MONDAY POSTER PRESENTATION

MP01 - Innovative Fractionation and Enrichment Techniques

MP01-001
Acid-based SCX fractionation for in-depth proteome and phosphoproteome analysis
Jun Adachi, National Institutes of Biomedical Innovation, Health and Nutrition, Japan

MP01-002
A new workflow for deep proteome profiling of the human sperm
Valdemir Carvalho, Fleury Group, Brazil

MP01-003
Comprehensive Analysis of Human Urinary Proteome through Ampholine@PM Fractionation Strategy
Yuanbo Chen, Key Laboratory of Separation Science for Analytical Chemistry, Dalian, China

MP01-004
Systematic comparison of sample complexity reducing methods in amniotic fluid proteomics
Petra Domasinska, Department of Biological and Biochemical Sciences, University of Pardubice, Czech Republic

MP01-005
Improved throughput of DIA quantitation using microflowLC
Gavin Fischer, Sciex, United States

MP01-006
Development of immobilized metal-ion affinity (IMA) monolith incorporated microfluidic device for plasma proteomics
Ashish Khaparde, Vit University, India

MP01-007
High throughput proteomic analysis using different OFFGEL fractionation panels
Sameh Magdeldin, Suez Canal University, Egypt

MP01-008
Automated pull-down of extracellular vesicles (EVs) on KingFisher[TM] using Dynabeads[TM] magnetic beads - standardizing EV capture and analysis
Axl Neurauter, Thermo Fisher Scientific, Norway

MP01-009
A Charge-Suppressing Strategy for Probing Protein Methylation
Zhibin Ning, Ottawa Institute of Systems Biology, BMI,, Faculty of Medicine, University of Ottawa, Canada

MP01-010
Identifying Novel Cancer Antigens using Immunoproteomics
Muneerah Smith, The University of Cape Town, South Africa

MP01-011
High pH Reversed-Phase Sample Fractionation for Phosphoproteomic and Glycoproteomic Workflows
Sergei Snovida, Thermo Fisher Scientific, United States

MP02 - Innovative Mass Spectrometry Techniques

MO02-001

MS1 based quantification optimization on DIA methods on a quadrupole-Orbitrap mass spectrometer

Yue Xuan, Thermo Fisher Scientific, Germany

MO02-002

Digging deeper into large SWATH MS1 windows using Gas Phase Fractionation SWATH-MS

Mark P Molloy, Australian Proteome Analysis Facility, Australia

MO02-004

All MS/MS ions monitoring acquired by data-dependent acquisition without dynamic exclusion: A new concept for in-depth protein quantification

Fei Fang, Key Laboratory of Separation Science for Analytical Chemistry, Dalian, China

MO02-005

Analyses of intact proteins by LC-FT-ICR mass spectrometry at 21 tesla

Lissa C. Anderson, Ion Cyclotron Resonance Program, National High Magnetic Field Laboratory, Tallahassee, FL, United States

MP02-001

Analysis of Peptides and Proteins Using Ion Mobility Separation, Electron-Based Dissociation and Mass Spectrometry

Catherine Costello, Boston Univ School of Medicine, United States

MP02-002

Extending the Depth of Coverage in SWATH® Acquisition with Deeper Ion Libraries

Joerg Dojahn, SCIEX Germany, Germany

MP02-003

Chemical cross-linking of NMDA receptor signaling complex: promising strategy of complexes characterisation

Elena Goltseva, Lund University, Sweden

MP02-004

The ETD-like fragmentation for secondary metabolites

Romain Huguet, Thermo Fisher Scientific, United States

MP02-005

Comparison of SWATH and iTRAQ in clinical study with multiple small protein samples

Antti Jylhä, Medical School, University of Tampere, Finland, Finland

MP02-006

Quantification of Low-Abundance Serological Proteins as Potential Colorectal Cancer Biomarkers by Pseudo-MRM with Peptide-Affinity Enrichment

Kwang Hoe Kim, Korea Basic Science Institute, South Korea

MP02-007

Shotgun proteomics using on-line Parallel Accumulation – Serial Fragmentation (PASEF)

Markus Lubeck, Bruker Daltonik, Bremen, Germany

MP02-008

Development of an Online 2D RP-RP LC/MRM-MS Method for Targeted and Comprehensive Analyses of the Human Plasma Proteome

Vincent Richard, Mcgill University - Lady Davis Institute, Canada

MP02-009

Improved Qualitative and Quantitative Analysis of the Human Mitochondrial Proteome by Hybrid Acquisition

Johannes Vissers, University of Rome Tor Vergata, Rome, Italy

MP02-010

Development of A Novel Method for Detection of Glycoprotein Using Lectin Decorated Diamond Nanoparticles and Mass Spectrometry

Chia-Chen Wang, Genomics Research Center, Academia Sinica, Taiwan

MP02-011

A simplified approach to fast and accurate, high throughput targeted MS2 quantitation using internal standards.

Vlad Zabrouskov, Thermo Fisher Scientific, United States

MP02-012

Comprehensive relative quantification of the cytochromes P450 by micro-LC and SWATH® acquisition and data processing using Cloud Computing.

Jason Neo, MRC Centre for Drug Safety Science, Dept Pathology, University of Liverpool, UK, United Kingdom

MO02-003

iST: Sample preparation for high throughput clinical proteomics- A novel, fast, sensitive and reproducible sample preparation for MS-based proteomics-

Garwin Pichler, Preomics GmbH, Germany

MO09-001

Structural characterization of protein phosphorylation and antibody complexes by top/middle-down mass spectrometry

Jingxi Pan, University of Victoria-Genome BC Proteomics Centre, Canada

MO09-002

Trapped Ion Mobility Spectrometry: An Additional Dimension of Separation for Proteomics Applications

Melvin Park, Bruker Daltonics, United States

MO09-003

Qualitative and Quantitative Characterization of a Novel Scanning Quadrupole DIA Method for Omics Analysis

Johannes Pc Vissers, Waters Corporation, United Kingdom

MO09-004

ProteusQC™: the Versatile Standard for Bottom-up Proteomics

Andrew Percy, Cambridge Isotope Laboratories, United States

MO09-005

Sampling of tissues for proteomics by soft laser ablation

Hartmut Schlueter, University Medical Center Hamburg-Eppendorf, Germany, Germany

WO07-005

Comprehensive draft of the HeLa proteome to a depth of more than 13,000 proteins.

