesis Finalist  
*Justin Sing, Canada*
- 14:55 3MT01.06: 3 Minute Thesis Finalist  
*Dafni Skiadopoulou, Norway*
- 15:00 3MT01.07: 3 Minute Thesis Finalist  
*Xue Sun, China*
- 15:05 3MT01.08: 3 Minute Thesis Finalist  
*Di Tang, Sweden*
- 15:10 3MT01.09: 3 Minute Thesis Finalist  
*Marvin Thielert, Germany*
- 15:15 3MT01.10: 3 Minute Thesis Finalist  
*Takehiro Tozuka, Japan*
- 15:20 3MT01.11: 3 Minute Thesis Finalist  
*Yun-Jung Yang, Taiwan*
- 15:25 3MT01.12: 3 Minute Thesis Finalist  
*Yu Zong, China*

**Session Date/Time: Monday, September 18, 2023 - 02:30 PM - 03:35 PM**

### **CS07: Extracellular Vesicles**

Chair

*Birgit Schilling, United States*

Chair

*Yong Tae Kwon, Republic of Korea*

- 14:31 CS07.01: Keynote Speaker - Proteomics in Mammalian and Bacterial Extracellular Vesicles and Integrated Database EVpedia  
*Yong Song Gho, Republic of Korea*
- 14:56 CS07.02: Prostate Cancer Reshapes the Secreted and Extracellular Vesicle Urinary Proteomes  
*Thomas Kislinger, Canada*
- 15:09 CS07.03: Proteogenomic Identification of Circulating Mutated Proteins in Extracellular Vesicles  
*Koji Ueda, Japan*





## PROGRAM

- 15:22 CS07.04: Mass Spectrometry Based Proteomic Profiling of Exosomal Proteins in Diabetic and Non-diabetic Ischemic Stroke Patients: A Case-Control Study  
*Muhammad Umar Sohail, Qatar*

**Session Date/Time: Monday, September 18, 2023 - 02:30 PM - 03:35 PM**

### CS08: Immunity and Immunopectidomics

Chair

*Wei Wu, Singapore*

Chair

*Aleksandra Nita-Lazar, United States*

- 14:31 CS08.01: Keynote Speaker - Great Expectations: Mass Spectrometry-Assisted Definition of the First Physiological Interactomes of TCR-like Antibodies  
*Nicola Ternette, United Kingdom*
- 14:56 CS08.02: Awesome Activities out there: Proteomics Discovery of Intercellular Signaling Circuits Regulating Inflammation  
*Felix Meissner, Germany*
- 15:09 CS08.03: Differential Enhancement of Antigen Presentation by Interferons in Lung Epithelia  
*Anthony Purcell, Australia*
- 15:22 CS08.04: The Impact of Varying Toll-like Receptor Activation on Intrinsic and Cross-presented MHC Peptidomes  
*Jessica Hung, United States*

**Session Date/Time: Monday, September 18, 2023 - 03:35 PM - 04:30 PM**

### PP01: Even Numbered Posters - Poster Viewing with Coffee Break

PP01.02: Extracellular Vesicles from  $\beta$ -thalassemia/HbE Reduced Endothelial Nitric Oxide Production  
*Pornthip Chaichompoo, Thailand*

PP01.04: Leveraging Deep Proteome Profiling of Plasma- and Serum-derived Extracellular Vesicles for Melanoma Biomarker Discovery and Disease Dissection  
*Yuehan Feng, Switzerland*

PP01.06: Proteomics Profiling of Tumor-derived Extracellular Vesicles for Triple-negative Breast Cancer Diagnosis  
*Juyong Hyon, Republic of Korea*

PP01.08: Small Extracellular Vesicle Protein Biomarker Profiles for Breast Cancer Diagnosis and Monitoring Progress  
*Yujin Lee, Australia*

PP01.10: Size-exclusion Purification of Extracellular Vesicles and Sample Characterization by Multiplex Fluorescent Western Blotting.  
*Kenneth Oh, United States*

PP01.12: The Involvement of Exosomes in Intercellular Communication During Chemotherapy-Induced Chemoresistance in Ovarian Cancer Cells  
*Polina Shnaider, Russian Federation*

## PROGRAM

PP01.14: Functional Characterization of EV Cargo and Surface Protein Complexes Towards Immunological and Organotropic Targeting in Vivo

*Wei Wu, Singapore*

PP01.16: pXg: Comprehensive Identification of Noncanonical MHC-I-associated Peptides from de Novo Peptide Sequencing using RNA-Seq Reads

*Seunghyuk Choi, Republic of Korea*

PP01.18: Unveiling the hidden potential of HLA-E in cancer immunity through a combinatorial approach to studying non-classical HLA-peptide repertoires

*Gabriel Goncalves, Australia*

PP01.20: Through a Direct Contact Mechanism, CD4 T Cell Can Generate FLT3LG, which Enables Them to Neutralize Cancer Effectively.

*Yeo Jin Im, Republic of Korea*

PP01.22: Efficient Identification of Immunopeptidomics and Clinically Relevant Neoantigens Presented on Lung Cancer by Mass Spectrometry

*Ziyi Li,*

PP01.24: Modulation of the Immunopeptidome by Serine Protease HtrA1

*Elizabeta Madzharova, Denmark*

PP01.26: The SystemMHC Atlas 2.0

*Wenguang Shao, China*

PP01.28: Enhanced Quantitative Analysis of Novel MHC-Peptides from Fusion Genes using Synthetic Polypeptide Sequences and High-Field Asymmetric Waveform Ion Mobility Spectrometry

*Zhaoguan Wu, Canada*

PP01.30: Discovery of Immunogenic Antigen Candidates Against Infectious Diseases for Vaccine Development and Diagnosis Platform Using Immunoproteomics Approach

*Jiyoung Yu, Republic of Korea*

PP01.32: A Complete, Deep Learning-driven and Quality-controlled Workflow for Tumor Antigen (TA) Discovery

*Qing Zhang, Canada*

PP01.34: Comprehensive Multi-omics Study Reveals Novel Colistin Resistance Profiles of *Acinetobacter Nosocomialis* Clinical Isolate, KAN02

*Hayoung Lee, Republic of Korea*

PP01.36: Accelerating the Development of Vaccines Against Nosocomial Infections: Proteomic Techniques Applied to AcinetoVax

*Gustavo Adolfo Sánchez-Corrales, Spain*

PP01.38: Multiproteomics Data Reveal Specific Associations between Plasma Proteomes and Auto/pathogen Immunoproteomes in a COVID-19 Timeline Study of ICU Patients

*Muhammad Umar Sohail, Qatar*

PP01.42: A Proteomics Insight into Streptolysin O's Multifunctionality: Unmasking Its Plasminogen Binding Role

*Di Tang, Sweden*

PP01.44: Novel Machine Learning Algorithm for Real-time Optimization of Mass Spectrometry-based Proteomics Data Acquisition to Improve Protein-protein Interaction Detection Sensitivity.

*Iryna Abramchuk, Canada*

PP01.46: Multi-layered Proteomics Approach to Elucidate Molecular Mechanisms of EGFR Signaling Diversity

*Akihiro Eguchi, Denmark*

## PROGRAM

- PP01.48: ChIP-MS Reveals the Local Chromatin Composition by Label-free Quantitative Proteomics  
*Dennis Kappei, Singapore*
- PP01.50: Global Interactome Mapping Reveals Pro-tumorigenic Interactions of NF- $\kappa$ B in Breast Cancer  
*Petr Lapcik, Czech Republic*
- PP01.52: Mass Spectrometry Analysis of the ADORA2A Interactome in a PDRN Environment Using LC-MS  
*Wonseok Lee, Republic of Korea*
- PP01.54: Interactome Profiling of UGP2 Splice-forms Differently Prevailing in Normal and Cancer Tissue  
*Ekaterina Poverennaya, Russian Federation*
- PP01.56: Flashlight into the Function of Unannotated C11orf52 Using Affinity Purification Mass Spectrometry  
*Yeji Yang, Republic of Korea*
- PP01.58: Unraveling Molecular Pathways and Implications of Triclosan Exposure on Adipocyte Dysfunction: Insights from Proteome Integral Solubility Alteration.  
*Susana Cristobal, Sweden*
- PP01.60: Transcriptome-wide Association Study Reveals Cholesterol Metabolism Gene Lpl is a Key Regulator of Cognitive Dysfunction  
*Wei Hu, China*
- PP01.62: Advances in Metabolomics using Untargeted Ion Chromatography Coupled with an Orbitrap Mass Spectrometer for Profiling.  
*Wai-Chi Man, United Kingdom*
- PP01.64: C18ORF25 is a Novel Exercise-Regulated AMPK Substrate Regulating Skeletal Muscle Function  
*Yaan Kit Ng, Australia*
- PP01.66: Analysis of m6A Modifications in HepG2 Cells  
*Viktoriiia Arzumanian, Russian Federation*
- PP01.68: ExpressVis: a Biologist-oriented Interactive Web Server for Exploring Multi-omics Data  
*Cheng Chang, China*
- PP01.70: Therapeutic Target Discovery Using Proteome-Wide Analyses in Large Population Health Studies Like the UK Biobank  
*Ray Chen, United States*
- PP01.72: Multiome Reveals the Molecular Regulation in Post-TKI Lung Adenocarcinoma  
*YiJing Hsiao, Taiwan*
- PP01.74: Building of a Massive Spectral Library Based on Experimental Data Applying Real Analysis Conditions  
*Dooun Jang, Republic of Korea*
- PP01.76: Proteogenomic Analysis of Longitudinal Trajectory of Glioblastoma Evolution  
*Kyung-Hee Kim, Republic of Korea*
- PP01.78: Deep Unbiased Interrogation of the Human Plasma Proteome in a Cancer Cohort of 3000 Subjects  
*Joon-yong Lee, United States*
- PP01.80: Proteogenomic Landscape of East-Asian Breast Cancer Reveals Pathogenesis and Subtypes for Prognostic and Therapeutic opportunities  
*Kuen-Tyng Lin, Taiwan*
- PP01.82: Drug Identification Using Genomic Feature, Kinase Activity Profiles, and Drug Screening with Patient-derived Models in Giant Cell Tumor of Bone  
*Rei Noguchi, Japan*



## PROGRAM

PP01.84: Omics Approaches for the Understanding of Herbs Used in Kampo Topical Medications

*Manon Paul-Traversaz, France*

PP01.86: The Effect of Exercise on the Serum Proteomes and Metabolomes of Elite-level Athletes in Different Sports Disciplines

*Yoondam Seo, Republic of Korea*

PP01.88: Integrating DIA-NN Software Analysis of Data-independent Acquisition Data into a Cloud Processing Pipeline

*Katherine Tran, Canada*

PP01.90: Understanding all of Biology: Simultaneous, High-throughput Si-Trap Multiomics Sample Preparation

*John Wilson, United States*

PP01.92: Transcriptional Landscape and Novel Candidate Genes in Heart Failure

*Fuyi Xu, China*

PP01.94: Targeted Detection of Protein Complexes by Mini-Complexome Profiling (mCP)

*Hugo Alejandro Amedei, Germany*

PP01.96: Standardized, High-throughput Platform for Automated, Rapid, and Extensive Plasma Proteome Characterization

*Manuel Bauer, Switzerland*

PP01.98: Solution-stabilized TMT & TMTpro Reagents in 96 Well Plates for High-throughput Sample Processing

*Ryan Bomgarden, United States*

PP01.100: Optimizing Experimental Design for Multi-kit TMT Labeling of Mixed Proteomes

*Jenna Cleyle, Canada*

PP01.102: BeatBox and iST for Standardized FFPE Tissue Processing: A robust, High-throughput, Xylene-free Sample Preparation for Proteomic Analysis

*Zuzana Demianova, Germany*

PP01.104: Ultra-fast Narrow Window DIA Approach for Quantitative Analysis of Comprehensive Proteomes with High Sequencing Depth and Quantitative Accuracy

*Ulises H Guzman, Denmark*

PP01.106: Proximity Extension Assay in Combination with Next Generation Sequencing continues to Increase throughput in Proteomics

*Sara Henriksson, Sweden*

PP01.108: A New High-Throughput Platform for Proteomics: Orbitrap unites with a Novel High-resolution Accurate Mass Analyzer

*Christian Hock, Germany*

PP01.110: Development of High Through-put Proteomics Using an LC-Quadrupole-Orbitrap Mass Spectrometer with Data-Independent Acquisition

*Masaki Ishikawa, Japan*

PP01.112: Human Biofluids Analysis Using a Scalable, Deep, Unbiased, Automated, Nanoparticle-based Proteomics Platform

*Wei Jiang, United States*

PP01.114: Spectra-Sum Method for Protein Quantification Using LC-MS/MS and TMT Labeling Data

*Haehyun Lee, Republic of Korea*

PP01.116: Comparison of Guinea Pig Retinal Proteomes Prepared Using S-Trap<sup>TM</sup> and EasyPep<sup>TM</sup> Protocols for Label-Free Proteomics

*Daqian Lu, Hong Kong*

## PROGRAM

PP01.118: Innovative High-throughput ENRICH-iST Workflow Facilitates Fast and Robust Plasma and Serum Proteome Profiling.

*Chloé Moritz, Germany*

PP01.120: Automated Data Analysis and Tools for Mass-Spectrometry-Based Omics: Introducing SpAC9 Data Foundry

*Gun Wook Park, Republic of Korea*

PP01.122: Label-Free Quantitation of Protein Mixtures Using Data-Independent Acquisition (DIA)

*Patrick Pribil, Canada*

PP01.124: Single-shot LC-MS Workflow for Comprehensive Proteome Identification on a Novel High-Resolution Accurate Mass Platform

*Julian Saba, Canada*

PP01.126: Data - Information - Knowledge Effortlessly: Combining timsTOF data with PaSER information and Mass Dynamics Knowledge to Accelerate Proteomic Discoveries

*Nobuyuki Shimura, Japan*

PP01.128: Next-Generation Protein Sequencing on Quantum-Si Platinum™: Advances in Protein Identification

*Kenneth Skinner, United States*

PP01.130: Nanoparticle Enrichment Mass-Spectrometry Proteomics Identifies Protein Altering Variants for Precise pQTL Mapping

*Karsten Suhre, Qatar*

PP01.132: High Throughput Plasma Proteome Profiling of Inflammatory Bowel Diseases Using a Novel High-resolution Accurate Mass Platform

*Jennifer Van Eyk, United States*

PP01.134: Unlocking the Potential of Large-cohort Proteomics Studies with a Novel High-resolution Accurate Mass Platform

*Yue Xuan, Germany*

PP01.136: Development of LC-MS/MS Analysis Method for High Throughput Screening of Protein Covalent Compounds and Verification Through Inter-laboratory Study

*Sanghyun Bae, Republic of Korea*

PP01.138: Understanding the Molecular Effects of Trilaciclib, a CDK4/6 Inhibitor, in the Treatment of FLT3-mutated Acute Leukaemia: Insights from Proteomic Analysis

*Amy George, United Kingdom*

PP01.140: Identifying the Anticancer Target of Ruthenium (III) Pyrazole Compounds in Colon Cancer by Chemoproteomics

*Jilin He, Hong Kong*

PP01.142: Unveiling the New Player in ER-Mitochondria Interactions by DARTS-LC-MS/MS Proteome Analysis

*Minjeong Ko, Republic of Korea*

PP01.144: High-Depth Multiplexed Drug Profiling with the Orbitrap Ascend

*Amanda Lee, United States*

PP01.146: A Proteomic Study on Traditional Chinese Medicine: Bavachinin Regulates Bone Homeostasis in T2DM via Inhibition of Ferroptosis Pathway.

