



### Poster Index

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## HUPO CoCONNECT 2021 Poster List

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Poster Board No.	Poster Theme	Poster Section No.	Poster Title	Presenter First Name	Presenter Last Name	Presenter Available at 16:00 - 17:00 UTC, Tuesday, November 16, 2021	Presenter Available at 04:30 - 05:30 UTC, Thursday, November 18, 2021
P01.01	10. The Future of Proteomics	1	Methylproteome and Phosphoproteome Crosstalk in the Maintenance and Differentiation of Glioma Cancer Stem Cells	Byron	Baron	Yes	No
P01.02	10. The Future of Proteomics	1	Cellular Protein Perturbations Identify Toxicity Pathways Associated with ZnO Nanoform Exposures	Premkumari	Kumarathasan	No	Yes
P01.03	10. The Future of Proteomics	1	Future Perspectives and Strategies for Data-Independent Acquisition on Orbitrap MS Instruments	Yansheng	Liu	No	Yes
P01.04	10. The Future of Proteomics	1	Progress Identifying and Analyzing the Human Proteome: 2021 Metrics from the HUPO Human Proteome Project	Gilbert S.	Omenn	Yes	No
P01.05	10. The Future of Proteomics	1	A TMTpro 18plex Proteomics Standard for Assessing Protein Measurement Accuracy and Precision	Bhavin	Patel	Yes	Yes
P02.01	03. Omics at Single Cell Resolution	1	Evaluation of Long Nanoflow Columns with Core-Shell Based Chromatographic Phases in Data Dependent Acquisition Workflows	Alexandra	Antonopolis	Yes	Yes
P02.02	03. Omics at Single Cell Resolution	1	Maximizing Sensitivity Gains with Ultra-low Nano-Flow LCMS Analysis Enabled by Next-Generation Low-Flow UHPLC System	Alexander	Boychenko	Yes	Yes

<b>P02.04</b>	03. Omics at Single Cell Resolution	<b>1</b>	Real-Time Search Assisted Acquisition on a Tribrid Mass Spectrometer Improves Coverage of Multiplexed Single-Cell Proteomics	Benjamin	Furtwängler	<b>Yes</b>	<b>No</b>
<b>P02.05</b>	03. Omics at Single Cell Resolution	<b>1</b>	A Highly Efficient and Automated Workflow for Label-Free and Multiplexed Single Cell Proteomics	David	Hartlmayr	<b>Yes</b>	<b>Yes</b>
<b>P02.06</b>	03. Omics at Single Cell Resolution	<b>1</b>	Digital Microfluidics for Proteomics Analysis of Few or Single Mammalian Cells	Jan	Leipert	<b>Yes</b>	<b>No</b>
<b>P02.07</b>	03. Omics at Single Cell Resolution	<b>1</b>	Streamlined Single-Cell Proteomics by the All-in-One Chip and Data-Independent Acquisition Mass Spectrometry	Hsiung-Lin	Tu	<b>No</b>	<b>Yes</b>
<b>P02.08</b>	03. Omics at Single Cell Resolution	<b>1</b>	Comparison of Epithelial and Stromal Proteomes from Colorectal Adenoma to Carcinoma	Keqiang	Yan	<b>No</b>	<b>Yes</b>
<b>P03.01</b>	12. Visualizing the Cell	<b>1</b>	Defining Mechanisms Underlying Virus Regulation of Mitochondrial Bioenergetics During Infection	Cora	Betsinger	<b>Yes</b>	<b>No</b>
<b>P03.02</b>	12. Visualizing the Cell	<b>1</b>	Cell-Surface Proteomics: Novel Methodology for Identifying Cell-Surface Proteins of Toxic Dinoflagellates	Kenrick Kai-yuen	Chan	<b>No</b>	<b>Yes</b>
<b>P03.03</b>	12. Visualizing the Cell	<b>1</b>	The Human Fallopian Tube Proteome	Andreas	Digre	<b>Yes</b>	<b>No</b>
<b>P03.04</b>	12. Visualizing the Cell	<b>1</b>	Identification of Cell Type-Specific Endometrial Markers through Integration of Single-Cell Transcriptomics and Spatial Proteomics	Åsa	Edvinsson	<b>Yes</b>	<b>No</b>
<b>P03.06</b>	12. Visualizing the Cell	<b>1</b>	System Wide Profiling of Protein Interaction Dynamics Links Host Innate Immunity and DNA Damage Responses	Joshua	Justice	<b>Yes</b>	<b>Yes</b>

<b>P03.07</b>	12. Visualizing the Cell	<b>1</b>	Spatial Proteomics Analysis of Ovaries from Women in Reproductive Age	Loren	Méar	<b>Yes</b>	<b>No</b>
<b>P03.08</b>	12. Visualizing the Cell	<b>1</b>	Differential Regulation of Promyelocytic Leukemia-Nuclear Body (PML-NB) Proteins during Oncogene Induced Senescence	Rodrigo	Mohallem Ferreira	<b>Yes</b>	<b>No</b>
<b>P03.09</b>	12. Visualizing the Cell	<b>1</b>	Combining SDS with Subcritical for Continuous Flowthrough Extraction of Proteins from Food Samples.	Hammam	Said	<b>Yes</b>	<b>No</b>
<b>P03.10</b>	12. Visualizing the Cell	<b>1</b>	Impacts of Intracellular-Advanced Glycation End Products in Pancreatic Ductal Epithelial Cells	Lakmini	Senavirathna	<b>No</b>	<b>No</b>
<b>P03.11</b>	12. Visualizing the Cell	<b>1</b>	Streamlined Use of Protein Structures and Virtual Reality to Analyse Variants	Neblina	Sikta	<b>Yes</b>	<b>Yes</b>
<b>P04.01</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Ghost Proteome Revealed Involved in Functional Regulator of Glioma Using Crosslink Mass Spectrometry	Tristan	Cardon	<b>Yes</b>	<b>No</b>
<b>P04.02</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Proteomic Investigation of Stress-Induced Neurological Changes in Brain Regions of an Alzheimer's Disease Transgenic Mouse Model	Amalie	Clement	<b>Yes</b>	<b>Yes</b>
<b>P04.03</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Deep Proteomic Profiling of Alzheimer's Disease CSF for Unbiased Biomarker Discovery and Subject Stratification	Yuehan	Feng	<b>Yes</b>	<b>No</b>
<b>P04.04</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Dynamics of Huntingtin Protein Interactions in the Striatum Identifies Candidate Modifiers of Huntington's Disease	Todd	Greco	<b>Yes</b>	<b>No</b>
<b>P04.05</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Brain Glycoproteomic Network Alterations in Alzheimer's Disease	Lian	Li	<b>Yes</b>	<b>No</b>

<b>P04.06</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Omics Insights into Gender Differences in Alzheimer Disease Subjects	Elisa	Maffioli	<b>Yes</b>	<b>Yes</b>
<b>P04.07</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Identification of Proteins Altered in Alzheimer's Disease by Mass Spectrometry That Could Be Key for the Understanding of the Disease	Ana	Montero Calle	<b>Yes</b>	<b>No</b>
<b>P04.08</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Proteomic Analysis of Three Brain Regions Isolated from Patients with Mesial Temporal Lobe Epilepsy Reveals Molecular Alterations beyond the Hippocampus	Amanda	Morato Do Canto	<b>Yes</b>	<b>No</b>
<b>P04.09</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Differential Proteomic Analysis of Astrocytes and Astrocytes-Derived Extracellular Vesicles from Control and Rai Knockout Mice: Insights into Neuroprotective Mechanisms	Enxhi	Shaba	<b>Yes</b>	<b>No</b>
<b>P04.10</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Assessment of IsoAsp7 Amyloid-beta Peptides as a Perspective Diagnostic Target of AD Progression by Proteomic MS Based Approaches	Polina	Strelnikova	<b>Yes</b>	<b>No</b>
<b>P04.11</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Proteomic Profiling Provides New Insights into the Role of Neuromelanin Granules in Neurodegenerative Processes	Maximilian	Wulf	<b>Yes</b>	<b>No</b>
<b>P04.12</b>	01. Brain Rewiring in Neurological Disorders	<b>1</b>	Mitochondrial, Cell Cycle Control and Neuritogenesis Alterations in an iPSC-Based Neurodevelopmental Model for Schizophrenia	Giuliana	Zuccoli	<b>Yes</b>	<b>Yes</b>
<b>P05.02</b>	05. Proteome-wide Structural Biology	<b>1</b>	A Survey of the Cancer Conformational Landscape Establishes Novel Anti-Cancer Drug Targets	Tom Casimir	Bamberger	<b>No</b>	<b>No</b>