Dorte Breinholdt Bekker-Jensen, University of Copenhagen, NNF Center for Protein Research, Denmark

MP03-001

A robust and sensitive capillary flow LC – high-resolution accurate-mass MS platform for discovery and targeted proteomics

Mike Baynham, Thermo Fisher Scientific, Germany

MP03-002

Application of baculovirus expression vector system in producing human high molecular weight kininogen, a highly glycosylated secretion protein.

Yating Chang, Molecular Medicine Research Center, Chang Gung University, Taiwan

MP03-003

Primary structure analyses for protein therapeutics using mass spectrometry-based methods

Ya-Fen Chen, Sun Jet Biotechnology Incorporation, Taiwan

MP03-004

Thermostable plasma proteome and its potential applications in biomarker discovery

Somchai Chutipongtanate, Department of Paediatrics, Ramathibodi Hospital, Mahidol University, Thailand

MP03-005

A new method for label free quantification in the Proteome Discoverer framework

Bernard Delanghe, Thermo Fisher Scientific, Germany

MP03-006

Studying protein phosphorylation with ultra-high temporal resolution using a microfluidic device

Margherita Dell´Aica, Protein Dynamics Group, Leibniz-institut Für Analytische Wissenschaften - Isas - E.v., Germany

MP03-007

Improving proteome coverage via efficient, complementary and automated digestion using high content magnetically immobilized Trypsin and Chymotrypsin

Isak Gerber, Resyn Biosciences, South Africa

MP03-008

2D-SWATH® mass spectrometry was applied in quantitation of membrane proteome of rat brain hippocampus

Lihai Guo, Sciex, China

MP03-009

Systematic exploration of subcellular redox status by methionine containing peptide enrichment

Ya-Ju Hsieh, Chang Gung University, Taiwan

MP03-010

Identification of metal species by ESI-MS/MS through release of free metals from the corresponding metal-ligand complexes

Yu-Chen Huang, Academia Sinica, Taiwan

MP03-011

Sensitive and accurate quantitation of phosphopeptides using TMT isobaric labeling technique

Xiaoyue Jiang, Thermo Fisher Scientific, United States

MP03-012

Quantitative analysis of methylation on histone H3 during cell cycle

Hong Jin, Fudan University, China

MP03-013

A Novel Tandem Quadrupole Mass Spectrometer for the Quantitative Analysis of Peptides using a Multi-point Internal Standard Calibration Method

James Langridge, Waters, United Kingdom

MP03-014

Streamlined hands-free sample preparation using Pressure Cycling and PCT µPestle sample containers for tissue biopsy profiling by SWATH-MS.

Alexander Lazarev, Pressure BioSciences, Inc., 14 Norfolk Ave., South Easton, MA 02375, United States

MP03-015

A zebrafish SWATH-MS platform for protease substrate identification

Qifeng Lin, Institute of Molecular & Cell Biology, Agency for Science, Technology & Research, Singapore

MP03-016

Multiplex Pseudo-Isobaric Dimethyl Labeling for Proteome Quantification

Jianhui Liu, Dalian Institute of Chemical Physics, Chinese Academy of Sciences., China

MP03-017

Reductive Amination Combining Dimethylation for Quantification of Early Stage Protein Glycation

Hao Jie Lu, Fudan University, China

MP03-018

Applications of solid phase peptide synthesis using the MultiPep Continuous Flow synthesizer with real-time UV-monitoring and automated feedback

Keren Liu, INTAVIS Bioanalytical Instruments AG, China

MP03-019

Development of a novel nano separation device for robust and accurate gradient delivery with intelligent diagnostics.

Jonathan Moss, Bruker Daltonics, Germany

MP03-020

A method for mass spectrometry-based absolute quantification reveals rhythmic variation of mouse circadian clock proteins

Ryohei Narumi, National Institutes of Biomedical Innovation, Health and Nutrition, Japan

MP03-021

The future of mass spectrometry-based protein clinical tests

Dobrin Nedelkov, Biodesign Institute, Arizona State University, United States

MP03-022

A novel method to separate high-molecular-mass proteins by an N, N' -methylenebisacrylamide gradient gel electrophoresis (BIS-gradient APAGE)

Masamichi Oishi, KItasato University Graduate School of Science, Japan

MP03-023

Precision and Accuracy in Proteomics

Magnus Palmblad, Leiden University Medical Center, Netherlands

MP03-024

Capillary Electrophoresis - Mass Spectrometry for Top Down Proteomics

Aran Paulus, Thermo Fisher Scientific, United States

MP03-025

Advanced peak detection, deconvolution, and centroiding algorithms improve MS/MS spectral quality and peptide identification

Jeff Peterson, Veritomyx, Inc., United States

MP03-026

Higher multiplexing with NeuCode SILAC metabolic labeling

John Rogers, Thermo Fisher Scientific, United States

MP03-027

Urine protein preparation workflow for urine proteomics

Suguru Saito, Biofluid Biomarker Center, Niigata University, Japan, Japan

MP03-028

Next Generation Protein Sequencing (NGPS) enables full-length *de-novo* protein and antibody sequence determination

Alon Savidor, Weizmann Institute of Science, Israel

MP03-029

Protons From Gas Phase Molecules Enhances the S/N of peptides in ESI

Kai Tang, Zhejiang Haochuang Biotech Co. Ltd., China

MP03-030

Detection and Quantification of Proteins From DIA Data without Spectral Libraries

Stephen Tate, Sciex, Canada

MP03-031

A "Solution" for High Sensitivity Phosphoproteomic Analysis with TMT Labeling

Chia-Feng Tsai, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

MP03-032

Performance considerations for ultraviolet photo-dissociation using the Nd:YAG 5th harmonic (213nm)

Chad Weisbrod, Thermo Fisher Scientific, United States

MP03-033

The SOMAscan° assay and SOMAmer° reagents: Translatable tools from high-throughput biomarker discovery to targeted.

