15th Human Proteome Organization World Congress

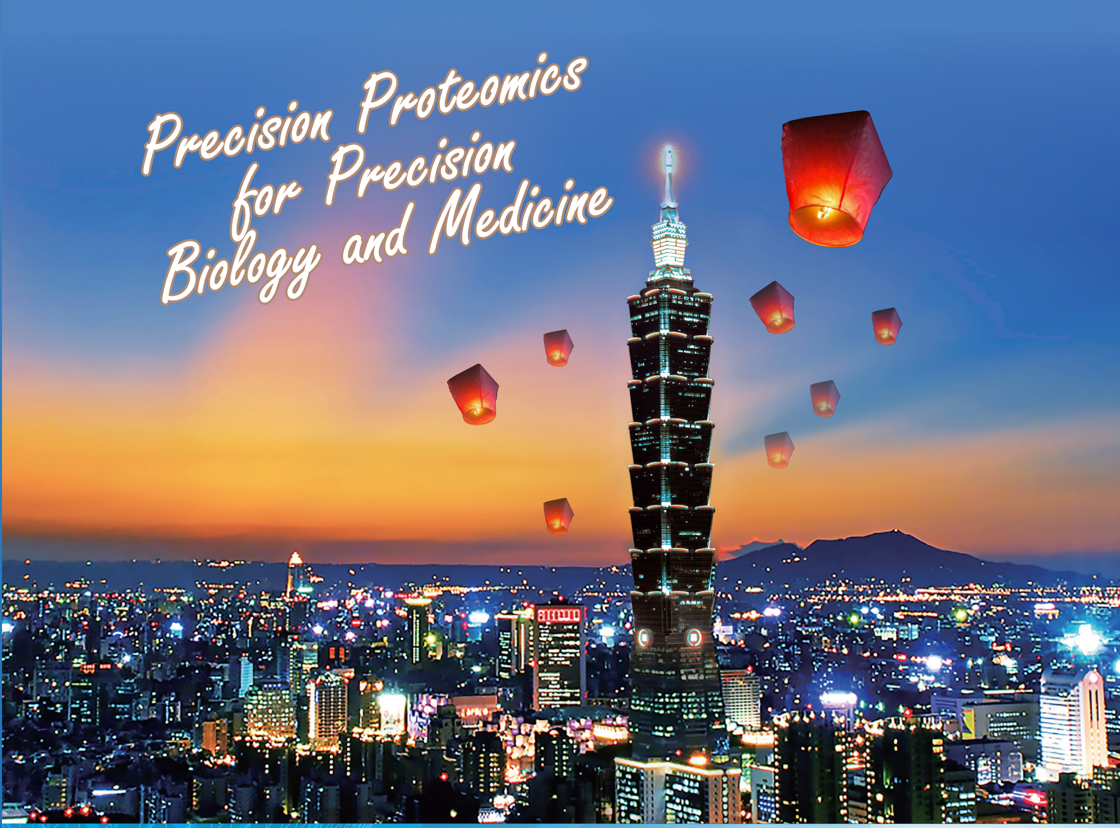
PROGRAM

2016 Taipei, Taiwan

2016 TAIPEI
HUPO

15th Human Proteome Organization World Congress

September 18-22, 2016 Taipei, Taiwan



Precision Proteomics for Precision Biology and Medicine

CONGRESS PROGRAM BOOK

HUPO
HUMAN PROTEOME ORGANIZATION
translating the code of life

TPS

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INTRODUCTION

Welcome Message from the Congress Chairs

Dear Colleagues and Friends,

On behalf of the Organizing Committee, we would like to extend a warm welcome to you all, especially those coming from afar, for attending the **15th Human Proteome Organization World Congress (HUPO 2016)** held in Taipei, Taiwan, from September 18 to 22, 2016.

Over the past several years, the annual international HUPO meeting has fast becoming one of the most prominent Congresses in the field with far reaching scientific impacts. This year in Taipei, we are expecting over 1,100 delegates coming from no less than 42 countries. In tune with the designated theme *"Precision Proteomics for Precision Biology and Medicine",* the Scientific Committee has organized a series of invited plenary lectures, concurrent pre-congress workshops and keynote sessions in parallel tracks, complete with poster viewing sessions, luncheon seminars and Bioinformatic Hubs, in what turns out to be a fully packed 4 days' program. We further encourage your participation in all social networking events to meet new friends and old, and visiting the exhibitions where our industry partners present tomorrow's science and technology.