<b>P05.03</b>	05. Proteome-wide Structural Biology	<b>1</b>	Proteomics and Large-Scale, Comparative Cross-Linking Mass Spectrometry Reveal Novel Roles for Ribosome Histidine Methylation	Tara	Bartolec	<b>No</b>	<b>Yes</b>
<b>P05.04</b>	05. Proteome-wide Structural Biology	<b>1</b>	Assessing Therapeutic Diet-Induced Succinylome Remodeling in Injured Kidney and Liver using Library-Free Data-Independent Acquisition	Joanna	Bons	<b>Yes</b>	<b>Yes</b>
<b>P05.05</b>	05. Proteome-wide Structural Biology	<b>1</b>	Interactome Analyses and HDX-MS Reveal Profound Proteasome Structural and Functional Rearrangements throughout Mammalian Spermatogenesis	Dušan	Živković	<b>Yes</b>	<b>Yes</b>
<b>P05.06</b>	05. Proteome-wide Structural Biology	<b>1</b>	A Structural Analysis of Heated Ovalbumin by Crosslink Proteomics	Mehdi	Cherkaoui	<b>Yes</b>	<b>No</b>
<b>P05.07</b>	05. Proteome-wide Structural Biology	<b>1</b>	N-Glycoproteome from a Cancer Cell Line and Its Non-tumorigenic Cell Line Combining Fbs1-GYR N-Glycopeptide Enrichment and Trapped-Ion-Mobility-Quadrupole-Time-of-Flight	Michael	Krawitzky	<b>Yes</b>	<b>No</b>
<b>P05.08</b>	05. Proteome-wide Structural Biology	<b>1</b>	Proteomics of A-to-I Rna Editing in Mouse and Human	Ksenia	Kuznetsova	<b>Yes</b>	<b>No</b>
<b>P05.09</b>	05. Proteome-wide Structural Biology	<b>1</b>	Mapping the Functional Proteome Landscape of Escherichia Coli with Thermal Proteome Profiling	André	Mateus	<b>Yes</b>	<b>No</b>
<b>P05.11</b>	05. Proteome-wide Structural Biology	<b>1</b>	HaDeX 2.0: Web-Server and R Package for the Hydrogen-Deuterium Exchange Mass Spectrometry Experiments Data	Weronika	Puchała	<b>Yes</b>	<b>No</b>
<b>P05.12</b>	05. Proteome-wide Structural Biology	<b>1</b>	Prolonged Exposure to Traffic-Related Particulate Matter and Gaseous Pollutants Implicate Distinct Molecular Mechanisms of Lung Injury in Rats	Denise Utami	Putri	<b>No</b>	<b>Yes</b>

<b>P06.01</b>	02. Combating COVID-19	<b>2</b>	Dysregulation of Plasma Proteome Induced by SARS-CoV-2 and MERS-CoV Infections Reveal Biomarkers for COVID-19 Patients Disease Outcomes	Ayodele	Alaiya	<b>Yes</b>	<b>Yes</b>
<b>P06.02</b>	02. Combating COVID-19	<b>2</b>	Proteomic Analysis of the Upper Respiratory Proteins from COVID 19 Patients: A Gel Based Approach.	Stefania	Angelucci	<b>Yes</b>	<b>No</b>
<b>P06.04</b>	02. Combating COVID-19	<b>2</b>	Targeted MS Based Multi-Omic Analysis of Blood Plasma from Hospitalized COVID-19 Patients Reveals Predictive Molecular Signatures of Survival	Vincent	Richard	<b>No</b>	<b>No</b>
<b>P06.05</b>	02. Combating COVID-19	<b>2</b>	The secretome signature for identifying biomarkers in COVID-19 severe forms	Sandrine	Bourgoin	<b>No</b>	<b>No</b>
<b>P06.06</b>	02. Combating COVID-19	<b>2</b>	Data-Independent Acquisition Mass Spectrometry (DIA-MS) Analysis Identifies a Neutrophil Proteomic Signature in COVID-19 Infection	Alejandro J.	Brenes	<b>Yes</b>	<b>No</b>
<b>P06.07</b>	02. Combating COVID-19	<b>2</b>	Quantitative Proteome and Phosphoproteome Analysis of A549-ACE2 Cells after Infection with Sars-COV2 – A Pilot Study	Fernando	Corrales	<b>No</b>	<b>No</b>
<b>P06.08</b>	02. Combating COVID-19	<b>2</b>	Glycopeptide Mapping for Comparison of CHO and HEK Cell Derived SARS-Cov-2 Spike Trimeric Protein Antigen	Caroline	Evans	<b>No</b>	<b>No</b>
<b>P06.09</b>	02. Combating COVID-19	<b>2</b>	Sex differences in Autoantibodies Response to SARS-CoV-2 Infection	Justyna	Fert-Bober	<b>Yes</b>	<b>No</b>
<b>P06.10</b>	02. Combating COVID-19	<b>2</b>	SARS-CoV-2 Infection Triggers Auto-Immune Response in ARDS	Manuel	Fuentes	<b>No</b>	<b>No</b>

<b>P06.11</b>	02. Combating COVID-19	<b>2</b>	Utilisation of Cyclic Ion Mobility with Multiple Pass Acquisition for the Analysis of Glycopeptides and Glycoforms Associated with SARS-CoV-2	Lee	Gethings	<b>Yes</b>	<b>No</b>
<b>P06.12</b>	02. Combating COVID-19	<b>2</b>	Longitudinal Proteomic Profiling of Dialysis Patients with COVID-19 Reveals Markers of Severity and Predictors of Death	Jack	Gisby	<b>Yes</b>	<b>No</b>
<b>P06.13</b>	02. Combating COVID-19	<b>2</b>	Large-Scale Discovery and Exploration of Virus-Host Interaction Motifs	Eszter	Kassa	<b>Yes</b>	<b>No</b>
<b>P06.14</b>	02. Combating COVID-19	<b>2</b>	Antibody Landscape against SARS-CoV-2 Proteome Revealed Significant Differences between Non-structural/ Accessory Proteins and Structural Proteins.	Dan Yun	Lai	<b>Yes</b>	<b>No</b>
<b>P06.15</b>	02. Combating COVID-19	<b>2</b>	Multi-omics Characterization of COVID-19 Reveals Risk Factors for One-year Sequelae	Xiao	Liang	<b>No</b>	<b>Yes</b>
<b>P06.19</b>	02. Combating COVID-19	<b>2</b>	Systematically Exploit the IgG Responses to SARS-CoV-2 at Amino Acid Level by AbMap	Huan	Qi	<b>No</b>	<b>Yes</b>
<b>P06.20</b>	02. Combating COVID-19	<b>2</b>	A COVID-19 Knowledge Graph for Therapeutic Discovery from Semantic Integration of Literature and Databases	Karen	Ross	<b>Yes</b>	<b>No</b>
<b>P06.22</b>	02. Combating COVID-19	<b>2</b>	Systematical Deciphering of SARS-CoV-2 Specific Humoral Immune Responses	Sheng-ce	Tao	<b>No</b>	<b>Yes</b>
<b>P07.01</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Saliva Protein Signatures of Smokers Enrolled in Lung Cancer Screening for Early Diagnosis and Clinical Management.	Stefania	Angelucci	<b>Yes</b>	<b>No</b>



<b>P07.02</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Connecting Molecular Pathology and Precision Oncology: Development and Validation of a Quantitative Immuno-MRB Assay for The PD-1/PD-L1 Axis	Vincent	Lacasse	<b>No</b>	<b>No</b>
<b>P07.03</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Extracellular Vesicle Protein Biomarkers of Cardiac AL Amyloidosis	Sandrine	Bourgoin	<b>No</b>	<b>No</b>
<b>P07.05</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Phospho-Proteome Analysis of Cerebrospinal Fluid Extracellular Vesicles in Primary Central Nervous System Lymphoma	Yuanyuan	Deng	<b>No</b>	<b>Yes</b>
<b>P07.06</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Mapping Isoform Abundance and Interactome of the Endogenous TMPRSS2-ERG Fusion Protein in Prostate Cancer	Andrei	Drabovich	<b>Yes</b>	<b>No</b>
<b>P07.08</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Proteomic Profiling of Ankylosing Spondylitis Patients Serum Reveals Biomarkers for Therapeutic Response Prediction and Associated Mechanistic Insights	Ana	Fernandes	<b>Yes</b>	<b>No</b>
<b>P07.11</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Cancer-Testis Antigen and Immune Profiling in Non-Small Cell Lung Cancer by Transcriptomics and Antibody-Based Proteomics	Feria	Hikmet Noraddin	<b>Yes</b>	<b>No</b>
<b>P07.12</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Cytokines and Chemokines Analysis of Malignant Pleural Effusions	Xiaomin	Hu	<b>No</b>	<b>Yes</b>
<b>P07.13</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Comprehensive Serum Proteome Analysis for Signatures Development in High-Grade Serous Ovarian Cancer	Un-Beom	Kang	<b>No</b>	<b>Yes</b>
<b>P07.14</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Diagnostic Value of Multiple Serum Protein Marker in Breast Cancer Based on Proteomics Technique	Yumi	Kim	<b>No</b>	<b>Yes</b>

<b>P07.15</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	The Effect of Storage Time and Temperature on MS Analysis of FFPE Tissue Sections	Jennifer	Koh	<b>No</b>	<b>Yes</b>
<b>P07.16</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Identification of Key Protein Markers of Colorectal Cancer for the Development of the Disease by TMT-Quantitative Proteomics	Ana	Montero Calle	<b>Yes</b>	<b>No</b>
<b>P07.17</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Automated Proteomics Sample Preparation of Extracellular Vesicles from Human Plasma and Serum	Satoshi	Muraoka	<b>No</b>	<b>Yes</b>
<b>P07.19</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Proteomic Profiles of Zika Virus-Infected Placentas Bearing Foetuses with Microcephaly	Mauricio	Quiñones-Vega	<b>Yes</b>	<b>No</b>
<b>P07.20</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Discovery of Prostate Cancer Biomarkers by Immunoaffinity Proteomics.	Yasmine	Rais	<b>Yes</b>	<b>Yes</b>
<b>P07.21</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	A Multi-Omics LC-MS Approach for Rational Selection of Neo-Antigens and Unbiased Detection of Corresponding Neo-Epitopes from Low Number of Cells	Mogjib	Salek	<b>No</b>	<b>No</b>
<b>P07.22</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Label-free Proteomics Profile from Spleens of Lupus-like cGVHD WT Mice Reflects a STAT-1-driven Type I IFN-signature	Jaime	Sancho	<b>Yes</b>	<b>No</b>
<b>P07.23</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Cardiac Sex Disparities are Established Prior to Gonad Formation	Xinlei	Sheng	<b>Yes</b>	<b>No</b>
<b>P07.24</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Serological Profiling of Crohn's Disease and Ulcerative Colitis Sera Reveal Microbial Antibody Markers	Mahasish	Shome	<b>Yes</b>	<b>No</b>