*Jingwen Liu, China*

PP01.148: Genetically Encodable Click Reactions(GEN-Click) for Spatially Restricted Protein and Metabolite Labeling

*Pratyush Mishra, Republic of Korea*



## PROGRAM

- PP01.150: Proteomic Characterization of Triple-negative Breast Cancer Treated with Nucleolin-targeting Aptamer AS1411  
*Hyoung Min Park, Republic of Korea*
- PP01.152: Proteomics Application in Discovering Therapeutic Effect of Dental Mesenchymal Stem Cell Secretome on Stroke.  
*Sehoon Park, Republic of Korea*
- PP01.154: Comprehensive Characterization of the Mechanism of Action of GSK3 Inhibitors in Stem Cells Using Functional Proteomics  
*Pierre Sabatier, Denmark*
- PP01.156: Time-resolved Phosphoproteomics of Colorectal Cancer Liver Metastases Resistant to Adjuvant Chemotherapy Reveals PI3K-PAK1 Axis as a Potential Therapeutic Target  
*Jun Adachi, Japan*
- PP01.158: Using Proteomics to Improve Risk Prediction Models for Common Diseases in Participants from the UK Biobank Pharma Proteomics Project  
*Shing Wan Choi, United States*
- PP01.160: Facilitating Precision Medicine through Targeted Proteomics Analysis of Dried Plasma from Fingerpricks  
*Andreas Hober, Sweden*
- PP01.162: Metabolomic Profiling Identified Serum Metabolite Biomarkers and Muscle Pathophysiology of Idiopathic Inflammatory Myopathy  
*Jihyun Kang, Republic of Korea*
- PP01.164: Proteomic Representation of the Genetic Architecture of Monogenic Diabetes  
*Ksenia Kuznetsova, Norway*
- PP01.166: Next Generation Proteomics of New Liquid Biopsy in Early Lung Cancer  
*Yoonha Park, Republic of Korea*
- PP01.168: A protein-based Prognostic Prediction Model to Stratify Pediatric Patients with Papillary Thyroid Carcinoma  
*Yaoting Sun, China*
- PP01.170: Mass Spectrometric Blood Metabogram: Characterization and Application to Disease Diagnostics  
*Oxana Trifonova, Russian Federation*
- PP01.172: Kitted Universal MAM: Automatable Sample Processing for all Stages of Biological Drugs  
*John Wilson, United States*
- PP01.174: Deciphering Deregulated Mechanisms Associated with Huntington's Disease and X-linked Dystonia Parkinsonism Pathogenesis in Human Medium Spiny Neuron Models  
*Joanna Bons, United States*
- PP01.176: Integrative Proteomic Analysis with Neurotransmitters for the Brain of PS19 Alzheimer's Disease Model Mice  
*Eunji Cho, Republic of Korea*
- PP01.178: Newly Synthesized Proteome of Parkinson's Disease Peripheral Blood Mononuclear Cells  
*Dani Flinkman, Finland*
- PP01.180: Rnf146 Disrupts Wnt/ $\beta$ -catenin Signaling Pathway in a VPA-induced Mouse Model of Autism Spectrum Disorder  
*Seoyeon Kim, Republic of Korea*
- PP01.182: Multiplexed Quantitative Proteomics Revealed Proteome Alterations in Two Types of Rodent Traumatic Brain Injury Models  
*Young Sik Kim, Republic of Korea*



## PROGRAM

- PP01.184: Plasma Proteomic Signature of Mild Cognitive Impairment Using Proteograph Workflow  
*Seung Joon Lee, Republic of Korea*
- PP01.186: Deep Plasma Proteomic Landscape of Alzheimer's Disease: An 1800-Sample Cohort Study  
*Khatereh Motamedchaboki, United States*
- PP01.188: Uncovering Brain Region-specific O-glycophenotypes of Mice with Depressive-like Behavior  
*Youngsuk Seo, Republic of Korea*
- PP01.190: Exploring Proteomic Alterations and Co-expression Modules Associated with Tau-induced Pathologies in Human Tau-transgenic Mice  
*Kazuya Tsumagari, Japan*
- PP01.192: A Routine Workflow of Spatial Proteomics on the 0.002mm<sup>2</sup> of FFPE Tissues  
*Hao Chen, China*
- PP01.194: Spatial Proteomics of a Human Brain Tumour  
*Simon Davis, United Kingdom*
- PP01.196: Development of Robust Spatial N-Glycomics and Proteomics Techniques for Human Tissue Analysis  
*Young Ah Goo, United States*
- PP01.198: A Spatiotemporal Single-cell Type Map of Human Tissues Based on High-resolution Antibody-based Imaging  
*Cecilia Lindskog, Sweden*
- PP01.198: Phosphoproteomic Analysis to Identify the Mechanism Underlying the Development of Childhood Autism on Prenatal VPA Exposure  
*Hazara Begum Mohammad, Republic of Korea*
- PP01.200: MitoAtlas, a Mitochondrial Proteome Map Created with Super-Resolution-Proximity-Labeling  
*Nirmali Sharma, Republic of Korea*

**Session Date/Time: Monday, September 18, 2023 - 04:30 PM - 05:35 PM**

### **CS09: Pharmaco/Chemical Proteomics**

Chair

*Tadashi Kondo, Japan*

Chair

*Garry Corthals, Netherlands*

- 16:31 CS09.01: Keynote Speaker - Unraveling Drug-Target-Phenotype Interaction Using Label-Free Small Molecules Based Chemical Proteomics and Its Translational Implications  
*Ho Jeong Kwon, Republic of Korea*
- 16:56 CS09.02: High-Throughput (Phospho)Proteomics Drug Screening in Triple-Negative Breast Cancer Cell Lines Uncovers Targetable Nodes for Rational Drug Combination Therapies  
*Kristina Bennet Emdal, Denmark*
- 17:09 CS09.03: Proteome-Wide Pharmacophore Selectivity Profiling by Chemical Proteomics  
*Polina Prokofeva, Germany*
- 17:22 CS09.04: Perturbation Proteomics: Insights from 16,000 Perturbed Triple-negative Breast Cancer Proteomes  
*Rui Sun, China*

## PROGRAM

**Session Date/Time: Monday, September 18, 2023 - 04:30 PM - 05:35 PM**

### CS10: Proteomics and Biology

Chair

*Peter Hoffmann, Australia*

Chair

*Sergio Encarnación-Guevara, Mexico*

- 16:31 CS10.01: A Protein-Based Differential Diagnosis Classifier for Follicular Thyroid Neoplasms  
*Yaoting Sun, China*
- 16:44 CS10.02: Measurement of Proteins at Scale Using Protein Identification by Short-epitope Mapping (PRISM)  
*Parag Mallick, United States*
- 16:57 CS10.03: Enhancing Consistent Quantification and Site-Localization of PTMs in Large-Scale DIA-MS Experiments using Dynamic Alignment and Ion Mobility  
*Justin Sing, Canada*
- 17:10 CS10.04: Different Impact of Oscillating, Transient, and Sustained Activations on the Same Kinase: An Optogenetic-Phosphoproteomic Study  
*Yansheng Liu, United States*

**Session Date/Time: Monday, September 18, 2023 - 04:30 PM - 05:35 PM**

### CS11: Metabolism and Regulation

Chair

*Fernando Corrales, Spain*

Chair

*Min-sik Kim, Republic of Korea*

- 16:31 CS11.01: Keynote Speaker: Proteome-Wide Systems Genetics Identifies UFMylation as a Regulator of Muscle Function  
*Benjamin Parker, Australia*
- 16:56 CS11.02: Integrated Multi-Omics Analysis Reveals Enhanced Branched-Chain Amino Acids Metabolism Alleviates Non-alcoholic Steatohepatitis  
*Hyeong Min Lee, Republic of Korea*
- 17:09 CS11.03: Integrated Multiomics Examinations in the Study of Obesity and Type 2 Diabetes  
*Eva Csoz, Hungary*
- 17:22 CS11.04: Identification of Secreted Unannotated Small ORF Microproteins from Adipocytes and in Plasma to Elucidate Function of Novel Gene Product Proteins  
*Christopher Barnes, United States*

**Session Date/Time: Monday, September 18, 2023 - 04:30 PM - 05:35 PM**

### CS12: Infectious Diseases

Chair

*Bernd Wollscheid, Switzerland*





## PROGRAM

Chair

*Junho Park, Republic of Korea*

- 16:31 CS12.01: Keynote Speaker - Defeating Human Host Cell Defences by Stealth SARS-CoV-2 Infection Executed by NSP5/3CLpro Main Protease.  
*Christopher Overall, Canada*
- 16:56 CS12.02: Lipopolysaccharide-induced Changes in the Macrophage RNA-binding Subproteome.  
*Aleksandra Nita-Lazar, United States*
- 17:09 CS12.03: Uncovering Novel Anti-virulence Strategies to Combat Fungal Infections  
*Brianna Ball, Canada*
- 17:22 CS12.04: Time Dependent Characterization and SRM Based Validation of Protein Profiles Induced by Chronic Infection With Lymphocytic Choriomeningitis Virus  
*Asif Manzoor Khan, Denmark*

**Session Date/Time: Monday, September 18, 2023 - 05:45 PM - 06:30 PM**

### **PL03: Plenary Session: Manuscript Competition**

- 17:45 PL03.01: Immobility-associated Thromboprotection is Conserved across Mammalian Species from Bear to Human  
*Johannes Bruno Müller-Reif, Germany*
- 18:00 PL03.02: Global Detection of Human Variants and Isoforms by Deep Proteome Sequencing  
*Pavel Sinitcyn, United States*
- 18:15 PL03.03: Dissecting the Blood Ecosystem in SARS-CoV-2 Omicron Patients  
*Hong Wang, China*

**Session Date/Time: Tuesday, September 19, 2023 - 08:00 AM - 09:00 AM**

### **ISS07: Bruker Seminar**

- 08:00 An Extended View on Targetable Tumour Antigens using de Novo Sequencing  
*Nicola Ternette, United Kingdom*
- 08:25 Optimal Metagenomic Data Annotation Pipeline Facilitates Deep Metaproteomic Coverage of Microbiota by TIMS-TOF PASEF  
*Liang Qiao, China*

**Session Date/Time: Tuesday, September 19, 2023 - 08:00 AM - 09:00 AM**

### **ISS08: Protein Analysis – Fast, Easy, Robust Sample Preparation Workflows for Every Protein Type. Every Matrix. Every User.**

- 08:00 Speaker  
*Debadeep Bhattacharyya, United States*
- 08:10 Speaker  
*Kyunggon Kim, Republic of Korea*
- 08:30 Speaker  
*Qifeng Lin, Singapore*

## PROGRAM

**Session Date/Time: Tuesday, September 19, 2023 - 08:00 AM - 09:00 AM**

### **ISS09: Evolution of Mass Spec Technologies Enables Next Generation Therapeutics**

- 08:00      Increasing Biological Insight using Alternative Fragmentation and High Sensitivity MS/MS on the SCIEX ZenoTOF 7600 System  
*Patrick Pribil, Canada*
- 08:30      Standardized Clinical Proteomics Enabled by a fully Automated Sample Preparation strategy and Powered by Zeno SWATH DIA  
*Dorte Bekker-jensen, Denmark*

**Session Date/Time: Tuesday, September 19, 2023 - 09:15 AM - 10:00 AM**

### **PL04: Plenary Session: Matthias Mann, Germany - Technological Advances in MS-based Proteomics Applied to Single Cell Type Analysis in Cancer Tissues**

Chair  
*Je Yoel Cho, Republic of Korea*

- 09:17      PL04.01: Plenary Speaker - Technological Advances in MS-based Proteomics Applied to Single Cell Type Analysis in Cancer Tissues  
*Matthias Mann, Germany*

**Session Date/Time: Tuesday, September 19, 2023 - 10:15 AM - 11:45 AM**

### **CS13: Technological Advancements**

Chair  
*Khatereh Motamedchaboki, United States*

Chair  
*Sara Ahadi, United States*

- 10:16      CS13.01: Keynote Speaker  
*Melanie White, Australia*
- 10:41      CS13.02: Keynote Speaker - Bottom-up Proteomics Using DIA  
*Lukas Reiter, Switzerland*
- 11:06      CS13.03: Quantitative Aspects of diaPASEF on Current and Novel Instrumentation Evaluated by Response Curve Analysis  
*Ben Collins, United Kingdom*
- 11:19      CS13.04: The Astral Analyzer: A Rising Star for Deep & High-Throughput Proteomics.  
*Hamish Stewart, Germany*
- 11:32      CS13.05: Robust and Scalable Single-Molecule Protein Sequencing With Fluorosequencing  
*Jagannath Swaminathan, United States*

**Session Date/Time: Tuesday, September 19, 2023 - 10:15 AM - 11:45 AM**

### **CS14: Clinical Proteomics/Biomarkers**

## PROGRAM

Chair

*Ji Eun Lee, Republic of Korea*

Chair

*Byoung Chul Park, Republic of Korea*

- 10:16 CS14.01: Keynote Speaker - Genetics Meet Proteomics: Challenges and Opportunities for GWAS with MS Proteomics  
*Karsten Suhre, Qatar*
- 10:41 CS14.02: Keynote Speaker - In-depth Plasma Proteomics for Cancer Biomarker Discovery  
*Ayumu Taguchi, Japan*
- 11:06 CS14.03: Mapping Early Serum Proteome Signatures of Liver Regeneration in Living Donor Liver Transplant Cases  
*Fernando Corrales, Spain*
- 11:19 CS14.04: Proteomics of Human Colon Adenocarcinoma Tissues and Tissue-Derived Primary Cell Lines Reveal Unique Functions of Tumours and New Potential Biomarkers  
*Lifeng Peng, New Zealand*
- 11:32 CS14.05: Comparative Evaluation of In-Depth Mass Spectrometry and Antibody-Based Proteomic Platforms for Plasma Biomarker Discovery  
*Noora Sissala, Sweden*