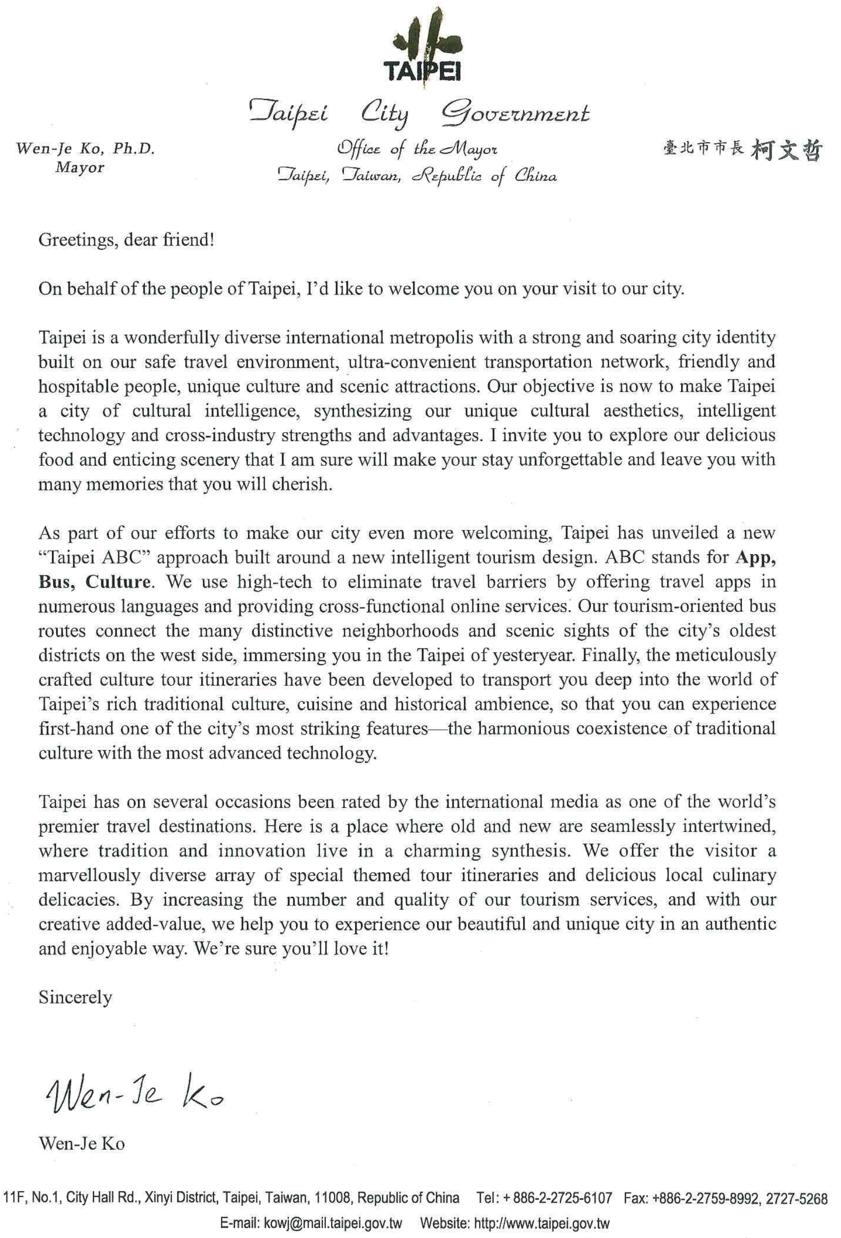
The Taipei International Convention Center sits right in the commercial center of Taipei, where selections of malls, restaurants and hotels are within walking distance while extensive public transport networks connect it to the rest of the city and beyond. From Taipei 101 to the National Palace Museum, from creative cultural park to temple and historic walks, the rich diversity of Chinese culture is amply represented not only by its modern architectures and historical buildings, but also the people. It is with such a fluid cultural mix and warm-hearted hospitality that Taipei, as a uniquely placed convention city in the Asia Pacific region, awaits your visit and exploring.

Enjoy your stay, and, welcome to Taiwan!