<b>P07.25</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Quantitative Proteome Profiling ties the Complement System to Amyloidosis	Christian	Treitz	<b>Yes</b>	<b>No</b>
<b>P07.26</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Clinical Mass Spectrometry Center Munich (CLINSPECT-M): Adding a Proteomic Component to Molecular Tumor Boards	Johanna	Tüshaus	<b>No</b>	<b>No</b>
<b>P07.27</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Peptide and Metabolite Profiling in Histological Variants of Papillary Thyroid Carcinoma	Yasemin	Ucal	<b>No</b>	<b>No</b>
<b>P07.28</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Serum Proteomic Analysis of Severe Eosinophilic Asthma Patients before and after Two New Biological Therapies	Lorenza	Vantaggiato	<b>Yes</b>	<b>No</b>
<b>P07.29</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Mass Spectrometry-Based Proteomic and Metabolomic Profiling of Serum Samples for Discovery and Validation of TB Diagnostic Biomarker	Ana	Varela Coelho	<b>Yes</b>	<b>No</b>
<b>P07.30</b>	04. Precision Pathology: Proteomics for Patients	<b>2</b>	Cell Type Deconvolution of Brain Proteomes (BrainDecon)	Theodore	Verhey	<b>Yes</b>	<b>Yes</b>
<b>P08.01</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Development of a Targeted Proteomics Method for Serum IGF-I, IGF-II, IGFBP-1, 2, 3, 4, 5 and 6.	Jakob	Albrethsen	<b>Yes</b>	<b>No</b>
<b>P08.03</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Bench-to-Bedside Alzheimer Disease's Detection by Biosensing Approaches Detecting Autoantibody Biomarkers Identified by Protein Microarrays-Based Proteomics	Rodrigo	Barderas	<b>Yes</b>	<b>No</b>
<b>P08.04</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Precision Analysis Reveals Diagnostic Protein Biomarkers of Japanese Encephalitis Virus Infection in Cerebrospinal Fluid	Tehmina	Bharucha	<b>Yes</b>	<b>No</b>

<b>P08.05</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Application of 16O/18O Labeling in Characterization of Thyroid Cancer Patient	Ing-Feng	Chang	<b>Yes</b>	<b>No</b>
<b>P08.06</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Tumor Outflow Pulmonary Blood Derived Exosome GCC2 act as a Clinically Informative Biomarker in Patients with Surgically Resected Lung Adenocarcinoma	Byeong Hyeon	Choi	<b>Yes</b>	<b>No</b>
<b>P08.07</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Multi-Staged Enrichment Method Capable of Quantifying Mutant Frameshift MUC1 in Urine from Patients with Autosomal Dominant Tubulointerstitial Kidney Disease (ADTKD-MUC1)	Kristen	Doucette	<b>Yes</b>	<b>No</b>
<b>P08.08</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Identification of Procalcitonin in Septic Patients Serum by Affinity Chips and Mass Spectrometry	Josef	Dvořák	<b>Yes</b>	<b>No</b>
<b>P08.09</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Proteomic Analysis of Synovial Liquid to Search for Severity Biomarkers in Osteoarthritis	Patricia	Fernandez Puente	<b>Yes</b>	<b>No</b>
<b>P08.10</b>	11. Translating Proteomics into the Clinic	<b>3</b>	An Intelligent Hybrid-Dia Data Acquisition Strategy for Cracking the Clinical Sample Complexity Challenge in Translational Proteotyping	Sandra	Goetze	<b>No</b>	<b>No</b>
<b>P08.11</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Cyclic Ion Mobility-Enabled Mass Spectrometer and Application to High Throughput Plasma Proteomics	Chris	Hughes	<b>No</b>	<b>No</b>
<b>P08.12</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Species-Specific Cutaneous Protein Signatures of Incision Injury and Correlation with Distinct Pain-Related Phenotypes in Humans	Christin	Kappert	<b>No</b>	<b>Yes</b>
<b>P08.13</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Proteomic Signature Associated with Prognosis in HPV-Related Oropharyngeal Squamous Cell Carcinoma	Jia (Jenny)	Liu	<b>No</b>	<b>Yes</b>

<b>P08.14</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Identification of Protein Biomarkers in FFPE Primary Tissues to Predict Recurrence in Endometrial Cancer	Carlos	López Gil	<b>Yes</b>	<b>No</b>
<b>P08.15</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Protein Biomarkers in Pipelle Biopsies to Diagnose the Histological Type and Grade of Endometrial Cancer and Predict Tumor Recurrence	Elena	Martinez Garcia	<b>Yes</b>	<b>No</b>
<b>P08.16</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Immunopeptidomics-Based Development of a Listeria mRNA Vaccine	Rupert	Mayer	<b>Yes</b>	<b>No</b>
<b>P08.17</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Regulation of Protein Cargo in Extracellular Vesicles during Cancer Onset	Orlando	Morales-tarré	<b>No</b>	<b>Yes</b>
<b>P08.19</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Evaluation of Melanoma Plasma Proteome Profile and the Modulation of Plasma Proteins Based on Tumor Proliferation	Natália	Pinto de Almeida	<b>Yes</b>	<b>No</b>
<b>P08.20</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Diagnosis of Pleural Effusions Using Mass Spectrometry-Based Targeted Proteomics	Aleksandra	Robak	<b>Yes</b>	<b>No</b>
<b>P08.21</b>	11. Translating Proteomics into the Clinic	<b>3</b>	An 8-Channel Automatic Glycan Profiling System Realized by The GlycoBIST Technology	Hiroko	Shimazaki	<b>No</b>	<b>Yes</b>
<b>P08.22</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Proteogenomics for Splicing Variation and Differential Expression: A Myotonic Dystrophy Type 1 Mouse Model Study	Elizaveta	Solovyeva	<b>No</b>	<b>Yes</b>
<b>P08.24</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Discovery of Soluble Pancreatic Cancer Biomarkers Using Innovative Clinical Proteomics and Statistical Learning.	Guillaume	Tosato	<b>Yes</b>	<b>Yes</b>
<b>P08.25</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Discovery of Candidate Stool Biomarker Proteins for Biliary Atresia Using Deep Proteome Analysis by Data-Independent Acquisition Mass Spectrometry	Eiichiro	Watanabe	<b>No</b>	<b>Yes</b>

<b>P08.26</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Large scale, deep and unbiased plasma proteomics profiling a sub-study of a multi-cancer cohort enabling biomarker discovery	Bruce	Wilcox	<b>Yes</b>	<b>No</b>
<b>P08.27</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Unbiased High-Throughput Mass Spectrometry-Based Plasma Proteomics for Detection of Early Stage Lung Cancer	Matthew	Willetts	<b>Yes</b>	<b>No</b>
<b>P08.28</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Proteomic Characterization of Primary Tumors and Brain Metastases in Lung Adenocarcinoma Patients	Nicole	Woldmar	<b>Yes</b>	<b>No</b>
<b>P08.29</b>	11. Translating Proteomics into the Clinic	<b>3</b>	A Pan-Cancer Proteomic Map of 960 Human Cell Lines	Qing	Zhong	<b>No</b>	<b>Yes</b>
<b>P08.30</b>	11. Translating Proteomics into the Clinic	<b>3</b>	A Fully Automated High-Throughput, Deep-Scale Quantitative Plasma Proteomics Workflow Enables Quantitatively Profile More Than 1000 Proteins Per Sample	Yu	Zhou	<b>Yes</b>	<b>No</b>
<b>P08.31</b>	11. Translating Proteomics into the Clinic	<b>3</b>	Accurate Quantitation of Clinically Approved Cancer Biomarkers Utilising SRM	Erin	Sykes	<b>No</b>	<b>Yes</b>
<b>P09.01</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Proteomics of the Acquired Resistance to Targeted Kinase Inhibition in Pancreatic Cancer Cells	Alain	Aguilar-Valdes	<b>Yes</b>	<b>No</b>
<b>P09.02</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Proteomic Characterization of two Extracellular Vesicle Subtypes Isolated from Human Glioblastoma Stem Cell Secretome by Sequential Centrifugal Ultrafiltration	Stefania	Angelucci	<b>Yes</b>	<b>No</b>

<b>P09.04</b>	08. Proteomics-guided Therapeutics	<b>3</b>	DIA-MS Identifies and Validates Transgelin as Protein Contributing to a Poor Response of Metastatic Renal Cell Carcinoma to Sunitinib Treatment	Pavla	Bouchalova	<b>No</b>	<b>No</b>
<b>P09.06</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Efficient Profiling of Protein Degradors by Specific Functional and Target Engagement Readouts	Alexey	Chernobrovkin	<b>Yes</b>	<b>Yes</b>
<b>P09.07</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Label Free Pharmacoproteomic Assays Enabled the Discovery of Cellular Pathways Involved in the Survival Of MCF-7 and K562 Cancer Cells	Cristina	Clement	<b>Yes</b>	<b>Yes</b>
<b>P09.09</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Proteomic Analysis of Equine Serum Antibody Repertoire against <i>Loxosceles</i> Venom.	Manuela Cristina	Emiliano Ferreira	<b>Yes</b>	<b>No</b>
<b>P09.10</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Discovering Substrates of PRMT5 and CDK4/6 In Human Melanoma Cells with Antibody-Based PTM Peptide Specific Enrichment Strategies.	Charles	Farnsworth	<b>Yes</b>	<b>No</b>
<b>P09.11</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Improved Middle-down Characterization of Antibodies Using Proton Transfer Charge Reduction on a Tribrid Orbitrap Mass Spectrometer	Luca	Fornelli	<b>No</b>	<b>No</b>
<b>P09.12</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Combatting Fungal Infections: Novel Anti-virulence Strategies and Reversing Antifungal Resistance.	Jennifer	Geddes- McAlister	<b>No</b>	<b>Yes</b>
<b>P09.13</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Proteomic Unraveling of the Hidden Regulators of Erythropoiesis	Sudip	Ghosh	<b>Yes</b>	<b>No</b>
<b>P09.14</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Effects of Salicornia-Based Cream Skin Application on a Human Experimental Model of Pain and Itch.	Rocco	Giordano	<b>Yes</b>	<b>No</b>