Sheri Wilcox, Somalogic, Inc., United States

MP03-034

New methods for qualitative and quantitative proteome analysis

Yukui Zhang, Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China

MP03-035

Ultralong and ultranarrow-bore capillary columns for proteome analysis

Lihua Zhang, Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China

MP03-036

Quantitative dot blot analysis (QDB), a low cost, high-throughput immunoblot method to complement Mass Spec studies in a regular lab.

Jiandi Zhang, Zestern Biotechnique Llc, United States

MP03-037

Simultaneous MRM quantitation of 200 proteins from a dried blood spot

Suping Zhang, University of Victoria-Genome BC Proteomics Centre, Canada

MP03-038

Ionic liquid-based filter-aided sample preparation for in-depth proteome analysis

Qun Zhao, National Chromatographic Research and Analysis Center, Dalian, China

MP03-039

High-throughput *de novo* proteome identification aided by translatome sequencing

Gong Zhong, Insitute of Life and Health Engineering, Jinan University, China

MP03-040

Comparison of different sample preparation protocols for protein and phosphopeptide identification

Ling Zhong, Bioanalytical Mass Spectrometry Facility, University of New South Wales, Australia

MP04 - Chemical Probes and Chemical Biology For Proteomics

MO03-001

Quantitative activity-based profiling of kinase inhibitor binding and selectivity on protein microarrays containing >300 human protein kinases

Jonathan Blackburn, Institute of Infectious Disease & Molecular Medicine, University of Cape Town, South Africa

MO03-002

Novel Hybrid Platform for Rapid, highly sensitive and specific quantification of proteins and their post-translational modifications

Liqi Xie, Fudan University, China

MO03-003

A highly sensitive probe for fucosylated glycans for biomarker discovery

Naoyuki Taniguchi, Systems Glycobiology Research Group, RIKEN, Japan

MO03-004

A novel set of isobaric peptide labeling reagent enabled proteomic quantification over 10 different samples

Yan Ren, BGI-SHENZHEN, Shenzhen, China

MO03-005

TMTcalibrator™ Enhances Biomarker Discovery in Peripheral Fluids

Hui-Chung Liang, Proteome Sciences Plc, United Kingdom

MP04-001

The mechanism of Nav1.7 regulating the metastasis of prostate cancer cells as revealed by toxin probes and proteomic analysis

Ping Chen, College of Life Sciences, Hunan Normal University, China

MP04-002

A deep proteome analysis of the hemolymph, brain, and antennae extends the mechanistic understanding of honeybee resistance to Varroa destructor

Han Hu, Chinese Academy of Agricultural Sciences, Institute of Apicultural Research, China

MP04-003

Functional and Proteomic Investigations Reveal Roles of Major Royal Jelly Protein 1 in Anti-hypertension in Mouse Vascular Smooth Muscle Cell

Jianke Li, Institute of Apicultural Research, Chinese Academy of Agricultural Sciences, China

MP05 - Phosphoproteomics, Kinome and Ptm Crosstalks

MO08-001

Drug resistance assessed by multi-proteomics approaches

Simone Lemeer, Biomolecular Mass Spectrometry and Proteomics, Utrecht University, Netherlands

MO08-002

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

Hsin-Yi Wu, Institute of Chemistry, Academia Sinica, Taiwan

MO08-003

Subtilisin for large scale (phospho)proteomics – the beginning of a wonderful love story?

Humberto Gonczarowska-Jorge, Leibniz-institut Für Analytische Wissenschaften - ISAS, Dortmund, Germany

MO08-004

Profiling Kinome Activities Using Kinase-Specific Substrate Peptides

Naoyuki Sugiyama, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

MO08-005

Tyrosine phosphorylation changes due to calcium signaling cascade post-sampling prevented by enzyme heat inactivation

Mats Borén, Denator, Sweden

MP05-001

Phosphotyrosine proteomics reveals modulation of kinase activity in colorectal cancer cell lines with the resistance to Cetuximab

Yuichi Abe, Lab of Proteome Res, Nat Inst of Biomedical Innovation, Health and Nutrition, Japan

MP05-002

Nuclear phosphoproteomic view unravel clade-specific signaling pathways and transcriptional dynamics

Subhra Chakraborty, National Institute of Plant Genome Research, India

MP05-003

Integrated analysis of phosphoproteome and global proteome reveals key protein phosphorylation by MCM2 in lung cancer cells

Chantal Hoi Yin Cheung, Institute of Molecular and Cellular Biology, National Taiwan University, Taiwan

MP05-004

Particulate matter dephosphorylates ezrin/radixin/moesin (ERM) protein on BEAS-2B cell

Moonhwan Choi, Department of Bioengineering, College of Engineering, Hanyang Univ., South Korea

MP05-005

Deep Phosphoproteome Analysis Reveals Neurobiological Underpinnings for Nurse and Forager Honeybee Workers (*Apis mellifera ligustica***)**

Bin Han, Institute of Apicultural Research, Chinese Academy of Agricultural Sciences, China