**Session Date/Time: Tuesday, September 19, 2023 - 10:15 AM - 11:45 AM**

### **CS15: Spatial and Imaging Proteomics**

Chair

*Lingjun Li, United States*

Chair

*Je-Hyun Baek, Republic of Korea*

- 10:16 CS15.01: Keynote Speaker - Bioorthogonal Chemistry-enabled Spatial-temporal Proteomics  
*Peng Chen, China*
- 10:41 CS15.02: Keynote Speaker - A Spatio-temporal Single-cell Type Map of Human Tissues  
*Cecilia Lindskog, Sweden*
- 11:06 CS15.03: Statistical Approach to Predict Lymph Node Metastasis in Endometrial Cancer using Mass Spectrometry Imaging  
*Peter Hoffmann, Australia*
- 11:19 CS15.04: Multiplex-DIA and Deep Visual Proteomics Enhances Spatially-Resolved Proteome Resolution to Uncover the Landscape of Pancreatic Islet Biology  
*Marvin Thielert, Germany*
- 11:32 CS15.05: Near Single Cell Proteomics on FFPE Tissue Sections Using Hydrogel-Based Tissue Expansion and DIA-Based Mass Spectrometry  
*Zhen Dong, China*

**Session Date/Time: Tuesday, September 19, 2023 - 10:15 AM - 11:45 AM**

### **CS16: Cell Biology**



## PROGRAM

Chair

*Kyunggon Kim, Republic of Korea*

Chair

*Bernd Wollscheid, Switzerland*

- 10:16 CS16.01: Keynote Speaker - Biophysical Proteomics  
*Mikhail Savitski, Germany*
- 10:41 CS16.02: Keynote Speaker - OSBPL2 Mutations Causes Hearing Loss via Proteinopathy  
*Heon Yung Gee, Republic of Korea*
- 11:06 CS16.03: Impact of Additional Chromosomes on Cellular Phosphoproteome  
*Barbora Salovska, United States*
- 11:19 CS16.04: Unveiling IRF4-steered Regulation of Context-Dependent Effector Programs in Th17 and Treg cells  
*Ute Distler, Germany*
- 11:32 CS16.05: Unlocking the Secrets: Using Secretomics for Exploring Cell-to-Cell Communications  
*Juan Manuel Sacnun, Austria*

**Session Date/Time: Tuesday, September 19, 2023 - 11:45 AM - 01:00 PM**

**PP03: Odd Numbered Posters - Poster Viewing with Coffee Break**

PP03.01: MaxLFQ Algorithm Enables Accurate Hybrid Precursor-fragment-based Quantification of plexDIA Data in MaxQuant

*Dmitry Alexeev, Germany*

PP03.03: Mass Spectrogram Decomposition of DIA Proteomics Datasets for Identification and Quantitation of Peptides and Proteins

*Jherico Geronca, Japan*

PP03.05: A New Bioinformatic Tool to Evaluate Biosimilarity of Antibody Drugs Using Intact Glycoprotein Analysis with LC-MS and Artificial Neural Network

*Heeyoun Hwang, Republic of Korea*

PP03.07: Real-Time Search Improves Sensitivity of TMTpro Complementary Ion Quantification

*Amanda Lee, United States*

PP03.09: DeepQuant, A Neural Network for Interference Correction of Precursor Quantities

*An-phi Nguyen, Switzerland*

PP03.11: Midia-PASEF Maximizes Information Content in Data-Independent Acquisition Proteomics and Uses Machine Learning Based-Deconvolution to Generate DDA Quality Spectra

*Stefan Tenzer, Germany*

PP03.13: Real-Time Proteome Identification Using Deep Learning

*qianzhou wei, China*

PP03.15: CAPE: Chromatogram Aware Pointwise Embeddings for Peak Group Identification in Multi-Run Multi-Transition Chromatogram-Based Data-Independent Acquisition Mass Spectrometry Data Analysis

*Leon Xu, Canada*

PP03.17: AIDIA: AI-Empowered Data-Independent Acquisition Proteomic Analytics for High-Throughput Phenotyping for Unexplored and Understudied Proteins Biomarkers

*Fangfei Zhang, China*

## PROGRAM

- PP03.19: SGLT2 Inhibition Reveals Kidney Reconfiguration and Metabolic Inter-Organ Communication  
*Anja Billing, Denmark*
- PP03.21: The Role of TRPA1 Cation Channel in Progression of Cardiac Fibrosis  
*Jessa Flores, Republic of Korea*
- PP03.23: Proteome-wide Interrogation of Idiopathic Pulmonary Arterial Hypertension  
*Sungseek Kim, Republic of Korea*
- PP03.25: KATP Channel Dependent Heart Multiome Atlas  
*Sungjo Park, United States*
- PP03.27: Proteotranscriptomic Analysis Identified Inducer and Driven Molecular Pathway for Calcific Aortic Valve Disease  
*Hung M. Vu, Republic of Korea*
- PP03.29: Proteome Analysis of Chrna7 Knock Out Mice Suggests an Involvement of Nicotinic Acetylcholine Receptors in the Regulation of Ovarian Functions  
*Karolina Caban, Germany*
- PP03.31: A Novel Role for RNA in Regulating the Maturation of Trigger Factor During the Initial Stages of Protein Folding  
*Yura Choi, Republic of Korea*
- PP03.33: Time-Resolved Proteome Profiling of Glioblastoma Cell Response to Type I Interferon Stimulation Using DirectMS1 Approach  
*Mark Ivanov, Russian Federation*
- PP03.35: RNA-binding as Chaperones of DNA Binding Proteins from Starved Cells: The Role of N-terminal Lysines in E. coli Dps Assembly  
*Yoontae Jin, Republic of Korea*
- PP03.37: The Study Based on Proteomics on the Specific Function of Transforming Growth Factor-  $\beta$ 2 in Human Umbilical Vein Endothelial Cells  
*Soohyeon Kim, Republic of Korea*
- PP03.39: The Effects of Conditional UHRF1 Knockout in CD4+ T Cell on Mammary Tumor  
*Jiyeon Kim, Republic of Korea*
- PP03.41: Proteomic Analysis of Human Dermal Fibroblasts Induced by Dermal Matrix Alteration  
*Sun Young Lee, Republic of Korea*
- PP03.43: USP-A Regulates p53 Through the DnaJ- $\alpha$  with Cisplatin  
*Yosuk Min, Republic of Korea*
- PP03.45: Establishment of Novel Cancer Stem-Like Cells of Cholangiocarcinoma. And Their Characterization by Proteomics  
*Orasa Panawan, Thailand*
- PP03.47: Assessing Human Stem Cell Models of Human Peri-Implantation Development While Contributing Towards the Chromosome-Centric HPP  
*Charles Pineau, France*
- PP03.49: Proteomic Analysis of Primary Human Nasal Epithelium Reveals the Allergic mechanisms by House Dust Mite and Diesel Exhaust Particles  
*Hoseok Seo, Republic of Korea*
- PP03.51: Elevated Expression of ANOS1 Induce Tamoxifen Resistance and Leads to Poor Prognosis in ER+ Breast Cancer  
*Hoonyoung Yoon, Republic of Korea*



## PROGRAM

PP03.53: Temporal Omics Profiling Using a Mouse Model of Nonalcoholic Steatohepatitis-Associated Hepatocellular Carcinoma.

*Yuichi Abe, Japan*

PP03.55: Identification of Stratifin as a Novel Biomarker for Interstitial Lung Disease by an Affinity Proteomics

*Noriaki Arakawa, Japan*

PP03.57: Population Serum Proteomics Uncovers Prognostic Protein Classifier and New Perspective on the Pathophysiology for Metabolic Syndrome

*Xue Cai, China*

PP03.59: Translating of Tissue Proteomics Profile Into Plasma Protein Biomarker Signature by DIA-MS-based Proteomics

*Yi-ju Chen, Taiwan*

PP03.61: Pushing DIA Proteomics Analyses of Neat Plasma to 1000 Protein Groups ID/h

*Moonju Cho, Republic of Korea*

PP03.63: Performance and Validation of “Proteome Panels” as Classifications Tools of Kidney Transplants in FFPE Tissues.

*Garry Corthals, Netherlands*

PP03.65: Proteomic Profiling of Cerebrospinal Fluid Reveals Protein A as a Potential Biomarker for Medulloblastoma

*Ki-soon Dan, Republic of Korea*

PP03.67: Proteomic Characterization of Blood Samples From Cystic Fibrosis Patients by Mass Spectrometry

*Kerstin Fentker, Germany*

PP03.69: Proteome Profiling of Clinically Relevant Pig Models for Duchenne Muscular Dystrophy: Disease Mechanisms and the Potential of Exon Skipping Therapies.

*Thomas Fröhlich, Germany*

PP03.71: Characterizing the Effect of Adiposity on Cardiometabolic Traits and the Circulating Proteome in Qatar Biobank

*Lucy Goudswaard, United Kingdom*

PP03.73: A Comparison of Sputum Proteome Analysis in Asthma Patients Receiving Different Biologic Treatments

*Jeong-yeon Hong, Republic of Korea*

PP03.75: Proteomics-Based Discovery of Salivary Biomarker Candidates Specific to Periodontal Disease.

*Kim Inyoung, Republic of Korea*

PP03.77: Plasma Proteome Profiling for Discriminating Major Depressive Disorder and Bipolar Disorder by Data Independent Acquisition Mass Spectrometry

*Eunji Jeon, Republic of Korea*

PP03.79: Multiple Biomarkers Identification to Diagnose Metastatic Carcinoma from Thyroid Cancer Patients Plasma Using High-precision Proteomics Approach

*Jinwoo Jung, Republic of Korea*

PP03.81: False Discovery Rates: Not Just a Matter of Getting the Science Right

*Daan Kenis, Belgium*

PP03.83: Integrated Analysis of Proteome, Phosphoproteome, and N-glycoproteome for Immuno-oncology Biomarker Discovery

*Kwang Hoe Kim, Republic of Korea*

PP03.85: Development of a Novel Serum Biomarker Panel for Early Diagnosis of Pancreatic Ductal Adenocarcinoma

*Hyeonji Kim, Republic of Korea*

## PROGRAM

- PP03.87: Optimized Biochemical and Analytical Workflow for High-Throughput Clinical Peptidome Profiling  
*Chien-Yun Lee, Germany*
- PP03.89: Comprehensive Spectral Library Generation for Primary Human Immune Cells Using Data-Dependent Acquisition  
*Hyeonjeong Lee, Republic of Korea*
- PP03.91: Serum Proteome Profiling for Biomarker Discovery of Current Depressive Episode  
*Jiyeong Lee, Republic of Korea*
- PP03.93: Proteomic Analysis of Tumor Tissues Reveals LCP1 as a Potential Regulator Involved in Oral Cancer Recurrence  
*Chiao-Rou Liu, Taiwan*
- PP03.95: An Empirical Study on Adenosine Triphosphate-binding Cassette (ABC) Transporter through RnsD Protein in Discovery of Biomarkers.  
*Shagufa Malik, Republic of Korea*
- PP03.97: A Shotgun Proteomics Approach to Reveal New Putative Therapeutical Targets in Nephropathic Cystinosis  
*Jesus Mateos, España*
- PP03.99: Investigating the Plasma Proteome of People Living with HIV (PLHIV) with ARV-associated Acute Kidney Injury in a South African Cohort.  
*Rethabile Mokoena, South Africa*
- PP03.101: Metabolic Phenotype of Leukemic Cells : A Major Determinant of the Prognosis of AML Patients  
*Pascal Mossuz, France*
- PP03.103: Discovery of Biomarkers Related to Chronic Kidney Disease Through Comparative Plasma Exosome Proteome Analysis Via SWATH LC-MS Platform  
*Yumi Oh, Republic of Korea*
- PP03.105: Optimization of LC-MRM Method for the Quantification of Core-Fucosylated AFP Glycopeptide Using Evosep One and Triple Quad 6500+ system  
*Juri Park, Republic of Korea*
- PP03.107: Compatibility of Plasma Collected Using Microsampling Devices with Olink® Proteomics Technology  
*Marijana Rucevic, Sweden*
- PP03.109: FAIMS PRM: Sub Attomole Sensitivity for Plasma Proteomics Analysis  
*Simonas Savickas, Switzerland*
- PP03.111: Quantifiable Peptide Library Enable Rapid Development of Blood Test for Breast Cancer Detection  
*Hyeonseok Shin, Republic of Korea*
- PP03.113: Investigation of Biomarkers in Osteosarcoma Chemoresistance Using Proteomics Technique  
*Nutnicha Sirikaew, Thailand*
- PP03.115: Development of an Ultrasensitive 2-Plex Immunoassay to Evaluate Serum Fucosylated PSA and GDF-15 for the Detection of Aggressive Prostate Cancer  
*Jin Song, United States*
- PP03.117: Comparative Study of LC-MRM Platforms for the Quantification of Core-Fucosylated AFP Glycopeptides in the Diagnosis of Hepatocellular Carcinoma (HCC)  
*Hanseul Suh, Republic of Korea*
- PP03.119: Identifying Patients With Rapid Progression From Hormone-Sensitive to Castration-Resistant Prostate Cancer: A Retrospective Study  
*Yaoting Sun, China*



## PROGRAM

- PP03.121: SWATH-MS-based Proteomics for Osteosarcoma Surface Target Identification From Patient-Derived Tumor Tissues  
*Viraporn Thepbundit, Thailand*
- PP03.123: Proteomics Assessment of Early Treated Adults With Phenylketonuria: A Perspective Sight to Personalized Medicine  
*Silvia Valentinuzzi, Italy*
- PP03.125: Multi-omics Precision Medicine Approach to Identify Effective Therapies for Advanced Cancer Patients  
*Juanjua Wang, China*
- PP03.127: Discovery of Urinary Proteins Correlating with HbA1c in Plasma by Quantitative Proteomics  
*Keiko Yamamoto, Japan*
- PP03.129: Discovery of Urine Biomarkers for Early Detection of Kidney Injuries in Diabetic Patients by Quantitative Proteomics  
*Kengo Yanagita, Japan*
- PP03.131: In-Depth Urinary and Exosome Proteome Profiling Analysis Identifies Novel Biomarkers for Diabetic Kidney Disease  
*Linhui Zhai, China*
- PP03.133: Early Urinary Candidate Biomarkers and Clinical Outcomes of Intervention in a Rat Model of Experimental Autoimmune Encephalomyelitis  
*Yameng Zhang, China*
- PP03.135: Toxicoproteomics for Evaluating the Toxicity of Pharmaceutical By-Products of Furosemide, a Widely-Used Diuretics  
*Sandrine Bourgoin-Voillard, France*
- PP03.137: Simultaneous Quantification of South Korea representative Allergenic Foods with Optimized HPLC-MS/MS Approaches  
*Minkyung Jun, Republic of Korea*
- PP03.139: Investigation of Soluble Protein Retention in Donor Human Milk After Holder Pasteurization, High-Pressure Process and UV-C Treatment  
*Bum-Jin Kim, United States*
- PP03.141: Phospho-proteomic Analysis of Microbe-Associated Molecular Patterns (MAMPs) Signalling in Plant Immunity  
*Jianan Lu, United Kingdom*
- PP03.143: Proteomics Analysis of Porcine Lens Epithelial Cells in Response to Lycium Barbarum Polysaccharide Against Oxidative Damage - iTRAQ Approach  
*Samantha Sw Shan, Hong Kong*
- PP03.145: Characterization of Potential Allergens in Different Forms of Krill and Whiteleg Shrimp by Shotgun Proteomics  
*Chantragan Srisomsap, Thailand*
- PP03.147: Effect of Postharvest Storage Conditions on Cellular Pathways in Kale (Brassica Oleracea)  
*Xin Ee Yong, Singapore*
- PP03.149: Development of Anion Exchange-mediated Glycopeptide Enrichment Methods for Characterization of Poly-LAcNAc-containing Glycoproteins in Malignant Melanoma Cells  
*Gege Xu, United States*
- PP03.151: Quantification Analysis of Site-specific N- and O-glycopeptides for Characterization of Fusion Protein Etanercept  
*Heeyoun Hwang, Republic of Korea*