<b>P09.15</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Transcriptional and Translational Dynamics Underlie Synergy in Endothelial Inflammation	Stijn	Groten	<b>Yes</b>	<b>No</b>
<b>P09.16</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Comprehensive Biological Characterization of Novel Antitumor Nanoconjugates by Newly Synthesized Proteomes with Bioorthogonal Non-canonical Amino-Acid Tagging.	Angela-Patricia	Hernandez	<b>Yes</b>	<b>No</b>
<b>P09.17</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Proteomic Basis for Understanding the Combination of Gemcitabine and Kinase Inhibitors to Kill Pancreatic Cancer Cells	Stefanie	Hoefler	<b>No</b>	<b>No</b>
<b>P09.18</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Developing and Validating a Set of Targeted Mass Spectrometry Assays for Pan-Herpesvirus Viral Protein Detection and Monitoring of Infection Progression	Michelle	Kennedy	<b>Yes</b>	<b>No</b>
<b>P09.19</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Target Identification of a Natural Compound Regulating Mitochondria-ER Interaction Using DARTS-LC-MS/MS	Minjeong	Ko	<b>No</b>	<b>Yes</b>
<b>P09.20</b>	08. Proteomics-guided Therapeutics	<b>3</b>	The Cell Membrane Proteome: From Cancer Hallmarks to Therapeutic Interventions	Iulia	Lazar	<b>Yes</b>	<b>No</b>
<b>P09.21</b>	08. Proteomics-guided Therapeutics	<b>3</b>	The Chemoproteomic Target Landscape of HDAC Inhibitors Highlights MBLAC2 as Common Off-Target	Severin	Lechner	<b>Yes</b>	<b>No</b>
<b>P09.22</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Label-Free Dia-PASEF Compared to TMT Quantitation for Thermal Proteome Profiling / Cellular Thermal Shift Assay	Johan	Lengqvist	<b>Yes</b>	<b>No</b>
<b>P09.23</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Proteomics Profiling of Systemic Effects of Bovine Colostrum Diet in Preterm Piglets - A Translational Model for Neonate Disease Pathology	Azra	Leto	<b>Yes</b>	<b>No</b>



<b>P09.24</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Target Identification, Selectivity Profiling and Mechanistic Insights of a Cdk9 Inhibitor Using Complementary Proteomics Methods	Daniel	Martinez Molina	<b>Yes</b>	<b>No</b>
<b>P09.25</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Systems-based Examination of DLK-MAPK Signaling in Human Stem Cell Derived Retinal Ganglion Cells during Cell Death	Joseph	Mertz	<b>Yes</b>	<b>No</b>
<b>P09.27</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Establishment and Characterization of a Novel Cancer Stem Cell Derived from Cholangiocarcinoma by Proteomics	Orasa	Panawan	<b>Yes</b>	<b>No</b>
<b>P09.28</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Dynamic Polygon for MHC Class I and II Immunopeptides	Francesco	Pingitore	<b>Yes</b>	<b>Yes</b>
<b>P09.29</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Metalloproteomic Analysis of Brazilian Snake Venoms as Proof of Concept for the Development of a Diagnostic Kit for Snakebites	Lucilene Delazari Dos	Santos	<b>No</b>	<b>Yes</b>
<b>P09.30</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Quantitative Proteomics Shows High Selectivity and Reveals the Mechanism-of-Action of a STAT3 Degradar	Yatao	Shi	<b>No</b>	<b>Yes</b>
<b>P09.31</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Kitted Universal MAM: Automated Sample Preparation for All Stages of Biological Drugs	John	Wilson	<b>Yes</b>	<b>Yes</b>
<b>P09.32</b>	08. Proteomics-guided Therapeutics	<b>3</b>	Integrated Proteomics Revealed Acetylation-Induced PCK Isoenzyme Transition Promotes Metabolic Adaptation of Liver Cancer to Systemic Therapy	Xiaohang	Zhao	<b>No</b>	<b>No</b>
<b>P10.01</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Global Proteome Expression Study of Patient-Derived Sarcoma Cell-Lines toward Optimization of Therapeutic Strategy Using Relocated Anti-cancer Drug	Taro	Akiyama	<b>Yes</b>	<b>Yes</b>

<b>P10.02</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	AI-Driven Glycoproteomics Liquid Biopsy in Nasopharyngeal Carcinoma: A Proof of Concept Study	Thin Thin	Aye	<b>Yes</b>	<b>No</b>
<b>P10.04</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Cell Surface Phenotyping of the Human Heart Reveals Cardiomyocyte-Specific Targets and Surfaceome Dynamics of Explanted Cardiac Fibroblasts	Linda	Berg Luecke	<b>Yes</b>	<b>No</b>
<b>P10.05</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	The Secretome Deregulations in a Rat Model of Endotoxemic Shock	Sandrine	Bourgoin	<b>No</b>	<b>No</b>
<b>P10.06</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Two Novel Serum Biomarkers Are Associated with the Serological Status of Rheumatoid Arthritis Patients: A Tool for Precision Medicine Strategies	Valentina	Calamia	<b>Yes</b>	<b>No</b>
<b>P10.08</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Development of a Standardized MRM Targeted Proteomics Method for Monitoring One-Carbon Metabolism Enzymes in Hepatocellular Carcinoma and Cirrhosis	Fernando	Corrales	<b>No</b>	<b>No</b>
<b>P10.09</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	The Proteomic Analysis of High Grade Serous Ovarian Cancer Reveals the Role of Tumor Microenvironment in Chemoresistance.	Kruttika	Dabke	<b>No</b>	<b>Yes</b>
<b>P10.10</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	A Quantitative Discovery Platform to Survey the Human Blood Plasma Proteome in Precision Oncology	Yuehan	Feng	<b>Yes</b>	<b>No</b>
<b>P10.12</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Functional Protein Discovery for the Early Diagnosis of Neonatal Sepsis	Julie	Hibbert	<b>No</b>	<b>Yes</b>
<b>P10.13</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Fast Library Generation Using Zeno MS/MS and Microflow Chromatography	Christie	Hunter	<b>Yes</b>	<b>Yes</b>

<b>P10.14</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Precise Quantitation of PTEN by Immuno-MRM: A Tool to Resolve the Breast Cancer Biomarker Controversy	Sahar	Ibrahim	<b>No</b>	<b>No</b>
<b>P10.16</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Development of a Parallel Reaction Monitoring Assay for the Quantification of Interferon Alpha Subtypes	Martha	Ingola	<b>No</b>	<b>No</b>
<b>P10.17</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Cancer SHooting ARrow Proteomics (cSHARP) to Target OnCo-proteogenomic Panels in a Quadrupolar Environment	Yasushi	Ishihama	<b>No</b>	<b>No</b>
<b>P10.18</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Biomarker Monitoring in Body Fluid by High Sensitivity and High Throughput FAIMS-Surequant™ Is Targeted Quantitation	Konstantinos	Kalogeropoulos	<b>Yes</b>	<b>No</b>
<b>P10.19</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Optimization of the protocol for collection and proteomic analysis of exhaled breath condensate for the lung cancer diagnostics	Anna	Kozyr	<b>No</b>	<b>No</b>
<b>P10.20</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	A Multi-Faceted System for Differential Glycoprotein Analysis: Toward the "Design Drawings" of GlyCo-targets for the Highly Specific Antibody Drug Development	Atsushi	Kuno	<b>Yes</b>	<b>No</b>
<b>P10.21</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Kinome Analysis of CIC-Rearranged Sarcoma Using Peptide Microarray; Global Investigation of Kinases Affected by Culture Condition	Yu	Kuwata	<b>No</b>	<b>Yes</b>
<b>P10.22</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Evaluation of Humoral Immune Dysfunction in Chronic Lymphocytic Leukemia by Affinity Proteomics.	Alicia	Ladeira Viñuela	<b>No</b>	<b>No</b>
<b>P10.23</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	A Large-Scale Assay Library for Targeted Protein Quantification in Renal Cell Carcinoma Tissues	Petr	Lapcik	<b>Yes</b>	<b>No</b>

<b>P10.24</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Discovery and Validation of Circulating Autoantibodies Associated with the ACPA Status in Early Rheumatoid Arthritis	Lucia	Lourido	<b>Yes</b>	<b>No</b>
<b>P10.25</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Integrated Proteomic and Glycoproteomic Signatures of Protein N-Glycosylation Aberrations in Ulcerative Colitis	Cheng	Ma	<b>Yes</b>	<b>No</b>
<b>P10.27</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Global Immunopeptidomics by Differential Ion Mobility Mass Spectrometry for Identification of Patient Specific HLA-Presented Antigens Directly from Clinical Tissues	Yuriko	Minegishi	<b>No</b>	<b>Yes</b>
<b>P10.29</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Immunoproteomics Characterization of Ligustrum Lucidum Pollen Allergens Causing Respiratory Allergies in Polysensitized Patients	Josaphat Miguel	Montero-Vargas	<b>Yes</b>	<b>No</b>
<b>P10.30</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Autoantigenomics in Neurology: Holistic Characterization of Autoantigen Repertoires Identifies Patient Subgroups and a Novel Target of Autoantibodies in CIDP	Christian	Moritz	<b>No</b>	<b>No</b>
<b>P10.31</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	The Urine Proteome/Degradome Using N-Terminomics with TMPP- Labelling on the Proteome and Peptidome Fractions	Leslie	MULLER	<b>Yes</b>	<b>No</b>
<b>P10.32</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	A Multi-Faceted System for Differential Glycoprotein Analysis: Toward the Discovery of Disease-Related Glycosylation Alterations Using Tissue Crude Samples	Chiaki	Nagai-Okatani	<b>No</b>	<b>Yes</b>
<b>P10.33</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Personalised Phosphoproteomics Identifies Functional Signalling	Elise	Needham	<b>No</b>	<b>Yes</b>