MP05-006

CHARACTRIZATION OF THE SIGNALING MECHANISMS IN PANCREATIC ISLETS ISOLATED FROM NORMAL AND OBESE DIABETIC *db/db* MICE

Taewook Kang, Department of Biochemistry and Molecular Biology, University of Southern Denmark, Denmark

MP05-007

Phosphate-affinity chromatographic micro-tip technology for enrichment of phosphopeptides towards phosphoproteomic study

Maho Kawaguchi, Hiroshima University, Japan

MP05-008

ModProt: A database for integrating laboratory and literature data concerning protein post-translational modifications

Yayoi Kimura, Advanced Medical Research Center, Yokohama City University, Japan

MP05-009

Phos-tag SDS-PAGE methodology that effectively uses phosphoproteomic data for profiling the phosphorylation dynamics of MEK1

Eiji Kinoshita, Hiroshima University, Japan

MP05-010

Dissection of protein kinase D signaling during thymocyte development using various phosphoproteomic strategies

Hidetaka Kosako, Fujii Memorial Institute of Medical Sciences, Tokushima University, Japan

MP05-011

Early phosphoproteomic dynamics for potential growth-regulating mechanisms in G-1 treated renal cell carcinoma cell line

Wei-Chi Ku, Cathay General Hospital, Taiwan

MP05-012

Carbon source dependent phosphoproteomic analysis of *Methanosarcina mazei* N2M9705

Shu-Jung Lai, Academia Sinica, Taiwan

MP05-013

Ultra-sensitive motif-targeting approach for stoichiometry measurement of drug-responsive tyrosine phosphorylation dynamics in EGFR

Yen-Chen Liao, Institute of Chemistry, Academia Sinica, Taiwan, Taiwan

MP05-014

Deep (Phospho)Proteome coverage of the archaea *P. furiosus* reveals the broad existence of fascinating ancestral protein kinase activity

Miao-Hsia Lin, Biomolecular Mass Spectrometry and Proteomics, Utrecht University, Utrecht, The Netherlands, Netherlands

MP05-015

Super-SILAC mix coupled with SIM/AIMS assays for targeted verification of phosphopeptides discovered in a large-scale phosphoproteome analysis of hepatocellular carcinoma.

Yu-Tsun Lin, Graduate Institute of Biomedical Sciences, Taiwan

MP05-016

Integrated analysis of genomics, proteomics, and phosphoproteomics in cells and tumor samples

Jason Mcdermott, Pacific Northwest National Laboratory, United States

MP05-017

Analysis of the phosphorylation of actinin-4 involved in cancer metastasis

Nami Miura, National Cancer Center Research Institute, Japan

MP05-018

Delineating mechanisms of Englerin A-induced cell death in renal cancer using multiple proteomics strategies

*Suat Peng Neo, Institute of Molecular and Cell Biology, A*star, Singapore*

MP05-019

Phospho-proteomics on pathways studies

Valentina Siino, Lund University, Sweden

MP05-020

Phosphoproteomics-based prediction of cellular protein kinome profiles

Chisato Takahashi, Graduate School of Pharmaceutical Sciences Kyoto University, Japan

MP05-021

Phosphoproteome analysis of the pathogenic *Helicobacter pylori* 26695

I-Fan Tu, Acedemia Sinica/ Institute of Biological Chemistry (ibc), Taiwan

MP05-022

Autophagy induces changes in the Sarcoma kinome and phosphoproteome in response to arginine starvation

Shin-Cheng Tzeng, Washington University School of Medicine, United States

MP05-023

Deep coverage phosphoproteome characterization of human colorectal cancer cell secreted exosomes and new phosphosite discovery

Tong Wang, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

MP05-024

Quantitative Phosphoproteomic Analysis Reveal Cyclic Stretch-induced Pathways in Human Lung Cancer and Normal Cells.

Wei-Hsuan Wang, Genome and Systems Biology Degree Program, National Taiwan University and Academia, Taiwan

MP05-025

Mining drug resistant targets from tyrosine kinase inhibitor-responsive phosphoproteome in non-small cell lung cancer

Shao-Hsing Weng, Genome and System Biology Degree Program,College of Life Science,National Taiwan University,Taipei, Taiwan

MP05-026

Phosphoproteome of *Spirulina platensis* C1 reveals the relevance of photosynthesis and chlorophyll biosynthesis in response to high-temperature stress

Wan-Ling Wu, Acedemia Sinica/ Institute of Biological Chemistry (ibc), Taiwan

MP05-027

Use of multiplexed kinase biosensor technology and SWATH-MS for monitoring chronic myelogenous leukemia (CML) signaling

Tzu-Yi Yang, University of Minnesota, United States

MP05-028

The ability to attack host iron acquisition pathways in Vibrio vulnificus YJ016 by phosphoproteomic analysis

Jhih-Tian/Oliver Yang, Institute of Biological Chemistry, Academia Sinica, Taiwan

MP06 - Bioinformatics and Computational Proteomics

MO07-001

Investigating the basic assumptions in protein abundance estimation using SWATH-MS data

Wenguang Shao, Institute of Molecular Systems Biology, ETH Zurich, Switzerland

MO07-002

Reactome - Interactive Pathway Analysis for Proteomics

Henning Hermjakob, EMBL-EBI, United Kingdom

MO07-003

MSCypher: A High-Throughput Peptide Identification Strategy for Complex Mixtures

Andrew Webb, The Walter and Eliza Hall Institute, Australia

MO07-004

neXtProt in the context of human proteomics projects

Lydie Lane, Sib Swiss Institute of Bioinformatics, Switzerland

MO07-005

A genetic algorithm to locate responsive subpathways for time-course proteomic data

Eu-Yu Lai, Bioinformatics Program, TIGP, Institute of Information Science, Academia Sinica, Taiwan

TO10-003

The HUPO-PSI Quality Control Working Group: making QC more accessible for biological mass spectrometry