Ming-Daw Tsai
Congress Chair,
HUPO 2016

Yu-Ju Chen
Congress Co-Chair,
HUPO 2016

WELCOME MESSAGE FROM THE MAYOR



TAIPEI
Taipei City Government
Office of the Mayor
Taipei, Taiwan, Republic of China

Wen-Je Ko, Ph.D.
Mayor

臺北市市長 柯文哲

Greetings, dear friend!

On behalf of the people of Taipei, I'd like to welcome you on your visit to our city.

Taipei is a wonderfully diverse international metropolis with a strong and soaring city identity built on our safe travel environment, ultra-convenient transportation network, friendly and hospitable people, unique culture and scenic attractions. Our objective is now to make Taipei a city of cultural intelligence, synthesizing our unique cultural aesthetics, intelligent technology and cross-industry strengths and advantages. I invite you to explore our delicious food and enticing scenery that I am sure will make your stay unforgettable and leave you with many memories that you will cherish.

As part of our efforts to make our city even more welcoming, Taipei has unveiled a new "Taipei ABC" approach built around a new intelligent tourism design. ABC stands for **App, Bus, Culture**. We use high-tech to eliminate travel barriers by offering travel apps in numerous languages and providing cross-functional online services. Our tourism-oriented bus routes connect the many distinctive neighborhoods and scenic sights of the city's oldest districts on the west side, immersing you in the Taipei of yesteryear. Finally, the meticulously crafted culture tour itineraries have been developed to transport you deep into the world of Taipei's rich traditional culture, cuisine and historical ambience, so that you can experience first-hand one of the city's most striking features—the harmonious coexistence of traditional culture with the most advanced technology.

Taipei has on several occasions been rated by the international media as one of the world's premier travel destinations. Here is a place where old and new are seamlessly intertwined, where tradition and innovation live in a charming synthesis. We offer the visitor a marvellously diverse array of special themed tour itineraries and delicious local culinary delicacies. By increasing the number and quality of our tourism services, and with our creative added-value, we help you to experience our beautiful and unique city in an authentic and enjoyable way. We're sure you'll love it!

Sincerely

Wen-Je Ko

Wen-Je Ko

11F, No.1, City Hall Rd., Xinyi District, Taipei, Taiwan, 11008, Republic of China Tel: + 886-2-2725-6107 Fax: +886-2-2759-8992, 2727-5268
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HUMAN PROTEOME ORGANIZATION (HUPO)

The Human Proteome Organization (HUPO) is an international scientific organization representing and promoting proteomics through international cooperation and collaborations by fostering the development of new technologies, techniques and training.

HUPO Mission Statement

To define and promote proteomics through international cooperation and collaborations by fostering the development of new technologies, techniques and training to better understand human disease.

Objectives

Foster global collaboration in major proteomics projects by gathering leading international laboratories in life sciences, bioinformatics, mass spectrometry, systems biology, pathology, and medicine;

Become the point of contact for proteomics research and commercialization activities worldwide;

Support large-scale proteomics projects that are aimed at:

- A mechanistic understanding of fundamental biological processes (often using model organisms and non human species);

- Directly studying human disease through proteomics techniques and technologies;

Coordinate and enable the fostering of communication among funding agencies and industry partners with the proteomics community and coordinate the activities of groups and organisations interested in HUPO's Scientific Initiatives

Coordinate the development of standard operating procedures related to:

- Sample preparation, analysis, and repetitions;
- Data collection, analysis, storage, and sharing;

Play a leading role in:

- Defining the location and functions of proteins in human health and disease by supporting the definition of common and specific standards for peptide and protein characterization from human and model organism specimen selection and phenotypic evaluation to data collection, storage and analysis allowing free and rapid exchange of data;

- The creation of country-based ethical and legal policy surrounding the handling, banking and use of human tissue specimens for large-scale proteomics projects.

HUMAN GOVERNANCE- COUNCIL

EXECUTIVE COMMITTEE 2016

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(ex-officio)

PRESIDENT-ELECT
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(2016)

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(2016-2017)

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(2014-2016)

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(2015-2016)

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MEMBER-AT-LARGE
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COMMITTEES

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Academia Sinica, Taiwan

Pan-Chyr Yang
National Taiwan University, Taiwan

Yun Yen
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LOCAL ORGANIZING COMMITTEE

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CONGRESS CO-CHAIR

Yu-Ju Chen
Academia Sinica, Taiwan

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National Taiwan University, Taiwan

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Yi-Sheng Wang
Academia Sinica, Taiwan