<b>P10.34</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Mass Spectrometry-Based Proteomics of Multiple Sites Reveals Signature of Lymph Node Metastasis for Head and Neck Cancer	Adriana	Paes Leme	<b>No</b>	<b>No</b>
<b>P10.35</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	MASTER INFORM Pro - Proteome Profiling for Personalized Oncology	Julia	Rechenberger	<b>Yes</b>	<b>No</b>
<b>P10.37</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Proteomics-Informed Two Stage Model of Resistance in Acute Myeloid Leukemia: Identification of Novel Therapeutic Targets to Inhibit Early Resistance	Karin	Rodland	<b>Yes</b>	<b>No</b>
<b>P10.38</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Differential Molecular Signatures in Synovial Membrane and Synovial Fluid from Patients with Rheumatoid Arthritis and Psoriatic Arthritis	Cristina	Ruiz-Romero	<b>Yes</b>	<b>No</b>
<b>P10.39</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Proteomic-Based Precision Medicine for Companion Diagnostics in Autoimmune Diseases	Jacob	Skallerup	<b>No</b>	<b>Yes</b>
<b>P10.40</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Aryl Hydrocarbon Receptor-Interacting Protein Regulates Tumorigenic and Metastatic Properties of Colorectal Cancer Cells Driving Liver Metastasis	Guillermo	Solís-Fernández	<b>No</b>	<b>No</b>
<b>P10.41</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Proteomic Analysis Identifies Unique Signatures in Small Cell Lung Cancer Subtypes.	Beáta	Szeitz	<b>Yes</b>	<b>No</b>
<b>P10.42</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Precision Proteomics in Allergy: Pecan Pollen Allergens	Luis M.	Teran	<b>Yes</b>	<b>Yes</b>
<b>P10.43</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Novel Candidate Drugs for Malignant Peripheral Nerve Sheath Tumor Revealed by Mass Spectrometry and Drug Screening Using Patient-Derived Cell Lines	Ryuto	Tsuchiya	<b>No</b>	<b>Yes</b>

<b>P10.44</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Patient-Derived Sarcoma Model; Pivotal Research Resource for Proteomics	Yuki	Yoshimatsu	<b>Yes</b>	<b>No</b>
<b>P10.45</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Urinary Proteins RAD23B and CORO1C Associated with Colorectal Cancer Progression and Metastasis	Xiaohang	Zhao	<b>No</b>	<b>No</b>
<b>P10.46</b>	07. Proteomics-driven Precision Medicine	<b>4</b>	Development of a Multiplexed Protein Panel Using a Targeted-Proteomics Approach for the Study of Resistance to CDK4/6-Inhibitors in Breast Cancer	Marta	Zurawska	<b>Yes</b>	<b>No</b>
<b>P11.01</b>	06. Proteomics Data Science and AI	<b>5</b>	Proteograph Analysis Suite: A Cloud-Scalable Software Suite for Proteogenomics Data Analysis and Visualization.	Harsharn	Auluck	<b>Yes</b>	<b>No</b>
<b>P11.02</b>	06. Proteomics Data Science and AI	<b>5</b>	HPPInspector: Automated Community-Scale Validation of Novel Protein Discoveries	Benjamin	Pullman	<b>Yes</b>	<b>No</b>
<b>P11.03</b>	06. Proteomics Data Science and AI	<b>5</b>	Proteome-Wide Analysis of Turnover Rates with TurnoverR and Skyline	Nathan	Basisty	<b>Yes</b>	<b>No</b>
<b>P11.04</b>	06. Proteomics Data Science and AI	<b>5</b>	DeepLC Can Predict Retention Times for Peptides That Carry As-Yet Unseen Modifications	Robbin	Bouwmeester	<b>Yes</b>	<b>No</b>
<b>P11.05</b>	06. Proteomics Data Science and AI	<b>5</b>	The Development of New Tools to Facilitate Proteomics Data Analysis; the UniProt Proteins API.	Emily	Bowler-Barnett	<b>Yes</b>	<b>No</b>
<b>P11.06</b>	06. Proteomics Data Science and AI	<b>5</b>	Comprehensive Cancer Tissue-Specific Neural Network Spectral Reference Library (SRL) Generation Using DIA-MS Acquisition	Daniel	Bucio Noble	<b>No</b>	<b>Yes</b>
<b>P11.07</b>	06. Proteomics Data Science and AI	<b>5</b>	Tissue Type Prediction Reveals Protein Expression Patterns	Tine	Claeys	<b>Yes</b>	<b>No</b>
<b>P11.08</b>	06. Proteomics Data Science and AI	<b>5</b>	Leveraging Large-Scale Comparative Proteomics across the Tree of Life to Improve Human Disease Models	Rachael	Cox	<b>Yes</b>	<b>No</b>

<b>P11.09</b>	06. Proteomics Data Science and AI	<b>5</b>	Power of prediction: MS <sup>2</sup> PIP and DeepLC-based rescoring dramatically boosts immunopeptide identification	Arthur	Declercq	<b>Yes</b>	<b>No</b>
<b>P11.11</b>	06. Proteomics Data Science and AI	<b>5</b>	Novel Statistics Tools for Reliable Proteome-Wide Quantification of Post-translational Modifications	Nina	Demeulemeester	<b>Yes</b>	<b>No</b>
<b>P11.12</b>	06. Proteomics Data Science and AI	<b>5</b>	ADPR Classification using DPA Clustering Algorithm	Maria	d'Errico	<b>No</b>	<b>No</b>
<b>P11.13</b>	06. Proteomics Data Science and AI	<b>5</b>	A Transformer for Prediction of MS <sup>2</sup> Spectrum Intensities	Markus	Ekvall	<b>Yes</b>	<b>No</b>
<b>P11.15</b>	06. Proteomics Data Science and AI	<b>5</b>	Extending INFERYYS' Capabilities to CID and TMT Data for (Non-)Tryptic Peptides	Siegfried	Gessulat	<b>Yes</b>	<b>Yes</b>
<b>P11.16</b>	06. Proteomics Data Science and AI	<b>5</b>	InfineQ: Real-time Cloud-Based DIA Data Processing For High-Throughput Proteomics	Arnoud	Groen	<b>No</b>	<b>No</b>
<b>P11.17</b>	06. Proteomics Data Science and AI	<b>5</b>	MAGPIE: A Machine Learning Approach for Deciphering Protein-Protein Interactions in Human Plasma	Emily	Hashimoto-Roth	<b>Yes</b>	<b>No</b>
<b>P11.18</b>	06. Proteomics Data Science and AI	<b>5</b>	PepGM: A Probabilistic Graphical Model for Taxonomic Profiling of Viral Proteomes and Metaproteomic Samples	Tanja	Holstein	<b>Yes</b>	<b>No</b>
<b>P11.19</b>	06. Proteomics Data Science and AI	<b>5</b>	Deep Plasma Proteomics at Scale: a Machine Learning Enhanced Multi-Nanoparticle Approach to Improve the Depth of Plasma Proteome Coverage	Daniel	Hornburg	<b>Yes</b>	<b>No</b>
<b>P11.20</b>	06. Proteomics Data Science and AI	<b>5</b>	Evolution of Protein Functional Annotation: Text Mining Study	Ekaterina	Ilgisonis	<b>Yes</b>	<b>No</b>
<b>P11.24</b>	06. Proteomics Data Science and AI	<b>5</b>	Introducing a Cloud Scalable Omics Data Analysis Pipeline with a Serverless Task Infrastructure for Large Scale Proteomics Studies	Hugo	Kitano	<b>Yes</b>	<b>No</b>

<b>P11.25</b>	06. Proteomics Data Science and AI	<b>5</b>	Increasing the Sensitivity of Neoantigen Identification in Mass Spectrometry-Based Immunopeptidomics Using Supervised Learning with Enhanced Peptide Features	Kevin	Kovalchik	<b>Yes</b>	<b>No</b>
<b>P11.26</b>	06. Proteomics Data Science and AI	<b>5</b>	Interactive Statistical and Functional Analysis of Phosphoproteomics Data with Phosphomatics	Michael	Leeming	<b>No</b>	<b>Yes</b>
<b>P11.27</b>	06. Proteomics Data Science and AI	<b>5</b>	A Computational Tool for Comprehensive Selection of Potential Cancer Protein Biomarkers in Blood Plasma	Huiyan	Li	<b>No</b>	<b>Yes</b>
<b>P11.28</b>	06. Proteomics Data Science and AI	<b>5</b>	Implementing Comet Search Engine into Proteome Discoverer to Improve TMT Real-Time Search Data Processing	Yang	Liu	<b>No</b>	<b>No</b>
<b>P11.29</b>	06. Proteomics Data Science and AI	<b>5</b>	AI Assisted Protein Identification and de Novo Sequencing in the Cloud	Bin	Ma	<b>Yes</b>	<b>No</b>
<b>P11.30</b>	06. Proteomics Data Science and AI	<b>5</b>	IcmsWorld: High-Performance 3D Visualization Software for Mass Spectrometry	Antony	McCabe	<b>Yes</b>	<b>No</b>
<b>P11.31</b>	06. Proteomics Data Science and AI	<b>5</b>	MASH-Native: A Universal and Comprehensive Software for Native Mass Spectrometry and Top-down Proteomics	Sean	McIlwain	<b>Yes</b>	<b>Yes</b>
<b>P11.33</b>	06. Proteomics Data Science and AI	<b>5</b>	Deep Plasma Protein Characterization Enabled by Mass Spectrometry (MS) Data Acquisition and Machine Learning (ML) Methods.	Iman	Mohtashemi	<b>Yes</b>	<b>No</b>
<b>P11.34</b>	06. Proteomics Data Science and AI	<b>5</b>	Improving the Sensitivity and Specificity of TMT-Labeled Phosphopeptide Identification Using Deep Learning	Seungjin	Na	<b>No</b>	<b>No</b>