Mathias Walzer, University of Tuebingen, Germany

WO07-001

Leaving shallow waters of protein identification: integrating taxonomic and functional information to tackle challenges in metaproteomic data analysis

Thilo Muth, Robert Koch Institute, Germany

WO07-002

HUPO Human Proteome Project Metrics for 2016

Gilbert Omenn, Department of Computational Medicine and Bioinformatics, University of Michigan, United States

WO07-004

ProDiGy: a Proteome Knowledge Discovery Gateway

Dong Li, Beijing Proteome Research Center, China

MP06-001

Omics Discovery Index - Discovering and Linking Public Omics Datasets

Mingze Bai, Embl-ebi, United Kingdom

MP06-002

DAPAR & ProStaR: software to perform statistical analyses in quantitative discovery proteomics

Thomas Burger, Université Grenoble Alpes, BIG-BGE, Grenoble, 38000, France

MP06-003

Combining Proteomics and RNASeq data for Biological Evaluation.

Mark Cafazzo, Sciex, Canada

MP06-004

iTop-Q: an intelligent top-down proteomics quantification tool using the DYAMOND algorithm for charge state deconvolution

Hui-Yin Chang, Institute of Information Science, Acdemia Sinica, Taiwan

MP06-005

Sensitive and Fast Identification of Bacteria by MALDI-TOF MS fingerprints

Zhuoxin Chen, Institute of Biomedical Science, Fudan University, China

MP06-006

A statistical method of automatically selecting optimal software package for detecting differential abundance in proteomics studies

Lin-Yang Cheng, Purdue University, United States

MP06-007

Updated Scores of Immunohistochemistry-based Expression Profiles in the Human Protein Atlas for Prioritizing Cancer Marker Candidates

Su-Chien Chiang, Institute of Biomedical Informatics, National Yang-Ming University, Taiwan

MP06-008

Epsilon-Q: Improved proteomic analysis tool based on extracted ion chromatogram and Combo-Spec search method

Jin-Young Cho, Department of Integrated Omics for Biomedical Science, Yonsei University, Seoul, South Korea

MP06-009

PECA2: new developments in the statistical modeling of protein concentration regulation in dynamic systems

Hyungwon Choi, New York University, United States

MP06-010

An Information System Enabling the Organization and Automatic Annotation of Proteomic Experiments with User-specific Proteins

Devin Drew, Thermo Fisher Scientific, United States

MP06-011

Entrapment sequences method for the evaluation of database search engines and quality control methods in shotgun proteomics

Xiaodong Feng, Beijing Proteome Research Center, National Center for Protein Sciences, China

MP06-012

Firmiana: A One-stop Proteome Data Processing and Integrated Omics Analysis Cloud Platform

Jinwen Feng, National Center for Protein Sciences (The PHOENIX center, Beijing), China

MP06-013

Analysis of the specific molecular networks of cancer stem cells using a novel data integration tool iPEACH

Yoshimune Yamasaki, Department of Tumor Genetics and Biology, Kumamoto University, Japan

MP06-014

Workflows for improving mass measurement accuracy in mass spectrometry

Arzu Tugce Guler, Center for Proteomics and Metabolomics, Leiden University Medical Center, Netherlands

MP06-015

An expert system for evaluating the validity of protein quantification in individual samples analyzed by high-sample-throughput SWATH-MS

Tiannan Guo, IMSB, ETH Zurich, Switzerland

MP06-016

Integration of Differentially Expressed Proteins and mRNAs with Deregulated microRNAs in Human Glioblastoma: 2-Dimensional Molecular Maps

Manoj Kumar Gupta, Institute of Bioinformatics, International Tech Park, Bangalore, India

MP06-017

DynaPho: a web tool for inferring the signaling dynamics from time-series phosphoproteomics data

Chia-Lang Hsu, Department of Life Science, National Taiwan University, Taiwan

MP06-018

Analysis Workflow for Quantitative Proteomics, Employing Triplex Dimethyl Labelling and Ion Mobility Assisted Data Independent Acquisition

Robert Tonge, Institute of Integrative Biology, University of Liverpool, United Kingdom

MP06-019

Bioinformatical analysis of depletion effect on SRM plasma profiling

Ekaterina Ilgisonis, Institute of Biomedical Chemistry, Russia

MP06-020

MIAPE-QC: a standard document for quality control of MS data

Jinmeng Jia, Shanghai Key Laboratory of Regulatory Biology,East China Normal University, Shanghai, China

MP06-021

Evaluation of search engines for phosphopeptide identification and quantitation

Olivia Yang, Thermo Fisher, United States

MP06-022

Implementation of flexible search for proteomics metadata

Shin Kawano, Database Center for Life Science, Research Organization of Information and Systems, Japan

MP06-023

QC portal for MRM-MS assay : Unified diagnostic assay guidelines for protein biomarkers

Jaenyeon Kim, Seoul National University College of Medicine, South Korea

MP06-024

Proteomic Cinderella: customized analysis of large amount of MS/MS data in one night

Olga Kiseleva, Orekhovich Institute of Biomedical Chemistry, Russia

MP06-025

EBprotV2: Statistical analysis of labeling-based quantitative proteomics data with applications to clinical data

Hiromi Koh, National University of Singapore, Singapore

MP06-026

LASH plot: A new tool for clinical biomarker discovery

Ching-Wan Lam, Department of Pathology, the University of Hong Kong, Hong Kong, China

MP06-027

PPICurator: a System for Extracting Protein-Protein Interaction Information from Literature

Mansheng Li, Beijing Proteome Research Center, Beijing, China

MP06-028

Critical transition and its regulatory network from chronic inflammation to hepatocellular carcinoma

Chen Li, Shanghai Institute for Biological Sciences, Chinese Academy of Sciences, China

MP06-029

PTMtopographer: a hidden Markov model-based tool for global post-translational modification prediction with in-protein false discovery rate estimation