## PROGRAM

PP03.153: Introducing the GlycoPaSER Prototype for Real-Time N-glycopeptide Identification on the PaSER Platform

*ShinKwon Kang, Republic of Korea*

PP03.155: Comparative Glycoprotein Analysis of Human and Porcine Red Blood Cells for Enhanced Xenotransfusion Compatibility

*Jae Ho Kim, Republic of Korea*

PP03.157: Detection of Pancreatic Ductal Adenocarcinoma-Associated Proteins in Serum

*Tung-Shing Mamie Lih, United States*

PP03.159: In-Depth Site-Specific O-Glycosylation Analysis of Glycoproteins in 3xTg-AD mouse model of Alzheimer's Disease

*Jiyoung Mun, Republic of Korea*

PP03.161: Advanced Assessment Through Intact Glycopeptide Analysis of Infliximab's Biologics and Biosimilar

*Yeseul Park, Republic of Korea*

PP03.163: Identification of Intact Sialylated N-glycopeptides using TiO<sub>2</sub> Chromatography in Combination with LC-MS/MS and Accurate Mass Matching Using the GPMW Glyco-tool

*Maria Kyung-Ah Petersen, Denmark*

PP03.165: Effective Mass Spectrometry-Based Methods for Comprehensive Characterization of Surface Glycoproteins and Their Dynamics in Immune Cells during the Infection

*Ronghu Wu, United States*

PP03.167: Search and Investigation of Potential Peptide Agents of Interaction Between Human Organism and Its Microbiome

*Georgij Arapidi, Russian Federation*

PP03.169: The Proteomic and Metaproteomic Analysis of the Infant Gut and Gut Microbiome in African HIV Exposed Infants

*Tara Miller, South Africa*

PP03.171: Accounting for Chimeric Spectra Boosts the Number of Identifications in Metaproteomics Without Impacting Sensitivity

*Tim Van Den Bossche, Belgium*

PP03.173: Some Lessons Learned on the Impact of the Storage and Injection of Samples on The GC-MS Reproducibility

*Ilya Kurbatov, Russian Federation*

PP03.175: Chromosome-Centric Human Proteome Study of Chromosome 11 Team

*Mina Park, Republic of Korea*

PP03.177: Highly Selective and Reproducible Glycopeptide Enrichment using ZIC-HILIC Chromatography in Human Serum

*Won Jun Yoo, Republic of Korea*

PP03.179: A Novel, Deep, Unbiased and Scalable Nanoparticle-Based Proteomics Workflow from Model Organisms with Limited Plasma/Serum Sample

*Shao-yung (Eric) Chen, United States*

PP03.181: Automated Pipeline for Robust and High Throughput Analyses of Low Input Proximity-Labeling Samples

*Therese Dau, Germany*

PP03.183: Protein and Peptide Signatures Separate Healthy Aging, Mild Cognitive Impairment and Alzheimer's Disease in a Paired CSF and Plasma Study

*Yuehan Feng, Switzerland*



## PROGRAM

PP03.185: onePOT, a Chaotrope-free Method for Near Single Cell Proteomics

*David Goodlett, Canada*

PP03.187: A Novel Online 3-Dimensional Separation for Comprehensive Phosphoproteome

*Chaewon Kang, Republic of Korea*

PP03.189: Discovery of Novel Bioactive Peptides in Plasma and Tissue Based on a High-Yield Peptide Extraction Method

*Yoshio Koderu, Japan*

PP03.191: Microflow 4D-Proteomics for Robust, High-Throughput Sample Analysis

*Kwangseon Lee, Republic of Korea*

PP03.193: Quadrupole Isolation and Characterization of Specific Proteoforms and Protein Complexes at a High m/z Range Using Orbitrap Ascend

*Rafael Melani, United States*

PP03.195: Development of PTMScan-HS Immunoaffinity Reagents and Standards for PTM Enrichment: High Sensitivity, High Specificity, Highly Simplified, and High Throughput

*Alissa Nelson, United States*

PP03.197: One-STAGE Tip Method for TMT based Proteomic Analysis of Minimal Amount of Cells

*Narae Park, Republic of Korea*

PP03.199: Improved SDS Depletion From Proteins With Automation and Minimal Sample Consumption by Transmembrane Electrophoresis.

*Hammam Said, Canada*

PP03.201: SP3 vs. SP4: A Practical Comparison of Cost, Handling, and Performance in a Core Facility.

*Marc Sylvester, Germany*

PP03.203: High-Throughput Proteomics at All Chromatographic Flow Rates

*Giorgi Tsiklauri, Germany*

PP03.205: Preparation of High-Density and Scalable Protein Arrays for Comprehensive Single-Molecule Proteomic Studies

*Sheri Wilcox, United States*

PP03.207: Shredder: A New Way to Sequence

*John Wilson, United States*

**Session Date/Time: Tuesday, September 19, 2023 - 01:15 PM - 02:15 PM**

**ISS10: New Insights into Analyzing Glycopeptides on Tribrid Mass Spectrometers**

13:15 Speaker

*Nicholas Riley, United States*

**Session Date/Time: Tuesday, September 19, 2023 - 01:15 PM - 02:15 PM**

**ISS11: Bruker Seminar**

13:15 Throughput without compromise in Immuno-peptidomics using timsTOF technology combined with EvoSep One

*Anthony Purcell, Australia*

## PROGRAM

- 13:40 Maximizing Information Content in Data-independent Acquisition using media-PASEF  
*Stefan Tenzer, Germany*

**Session Date/Time: Tuesday, September 19, 2023 - 01:15 PM - 02:15 PM**

### ISS12: Olink Seminar

- 13:15 Olink® Explore HT – A New Era in Proteomics  
*Andrea Ballagi, Sweden*
- 13:35 Olink® Explore HT – Proven Technology, Validated by Scientists  
*Jenny Samskog, Sweden*
- 13:55 Translating Millions of Datapoints to Actionable Insights  
*Per Eriksson, Sweden*

**Session Date/Time: Tuesday, September 19, 2023 - 01:15 PM - 02:15 PM**

### ISS13: Disease Risk Visualization by SomaScan® Assay

- 13:15 Speaker  
*Iwao Waga, Japan*

**Session Date/Time: Tuesday, September 19, 2023 - 02:30 PM - 03:35 PM**

### CS17: Standardization and Harmonization

- Chair  
*Sang-Won Lee, Republic of Korea*
- Chair  
*Lydie Lane, Switzerland*
- 14:31 CS17.01: Keynote Speaker - Exploring Public Data Repositories by Integration and Sharing of Proteome Data  
*Yasushi Ishihama, Japan*
- 14:56 CS17.02: lesSDRF Is More: Maximizing The Value Of Proteomics Data Through Streamlined Metadata Annotation  
*Tine Claeys, Belgium*
- 15:09 CS17.03: MassSpecPreppy - Cost-Effective End-To-End Solution for Automated & Flexible Sample Preparation for Proteome Profiling by Mass Spectrometry  
*Stephan Michalik, Germany*
- 15:22 CS17.04: Sample Preparation to Match Analytical Advances: 384-well S-Trap plates  
*John Wilson, United States*

**Session Date/Time: Tuesday, September 19, 2023 - 02:30 PM - 03:35 PM**

### CS18: Glycoproteomics



## PROGRAM

Chair

*Nicolle Packer, Australia*

Chair

*Morten Thaysen-andersen, Australia*

- 14:31 CS18.01: Keynote Speaker - Small but Giant Leaps towards Neuroglycomics: Spatial and Temporal Diversity of Glycome Expression in Mammalian Brain  
*Hyun Joo An, Republic of Korea*
- 14:56 CS18.02: GlycopeptideAtlas: A Comprehensive Database and Analysis Tools for Glycoproteomic Characterization in Disease Studies  
*Yingwei Hu, United States*
- 15:09 CS18.03: Deep Quantitative Glycoproteomics Reveals Gut Microbiome Induced Remodeling of the Brain Glycoproteome  
*Clement Potel, Germany*
- 15:22 CS18.04: Distinctive Antibody Glycosylation Profiles in ESRD Patients with Divergent Immune Responses to COVID-19 Vaccination  
*Yun-Jung Yang, Taiwan*

**Session Date/Time: Tuesday, September 19, 2023 - 02:30 PM - 03:35 PM**

### **CS19: Microbial Proteomics, Microbiome and Metaproteomics**

Chair

*Tim Van Den Bossche, Belgium*

Chair

*Uwe Völker, Germany*

- 14:31 CS19.01: Keynote Speaker - Proteomics of One Health  
*Jennifer Geddes-McAlister, Canada*
- 14:56 CS19.02: The Acetylome of Campylobacter jejuni Shows Lysine Acetylation of the CadF Adhesin Regulates Host Cell Binding  
*Stuart Cordwell, Australia*
- 15:09 CS19.03: Untargeted Data-Independent Acquisition for Metaproteomics of Complex Microbial Samples  
*Laura Elo, Finland*
- 15:22 CS19.04: metaExpertPro: A Computational Workflow for Data-Independent Acquisition Mass Spectrometry-Based Metaproteomics Data Analysis  
*Yingying Sun, China*

**Session Date/Time: Tuesday, September 19, 2023 - 02:30 PM - 03:35 PM**

### **MS02: Mentoring Session 2 - Promoting Your Science**

Chair

*Daniel Garama, Australia*

Chair

*Mathieu Lavallée-Adam, Canada*



## PROGRAM

MS02.01: Panelist

*Alexey Nesvizhskii, United States*

MS02.02: Panelist

*Hyun Woo Park, Republic of Korea*

MS02.03: Panelist

*Stephen Pennington, Ireland*

MS02.04: Panelist

*Paula Burton, Australia*

**Session Date/Time: Tuesday, September 19, 2023 - 03:35 PM - 04:30 PM**

**PP03: Even Numbered Posters - Poster Viewing with Coffee Break**

PP03.02: PandaNovo: An Efficient and Accurate Transformer-Based Model for de Novo Peptide Sequencing

*Cheng Chang, China*

PP03.04: Harnessing Machine Learning to Correct Peptides Intensity Heterogeneity and Enhance Mass Spectrometry Data Analysis

*Daniel Hornburg, United States*

PP03.06: Transfer Learning Model Based Nt-Arginylome Analysis Reveals Organelle Specific Novel Arg/N-degrons

*Shinyeong Ju, Republic of Korea*

PP03.08: A Novel Denovo Model based on Transformer for Proteomics Research

*Ziyi Li,*

PP03.10: DeepMRM: Deep Learning-Based Object Detection Model for Targeted Proteomics Data and Its Extension to Untargeted Proteomics Data

*Jungkap Park, Republic of Korea*

PP03.12: Data Mining Antibody Sequences for Database Searching in Proteomics Data

*Xuan-Tung Trinh, Denmark*

PP03.14: A Complete Software Suite for de Novo Sequencing and Predicting the Immunogenicity of Class 1 and Class 2 Neoantigens

*Lei Xin, Canada*

PP03.16: MSFragger-WWA Coupled With Fragpipe Enables Fast and Easy Wide-Window Acquisition Data Analysis

*Fengchao Yu, United States*

PP03.18: DeepFLR Facilitates False Localization Rate Control in Phosphoproteomics

*Yu Zong, China*

PP03.20: Omics Approaches to Right Ventricular Maladaptive Hypertrophy in Chronic Pulmonary Hypertension

*Emilio Camafeita, Spain*

PP03.22: Mitochondrial Creatine Kinase Rescues the Heart from Ischemic Injury

*Maria Victoria Faith Garcia, Republic of Korea*

PP03.24: MDH2 Phosphorylation Renders Cardioprotection Against Hypoxia/Reoxygenation Injury

*Jubert Marquez, Republic of Korea*

## PROGRAM

PP03.26: Towards Deciphering the Molecular Signature Particular for Peripartum Cardiomyopathy Through a Data-Driven Multi-Omics Strategy

*Carolin Sailer, Denmark*

PP03.28: Effects of Rice Germ on Chronic Unpredictable Mild Stress-Induced Depressive-like Behavior: Alleviation through Neuroinflammation Reduction

*Sosorburam Batsukh, Republic of Korea*

PP03.30: Comprehensive Characterization of Protein Turnover by Comparative SILAC Labeling Analysis in 3T3-L1 Adipocytes

*Sunkyoo Choi, Qatar*

PP03.32: Liver Proteomics Profile to Unveil the Biological Role of BAG3 through Tissue-specific BAG3 Knockout Mouse Models

*Federica Di Marco, Italy*

PP03.34: LC-MS/MS-based Proteomic Analysis of Three-Dimensional Spheroids Derived From Human Primary Cells Exposed to Urban Particulate Matter

*Young June Jeon, Republic of Korea*

PP03.36: Mitochondrial Intracristal Space (ICS) Proteome Was Revealed by Mass Detection of Isotope-Coded Post-translational Modification by APEX

*Myeong-gyun Kang, Republic of Korea*

PP03.38: Highly Expressed QSOX2 in Triple-Negative Breast Cancer Overly Stabilizes Integrin- $\beta$ 1 for Rapid Migration and Proliferation of Tumor Cells

*A-In Kim, Republic of Korea*

PP03.40: Analysis of Resistance Biomarkers after EGFR TKI Treatment on NSCLCs

*Hyung Joon Kwon, Republic of Korea*

PP03.42: iTF-seq: Systematic Mapping of TF-mediated Cell Fate Changes by a Pooled Induction Coupled with scRNA-seq and Multi-omics Approaches

*Muyoung Lee, United States*

PP03.44: The Role of Ferroptosis Progress and Some Related Genes in Psoriasis Disease.