P11.35	06. Proteomics Data Science and AI	5	"Oncoprogrx": Innovative Proteogenomic Software Generating Sample-Specific Database for Mass Spectrometric Protein Identification	Rei	Noguchi	No	Yes
P11.36	06. Proteomics Data Science and AI	5	Expanding the Boundaries of Proteomics Data Integration and Visualization in Uniprot.	Sandra	Orchard	Yes	No
P11.37	06. Proteomics Data Science and AI	5	Combination of Library Search and Database Search on DIA Data	Robin	Park	Yes	Yes
P11.38	06. Proteomics Data Science and AI	5	Application of TIMScore to De Novo Search Engine, DeepNovo in PaSER	Robin	Park	Yes	Yes
P11.39	06. Proteomics Data Science and AI	5	The Selection of Knockout Targets: HepG2 Multi-omics Profiling and Meta-Analysis	Elena	Ponomarenko	No	Yes
P11.40	06. Proteomics Data Science and AI	5	PTMeXchange: Reanalysis of Post-translational Modifications and Independent Estimation of False Localisation Rates	Kerry	Ramsbottom	Yes	No
P11.41	06. Proteomics Data Science and AI	5	RHybridFinder: An R Package to Process Immunopeptidomic Data for Putative Hybrid Peptide Discovery	Frederic	Saab	Yes	Yes
P11.42	06. Proteomics Data Science and AI	5	SAPID-MSI: Spatially-Aware Protein Identification Algorithm for Mass Spectrometry Imaging	Soroush	Shahryari Fard	Yes	No
P11.43	06. Proteomics Data Science and AI	5	Deep Learning Algorithm for CID Peptide Fragmentation Prediction	Hyeonseok	Shin	No	Yes
P11.44	06. Proteomics Data Science and AI	5	MetaProClust-MS1: An MS1 Profiling Approach to Metaproteome Screening	Caitlin	Simopoulos	Yes	No
P11.45	06. Proteomics Data Science and AI	5	TIMS Viz for Mobility Offset Mass Aligned Interrogation of Complex Samples	Philipp	Strohmidel	Yes	No
P11.47	06. Proteomics Data Science and AI	5	Glycan de Novo Sequencing by Deep Learning	Ngoc Hieu	Tran	No	Yes

<b>P11.48</b>	06. Proteomics Data Science and AI	<b>5</b>	MS2ReScore: Using Predicted Fragment Ion Intensities and Retention Times to Increase Identification Rates in Metaproteomics without Impacting Sensitivity	Tim	Van Den Bossche	<b>Yes</b>	<b>Yes</b>
<b>P11.49</b>	06. Proteomics Data Science and AI	<b>5</b>	Identification of Murine Protein Homologs in the Chinese Hamster Proteome via Sequence Alignment and Machine Learning	Junmin	Wang	<b>Yes</b>	<b>No</b>
<b>P11.50</b>	06. Proteomics Data Science and AI	<b>5</b>	Enhancement of MaCPepDB (Mass Centric Peptide Database)	Dirk	Winkelhardt	<b>Yes</b>	<b>No</b>
<b>P11.51</b>	06. Proteomics Data Science and AI	<b>5</b>	The R-Package Profqca for Proteomics Label-Free Quantification Data Analysis	Witold	Wolski	<b>Yes</b>	<b>No</b>
<b>P11.52</b>	06. Proteomics Data Science and AI	<b>5</b>	CHIMERYYS: An AI-Driven Leap Forward in Peptide Identification	Daniel	Zolg	<b>No</b>	<b>Yes</b>
<b>P12.A01</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	The HUPO-PSI Universal Spectrum Identifier (USI) For Mass Spectra	Alexandra	Antonoplis	<b>Yes</b>	<b>Yes</b>
<b>P12.A02</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	ProtView: A Software Tool for Protease Selection to Optimise Shotgun Proteomics and Investigate Transcript Activities	Sophia	Puliasis	<b>Yes</b>	<b>No</b>
<b>P12.A03</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	PaSER Ex: Real Time Exclusion List	Patrick	Garrett	<b>Yes</b>	<b>Yes</b>
<b>P12.A05</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	Using Multilayer Heterogeneous Networks to Infer Functions of Phosphorylated Sites	Joanne	Watson	<b>Yes</b>	<b>No</b>

<b>P12.A06</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	Real-Time Selection of Glycopeptide Dissociation Methods by Matching Oxonium Patterns Using a Real-Time Library Search	Nicholas	Riley	<b>Yes</b>	<b>No</b>
<b>P12.A07</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	Unipept Desktop: Getting Unipept Ready for Proteogenomics	Pieter	Verschaffelt	<b>Yes</b>	<b>No</b>
<b>P12.A09</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	Alignment Strategies of Dia Data and Their Effect on the Quantification Table	Shubham	Gupta	<b>Yes</b>	<b>No</b>
<b>P12.A10</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	Real-Time Modification-Tolerant Matching of MS/MS Spectra at the Repository Scale	Benjamin	Pullman	<b>Yes</b>	<b>No</b>
<b>P12.A11</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	PRM-LIVE with Trapped Ion Mobility Spectrometry and Its Application in Selectivity Profiling of Kinase Inhibitors	He	Zhu	<b>Yes</b>	<b>No</b>
<b>P12.A12</b>	09. Technological Advancements in Proteomics - Data Processing / informatics	<b>6</b>	Mass Dynamics 1.0: Growing a Streamlined, Web-Based Environment for Analyzing, Sharing and Integrating Proteomics Data.	Joseph	Bloom	<b>Yes</b>	<b>Yes</b>
<b>P12.B01</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	MS <sup>3</sup> Analysis of Glycopeptides Using MALDImini™-1 Compact MALDI Digital Ion Trap Mass Spectrometer	Andreas	Baumeister	<b>Yes</b>	<b>Yes</b>
<b>P12.B02</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	High Throughput Single-Shot Proteomics on the Timstof Pro 2	Verena	Tellstroem	<b>No</b>	<b>No</b>

<b>P12.B03</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Doubly Functionalized Magnetic Microspheres with Immobilized Trypsin and LysC Enabling Fast, Easy and Automatable LC-MS Sample Preparation	Jasmin	Johansson	<b>No</b>	<b>No</b>
<b>P12.B05</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Deep Metaproteome Analysis using a Vanquish Neo UHPLC System Coupled to an Orbitrap Eclipse Tribrid with FAIMS Pro Interface	Amirmansoor	Hakimi	<b>No</b>	<b>No</b>
<b>P12.B06</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Rethink Tissue Lysis: High-Throughput Tissue Lysis Workflow Using the 'BeatBox' Platform for in-Depth Proteomic Coverage	Berit	Mang	<b>Yes</b>	<b>No</b>
<b>P12.B08</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Evaluation of Dia-PASEF Using Library and Library Free Approaches for Different Gradients	Diego	Assis	<b>No</b>	<b>No</b>
<b>P12.B09</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	The Impact of a Plug and Play Microflow Ionization Source on High Throughput Proteomics	Dylan	Xavier	<b>No</b>	<b>Yes</b>
<b>P12.B10</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Exploring Human Brain Proteome with Alzheimer's Disease (AD) With MALDI Imaging Mass Spectrometry in Combination with Shotgun Proteomics	Yumiko	Toyama	<b>No</b>	<b>Yes</b>
<b>P12.B11</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Absolute Quantification of 500 Human Plasma Proteins in Colon Cancer Plasma Samples by Prm-PASEF	Pierre-Olivier	Schmit	<b>No</b>	<b>No</b>
<b>P12.B12</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Comparative Evaluation of a New Processing Pipeline for Pasef Label-Free Quantification Analysis.	Aurelie	Meme	<b>Yes</b>	<b>Yes</b>

<b>P12.B13</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	The Next-Generation All-in-One Nano-, Capillary- And Micro-Flow LC System Is Paving the Way for Robust, Fast, and Deep LC-MS Proteomics	Alexander	Boychenko	<b>Yes</b>	<b>Yes</b>
<b>P12.B14</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Multicentric Evaluation of High-Throughput Low-Flow LC-MS Proteomic Profiling of Cell Lysates and Biofluids	Alexander	Boychenko	<b>Yes</b>	<b>Yes</b>
<b>P12.B15</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Impact of Improved MS/MS Duty Cycle On Protein Identification Efficiency using Data Independent Acquisition On a New QTOF Platform	Ihor	Batruch	<b>Yes</b>	<b>No</b>
<b>P12.B16</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Benchmark of Micro-flow Chromatograph for Robust Proteomics Analysis	Yang	Liu	<b>No</b>	<b>No</b>
<b>P12.B18</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Rapid and Reproducible Phosphoenrichment Using Fe-NTA Magnetic Beads	Bhavin	Patel	<b>Yes</b>	<b>Yes</b>
<b>P12.B19</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	SureQuant Targeted Mass Spectrometry Standards and Assay Panel for Quantitative Analysis of Phosphorylated Proteins from Multiple Signaling Pathways	Bhavin	Patel	<b>Yes</b>	<b>Yes</b>
<b>P12.B20</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Engineered Multi-Nanoparticle Panels Enable Unmatched Depth and Sensitivity in Plasma Proteomics in Combination with Trapped Ion Mobility Mass Spectrometry	Moaraj	Hasan	<b>Yes</b>	<b>No</b>
<b>P12.B22</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Low Abundance Protein Detection after Acetone Precipitation Using the ProTrap XG	Victoria Ann	Miller	<b>Yes</b>	<b>No</b>