Ginny X.H Li, Saw Swee Hock School of Public Health, National University of Singapore, Singapore

MP06-030

Evaluation of false discovery rate-controlling strategies for proteogenomic search

Honglan Li, School of Computer Science and Engineering, South Korea

MP06-031

Development of Universal MS Signal Processor for Improved Data Independent Acquisition Performance

Chung-Hao Li, Institute of Biotechnology, National Taiwan University, Taiwan

MP06-032

MAGIC-web: a platform for untargeted and targeted N-linked glycoprotein identification

Tung-Shing Lih, Institute of Information Science, Academia Sinica, Taipei 11529, Taiwan

MP06-033

Characterization of a large-scale phosphorylation motifs in human proteome

Yiwei Ling, Niigata University, Japan

MP06-034

New functionality for the Trans-Proteomic Pipeline: tools for the analysis of proteomics data

Luis Mendoza, Institute for Systems Biology, United States

MP06-035

jPOST: Current Status in 2016

Yuki Moriya, Database Center for Life Science, Japan

MP06-036

A virtual-experimental 2DE together with ESI LC-MS/MS as an efficient approach for study of proteome heterogeneity and dynamics

Stanislav Naryzhny, Petersburg Nuclear Physics Institute, Russia

MP06-037

Improved peptide feature detection in the OpenMS software framework.

Lars Nilse, Freiburg University, Institute of Molecular Medicine and Cell Research, Germany

MP06-038

jPOST: repository opened

Shujiro Okuda, Niigata University, Japan

MP06-039

Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets available in the PRIDE Archive database

Yasset Perez-Riverol, European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Trust, United Kingdom

MP06-040

Proteoforms space odyssey: strategy of scouting

Ekaterina Poverennaya, Institute of Biomedical Chemistry, Russia

MP06-041

Targeting Peptidoforms via SWATH-MS: Quantification of PTM Variability in Human Blood Plasma

George Rosenberger, Institute of Molecular Systems Biology, ETH Zurich, Switzerland

MP06-042

Reproducible protein quantification with TRIC: An automated alignment strategy for comprehensive data matrices in targeted proteomics

Hannes Röst, Stanford University, United States

MP06-043

Proteomic Data Sharing by the "ProteoMap Online"

Takayoshi Suzuki, Div. Molecular Target and Gene Therapy Products, National Institute of Health Sciences, Japan

MP06-044

A protein quantification modified algorithm for the improvement of tandem mass spectra usage

Jun Tang, East China Normal University, China

MP06-045

Rapid and Efficient Quantification of Proteins Using Routine Proteomics Identification Workflows

Lorne Taylor, Research Institute - McGill University Health Center, Canada

MP06-046

High quantification efficiency for targeted proteomics using Q-TOF instruments and sophisticated data processing
Alex (Lien-Yung) Wang, Bruker Daltonics, Germany
MP06-047
FeatureFinderIdentification: Targeted feature detection for data-dependent shotgun proteomics
Hendrik Weisser, Wellcome Trust Sanger Institute, United Kingdom
MP06-048
An efficient and accurate feature-based label-free quantification software tool for SWATH MS data
Long Wu, The Hong Kong University of Science and Technology, Hong Kong, China
MP06-049
jPOST: Re-analysis Protocol
Akiyasu C. Yoshizawa, Bioinformatics Center, Institute for Chemical Research, Kyoto University, Japan
MP06-050
Label Free Quantitation using Peptide Isotope Peak Intensities in Mass Spectrometry
Kina Yun, Biomedical Omics group, Korea Basic Science Institute, South Korea
MP06-051
Diffacto: a robust and accurate quantification-centered proteomics method for large-scale differential analysis
Bo Zhang, Karolinska Institutet, Sweden
MP06-052
Optimal integration strategy of multi-engine MS spectra search results
Panpan Zhao, Institute of Life and Health Engineering, Key Laboratory of Functional Protein Research of Guangdong Higher Education Institutes, Jinan University, Guangzhou, China, China
MP06-053
CNHPP Data Portal: an integrated framework for proteome-centric pan-omics data
Weimin Zhu, Laboratory of Data Sciences, China

MP07 - Immunity, Inflammation and Infectious Diseases

MO06-001

The human immunopeptidome: can big data improve the precision of immunotherapy?

Anthony Purcell, Monash University, Australia

MO06-002

Quantitative host-pathogen protein network analysis using data-independent acquisition mass spectrometry analysis

Johan Malmström, Lund University, Sweden

MO06-003

Proteomic of host-microbiome interactions in a pediatric inflammatory bowel disease inception cohort to identify protein biomarkers

Daniel Figeys, University of Ottawa, Canada

MO06-004

Challenges of biomarker discovery in developing countries: A proteomics investigation to identify unique disease signatures in infectious diseases

Sanjeeva Srivastava, Indian Institute of Technology Bombay, India

MO06-005

Robust temporal profiling of GRB2 protein complexes in primary T lymphocytes using SWATH mass spectrometry

Etienne Caron, Eth Zurich, Switzerland

MP07-001

Extracellular vesicles as potential biomarkers in female patients with suspected adverse effects to the quadrivalent Human Papilloma Virus vaccine

Rikke Baek, Department of Clinical Immunology, Aalborg University Hospital, Denmark

MP07-002

Digging into meningitis proteome profiles in human cerebrospinal fluid using DIA-MS.