*Thien Nguyen Huu, Việt Nam*

PP03.46: Specific Tumor Immune Microenvironment(TIME) Profile Influences the Awakening of Dormant Cancer Cells

*Jong Hyeok Park, Republic of Korea*

PP03.48: The Use of Hydrophilic Magnetic Beads for Mass Spec Sample preparation as part of Complex Proteomic Workflows

*Michael Rosenblatt, United States*

PP03.50: Quantitative Analysis of Early Signaling Pathways in Lens-induced Myopia in C57BL/6J Mice Retina Proteome by SWATH-MS

*Ying Hon Sze, Hong Kong*

PP03.52: Investigating the Insulin Secretion Mechanism Regulated by AC9 with Pancreatic  $\beta$ -cell-specific AC9 Knockout Mice Through Proteomics

*Yanpu Zhao, China*

PP03.54: Unmasking Hidden Systemic Effects of Neurodegenerative Diseases: A Two-Pronged Approach to Biomarker Discovery

*Sandra Anjo, Portugal*

PP03.56: Multi-omics Approach to the Identification of Biomarkers for Progression from Psoriasis to Psoriatic Arthritis

*Annika Bendes, Sweden*

## PROGRAM

PP03.58: Integrated Proteomic and Transcriptomic Analysis Uncovers CASP as A Novel Oncogenic Player in Colorectal Cancer

*Ting Chen, China*

PP03.60: A Novel MALDI-TOF Platform for the Simultaneous Detection of Multiple Target Proteins in Clinical Microbiology

*Donghuey Cheon, Republic of Korea*

PP03.62: Enhanced Performance of MALDI-TOF MS Analysis for Proteins by Graphene-coated Silicon Wafer Plate

*YoonKyung Choi, Republic of Korea*

PP03.64: Integrated Fast Analysis of Transplant Biopsy Tissues with Histopathology to Improve Patient Outcome

*Garry Corthals, Netherlands*

PP03.66: Bench, Bedside, and Beyond: Navigating Ethics in Large-Scale Clinical Proteomics Research

*Ina Devos, Belgium*

PP03.68: Mass Spectrometry-based Profiling of Small FFPE Tissue Areas

*Marius Fraefel, Germany*

PP03.70: Viewing Amyloid Through the Proteomic Microscope: Characterization of Two Protein Misfolding Diseases Targeting the Heart

*Juliane Gottwald, Germany*

PP03.72: An In-Depth Plasma Proteomics Workflow Powered by Orbitrap Astral Mass Spectrometer

*Amirmansoor Hakimi, United States*

PP03.74: Proteomic Landscape Reveals Potential Protein Signature Independent of Helicobacter Pylori Infection in Gastric Cancer

*Hsiang-en Hsu, Taiwan*

PP03.76: Optimization of MALDI-TOF MS for CTX-M Subtype Detection From Clinical Isolates

*Heejung Jang, Republic of Korea*

PP03.78: Membrane Proteogenomics Analysis of CRISPR-9 Edited Non-small Cell Lung Cancer Cells

*Yu Teng Jheng, Taiwan*

PP03.80: Avian Model of Experimental Keratoconus: A Preliminary Proteomic Analysis of Corneal Limbus in Chicks

*Byung Soo Kang, Hong Kong*

PP03.82: Discovery of MDR-TB Biomarker Signature by Secretome Analysis and Quantitative Proteomics

*Hye-Jung Kim, Republic of Korea*

PP03.84: LC-MS based Discovery of Plasma Phosphopeptide Markers for Alzheimer's Disease Staging and Clinical trials

*Kyungdo Kim, Republic of Korea*

PP03.86: Targeted Mass Spectrometry-based Validation Race-specific Disease Diagnostic Protein Profiling in Laboratory Developed Tests

*Woojin Kim, Republic of Korea*

PP03.88: Discovery, Verification, and Validation of Walnut Protein Marker Peptides Using LC-MS Approaches

*Dain Lee, Republic of Korea*

PP03.90: Development of an Efficient Detection Method for Monoclonal Protein using MALDI-TOF Mass Spectrometry

*Jikyoo Lee, Republic of Korea*



## PROGRAM

- PP03.92: Serum Proteome Profiling of Sarcopenia Through Integration of Proteograph™ Workflow  
*Jiyeong Lee, Republic of Korea*
- PP03.94: Candidate Protein Biomarkers Associated with Glomerular Filtration Rate in Chronic Kidney Disease: a Proteomics Cohort Study  
*Zhalaliddin Makhammajanov, Kazakhstan*
- PP03.96: Identification of Prognostic Protein Biomarkers in Tears From Non-infectious Uveitis Patients Undergoing Biologic Treatment as a Prelude to Personalized Medicine.  
*Jesus Mateos, España*
- PP03.98: Single-Glomerular Spatial Proteomics Profiles Glomerular Heterogeneity in Chronic Kidney Disease  
*Liyuan Meng, China*
- PP03.100: Deeper Plasma Proteome Coverage Enables Identification of Novel Biomarkers and Classification of Diseases  
*Jonathan Moss, Australia*
- PP03.102: Unravelling the Pathomechanisms of Uterine Fibroids and Associated Heavy Menstrual Bleeding through Systems Biology  
*Darragh O'Brien, United Kingdom*
- PP03.104: Development of Diagnostic Multimarkers for Glioblastoma at Early Stages Using Quantitative Proteomic Method  
*Hyeonji Park, Republic of Korea*
- PP03.106: Machine Learning Applied to Molecular Protein Patterns for Diagnosis of Motor Neuron Disease  
*Livia Rosa-fernandes, Australia*
- PP03.108: Optimized Methods to Investigate the Human Lysosomal Proteome by Targeted Proteomics  
*Shigeru Sakamoto, Japan*
- PP03.110: Quantitative Analysis of Endogenous Native Peptides in Urine by DIA-NN after Generating a Comprehensive Spectral Library from DDA Mascot Data.  
*Amr shalaby, Japan*
- PP03.112: Comparative Proteoinformatics for Discovering the Potential Pathogenic Mechanisms of Oligozoospermia  
*Timur Shkrigunov, Russian Federation*
- PP03.114: Investigating the Role of Proteins in Regulating Breast Density in Premenopausal Breast Cancer Patients  
*Minsoo Son, United States*
- PP03.116: Utilizing HRAM Orbitrap MS to Quantify Therapeutic Monoclonal Antibodies (mAbs) in Human Serum for Clinical Research  
*Yvonne Song, United States*
- PP03.118: Proteomic Characterization Reveals a Prognosis Panel of Primary Prostate Cancer  
*Rui Sun, China*
- PP03.120: Quantitation of Clinically Approved Breast Cancer Biomarkers Utilising Selected Reaction Monitoring  
*Erin Sykes, Australia*
- PP03.122: Quantitative DIA Proteomics of Urinary Proteins for Identification of Gender and Ages, and for Biomarker Discovery in the Future  
*TOMOHIRO UCHIMOTO, Japan*
- PP03.124: Exploring Sample Preparation Methods for Plasma Proteomics  
*Iolanda Vendrell, United Kingdom*



## PROGRAM

PP03.126: Proteomic Profiling of Extracellular Vesicles and Particles From Prostate Cancer Cell Lines and Plasma Samples for Diagnosis and Risk Stratification

*Qi Wang, Australia*

PP03.128: Discovery of Urine Biomarkers for Diabetic Nephropathy Detectable Earlier Than Microalbuminuria Development

*Tadashi Yamamoto, Japan*

PP03.130: Quantitative Proteomics Approach Reveals ARCN1 as Potential Therapeutic Target of LUAD

*Chunhua Yang, China*

PP03.132: Exploration towards the Novel Biomarkers of Human Cystic Echinococcosis based on coupling of LC-MS/MS and Immunoassay

*Congmin Zhang, China*

PP03.134: Characterization of the Epigenetic Profile of Epidermis in Response to Co-exposure to Ultraviolet Radiations and Benzo[a]pyrene

*Sandrine Bourgoin-Voillard, France*

PP03.136: Exposure of Aged Microplastic Induces Changes in the Proteome of Daphnia Magna – A Comprehensive Ecotoxicoproteomic Study

*Thomas Fröhlich, Germany*

PP03.138: Identification of Cadmium-Responsive Proteins as Potential Biomarkers for Environmental Hazard Exposure

*Hee-Gyoo Kang, Republic of Korea*

PP03.140: Proteome Profiling of Alternative Proteins in Food Safety

*Qifeng Lin, Singapore*

PP03.142: Proteomic Mechanisms Underlying Lung Injury in Aging Rat Model Exposed to Fine Particular Matter Air Pollution

*Manh Quan Nguyen, Taiwan*

PP03.144: Crosslinking Mass Spectrometry for Rabbit Calicivirus Receptor Identification

*Elena Smertina, Australia*

PP03.146: Bee Metaproteomics as the Toolbox for Assessing Microbial Dynamics of One-Health Relevance.

*Bruno Tilocca, Italy*

PP03.148: Algorithm Development for Analysis of O-GlcNAcylated Protein using LC-MS/MS

*Dasom An, Republic of Korea*

PP03.150: Identifying Glycan Profile Differences of CD33 expressed in HEK293 and CHO Cells

*Kyle Hoffman, Canada*

PP03.152: Site-Specific Glycan Microheterogeneity Evaluation of Aflibercept Fusion Protein by Glycopeptide-Based LC-MS/MS Mapping

*Seoyoung Hwang, Republic of Korea*

PP03.154: A New Strategy for Glycopeptide Enrichment Using Combining ZIC-HILIC and Molecular Weight Cut-off

*Ji Hyun Kang, Republic of Korea*

PP03.156: N-glycomic Identification of Novel Soft Tissue Prognostic Biomarkers for Oral Cancers

*Ilya Kurbatov, Russian Federation*

PP03.158: Characterizing Degradation Products from Bacteroides Thetaiotaomicron to Understand Bacterial Dextran Utilization in the Gut.

*Wai-Chi Man, United Kingdom*



## PROGRAM

- PP03.160: Proteomic Analysis of Human Tissue and Organoids Derived From Hepatocellular Carcinoma  
*Ye Eun Park, Republic of Korea*
- PP03.162: High-resolution MS-based Glycoproteomics Analysis of Esophageal Cancer Lines Reveal Potential Link Between Estrogen Signaling and Esophageal Cancer  
*Chao Peng, China*
- PP03.164: Improvements in Glycoproteomics Through Architecture Changes to the Tribrid MS Platform  
*Nicholas Riley, United States*
- PP03.166: Proteome-Wide Discovery of Human Brain Protein Glycoforms and Glycan Modification Changes in Alzheimer's Disease  
*Qi Zhang, United States*
- PP03.168: Unveiling the Performance of a Novel High-Resolution Accurate Mass Platform for Proteomics Applications  
*Tabiwang N. Arrey, Germany*
- PP03.170: Generation of Amino Acid Sequences of Unknown Species for Metaproteomics Using Phylogenetic Relationships of Known Species  
*Nobuaki Miura, Japan*
- PP03.172: A Complete and Automated End-To-End Sample Preparation Strategy for High-Throughput and Standardized Proteomics With High Sensitivity  
*Dorte Bekker-jensen, Denmark*
- PP03.174: Operating, Maintaining, and Troubleshooting the Sensitivity and Robustness of timsTOF Platforms for Proteomics Studies  
*Xianming Liu, China*
- PP03.176: S-Trap Turbo: From Sample Prep to Analysis in Record Time  
*John Wilson, United States*
- PP03.178: A Unified Approach for Comprehensive Characterization of Intracellular and Extracellular Proteome Remodeling, Specifically Thiol-based, in Response to Oxidative Stress  
*Sandra Anjo, Portugal*
- PP03.180: Utilization of the Speed, Sensitivity and Accuracy of the ZenoTOF 7600 to Enhance Protein Identifications From Packed Emitter Columns  
*Jenna Cowen, Australia*
- PP03.182: A Comparative Investigation of Human Plasma Proteome Profiling With State-Of-The-Art Mass Spectrometry and Affinity-Based Assays  
*Yuehan Feng, Switzerland*
- PP03.184: Analysis of Peptides and Proteins by Native and SDS Capillary Gel Electrophoresis Coupled to Electrospray Ionization Mass Spectrometry  
*Enikő Gebri, Hungary*
- PP03.186: Critical micelle considered Filter-Aided Sample Preparation Method Combined with LC-MS/MS Allows Comprehensive Global Proteomic Profiling of Adipocytes  
*Jiwon Hong, Republic of Korea*
- PP03.188: An Approach Using Peptide Barcodes for Quantification of Duplicated Gene Products With Identical Sequence to Study the Evolutionary Significance  
*Keiji Kito, Japan*
- PP03.190: Single Drop Microextraction for Enhanced Detection in Glycan Analysis by Capillary Electrophoresis  
*Ilya Kurbatov, Russian Federation*



## PROGRAM

PP03.192: Improving Mass Accuracy in MALDI-TOF MS Analysis of Pathogenic Proteins Using 6xHIS-Tagged Internal Calibration

*Saeyoung Lee, Republic of Korea*

PP03.194: Approaching Single-Shot, Full Proteome Coverage Using Packed Emitter Columns

*Yanxiang Meng, Australia*

PP03.196: Quantifying 1000 Protein Groups per Minute of Microflow LC Gradient Using Data-Independent Acquisition (DIA)

*Jason Neo, Singapore*

PP03.198: AbMap: A High-Throughput Platform for Antibody Decoding

*Huan Qi, China*

PP03.200: Unlocking the Full Potential of the timsTOF Platform Using Packed Emitter Columns

*Jarrod Sandow, Australia*

PP03.202: Specific Pupylation as IDENTITY Reporter (SPIDER) for the Identification of Protein-Biomolecule Interactions

*Sheng-ce Tao, China*

PP03.204: Novel Tandem Nano and Capillary Flow LC-MS Based Approach for Ultra-High Performance Proteome Profiling With Near 100% MS Utilization

*Alec Valenta, United States*

PP03.206: BCA-no-more: Seamless, High Throughput Protein Quantification Directly on S-Trap Plates

*John Wilson, United States*

PP03.208: AccelerOme Automatic Sample Preparation Enables Highly Reproducible Quantitative Proteomics Analysis in Velocity Data-independent Acquisition (DIA) Workflow

*Kevin Yang, United States*

**Session Date/Time: Tuesday, September 19, 2023 - 04:30 PM - 05:35 PM**

### CS20: AI and MS Analysis

Chair

*Nuno Bandeira, United States*

Chair

*Laura Elo, Finland*

16:31 CS20.01: Keynote Speaker - Towards Sensitivity and Quantitative Accuracy in DIA Proteomics

*Vadim Demichev, Germany*

16:56 CS20.02: Deep Neural Networks for Combining Heterogeneous Features of Peptides in Data Independent Acquisition Mass Spectrometry

*Namgil Lee, Republic of Korea*

17:09 De Novo Peptide Sequencing With Instanovo: Highly Accurate, Database-Free Peptide Identification for Large Scale Experiments

*Timothy Jenkins, Denmark*

17:22 CS20.04: MAGPIE: Using Machine Learning to Assess the Confidence of Protein-Protein Interactions in Human Plasma

*Emily Hashimoto-Roth, Canada*

**Session Date/Time: Tuesday, September 19, 2023 - 04:30 PM - 05:35 PM**



## PROGRAM

### CS21: Food/Environmental Impact

Chair

*Tae-Young Kim, Republic of Korea*

Chair

*Eva Csoz, Hungary*

16:31 CS21.01: Keynote Speaker - Proteomics on the verge of One Health Approach  
*Paola Roncada, Italy*