<b>P12.B23</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Combining the Data-Driven and Hypothesis-Driven Approaches in One Go via a Novel Intelligent Data Acquisition Hybrid-Dia Mass Spectrometry Strategy	Sean	Mcllwain	<b>Yes</b>	<b>No</b>
<b>P12.B24</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Reproducibility and Sensitivity of a Targeted Quantitative Assay for 804 Peptides in Plasma Using a 20 Min Microflow Gradient	Christie	Hunter	<b>Yes</b>	<b>Yes</b>
<b>P12.B25</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Increased Protein and Peptide Identifications using Zenon MS/MS in Data Dependent Acquisition Workflows	Alexandra	Antonoplis	<b>Yes</b>	<b>Yes</b>
<b>P12.B26</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	S-Trap Turbo: From Sample Prep to Analysis in Record Time	John	Wilson	<b>Yes</b>	<b>Yes</b>
<b>P12.B27</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	Sample Preparation to Match Analytical Advances: 384-Well S-Trap Plates	John	Wilson	<b>Yes</b>	<b>Yes</b>
<b>P12.B28</b>	09. Technological Advancements in Proteomics - Product Development	<b>6</b>	BCA-No-More: Seamless, High Throughput Protein Quantification Directly on S-Trap Plates	John	Wilson	<b>Yes</b>	<b>Yes</b>
<b>P12.C01</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Can the Ultra-fast Proteomics Be Quantitative: Benchmarking directMS1 Method against Label-Based and Label-Free Approaches	Julia	Bubis	<b>Yes</b>	<b>No</b>
<b>P12.C02</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	SMART-CARE: A Systems Medicine Approach to Stratification of Cancer Recurrence Facilitated by Automated MS-Based Clinical Proteomics	Torsten	Müller	<b>Yes</b>	<b>No</b>

<b>P12.C03</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Systematic Identification of ALK Substrates by Phosphoproteome and Interactome Analysis	Jun	Adachi	<b>No</b>	<b>Yes</b>
<b>P12.C05</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Targeted UHPLC-MS/MS Proteomic Analysis Using QPrEST and Single Point Calibration with Application to the Determination of Apolipoproteins in Human Plasma.	Hatem	Elmongy	<b>Yes</b>	<b>No</b>
<b>P12.C07</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Analyzing Protein Fluorosequencing Data, a New Technology for Single Molecule Proteomics	Matthew	Smith	<b>Yes</b>	<b>Yes</b>
<b>P12.C09</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	New Method to Construct a Reference Amino Acid Sequence Database for Metaproteome Analysis	Nobuaki	Miura	<b>No</b>	<b>Yes</b>
<b>P12.C10</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Label-Free Quantification of Oxidized Peptides in eHAP Cell Lines via a High-Throughput DiPASEF Workflow	Romano	Hebeler	<b>Yes</b>	<b>No</b>
<b>P12.C11</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Data-Independent Acquisition Method for Ubiquitinome Analysis Reveals Regulation of Circadian Biology	Fynn	Hansen	<b>Yes</b>	<b>No</b>
<b>P12.C12</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	The Number of «Missing» Proteins Is a Function of the Analytical Sensitivity of Proteomic Analysis	Ekaterina	Ilgisonis	<b>Yes</b>	<b>No</b>
<b>P12.C13</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Streamlined SDS-based Workflows in the ProTrap XG for Top-down or Bottom-up Proteomics	Alan	Doucette	<b>No</b>	<b>No</b>
<b>P12.C14</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Assessment of Bacterial Metaproteome Using Ultra-fast MS/MS-Free Proteomics	Elizaveta	Kazakova	<b>Yes</b>	<b>No</b>

<b>P12.C15</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Number of Detected Proteins as the Function of the Sensitivity of Proteomic Technology in Human Liver Cells	Nikita	Vavilov	<b>Yes</b>	<b>No</b>
<b>P12.C16</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	A Comprehensive Quality Control Pipeline for Clinical Biomarker Discovery	Natasha	Lucas	<b>No</b>	<b>Yes</b>
<b>P12.C18</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Comparison of Sample Preparation Methods and Instrumental Platforms for Proteomic Analysis of Murine Brain Tissues and Isolated Brain Cell Types	Jeewan Babu	Rijal	<b>Yes</b>	<b>No</b>
<b>P12.C19</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	PEPPI-MS Workflow for Bottom-Up Proteomics	Nobuaki	Takemori	<b>No</b>	<b>Yes</b>
<b>P12.C20</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Specific Cysteine Sulfenic Acid Biomarker Screening by Coupling Mass Spectrometry with Laser Induced Dissociation Applied to Alzheimer's Disease and COVID-19.	Jean-valery	Guillaubez	<b>Yes</b>	<b>No</b>
<b>P12.C21</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Automated High Throughput DIA-MS Workflow for Plasma Proteomics with Novel Quality Control Procedure	Annie	Moradian	<b>Yes</b>	<b>Yes</b>
<b>P12.C22</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Critical Assessment of Salt Ions on the Recovery of Proteins through Solvent-Based Precipitation	Ziheng	Dang	<b>Yes</b>	<b>No</b>
<b>P12.C24</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Enhanced Nano-Bio Interaction Enables Deep Plasma Proteomics at Scale, with Enhanced Precision, and Depths of Coverage.	Shadi	Ferdosi	<b>Yes</b>	<b>No</b>



<b>P12.C25</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Neoantigens Identification and Personalized Vaccines Development from Immunopeptidomics Characterization	Pablo	Juanes-Velasco	<b>Yes</b>	<b>No</b>
<b>P12.C27</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	The Isotopic AC-IP Tag Enables Multiplexed Proteome Quantification in Data-Independent Acquisition Mode	Xiaobo	Tian	<b>Yes</b>	<b>No</b>
<b>P12.C28</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	FLASHIda: Intelligent Data Acquisition for Top-down Proteomics That Doubles Proteoform Identification Count	Kyowon	Jeong	<b>Yes</b>	<b>Yes</b>
<b>P12.C29</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Quantitative Assessment of Enzyme Activity in the Presence of Surfactants: Implications for Bottom-Up Proteomics	Jessica	Nickerson	<b>Yes</b>	<b>No</b>
<b>P12.C30</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Rapid Sample Preparation of Cancer Tissue Microarray Sections and FFPE Blocks for Clinical Analysis	Steven	Williams	<b>Yes</b>	<b>No</b>
<b>P12.C31</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Automated Solid-Phase Extraction Methods for High-Throughput Proteomic Sample Preparation	Erin	Humphries	<b>No</b>	<b>No</b>
<b>P12.C32</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Targeted Analysis of Protein Biomarkers in Biological Fluids by on-Line Aptamer-Affinity Solid-Phase Extraction Capillary Electrophoresis-Mass Spectrometry	Roger	Pero-Gascon	<b>Yes</b>	<b>No</b>
<b>P12.C34</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Using of SILAC Technique for Studying Therapy-Induced Cell Communication in Ovarian Cancer Cells	Polina	Shnaider	<b>No</b>	<b>No</b>

<b>P12.C36</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Glycoprotein Characterization Through Sensitive Analysis Of Glycopeptides By On-line Solid-phase Extraction Capillary Electrophoresis-Mass Spectrometry	Estela	Giménez	<b>Yes</b>	<b>No</b>
<b>P12.C38</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Quantitative Proteomics Identifies Redox Switches That Regulate Fetal and Adult Hematopoiesis	Kristyna	Pimkova	<b>Yes</b>	<b>No</b>
<b>P12.C39</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Development of Immunoaffinity-Selected Reaction Monitoring Assays for the Differential Quantification of Human Endogenous Retrovirus Proteins	Delaram	Dara	<b>Yes</b>	<b>No</b>
<b>P12.C40</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Development of a Peptidome Analysis Method for Submilligram Brain Tissue	Yoshio	Kodera	<b>No</b>	<b>No</b>
<b>P12.C42</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Comprehensive Proteomic Characterization of the Intra- And Extracellular Adaptations in Response to Oxidative Stress by OxSWATH	Sandra	Anjo	<b>No</b>	<b>No</b>
<b>P12.C44</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Automated, Parallel Protein Extraction for Analysis of Low Input FFPE, Fresh Tissue and Cells Clinical Samples with Adaptive Focused Acoustics	Nicolas	Autret	<b>Yes</b>	<b>No</b>
<b>P12.C45</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	HTPS: A Proteomic High-Throughput Screen to Map Specificity, Cleavage Entropy, Allosteric Changes and Substrates of Proteases	Federico	Uliana	<b>No</b>	<b>No</b>
<b>P12.C47</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Mapping Protein Complexes for Unraveling the Hidden Proteome in Ovarian Cancer.	Diego Fernando	Garcia Del Rio	<b>Yes</b>	<b>No</b>