Anahita Bakochi, Division of Infection Medicine, Department of Clinical Sciences Lund, Lund University, Sweden

MP07-003

Direct identification of viral epitopes from MHC I molecules by mass spectrometry

Renata Blatnik, German Cancer Research Center (DKFZ), Immunotherapy and -prevention, Heidelberg, Germany

MP07-004

Defective wound healing as observed through clinical and proteome measurements

James Broadbent, Queensland University of Technology, Australia

MP07-005

Identifying the endomembrane system and organelle proteomic analysis in protozoan parasite, *Trichomonas vaginalis.*

Chien-Hsin Chu, Academia Sinica, Taiwan

MP07-006

In depth proteomic characterization of classical and non-classical monocyte subsets

Fernando J. Corrales, Proteomics, Genomics and Bioinformatics Unit, CIMA, University of Navarra, Spain

MP07-007

Quantitative Proteomics Study of Macrophage Kinases after Interaction with *Candida albicans*

Concha Gil, Department of Microbiology, Fct. of Pharmacy, Complutense University of Madrid and Irycis, Spain, Spain

MP07-008

Proteomic Study of Monocyte Chemoattractant Protein-1 Induced polarisation

Cheng Huang, Department of Biochemistry and Molecular Biology, Monash University, Australia

MP07-009

Proteomic analysis of murine norovirus-infected Raw264.7 cells reveals the induced expression of host immune response proteins

Ju-Suk Kim, Biological Disaster Analysis Group, Korea Basic Science Institute, Daejeon 34133, South Korea

MP07-010

Proteomic analysis of human saliva samples obtained from caries-free and caries-susceptible people

Lucie Kulhavá, Department of Analytical Chemictry, Faculty of Science, Charles University in Prague, Czech Republic

MP07-011

Quantitative Proteomic Analysis of Different Clinical Manifestation of Severe Falciparum Malaria Patients

Vipin Kumar, Indian Institute of Technology-Bombay, India

MP07-012

Quantitative Proteomic Analysis from Acute to Chronic Stages Hepatitis C Virus Infection by iTRAQ Technology

Tze-Yu Lin, Department of Chemistry, National Taiwan Normal University, Taiwan

MP07-013

Serum Proteome and Cytokine Analysis in a longitudinal cohort of Dengue Fever Patients for Identification of Predictive Markers

Monalisha Nayak, Indian Institute of Technology Bombay, India

MP07-014

Phosphoproteomics and proteomics profiling of macrophage cells infected with dengue virus

Victoria Pando-Robles, Centro de Investigación sobre Enfermedades Infecciosas. Instituto Nacional De Salud Publica, Mexico

MP07-015

Multipronged Quantitative Proteomics Analysis Reveal Oxidative Stress and Cytoskeletal Proteins as Possible Markers for Severe Vivax Malaria

Sandip Patel, Indian Institute of Technology Bombay, India

MP07-016

Characterization of specific antibody-peptide sequences in glaucoma sera using discovery proteomic strategies.

Carsten Schmelter, Experimental Ophthalmology, University Medical Center of the Johannes Gutenberg University Mainz, Germany

MP07-017

Delineation of the human Ramos B cell proteome and the substrate network of the protein tyrosine phosphatase 1B by quantitative proteomics

Jennifer Schwarz, Department of Biochemistry and Functional Proteomics, Institute of Biology II, Freiburg University, Germany

MP07-018

Selective modulation of host cellular and mitochondrial proteome during time resolved phagocytosis of MSSA and MRSA *Staphylococcus aureus*

Alessio Soggiu, Department of Veterinary Medicine , University of Milan, Milan, Italy

MP07-019

Attenuation of Coactosin-like Protein-1 Protects Liver from Steatosis and Injury

Ai-Hua Sun, Beijing Proteome Research Center, China

MP07-020

Investigation of IgG heavy chain variable region peptides for differential diagnosis of autoimmune pancreatitis and pancreatic adenocarcinoma

I-Lin Tsai, Department of Biochemistry and Molecular Cell Biology, School of Medicine, College of Medicine, Taipei Medical University, Taiwan

MP07-021

HLA class I peptidedome analysis to identified allergic peptides for drug hypersensitivity

Chun-Yu Wei, Institute of Biomedical Sciences, Academia Sinica, Taiwan

MP07-022

Quantitative shifts in the influenza immunopeptidome reveal the relative contributions of direct and cross-presentation to T cell mediated immunity

Ting Wu, Infection and Immunity Program, Biomedicine Discovery Institute, Monash University, Australia

MP07-023

Interactome analysis of the NS1 protein encoded by influenza A virus reveals a positive regulatory role of host protein PRP19 in viral replication

Chih-Ching Wu, Department of Medical Biotechnology and Laboratory Science, Chang Gung University, Taiwan

MP07-024

Temporal regulation of Lsp1 *O* -GlcNAcylation and phosphorylation during apoptosis of activated B cells

Jung Lin Wu, Grc, Academia,sinica, Taiwan

MP07-025

Inorganic nanomaterials react with tumor infiltrating immune cells to modulate tumor progression

Ren-In You, Department of Laboratory Medicine and Biotechnology, Tzu Chi University, College of Medicine, Taiwan

MP08 - Brain and Eyeome: Connecting Two Images

MO05-001

Proteomics reveals individual patient responses to therapeutic treatment for dry eye

Roger Beuerman, Singapore Eye Research Institute, Duke-nus, Singapore

MO05-002

A comprehensive inter-grade proteomic analysis of serum, CSF and tissue in glioma

Manubhai Kp, Indian Institute of Technology Bombay, India

MO05-003

Building a comprehensive chick retinal proteome dataset by liquid chromatography (LC) fractionation for tandem MS and SWATH analysis

Hu Xiao, Laboratory of Experimental Optometry, Centre for Myopia Research, Hong Kong Polytechnic University, Hong Kong, China

MO05-004

Do Platelet-derived extracellular vesicles contain specific biomarkers allowing for early diagnostics of Alzheimer's Disease?

