



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

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

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

PCT02: Protein Interactions/Spatial Proteomics (Ticketed Session)



PROGRAM

- 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 π -HuB Project: The Proteomic Navigator of the Human Body (Ticketed Session)



PROGRAM

- 10:15 PS03.01: Opening Introduction, π -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

- 12:30 PCT04.01 - Review of the History of How We Came to Use NanoLC-MS for Bottom-Up Proteomics
David Goodlett, Canada



PROGRAM

- 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

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



PROGRAM

- 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

18:00 PL01.01 Opening Remarks

Je Yoel Cho, Republic of Korea



PROGRAM

- 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

ISS01: Standardization is Key – Proteomics for Everyone

- 08:00 Single Cell and Plasma Proteomics on the Evosep: Bringing Proteomics to the Clinic
Matthias Mann, Germany
- 08:30 Slice-PASEF and Evosep One for Sensitive High-Throughput Proteomics
Vadim Demichev, Germany

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



PROGRAM

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

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



PROGRAM

- 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

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

Jong Bae Park, Republic of Korea

Chair

Chien-Yun Lee, Germany

- 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

PROGRAM

- 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

- 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 β -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

PROGRAM

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

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 NULISAsq Proteomic Technologies Applied to a COVID-19 Case-control Cohort Showed High Similarity Between the Two Technologies.

Frank Schmidt, 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

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

Junbiao Xue, China

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

Fábio Nogueira, Brazil

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

PP01.53: Phosphoproteomic Analysis to Identify the Mechanism Underlying the Development of Childhood Autism on Prenatal VPA Exposure

Hazara Begum Mohammad, Republic of Korea

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



PROGRAM

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, China

PP01.65: The Role of AC9 in Glucagon Secretion in Islet α 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

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

PROGRAM

- 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
- 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



PROGRAM

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

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 Degraders 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

PROGRAM

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

Poorichaya Somporn, 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

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 β -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



PROGRAM

PP01.201: Mapping the Spatial Proteome: Exploring Tissue Heterogeneity Through TMT Labeling and Multiplexed Mass Spectrometry Analysis

Yuanwei Xu, United States

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

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

13:15 Speaker

Daniel Hornburg, United States

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

ISS05: Seminar Supported by Bruker

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: Complementing Mass Spectrometry with Immunoaffinity Techniques

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



PROGRAM

- 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

- 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



PROGRAM

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
- 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 Immunopeptidomics

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 β -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



PROGRAM

- 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
- 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
Joshua Fehring,
- 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, China
- 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
Frank Schmidt, Qatar



PROGRAM

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

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- κ 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

PROGRAM

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

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

PROGRAM

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

Hahyun Lee, Republic of Korea

PP01.116: Comparison of Guinea Pig Retinal Proteomes Prepared Using S-TrapTM and EasyPepTM Protocols for Label-Free Proteomics

Daqian Lu, Hong Kong

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 PlatinumTM: 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

PROGRAM

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

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



PROGRAM

- PP01.178: Newly Synthesized Proteome of Parkinson's Disease Peripheral Blood Mononuclear Cells
Dani Flinkman, Finland
- PP01.180: Rnf146 Disrupts Wnt/ β -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
- 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 0.002mm² 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
- PP01.200: 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



PROGRAM

- 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

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

PROGRAM

CS12: Infectious Diseases

Chair

Bernd Wollscheid, Switzerland

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: Seminar Supported by Bruker

- 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



PROGRAM

08:10 Speaker
Kyunggon Kim, Republic of Korea

08:30 Speaker
Qifeng Lin, Singapore

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 - Finding The Connection: Multi-omics To Provide Dimensionality To The Proteome
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

PROGRAM

- 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

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

Je Yoel Cho, Republic of Korea

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

PROGRAM

- 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

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



PROGRAM

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

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- β 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- α 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

PROGRAM

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

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

PROGRAM

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

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

PROGRAM

- 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
- 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 Sigh 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



PROGRAM

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

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 TiO₂ Chromatography in Combination with LC-MS/MS and Accurate Mass Matching Using the GPMaw 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



PROGRAM

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

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 Kodera, 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: Seminar Supported by Bruker



PROGRAM

- 13:15 Throughput without compromise in Immunopeptidomics using timsTOF technology combined with EvoSep One
Anthony Purcell, Australia
- 13:40 Maximizing Information Content in Data-independent Acquisition using midia-PASEF
Stefan Tenzer, Germany

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

ISS12: A New Era in Proteomics, Introducing Olink Explore HT

- 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: IesSDRF 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



PROGRAM

CS18: Glycoproteomics

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



PROGRAM

Chair

Mathieu Lavallée-Adam, Canada

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, China

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

PROGRAM

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

Jubert Marquez, Republic of Korea

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

Sunky 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- β 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 β -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



PROGRAM

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

Annika Bendes, Sweden

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

PROGRAM

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

Jikyo Lee, Republic of Korea

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

PP03.120: 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
Enikő Gebri, Hungary
- 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

Enikő Gebri, Hungary



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 Ca²⁺-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 - N-Terminal Formyl-Methionine: a Critical Determinant for Ribosome and Protein Quality Control in Eukaryotes
Cheol-Sang Hwang,
- 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 Degroove, 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
- PP05.16A: Single-cell Proteomics Methodologies on the Orbitrap Tribird Platform for Increased Throughput and Extended Coverage
Amanda Lee, United States
- PP05.16: Increasing the Depth of Single Shot Proteomics with Enhanced Data Acquisition and Processing Strategies Using Orbitrap Ascend MS
Amanda Lee, United States
- PP05.17: 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 Urzabakhtin, 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- κ 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 β -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

PP05.75: 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

PP05.80: 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

PP05.91: The Small Open Reading Frame-encoded Peptides: Method Development and Functional Studies

Qian Zhao, Hong Kong

PROGRAM

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

PP05.95A: Uncovering a Neurological Protein Signature for Severe COVID-19

Houari Abdesslem, Qatar

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 α and p38 β

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 Sintés, 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, China

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: Expanding Proteomic Horizons with Single-Molecule Analysis at Scale

13:15 Single-molecule Proteome Analysis using Protein Identification by Short-epitope Mapping

Parag Mallick, United States

13:45 A deep dive into proteome changes with acute and chronic kidney injury in mice and non-human primates

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
Je Yoel Cho, Republic of Korea
- 16:30 PL07.01: Congress Summary
Youngsoo Kim, Republic of Korea
- 16:40 PL07.02: ECR Summary and Announcement of ECR Award Winners
Ruth Huttenhain, United States
- 16:40 PL07.02: ECR Summary and Announcement of ECR Award Winners
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



See you in Busan!
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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
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 π -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