<b>P12.C48</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Developing a Targeted Mass Spectrometry Workflow for Investigating the Tear Proteome from Healthy Volunteers	Maggy	Lépine	<b>Yes</b>	<b>No</b>
<b>P12.C49</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Phosphoproteomic Workflow Optimization for the Analysis of FFPE Tissue Sections	Gábor	Tóth	<b>No</b>	<b>No</b>
<b>P12.C50</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	Comparison of In-Solution and S-Trap <sup>TM</sup> Based Sample Preparation for Tear Proteomics Study	Sung-hei Jimmy	Tse	<b>No</b>	<b>Yes</b>
<b>P12.C51</b>	09. Technological Advancements in Proteomics - Methodology	<b>7</b>	DeGlyPHER: An Ultrasensitive Method for Analysis of Viral Spike N-Glycoforms	Sabyasachi	Baboo	<b>No</b>	<b>Yes</b>
<b>P13.02</b>	13. Other	<b>8</b>	Identifying Disease-Induced Interactome Changes in the Honey Bee Midgut	Mopelola	Akinlaja	<b>Yes</b>	<b>No</b>
<b>P13.03</b>	13. Other	<b>8</b>	Molecular Weight-Based Proteome Fractionation by Stepwise Organic Solvent Precipitation	Venus	Baghalabadi	<b>Yes</b>	<b>No</b>
<b>P13.04</b>	13. Other	<b>8</b>	Conservation and Conditional Regulation of Protein Ubiquitination	Inigo	Barrio-Hernandez	<b>Yes</b>	<b>No</b>
<b>P13.05</b>	13. Other	<b>8</b>	Proteome Analysis Reveals Pathways of Corticoid- And Shape Constraint-Induced Transdifferentiation of HepaRG Cells	Charlotte	Brun	<b>Yes</b>	<b>No</b>
<b>P13.06</b>	13. Other	<b>8</b>	Cancer Stem Cell Marker DCLK1 Reprograms Small Extracellular Vesicles toward Migratory Phenotype in Gastric Cancer Cells	Annalisa	Carli	<b>No</b>	<b>Yes</b>

<b>P13.07</b>	13. Other	<b>8</b>	Quantitative Phosphoproteomics Reveals Ectopic ATP Synthase on Mesenchymal Stem Cells to Promote Tumor Progression via ERK/c-Fos Pathway Activation	Yi-Wen	Chang	<b>No</b>	<b>Yes</b>
<b>P13.09</b>	13. Other	<b>8</b>	NanoLC-nESI/MS/MS Analysis of Malondialdehyde-Induced Post-Translational Modifications in Breast Cancer Patients	Hauh-Jyun	Chen	<b>No</b>	<b>Yes</b>
<b>P13.10</b>	13. Other	<b>8</b>	A Virus-Host Protein Interactome Comparison of Differentially Pathogenic Arenaviruses	Bahne	Christiansen	<b>Yes</b>	<b>No</b>
<b>P13.11</b>	13. Other	<b>8</b>	New Proteomics Insights in the Characterization of FACs-Sorted Leukocyte-Derived Extracellular Vesicles as “Liquid Biopsy” of Immune Response	Maria Concetta	Cufaro	<b>Yes</b>	<b>No</b>
<b>P13.15</b>	13. Other	<b>8</b>	The Effects of Testosterone Replacement in a Pharmacologically Induced Hypogonadism Cohort: A Controlled Study with Healthy Young Males	Jéssica	Guedes	<b>Yes</b>	<b>No</b>
<b>P13.16</b>	13. Other	<b>8</b>	SpatialOMx on Intracellular Bacteria Reveals Metabolic and Proteomic Phenotypes In-situ	Corinna	Henkel	<b>Yes</b>	<b>No</b>
<b>P13.19</b>	13. Other	<b>8</b>	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation	Anton	Kalyuzhnyy	<b>Yes</b>	<b>No</b>
<b>P13.20</b>	13. Other	<b>8</b>	Phospho-proteomic Analysis of Microbe-Associated Molecular Patterns (MAMPs) Signalling in Food Security	Jianan	Lu	<b>Yes</b>	<b>No</b>
<b>P13.21</b>	13. Other	<b>8</b>	Towards Nanopore based Single-Molecule Bottom-Up Proteomics	Florian	Lucas	<b>Yes</b>	<b>No</b>
<b>P13.22</b>	13. Other	<b>8</b>	Representing Proteins and Peptides with Variational Feature Information in Graphs using ProtGraph	Dominik	Lux	<b>Yes</b>	<b>No</b>

<b>P13.23</b>	13. Other	<b>8</b>	Unveiling New Proteoforms of the Industrial Workhorse <i>Corynebacterium Glutamicum</i> through Top-down Proteomics	Reynaldo	Magalhães Melo	<b>Yes</b>	<b>No</b>
<b>P13.25</b>	13. Other	<b>8</b>	Identification of Interaction Partners of Calcitonin Receptor-like Receptor in Primary Human Dermal Lymphatic Endothelial Cells.	Dimitrios	Manolis	<b>Yes</b>	<b>No</b>
<b>P13.27</b>	13. Other	<b>8</b>	Use of Proteomics to Study the Antifungal Effect of Metformin on <i>C. albicans</i>	Gloria	Molero	<b>Yes</b>	<b>No</b>
<b>P13.28</b>	13. Other	<b>8</b>	Toward Better Pre-clinical Sarcoma Model Using Decellularized Extracellular Matrix	Takuya	Ono	<b>No</b>	<b>Yes</b>
<b>P13.30</b>	13. Other	<b>8</b>	1DE Gel-Concentration Procedure for LC-MS/MS Analysis of Sds-Extracts of Human Chorionic Villus	Natalia	Petushkova	<b>Yes</b>	<b>No</b>
<b>P13.31</b>	13. Other	<b>8</b>	Characterization of Biological and Metabolic Responses to PH Changes in <i>Staphylococcus Epidermidis</i>	Susana	Santos	<b>Yes</b>	<b>No</b>
<b>P13.32</b>	13. Other	<b>8</b>	Proteomic analysis of mouse hearts treated with rattlesnake venom revealed modulation of proteins associated with mitochondria and cardiomyopathies	Wellington da Silva	Santos	<b>Yes</b>	<b>No</b>
<b>P13.33</b>	13. Other	<b>8</b>	Proteomic Analysis to Identify Candidate Biomarkers Associated with Skin Co-exposure to Ultraviolet Radiations and Benzo[A]Pyrene	Michel	Seve	<b>Yes</b>	<b>No</b>
<b>P13.34</b>	13. Other	<b>8</b>	High-throughput Lipidomics using Ion-mobility enhanced DDA and DIA Mass Spectrometry	Premy	Shanthamoorthy	<b>No</b>	<b>Yes</b>

<b>P13.35</b>	13. Other	<b>8</b>	Establishment and Characterization of a Novel Cell Line, NCC-MPNST6-C1, Of Malignant Peripheral Nerve Sheath Tumor	Yooksil	Sin	<b>No</b>	<b>Yes</b>
<b>P13.36</b>	13. Other	<b>8</b>	Developing a Pipeline for Isoform-Level Multi-Omics Data Analysis	Manika	Singh	<b>No</b>	<b>Yes</b>
<b>P13.37</b>	13. Other	<b>8</b>	Metabolomic Analysis of Amniotic Fluid Samples Infected by Zika Virus: Microcephalic versus Non-microcephalic Fetuses	Patricia	Sosa Acosta	<b>Yes</b>	<b>No</b>
<b>P13.38</b>	13. Other	<b>8</b>	GSH Mediated Alleviation of AAL Induced Stress in Plants- A Proteomic Approach in Solving the Cryptex of Plant Stress Signaling	Asma	Sultana	<b>Yes</b>	<b>No</b>
<b>P13.39</b>	13. Other	<b>8</b>	Dried Blood Spot as a Biomarker Source: A Bridge between Proteins and Metabolites in the Omics Era	Silvia	Valentinuzzi	<b>Yes</b>	<b>No</b>
<b>P13.40</b>	13. Other	<b>8</b>	The Metaproteomics Initiative: Coordinating International Efforts for Propelling the Functional Characterization of Microbiomes	Tim	Van Den Bossche	<b>Yes</b>	<b>Yes</b>
<b>P13.42</b>	13. Other	<b>8</b>	Glycoproteomic Study of Saccharomyces Cerevisiae Yeast Cell Wall Mannoproteins Reveals a Dynamic Molecular Change Depending on Culture Strategy and Conditions	Marie	Yamine	<b>No</b>	<b>Yes</b>
<b>C.P.01</b>	14. Corporate Posters	<b>8</b>	Precision Pathology: Mass Spectrometry Proteomics for Early Cancer Detection in Esophageal Disease	Joe Abdo Stella Diagnostics Inc		<b>Yes</b>	<b>Yes</b>
<b>C.P02</b>	14. Corporate Posters	<b>8</b>	IonOpticks packed emitter columns. Your data is only as good as your chromatography	Jarrod Sandow IonOpticks		<b>Yes</b>	<b>Yes</b>

<b>C.P.03</b>	14. Corporate Posters	<b>8</b>	Improving Nano-LC-MS/MS Data Quality Using a Trap-and-Elute Methodology	Phenomenex	<b>Yes</b>	<b>Yes</b>
<b>C.P.04</b>	14. Corporate Posters	<b>8</b>	Leveraging the Power of a Core-Shell Particle to Improve Micro and Nano Flow Separations	Phenomenex	<b>Yes</b>	<b>Yes</b>
<b>C.P.05</b>	14. Corporate Posters	<b>8</b>	Release the Power of Precise Proteomics	Susan Mockus, Precision Biomarker Laboratories	<b>Yes</b>	<b>Yes</b>
<b>C.P.06</b>	14. Corporate Posters	<b>8</b>	Plasma protein signatures of multi-organ disease states as predictors of COVID-19 outcome severity	Clare Paterson SomaLogic	<b>Yes</b>	<b>Yes</b>
<b>C.P.07</b>	14. Corporate Posters	<b>8</b>	Progress Towards A Proteomic Surrogate Endpoint for Cardiovascular Outcomes	Clare Paterson SomaLogic	<b>Yes</b>	<b>Yes</b>
<b>C.P.08</b>	14. Corporate Posters	<b>8</b>	A Standardized Separation Tool for Clinical Omics	Dorte Bekker-Jensen Evosep ApS	<b>Yes</b>	<b>Yes</b>
<b>C.P.10</b>	14. Corporate Posters	<b>8</b>	Publish with Expert Review of Prote	James Crosby Expert Review of Proteomics	<b>Yes</b>	<b>Yes</b>