16:56 CS21.02: Predicting the Impact of Chemical Mixtures Through Proteome Integral Solubility Alteration and Intrinsic Properties of Protein Targets  
*Susana Cristobal, Sweden*

17:09 CS21.03: The Proteomes that Feed the World  
*Genc Haljiti, Germany*

17:22 CS21.04: Proteomic Study on the Physiological Responses of Marine Ectotherm Under Temporal and Spatial Variation of Temperature Stress  
*Woo-young Song, Republic of Korea*

**Session Date/Time: Tuesday, September 19, 2023 - 04:30 PM - 05:35 PM**

### CS22: Clinical Proteomics

Chair

*Polina Prokofeva, Germany*

Chair

*Stephen Pennington, Ireland*

16:31 CS22.01: Multi-Omics Analyses Reveal Novel Regulators for Age-Associated Deterioration of Musculoskeletal System  
*Eun-Soo Kwon, Republic of Korea*

16:44 CS22.02: Proteomic Signatures of Drug Susceptibility in Cancer  
*Priya Ramarao-milne, Australia*

16:57 CS22.03: Clinical Proteogenomics, a Powerful New Tool for Understanding Response and Resistance to Therapies for Breast Cancer  
*Shankha Satpathy, United States*

17:10 CS22.04: Tear Proteomic Profile in Response to Fenofibrate Treatment in Diabetic Corneal Neuropathy  
*Lei Zhou, Hong Kong*

17:23 CS22.05: In-Depth Serum Proteomics Reveals the Trajectory of Hallmarks of Cancer in Hepatitis B Virus-Related Liver Diseases  
*Xiaobo Yu, China*

**Session Date/Time: Tuesday, September 19, 2023 - 04:30 PM - 05:35 PM**

### CS23: Cardiovascular

Chair

*Rebekah Gundry, United States*



## PROGRAM

Chair

*Anthony Gramolini, Canada*

- 16:31 CS23.01: Keynote Speaker - Identifying Protein Targets to Mitigate Pathological Remodeling in Hearts by Proteomics Investigations  
*Alicia Lundby, Denmark*
- 16:56 CS23.02: Disruption of Protein Complexes involved in Ca<sup>2+</sup>-Handling and Mitochondrial Function is an Early Hallmark of R14del-Phospholamban Cardiomyopathy  
*Brian Foo, Germany*
- 17:09 CS23.03: Insights Into Mode of Action of Empagliflozin to Prevent Heart Failure Using Large-Scale Proteomics in Participants in the EMPEROR Trials  
*Marijana Rucevic, Sweden*
- 17:22 CS23.04: High Throughput Label-Free Quantitative Plasma Proteomic Profiling for Abdominal Aortic Aneurysm Biomarker Discovery in a Large Patient Cohort  
*Santosh Renuse, United States*

**Session Date/Time: Tuesday, September 19, 2023 - 05:45 PM - 06:30 PM**

**PL05: Plenary Session: Kathryn Lilley, UK - The Orchestration of Subcellular Processes through RNA and Protein Interactions**

Chair

*Jin Han, Republic of Korea*

- 17:47 PL05.01: Plenary Speaker - The Orchestration of Subcellular Processes through RNA and Protein Interactions  
*Kathryn Lilley, United Kingdom*

**Session Date/Time: Wednesday, September 20, 2023 - 09:15 AM - 10:00 AM**

**PL06: Plenary Session: Hee-Sup Shin, Korea - Neural Mechanism Underlying Observational Fear, a Rodent Model of Affective Empathy**

Chair

*Uwe Völker, Germany*

- 09:17 PL06.01: Plenary Speaker - Neural Mechanism Underlying Observational Fear, a Rodent Model of Affective Empathy  
*Hee-Sup Shin, Republic of Korea*

**Session Date/Time: Wednesday, September 20, 2023 - 10:15 AM - 11:45 AM**

**CS24: Structural Proteomics**

Chair

*Dina Schuster, Switzerland*

Chair

*Francis O'Reilly, United States*

- 10:16 CS24.01: Keynote Speaker - Structure and Function of TMEM87A, A Unique Voltage-Gated Cation Channel in the Golgi  
*Ho Min Kim, Republic of Korea*



## PROGRAM

- 10:41 CS24.02: Keynote Speaker - Developing Structural Interactomics and its Application in Cell Biology  
*Fan Liu, Germany*
- 11:06 CS24.03: Integrative Approach for Large-Scale Protein-Protein Interaction Analysis Using Deep Learning and Proteomics  
*Martin Garrido Rodriguez-Cordoba, Germany*
- 11:19 CS24.04: Validation of a Zero Degrees Celsius Capillary Electrophoresis Platform for Hydrogen Exchange Mass Spectrometry  
*Jordan Aerts, Sweden*
- 11:32 CS24.05: In-Cell LiP-MS: Detecting Protein Structural States in their Native Environment  
*Franziska Elsässer, Switzerland*

**Session Date/Time: Wednesday, September 20, 2023 - 10:15 AM - 11:45 AM**

### CS25: PTMs

Chair

*Jennifer Geddes-McAlister, Canada*

Chair

*Minjia Tan, China*

- 10:16 CS25.01: Keynote Speaker - Revving an Engine of Human Metabolism: Activity Enhancement of Triosephosphate Isomerase via Hemi-Phosphorylation  
*Neil Kelleher, United States*
- 10:41 CS25.02: Keynote Speaker - A Novel Mass Spectrometry-Based Method for Large-Scale Qualitative and Quantitative Analysis of Citrullinated Proteins From Complex Biological Samples  
*Lingjun Li, United States*
- 11:06 CS25.03: decryptM: Decrypting Drug Actions and Protein Modification by Dose- and Time-resolved Proteomics  
*Matthew The, Germany*
- 11:19 CS25.04: Mining the Dark Proteome: Uncovering Wide Lactylation in Human With Cyclic Immonium Ions  
*Hui Ye, China*
- 11:32 CS25.05: PTMeXchange : Globally Harmonized Re-Analysis and Sharing of Data on Post-translational Modifications  
*Juan Antonio Vizcaino, United Kingdom*

**Session Date/Time: Wednesday, September 20, 2023 - 10:15 AM - 11:45 AM**

### CS26: Cancer Proteomics

Chair

*Hui Zhang, United States*

Chair

*Cheolju Lee, Republic of Korea*

- 10:16 CS26.01: Keynote Speaker - Immunological Impact on Internal Proteomics Cancer Heterogeneity  
*Tami Geiger, Israel*



## PROGRAM

- 10:41 CS26.02: Keynote Speaker - Functional Studies on Melanoma Cancer: Assessing Drug Impact and Correlation with Survival  
*György Marko-Varga, Sweden*
- 11:06 CS26.03: Extensive Proteogenomic Analysis on Human Pancreatic Ductal Adenocarcinoma (PDAC) In an Asian Population Identified Six PDAC Subtypes  
*Dowoon Nam, Republic of Korea*
- 11:19 CS26.04: Analysis of Therapeutic Target Networks of Cancer Stem Cells by Proteomics-Based Multi-Omics  
*Norie Araki, Japan*
- 11:32 CS26.05: Pan-Cancer Proteogenomics Expands the Landscape of Therapeutic Targets  
*Jonathan Lei, United States*

**Session Date/Time: Wednesday, September 20, 2023 - 10:15 AM - 11:45 AM**

### CS27: Single Cell

Chair

*Jennifer Van Eyk, United States*

Chair

*Takeshi Masuda, Japan*

- 10:16 CS27.01: Keynote Speaker - Is it Possible to Analyze 5000 Proteins from a Single Human Cell?  
*Karl Mechtler, Austria*
- 10:41 CS27.02: Keynote Speaker - Interfacing Optics, Microfluidics, and Mass Spectrometry to Advance Single-cell and Spatial Proteomics  
*Ying Zhu, United States*
- 11:06 CS27.03: Single Cell Proteomics Study of Drugs Responses  
*Bogdan Budnik, United States*
- 11:19 CS27.04: Platform for Single Cell Science (PSCS) Repository Enables No-Code Single Cell Proteomic Data Analysis and Sharing  
*Alexandre Hutton, United States*
- 11:32 CS27.05: Spatial Proteomic Approaches for Triple-Negative Breast Cancer on Single-Cell Resolution  
*Gangsoo Jung, Republic of Korea*

**Session Date/Time: Wednesday, September 20, 2023 - 11:45 AM - 01:00 PM**

### PP05: All Posters - Poster Viewing with Coffee Break

PP05.01: Enhanced Insight Generation Through Automated Transformation of Historical Experiments Into Quantitative Knowledge Base

*Mark Condina, Australia*

PP05.02: Protein Language Models for Phosphorylation Site Prediction from LC-MS/MS data

*Sven Degroeve, Belgium*

PP05.03: The 2023 Report on the Human Proteome from the HUPO Human Proteome Project

*Eric Deutsch, United States*

PP05.04: Improved Library-Free Proteomics Analysis for dia-PASEF using directDIA+ in Spectronaut

*Sira Echevarria, Switzerland*

## PROGRAM

- PP05.05: Synchronizing Analysis With Acquisition for Significantly Faster Library Free Analysis of DIA  
*Tejas Gandhi, Switzerland*
- PP05.06: Evaluating Network Methods to Understand Cellular Signaling From Phosphoproteomics Data  
*Martin Garrido Rodriguez-Cordoba, Germany*
- PP05.07: Normalization to External Reference for Reduction of Technical Variation  
*Yolanda Hagar, United States*
- PP05.08: Proteogenomics Data Integration to Assess Clinical Potential of Protein Sequence Variants  
*Peter Horvatovich, Netherlands*
- PP05.09: PaxDB 5.0: Curated Protein Quantification Data Suggests Adaptive Proteome Changes in Yeasts  
*Qingyao Huang, Switzerland*
- PP05.10: MOLE: MultiOmics Learning to Extrapolate Proteome Expression  
*Ekaterina Ilgisonis, Russian Federation*
- PP05.11: Reaching Methodological Agreement in Proteomics – A Thematic Analysis Scoping Downstream Data Analysis Workflows  
*Somya Iqbal, United Kingdom*
- PP05.12: Enhanced TMT Data Analysis with AI-driven Workflows Utilizing CHIMERY5 and INFERY5 Algorithms  
*Anas Kamleh, Netherlands*
- PP05.13: dia-PASEF Tools: a Shiny App for Data Visualization and Exploration of dia-PASEF Data  
*Kyoko Kato, Japan*
- PP05.14: PPIAT: Targeted Mass Spectrometry-Based Analysis Tool for Protein-Protein Interactions  
*Hyunsoo Kim, Republic of Korea*
- PP05.15: FLASHViewer: a Web Application for Visualizing Deconvolved Signals in Top-down Mass spectrometry-based Proteomics  
*Jihyung Kim, Germany*
- PP05.16: Increasing the Depth of Single Shot Proteomics with Enhanced Data Acquisition and Processing Strategies Using Orbitrap Ascend MS  
*Amanda Lee, United States*
- PP05.16A: Single-cell Proteomics Methodologies on the Orbitrap Tribird Platform for Increased Throughput and Extended Coverage  
*Amanda Lee, United States*
- PP05.17: Retention Time-Free (RT-free) using Featured Ion-Guided Stoichiometry (FIGS) Enables Peptide Identification and Quantification by Data-Independent Acquisition  
*Qingrun Li, China*
- PP05.18: A Target-decoy Competition Approach to Control for False Discoveries in Nautilus PrISM Data  
*Parag Mallick, United States*
- PP05.19: A Novel Deep Learning Approach to Predict Protein O-GlcNAcylation Sites  
*Jia Mi, China*
- PP05.20: The PBMC Methylome Landscape in CMTs Reveals the Epigenetic Regulation of Immune Genes and its Application in Predicting Tumor Malignancy  
*Areum Nam, Republic of Korea*
- PP05.21: iDeepLC: A Deep Learning-based Retention Time Predictor for Unseen Modified Peptides with a Novel Encoding System  
*Alireza Nameni, Belgium*



## PROGRAM

PP05.22: Updates to FragPipe Computational Platform: New Capabilities, Tools, and Workflows

*Alexey Nesvizhskii, United States*

PP05.23: Search Engine Optimization for mediaPASEF Data Independent Acquisition (DIA)

*Robin Park, United States*

PP05.24: Analyzing Data-independent Acquisition (DIA) Data One Experimental Spectrum at a Time

*Patroklos Samaras, Germany*

PP05.25: Identification of Senescence Signatures and Senescence Characterization in High-grade Serous Ovarian Carcinoma

*Dongjun Shin, Republic of Korea*

PP05.26: A Cloud-based QC Platform for Comprehensive Examination of MS-based Proteomics Data

*Yourae Shin, Republic of Korea*

PP05.27: Identifying Protein Products of Germline Variation Using Mass Spectrometry

*Dafni Skiadopoulou, Norway*

PP05.28: Precise and Accurate Real-time de Novo Sequencing of TimsTOF data with the Novor Algorithm on the Bruker ProteoScope Platform

*Tharan Srikumar, Canada*

PP05.29: TRIMQuant: Precise and Scalable MS1 Quantification for DDA and DIA using Transfer Learning, Targeted Analysis and Semi-supervised Machine Learning

*Tharan Srikumar, Canada*

PP05.30: Reproducibility-optimized Multi-group Statistic and Survival Analysis

*Tomi Suomi, Finland*

PP05.31: XMass: XGBoost-based Peptide Spectral Library Prediction Integrated into MaxQuant for DDA and DIA Data Analysis

*Shamil Urazbakhtin, Germany*

PP05.32: BatchDesigner: Streamlining Metadata Management for Efficient Experimental Design and Data Quality Control in Mass Spectrometry Analysis

*Dhonggeon Won, Republic of Korea*

PP05.33: Accurate in Silico Functional Annotation for Entire Proteomes

*Gong Zhang, China*

PP05.34: Fully Automated and Spectrum-centric Processing of Parallel Reaction Monitoring (PRM) Data

*Daniel Zolg, Germany*

PP05.35: Comprehensive Proteomic Analysis of FFPE Specimens in Hepatocellular Carcinoma for Investigating Recurrence Mechanism

*Yuki Adachi, Japan*

PP05.36: Global Proteome Expression Study of Patient-derived Pleomorphic Sarcoma Cell-lines Toward Optimization of Therapeutic Strategy Using Trabectedin and Eribulin

*Taro Akiyama, Japan*

PP05.37: Secretome Landscape of Triple Negative Breast Cancer Unravels Subclass-specific Functional Intricacies

*Asfa Alli-Shaik, Singapore*

PP05.38: Proteomic Discovery of the Correlation between Anticancer Drug and NK Immunotherapeutic Resistance in hABCB1-expressing A549 Cells

*Geul Bang, Republic of Korea*

## PROGRAM

PP05.39: Investigation of Potential Chemoresistant Breast Cancer Targets by Proteomics and Phosphoproteomics Approaches