Helmut Erich Meyer, Leibniz-Institut Für Analytische Wissenschaften - Isas - e.V., Germany

MO05-005

Generating a Proteomic Profile of Neurogenesis, through a quantitative comparison of neuroepithelial and radial glial like stem cells

Shaun Garnett, University of Cape Town, South Africa

MP08-001

Comparison of protein extraction protocols for label free proteomic studies in retinal tissue.

Jingfang Bian, School of Optometry, The Hong Kong Polytechnic University, Hong Kong, China

MP08-002

Comparison of fixed Sequential Windowed Acquisition of All Theoretical Fragment Ion Mass Spectra (SWATH) windows for normal chick vitreous proteome

Ka Wai Cheung, School of Optometry, Hong Kong Polytechnic University, Hong Kong, China

MP08-003

Discovering protein regulations of human trabecular meshwork in response to corticosteroids using SWATH acquisition and MRMHR

Samantha Sze Wan Shan, School of Optometry, Hong Kong Polytechnic University, Hong Kong, China

MP09 - Diabetes and Cardiovascular Diseases: Energy Balance in Disease Phenotypes

MO10-001

Changes in protein expression patterns in islets of Langerhans: implications for treatment of children with obesity and type 2 diabete

Peter Bergsten, Uppsala University, Sweden

MO10-002

Proteomic Phenotyping of Human Arterial Samples Identifies Novel Markers of Early Atherosclerosis

David Herrington, Wake Forest School of Medicine, United States

MO10-003

Proteomic Analysis of Membranes in Mouse And Human Cardiovascular Tissues

Anthony Gramolini, University of Toronto, Ted Rogers Centre for Heart Research, Canada

MO10-004

Glycoproteomics of the Aortic Extracellular Matrix: An Approach for Studying Diabetes and Cardiovascular Risk

Ferheen Baig, King's College London, United Kingdom

MO10-005

Phosphoproteomics Identifies CK2 as a Negative Regulator of Beige Adipocyte Thermogenesis and Energy Expenditure

Kosaku Shinoda, Ucsf School of Medicine, United States

MO10-006

Protective effects of GLP-1 analogues against cellular stress: An *in vitro* proteomic study

Ali Tiss, Dasman Diabetes Institute, Kuwait

MO10-007

Poorly controlled diabetes mellitus is associated with decreased aspirin-mediated acetylation of platelet cyclooxygenase 1 (COX-1) at serine 529

Jean-Charles Sanchez, Geneva University, Switzerland

MP09-001

SILAC-BASED PROTEOMICS OF HUMAN KIDNEY CELLS REVEALS A NOVEL LINK BETWEEN MALE SEX HORMONES AND IMPAIRED ENERGY METABOLISM IN DIABETIC KIDNEY DISEASE

Sergi Clotet, University Health Network, Toronto, Canada

MP09-002

Quantitative simultaneous multiple PTMomics characterization of arteries from patients with atherosclerosis and type 2 diabetes

Honggang Huang, University of Southern Denmark, Denmark

MP09-003

A quantitative proteomic analysis of liver samples from liraglutide vs. placebo treated GIPR[dn] pigs

Erik Ländström, Laboratory for Functional Genome Analysis (LAFUGA), Gene Center, LMU-Munich, Germany

MP09-004

Differential Membrane Proteomics of Diet-induced Insulin Resistance Mice featured by Disorganized Actin and Myocardial Dysfunctic

Szu-Hua Pan, National Taiwan University College of Medicine, Taiwan

MP09-005

The changes of proteomic profiling in the human four chambers from heart failure and additional insights in their biological function

Liu Shanshan, Fudan University, China

MP09-006

Glycoproteomics of Aortas from Patients with Marfan Syndrome

Xiaoke Yin, King's College London, United Kingdom

MP10 - Missing Proteins-Identification, Validation and Functional Characterization (CHPP)

MP10-001

Proteome identification of human beta-defensins in male reproductive system, and induced expression by epigenetic regulation

Yang Liu, Fudan University, China

MP10-002

Looking for missing proteins in the proteome of human spermatozoa: an update

Yves Vandenbrouck, CEA, Biosciences and Biotechnology Institute of Grenoble, INSERM, UGA, France

MP10-003

State of the Chromosome 18-centric HPP in 2016: Transcriptome and Proteome Profiling of Liver Tissue and HepG2 Cells

Alexander Archakov, Institute of Biomedical Chemistry, Russia

MP10-004

Mining Missing Membrane Proteins by High-pH Reverse Phase StageTip Fractionation and Multiple Reaction Monitoring Mass Spectrometry

Reta Birhanu Kitata, Institute of Chemistry, Academia Sinica, Taipei, Taiwan

MP10-005

The Spanish HPP: Detection of chromosome 16 missing proteins by targeted proteomics

Targeted Proteomics Working Group Proteored, Plataforma de Recursos Biomoleculares y Bioinformáticos-ISCIII, Spain

MP10-006

Detection of missing proteins using the PRIDE database as a source of mass-spectrometry evidence

Victor Segura, Proteomics and Bioinformatics Unit, CIMA, University of Navarra, Spain

MP10-007

Proteomic Analysis of Human Placenta Stem Cell in Search of Missing Proteins

Jong-Sun Lim, Yonsei Proteome Research Center, South Korea

MP11 - Functional Roles of Alternative Splicing Varients (CHPP)

MP11-001

Functional characterization of a novel oncogene C20orf24 in colorectal carcinoma

Yang Wang, Jinan University, China

MP12 - Snps And Ptms (Identification, Validation and Functional Consequences) (CHPP)

MP12-001

FROM SNP TO GLYCOSYLATION: A COMPREHENSIVE GENO-GLYCOMIC APPROACH TO DISCOVER NEW LUNG DISEASE

Andras Guttman, Sciex, United States

MP12-002

Establishment of an omics database to study AOM/DSS mouse model of colorectal cancer

Qingfei Pan, Beijing Institute of Genomics, Chinese Academy of Sciences, China