*Praneeta Bhavsar, India*

PP05.40: A Novel S-Capped Cysteine and its Utilization for Targeted Proteomics

*Kwon Hee Bok, Republic of Korea*

PP05.41: The Effect of gp120 in Glioblastoma: Targeting UPR Survival Proteomics Signatures

*Nawal Boukli, Puerto Rico*

PP05.42: Data-independent Acquisitions of Human Breast Cancer Tissue Subtypes Explore Molecular Profiles to Identify Potential Targets for Stratification and Stromal Reprogramming

*Jordan Burton, United States*

PP05.43: Proteomics Profiling of Tumor Tissues Reveals a Promoting Role of ENAH in Progression of Oral Cancers

*Xiu-ya Chan, Taiwan*

PP05.44: Targeting Drug Resistance in Colorectal Cancer Through the Lens of Multiomics Analysis

*Hsin-Yi Chang, Taiwan*

PP05.45: Histopathologically Contextualized Proteomic Analysis of Prostate Cancer Whole-Mount Patient Specimens Leveraging Ion Mobility Mass Spectrometry

*Matthew Chang, United States*

PP05.46: Next Generation Proteomics Reveals Signature for Metastatic Cancer Years prior to Diagnosis Enabled by a Longitudinal Wellness Cohort

*Ray Chen, United States*

PP05.47: Activity-Based Protein Profiling and Global Proteome Analysis Reveal MASTL-NEDD4-1 Axis Promotes Gastric Cancer Tumorigenesis

*Kyoung-Min Choi, Republic of Korea*

PP05.48: Molecular Phenotyping of 3D Cultured Triple-Negative Breast Cancer Cells Reveals Pathways Influenced by Culture System

*Luis Coy, United Kingdom*

PP05.49: New Proteomics Insights in the Characterization of Pancreatic Cancer Extracellular Vesicles as Lymphocyte Immune Activators

*Federica Di Marco, Italy*

PP05.50: ANKRD1 Promotes Breast Cancer Metastasis via NF- $\kappa$ B-MAGE-A6

*Penchatr Diskul Na Ayudthaya, Thailand*

PP05.51: Mitochondrial Proteome and Acetylome in Glioblastoma Cells with Contrasting Metabolic Phenotypes

*Sergio Encarnación-Guevara, Mexico*

PP05.52: Plasma Proteomic Signature of Ovarian Cancer: Precise Biomarkers for Early Detection

*Stefan Enroth, Sweden*

PP05.53: Pan-Cancer N-Glycoproteomic Atlas of Patient Derived Xenografts for Therapeutic Target and Serum Biomarker Discovery

*Meinusha Govindarajan, Canada*

PP05.54: Mouse Stromal Cells Confound Proteomic Characterization and Quantification of Xenograft Models

*Piliang Hao, China*

PP05.55: Silencing DTX3L Inhibits the Progression of Cervical Carcinoma by Regulating PI3K/AKT/mTOR Signaling Pathway

*Wei Hu, China*

## PROGRAM

PP05.56: Targeting Cholesterol Esters Synthesis Combats Colorectal Cancer

*Tsui-chin Huang, Taiwan*

PP05.57: Integrative Multi-omics Analysis Prioritizes Potential Therapeutic Targets in TNBC Stem Cells

*Sunghyun Huh, Republic of Korea*

PP05.58: Proteomic and Proteogenomic Characterization of Triple Negative Breast Cancer

*Henrik Johansson, Sweden*

PP05.59: A Novel Therapeutic Strategy: Overcoming AKT inhibitor-induced Cell Migration via  $\beta$ -catenin Targeting in CRC

*Yonghyo Kim, Republic of Korea*

PP05.60: The Regulatory Roles of Mitochondrial Metabolism Dynamics and Mitochondria Calcium Uniporter (MCU) in Bevacizumab Resistance of GBM

*Yejin Kim, Republic of Korea*

PP05.61: Functional Study of Nucleus-localized Proteins in Temozolomide-resistant Glioblastoma

*Chanil Kim, Republic of Korea*

PP05.62: Proteomic Analysis of Non-Canonical Proteins in Non-Small Cell Lung Cancer.

*Dae Ho Kim, Republic of Korea*

PP05.63: Differential Expression of Deubiquitinating Enzymes in Cisplatin-treated Lung Cancer Cells

*Tae-Woo Kim, Republic of Korea*

PP05.64: Discovery and Validation of Immuno-oncology Therapeutic Targets in Human Immune Cells by Mass Spectrometry Based Proteomics

*amaury lachaud, Switzerland*

PP05.65: Novel Insights into the Mechanisms of Tumorigenesis through Proteome and Glycoproteome Analysis of Secretome from EGFR TKI-Resistant Lung Cancer Cells

*Ju Yeon Lee, Republic of Korea*

PP05.66: Repurposing Neuroactive Drugs for Brain Cancer Drug Discovery

*Sohyon Lee, Switzerland*

PP05.67: HER2 Expression in Breast Cancer by Proteomics Analysis

*Gi Yeon Lee, Republic of Korea*

PP05.68: Secretome Analysis Reveals Potential Driver of Tumorigenesis Driven by EGFR-TKI Resistant Lung Cancer

*Su-Min Lee, Republic of Korea*

PP05.69: Proteome Profiling of Peripheral Blood Mononuclear Cells in dog with Mammary Gland Tumor

*Jeong Woon Lee, Republic of Korea*

PP05.70: Sonication-assisted Protein Extraction from Tumor Tissues Improves Proteomic Detection of DNA- and Plasma Membrane-associated Proteins

*Qing Kay Li, United States*

PP05.71: Laser Capture Microdissection-based Trace Proteomics Accurately Defines the Characteristics of Esophageal Squamous Cell Carcinoma Progression

*Xumiao Li, China*

PP05.72: Decoding the Immune Microenvironment of High-Grade Serous Ovarian Cancer

*Loren Méar, Sweden*

PP05.73: A Comparison of Tribrid Mass Spectrometer Architectures for Deep Blood Plasma Proteomics

*Rafael Melani, United States*

## PROGRAM

PP05.74: Proteomic Analysis of the Function of IMPDH2 in Osteosarcoma Metastasis

*Sutpirat Moonmuang, Thailand*

PP05.74: Multi-omics Profiling of Metastatic Spread in a Large Breast Cancer Patient Cohort

*Sergio Mosquim Junior, Sweden*

PP05.76: S100A10 is Associated with Ovarian Cancer Progression and Chemotherapy Resistance

*Tannith Noye, Australia*

PP05.77: Proteomic Analysis to Identify the Molecular Differences between Dermatofibrosarcoma Protuberans and Fibrosarcomatous Dermatofibrosarcoma Protuberans

*Takuya Ono, Japan*

PP5.078: Development of Treatments for CIC-rearranged Sarcomas: Multiplex Kinase Activity Analysis and Drug screening Using Patient-derived Cancer Models

*Julia Osaki, Japan*

PP05.79: Estrogen Signaling as a Putative Target for Never-Smoker Lung Adenocarcinoma Patients without EGFR Mutation and ALK Fusion from Proteogenomic Characterization

*Seung-jin Park, Republic of Korea*

PP05.80: Oxidative PTM by Exogenous ROS at Lysosome as a Chemical Leverage to Regulate Autophagy

*Mingyu Park, Republic of Korea*

PP05.81: Establishing Proteome Divergence between Chemo Naïve High-grade Serous Ovarian Tumors and Patient-derived Xenograft Experimental Models

*Jesenia Perez, United States*

PP05.82: Integrative Proteomic Characterization of Epithelial Ovarian Cancer

*Liuqia Qian, China*

PP05.83: Olink Insight and Human Disease Blood Atlas to Uncover Human Disease Proteome and Accelerate Adoption of Proteomics

*Marijana Rucevic, Sweden*

PP05.84: Proteogenomic Landscape of Non-small Cell Lung Cancer

*Adrianna Seredynska, Germany*

PP05.85: Proteomics-based Identification of S100 Protein Members in Pancreatic Tumor Secretome and its Potential Role in Collective Invasion of Cancer Cells

*Dongwoo Son, Republic of Korea*

PP05.86: Mutual phosphorylation of FAK and SRC is Involved in Osimertinib Resistance in Non-small Cell Lung Cancer

*Takehiro Tozuka, Japan*

PP05.87: Sources of Technical Variability in Manual Proteomic Sample Preparation Workflows Incorporating Multiplexed Isobaric Labeling and LC-MS/MS Analysis

*Carly Twigg, United States*

PP05.88: Unique Protein Patterns Identified from Multilevel Proteomic Characterization of Intraductal Papillary Mucinous Neoplasms of the Pancreas

*Yuefan Wang, United States*

PP05.89: Label-free Quantitative Proteomics of Nicotine-treated A549 Cells Reveal a Potential Therapeutic Target for Metastatic Lung Cancer

*Churat Weeraphan, Thailand*

PP05.90: The Effect of Allelic Bias in Cancer Cell Line Proteomes

*James Wright, United Kingdom*

## PROGRAM

- PP05.91: The Small Open Reading Frame-encoded Peptides: Method Development and Functional Studies  
*Qian Zhao, Hong Kong*
- PP05.92: Integrating Multiplex Staining and Multiplex-DIA: Profiling the Tumor Microenvironment Proteome for Precision Cancer Research  
*Xiang Zheng, Denmark*
- PP05.93: Data-driven Exploration of the Inflammatory Proteome Associated with SARS-CoV-2 Infection and/or Vaccination from Home-sampled Blood Spots  
*Leo Dahl, Sweden*
- PP05.94: Super-resolution Proximity Labeling Reveals Antiviral Protein Network and its Structural Changes against SARS-CoV-2 Viral Proteins  
*Yun-bin Lee, Republic of Korea*
- PP05.95: Antiviral Activity of a Nanoscale Phospholipid Dosage Form Containing an Antiviral Component against SARS-COV-2  
*Yuliya Romashova, Russian Federation*
- PP05.96: Systematic Analysis of Specific Antibody Response to SARS-CoV-2  
*Sheng-ce Tao, China*
- PP05.97: Characterization of Lymphocytes Protein Cargo in Covid-19: Unveiling the Impaired Coagulation  
*Silvia Valentinuzzi, Italy*
- PP05.98: Viable Single Cardiomyocytes Applications in Proteomics  
*Aleksandra Binek, United States*
- PP05.99: Exploring the Human Aging Blood Proteome  
*Dohun Lee, Republic of Korea*
- PP05.100: Tandem Mass Tag-based Quantitative Proteomic Profiling Identifies Candidate Biomarkers of Aging-induced Hematopoietic Stem Cells  
*VAN DUC PHAM, Republic of Korea*
- PP05.101: Differential Modulation of the Phosphoproteome by the MAP Kinases Isoforms p38 $\alpha$  and p38 $\beta$   
*Arie Admon, Israel*
- PP05.102: Characterizing Serine ADP-ribosylation in Breast Cancer Cell Lines After DNA Damage Stimulation Using Mass Spectrometry  
*Holda Anagho, Denmark*
- PP05.103: How Does the Conventional Cell Culturing at Atmospheric Oxygen Influence the Response to Oxidative Stress and the Thiol-based Proteome Remodeling?  
*Sandra Anjo, Portugal*
- PP05.104: Targeted Cancer Treatment Using Cell-Penetrating Peptide-Conjugated vDUB  
*Kwang-Hyun Baek, Republic of Korea*
- PP05.105: Exploring the Role of Post-translational Modifications in Tardigrade Cryptobiosis  
*Samantha Balboa, United States*
- PP05.106: Combining Time-resolved Phosphoproteomics and Causal Network Models Elucidates Deregulated Signaling Mechanisms in Cancer  
*Mira Lea Burtscher, Germany*
- PP05.107: Investigating Proteome-wide Effect of PARP Inhibitor in Human Cancer Cells using Quantitative Mass-spectrometry  
*Hayoung Cho, Denmark*

## PROGRAM

PP05.108: Pro-apoptosis Protein Bax is Regulated by Deubiquitinating Enzymes

*Hae-seul Choi, Republic of Korea*

PP05.109: Proteoform Detection in Deep Plasma Proteomics using Peptide Expression Correlation

*Jennifer D'Angelo, United States*

PP05.110: Label Free and Isobaric Labeling Mass Spectrometry to Monitor Ubiquitination Dynamics upon Modulation by Small Molecule Inhibitors.

*Jeroen Demmers, Netherlands*

PP05.111: Investigating the Impact of Lysine Acetylation on Short-Chain Fatty Acid Production in the Human Gut Microbiome

*Haonan Duan, Canada*

PP05.112: A New Simple Glyco-check with Lectin/antibody Dotcoding using a Fully Automated System

*Sayaka Fuseya, Japan*

PP05.113: Proteomics Analysis of Pathological Alpha synuclein in Synucleinopathies in Search for New Biomarkers and Therapeutic Targets

*Belén García Sintes, Denmark*

PP05.114: Ubiquitome Profiling in Dozens of Cells without Enrichment using a Boosting Channel

*Minsang Hwang, Republic of Korea*

PP05.115: Global, in Vivo, and Site-specific Profiling of Protein Lipidation

*Koshi Imami, Japan*

PP05.116: Investigation of Brain N-glycosylation Alteration in Acute Social Isolation Models using Mass Spectrometry Imaging (MSI)

*Hyun Jun Jang, Republic of Korea*

PP05.117: Global Oxidative Modifications and Molecular Alterations in the Heart after Ischemia-reperfusion Injury

*Inmaculada Jorge, Spain*

PP05.118: Fe-IMAC phosphopeptide Enrichment of Plasma Phosphoproteome for Diagnosis of AD

*Seunghyeon Jung, Republic of Korea*

PP05.119: ReCom: A Semi-Supervised Approach to Ultra-Tolerant Database Search for Improved Identification of Modified Peptides

*ANDREA LAGUILLO GOMEZ, España*

PP05.120: Analysis of Oxidized Proteomes in Two Cellular Organelles Exhibiting Synergistic Cell Death

*Chae Gyu Lee, Republic of Korea*

PP05.121: Evaluating Data Analysis Pipelines for Large-Scale Citrullination Proteomics

*Chien-Yun Lee, Germany*

PP05.122: Unveiling Organ-Specific Glycan Profiles in Porcine Xenograft Model: Insights into Non-Human Glycan Antigens

*Daum Lee, Republic of Korea*

PP05.123: Proteome-wide Analysis of Post translational Modification Reveals Dynamic Alterations in Protein Function During Lipopolysaccharide-induced Neuroinflammation in Microglia.

*GEEEUN LEE, Republic of Korea*

PP05.124: Optimization of Peptide-to-bead Ratios for In-depth Phosphoproteomic Analysis

*Jung-hyun Lee, Republic of Korea*

PP05.125: A Tip-Based N-terminal Proteome Enrichment Method and Its Applications

*Seonjeong Lee, Republic of Korea*

## PROGRAM

- PP05.126: Identification of Histone Lysine Acetoacetylation as a Dynamic Post-translational Modification Regulated by HBO1  
*Sangkyu Lee, Republic of Korea*
- PP5.127: Global Characterization of Lysine Acetylation and Lactylation in Kupffer Cells  
*Sangkyu Lee, Republic of Korea*
- PP05.128: An Improved Workflow for Robust and Comprehensive Lysine Acetylome Analysis  
*Tao Liu, United States*
- PP05.129: Exposing the Molecular Heterogeneity of Glycosylated Biotherapeutics  
*Rafael Melani, United States*
- PP05.130: Real-time Instrument Methods to Resolve Chimeric Spectra and Post-translational Modifications in Multiplexed Proteomics  
*Rafael Melani, United States*
- PP05.131: Flavone-induced S-Nitrosylated Proteins Facilitate Schwann Regeneration  
*Shirley Thy Nguyen, Republic of Korea*
- PP05.132: Disentangling the Tubulin Code: Characterization of Tubulin Polyglutamylation in the Flagellum of *Trypanosoma Brucei*  
*Marija Nisavic, France*
- PP05.133: Unraveling Nitration Signaling in Early Onset Gastric Cancer: Insights from Nitroproteomics Analysis  
*JaeWon Oh, Republic of Korea*
- PP05.134: Proteomic and Phosphoproteomic Profiling of Transglutaminase 2 Inhibition in Human Kidney Tubular Epithelial Cells  
*Hong-Beom Park, Republic of Korea*
- PP05.135: Label-free Quantitative Phosphoproteomics of Isogenic Cholangiocarcinoma Cell Lines Reveal the Crucial Protein Phosphorylation as Potential Therapeutic Targets for Metastatic Cancer  
*Metarsit Patchimaekapol, Thailand*
- PP05.136: MSFragger-Labile: Improving Analysis of Post-translationally Modified Peptides  
*Daniel Polasky, United States*
- PP05.137: Scop3PTM: a Knowledgebase on Human Post-translational Modifications of Proteins Built by Reprocessing and Reusing Public Proteomics Experiments  
*Pathmanaban Ramasamy, Belgium*
- PP05.138. Digging Deeper into Phosphoproteomes through AI-driven Deconvolution of Chimeric Spectra  
*Florian Seefried, Germany*
- PP05.139: Protein Arginylation: A New Key Player in SARS-CoV-2 Infection  
*Janaina Silva, Brazil*
- PP05.140: Interactome of Intact Chromatosome Variants with Site-specifically Ubiquitylated and Acetylated Linker Histone H1.2  
*Florian Stengel, Germany*
- PP05.141: Structural Characterization of SARS-CoV-2 Dimeric ORF9b Reveals Potential Fold Switching Trigger Mechanism  
*Xue Sun, China*
- PP05.142: The Protein Methylation Network in Yeast: a Landmark in Completeness for a Eukaryotic Post-translational Modification  
*Marc Wilkins, Australia*



## PROGRAM

PP05.143: Pushing the Boundaries for Robust and High-throughput Single Cell Analysis with Whisper Flow Technology Powered by dia-PASEF

*Dorte Bekker-jensen, Denmark*

PP05.144: Identification of Causal Genes for Nonalcoholic Fatty Liver Disease using Multi-omics Based Single-cell Analysis

*Sung Eun Hong, Republic of Korea*

PP05.145: Single-nucleus RNA-seq Reveals Key Contributors in Duchenne Muscular Dystrophy

*Eun Young Jeon, Republic of Korea*

PP05.147: Single Cell Proteome Analysis with Ultra-high sensitivity Using a timsTOF Mass Spectrometer

*Christoph Krisp, Germany*

PP05.148: Increasing Proteomic Depth of Single-Cell Analysis by Feature Matching in diaPASEF data

*Karl Kristian Krull, Germany*

PP05.150: Novel Developments in Single-Cell Proteomics: Clustering Analysis of Human PBMCs and High-Throughput LC-MS/MS Platform

*Ziyi Li,*

PP05.151: Single-cell and Low-input Proteomics Depicted an In-depth Landscape for Mouse Maternal-to-zygotic Transition

*Chen Li, China*

PP05.152: Time-resolved Metabolite and Lipid Profiling Depicts Macrophage Continuum with Apoptotic and Ferroptotic Heterogeneity along Foam Cell Formation

*Ling Lin, China*

PP05.153: Water Droplet-in-oil Digestion Method with Enhanced Throughput for Single-cell Proteomics

*Takeshi Masuda, Japan*

PP05.154: Discovery of Post-translationally Modified and Variant Peptides in Single cell Proteomics Experiments

*Dong-Gi Mun, United States*

PP05.155: Evaluating Linear Ion Trap for MS3-based Multiplexed Single-cell Proteomics

*Junho Park, Republic of Korea*

PP05.156: Single-cell Proteomics Reveals the Difference on Early Tumor Evolution between dMMR and pMMR Colorectal Cancer Organoids

*Yan Ren, China*

PP05.157: Single-cell Proteomics Reveals Changes in Expression during Colorectal Cancer Organoids Development

*Yan Ren, China*

PP05.158: Single-cell Proteomics by Mass spectrometry with Spatial Context in Mammalian Liver

*Florian A Rosenberger, Germany*

PP05.159: Accessible Low Input Proteomics Reveals Relationship Between Mitochondrial Potential, Lipid Metabolism, and Progenitor Associated Phenotype in the Basal Mammary Epithelium

*Matthew Waas, Canada*

PP05.160: Optimized Data-independent Acquisition Approach for Proteomic Analysis at Single-cell Level

*Yuefan Wang, United States*

PP05.161: A High-sensitivity Low-nano -Flow LC-MS Configuration for High-throughput Sample-limited Proteomics

*Runsheng Zheng, Germany*





## PROGRAM

PP05.162: High Throughput XL-MS Analysis on a New High-resolution Accurate Mass Platform

*Yi He, United States*

PP05.163: Differential N-Glycosylation Site Occupancy Depends on Distinct Amino Acid Sequence Features of Oligosaccharyltransferase and Acceptor Polypeptides

*Marium Khaleque, Australia*

PP05.164: Probing Protein Interactome Dynamics using an Experimental Library of Protein Complex Interfaces

*Cathy Marulli, Switzerland*

PP05.165: deMix\_GUI Provides a Solution for Automatically Analyzing HDX-MS Data and Investigating Protein Conformational Changes

*Seungjin Na, Republic of Korea*

PP05.166: Structural Premise of Selective Deubiquitinase USP30 Inhibition by Small-Molecule Benzosulfonamides; Implications for Mitophagy and Neurodegeneration

*Darragh O'Brien, United Kingdom*

PP05.167: Identification of Novel Protein Metal-Binding Sites Using Limited Proteolysis-Coupled Mass Spectrometry (LiP-MS)

*Jan-philipp Quast, Switzerland*

PP05.168: Molecular Organization of Signaling at the Plasma Membrane in Mouse Brain Revealed by High-Resolution Complexome Profiling

*Uwe Schulte, Germany*

PP05.169: How to Study Flexible Domains on Membrane Proteins - Combining Cryo-EM, Limited Proteolysis-coupled and Crosslinking Mass Spectrometry

*Dina Schuster, Switzerland*

PP05.170: Quantifying the Direct Human DNA Interactome in Response to Transcription-Modulating Drugs

*Jakob Trendel, Germany*

**Session Date/Time: Wednesday, September 20, 2023 - 01:15 PM - 02:15 PM**

### **ISS14: Nautilus Biotechnology Seminar**

13:15 Expanding Proteomic Horizons with Single

*Parag Mallick, United States*

13:45 Molecule Analysis at Scale

*Birgit Schilling, United States*

**Session Date/Time: Wednesday, September 20, 2023 - 02:30 PM - 03:35 PM**

### **CS28: AI and Bioinformatics**

Chair

*Eunok Paek, Republic of Korea*

Chair

*Alexey Nesvizhskii, United States*

14:31 CS28.01: Keynote Speaker - Ending Brute Force Mass Spectrometry-Based Proteomics Data Acquisition Using Machine Learning

*Mathieu Lavallée-Adam, Canada*

## PROGRAM

- 14:56 CS28.02: Completing the Human Functional Proteome Together!  
*Lydie Lane, Switzerland*
- 15:09 CS28.03: A Multi-Scale Map of Proteome Organization From Integration of Protein Interactions and Images  
*Leah Schaffer, United States*
- 15:22 CS28.04: Deep Learning Based Mass Spectra Prediction Facilitates Proteomics Data Analysis  
*Liang Qiao, China*

**Session Date/Time: Wednesday, September 20, 2023 - 02:30 PM - 03:35 PM**

### CS29: Covid and Long Covid

Chair

*Robyn Kaake, United States*

Chair

*Daesub Song, Republic of Korea*

- 14:31 CS29.01: Keynote Speaker - Multi Omics Analysis of SARS-CoV2 Infected Mouse  
*Je Kyung Seong, Republic of Korea*
- 14:56 CS29.02: COVID-eQTL: Genetic Dissection of COVID-19 Susceptibility  
*Jeongha Lee, Republic of Korea*
- 15:09 CS29.03: High-Throughput Mining of Proteomics Datasets for Evidence of Proteolysis during SARS-CoV-2 infection  
*Peter Bell, Canada*
- 15:22 CS29.04: Persistent and Prevalent New-Onset Autoantibodies in Mild to Severe COVID-19  
*August Jernbom Falk, Sweden*

**Session Date/Time: Wednesday, September 20, 2023 - 02:30 PM - 03:35 PM**

### CS30: Epigenetic and Aging

Chair

*Je Yoel Cho, Republic of Korea*

Chair

*Christina King, United States*

- 14:31 CS30.01: Keynote Speaker - The Aging Brain Proteome  
*Alessandro Ori, Germany*
- 14:56 CS30.02: Proteomic and Functional Exploration of Anti-aging Molecules  
*Haiteng Deng, China*
- 15:09 CS30.03: USP7 regulates the ncPRC1 Polycomb Axis to Stimulate Genomic H2AK119ub1 Deposition Uncoupled from H3K27me3  
*Jeroen Demmers, Netherlands*
- 15:22 CS30.04: Functional Phosphoproteomic Analysis of Insulin Signalling in Ageing Bone  
*Mriga Dutt, Australia*



## PROGRAM

**Session Date/Time: Wednesday, September 20, 2023 - 02:30 PM - 03:35 PM**

**MS03: Mentoring Session 3 - Geographical Differences for Academic (Postdoc-PI) Job Applications (Asia, Europe, Africa, Americas)**

Chair

*Livia Rosa-fernandes, Australia*

Chair

*Andreas Hober, Sweden*

MS03.01: Panelist

*Nicolle Packer, Australia*

MS03.02: Panelist

*Uwe Völker, Germany*

MS03.03: Panelist

*Yu-Ju Chen, Taiwan*

MS03.04: Panelist

*Birgit Schilling, United States*

**Session Date/Time: Wednesday, September 20, 2023 - 04:30 PM - 06:30 PM**

**PL07: HUPO Awards Ceremony and Closing Session**

- 16:30 PL07.01: Congress Summary & Thank You from KHUPO  
*Je Yoel Cho, Republic of Korea*
- 16:30 PL07.01: Congress Summary & Thank You from KHUPO  
*Youngsoo Kim, Republic of Korea*
- 16:40 PL07.02: ECR Summary and Announcement of Various Award Winners + Photo Opp  
*Ruth Huttenhain, United States*
- 16:40 PL07.02: ECR Summary and Announcement of Various Award Winners + Photo Opp  
*Mathieu Lavallée-Adam, Canada*
- 17:05 PL07.03: Rising Star Award - Presentation  
*Nicholas Riley, United States*
- 17:20 PL07.04: Clinical & Translational Proteomics Sciences Award - Presentation  
*Rebekah Gundry, United States*
- 17:32 PL07.05: Discovery in Proteomic Sciences Award - Presentation  
*Hannes Röst, Canada*
- 17:44 PL07.06: Distinguished Achievement in Proteomic Sciences Award - Presentation  
*Bernhard Küster, Germany*
- 17:56 PL07.07: Distinguished Service Award - Presentation  
*Henning Hermjakob, United Kingdom*
- 18:08 PL07.08: Science & Technology Award - Presentation  
*Alexey Chernobrovkin, Sweden*



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## PROGRAM

- 18:08 PL07.08: Science & Technology Award - Presentation  
*Tomas Friman,*
- 18:18 PL07.09: Closing Remarks  
*Jennifer Van Eyk, United States*
- 18:23 PL07.10: HUPO 2024 Invitation + Video  
*Uwe Völker, Germany*



**See you in Busan!**  
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## HPP Day (September 21, 2023) – Emerging Strategies to Address Protein Functions

### Registration Fee: 100 USD

The Human Proteome Project (HPP) is HUPO's flagship project. It is designed to map the entire human proteome in a systematic effort using currently available and emerging techniques. In 2021, the HPP launched the Grand Challenge, the objective of which is to identify a function for every human protein. During the HPP Day at HUPO 2023, different strategies to predict or address the functional properties of proteins in the context of cells will be presented and discussed.

Be sure to register for this outstanding program! All HUPO 2023 delegates are welcome to attend.

### 08:00 – 10:30 Session 1: Mission and Current Status

- 08:00 Welcome and Introduction – Charles Pineau, France & Cecilia Lindskog, Sweden
- 08:05 Overview of the Grand Challenge and Reflections from 2022 – Charles Pineau, France
- 08:15 2nd Update on the  $\pi$ -Hub Project – Fuchu He, China
- 08:45 2nd Update on the Chinese Westlake Pilot Project – Tiannan Guo, China
- 09:00 The HPP-ChemBioFrance Pilot Project – Charles Pineau, France
- 09:15 Proteins in Time and Space – Spatial Proteomics for Predicting Function – Cecilia Lindskog, Sweden
- 09:30 TBC – Gong Zhang, China
- 09:45 Involving Undergraduates in the HPP Grand Challenge: The Functionathon Experience at the University of Geneva – Lydie Lane, Switzerland

### 10:30 - 10:45 Coffee Break

### 10:45 – 12:30 Session 2: How Should We Get Organized to Contribute to the Grand Challenge?

- 10:45 Current HPP Structure and Suggestions of Future Directions – Charles Pineau, France
- 11:00 4x Breakout Sessions
- 11:30 Summaries from the Different Sessions and General Discussion

### 12:00 - 13:00 Lunch Break

### 13:00 – 15:30 Session 3: Moving Forward – Strategies and Initiatives to Predict Protein Function(s)

- 13:00 How to Propose Protein Function Based on Cellular Localization – Kathryn Lilley, UK
- 13:30 Proteomics and Protein Function in Clinical Precision Medicine and Pathology – Michael Roehrl, USA
- 14:00 Location matters! Position-specific Glycosylation Impacts Protein Function - Morten Thaysen-Andersen, Australia
- 14:30 Discussion on Future Directions - All
- 15:25 Wrap Up – Charles Pineau, France