Chia-Jung Yu
Chang-Gung University, Taiwan

Jau-Song Yu
Chang-Gung University, Taiwan

SCIENTIFIC ORGANIZING COMMITTEE

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Academia Sinica, Taiwan

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University of Southern Denmark, Denmark

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KTH Royal Institute of Technology, Sweden

Alexey Nesvizhskii
University of Michigan, USA

Jun Qin
National Center for Protein Sciences, Beijing , China

Jau-Song Yu
Chang-Gung University, Taiwan

ACKNOWLEDGEMENTS

HUPO and the 15th World Congress would like to take this opportunity to acknowledge, with sincere appreciation, the generous contributions and support of the following sponsors:

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Journal of PROTEOMICS ELSEVIER

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SiC
Supra Integration and Incubation Center

TBI

TPP 台灣蛋白質計畫

TPS
Taiwan Proteomics Society

TSMS
台灣質譜學會
Taiwan Society for Mass Spectrometry

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TAIPEI 觀光傳播局 Department of Information and Tourism

GENERAL INFORMATION

2016 TAIPEI HUPO

GENERAL INFORMATION

In alphabetical order

Awards

Award winners will be awarded during the closing plenary session on Wednesday, September 21 in the Plenary Hall (3rd Floor). Awardees must appear in person for promulgation.

Badges

All participants are required to wear a badge to attend sessions or enter the exhibition area all the time during the Congress period for recognition.

Supported by: BRUKER

Camera and Recording

Any electronic recording as well as photograph taking are NOT allowed in all sessions.

Congress Materials

Program is included in the Congress bag and delivered to fully registered delegates.

Emergencies

For emergencies, dial 110 (police) or 119 (fire) from any phone.

Exhibition

The exhibits are located in Room 201 (2nd Floor) and Banquet Hall (3rd Floor).
Industrial exhibition will be open as follows:

Sunday, September 18, 2016	20:00-21:30 (Welcome Reception)
Monday, September 19, 2016	09:30-17:30
Tuesday, September 20, 2016	09:30-17:30
Wednesday, September 21, 2016	09:30-15:30

Food and Beverage

Light meals are available at the Taipei Garden Café and Jade Restaurant on the 1st & 2nd floor of TICC on individual's own expense. There are many restaurants choices in Taipei, and a food court is located right in the basement floor of Taipei 101.

Housing

Any changes to hotel reservations should be made directly with the hotel.

Information (Lost & Found)

Information counter will be in service in the registration area during service hours and provide the relevant information on the Congress and Taipei.
Any missing or unattended personal belongings will be taken to the same counter.

Internet Service

WiFi for mobile phones, tablets, and laptops will be accessible within the Center by selecting the SSID: HUPO2016. Neither a special registration process nor fees are necessary.

Language

The official language of the Congress is English.

Liability and Insurance

The Organizing Committee and HUPO shall not be liable for personal accidents, illness, losses or damage to private property of registered delegates of the Congress. It is therefore recommended that delegates and accompanying persons arrange appropriate travel and health insurance before traveling.

Message Board

Message board will be set up on the 1st floor for participants to exchange messages or obtain the Congress updates.

Mobile Phones

Put the mobile phone into silent mode or switch it off during all sessions.

Networking Breaks and Poster Viewing

Networking Breaks will take place in Room 201 (2nd Floor) and Banquet Hall (3rd Floor) at the following times. Refreshments will be provided.

Monday, September 19, 2016	09:30-10:30 and 15:30-16:30
Tuesday, September 20, 2016	09:30-10:30 and 15:30-16:30
Wednesday, September 21, 2016	09:30-10:30 and 12:30-13:30

Registration Counter

Onsite registration is acceptable during the service hours listed below. Only TWD (aka NTD: New Taiwan Dollar) cash and credit cards (VISA, Master and JCB) will be accepted for payment.

Sunday, September 18, 2016	07:30-19:30
Monday, September 19, 2016	07:30-17:30
Tuesday, September 20, 2016	08:00-17:30
Wednesday, September 21, 2016	08:00-16:00

Secretariat Office

Secretariat office will be at Room 105 during the service hours.

Sunday, September 18, 2016	07:30-19:30
Monday, September 19, 2016	07:30-17:30
Tuesday, September 20, 2016	08:00-17:30
Wednesday, September 21, 2016	08:00-16:00

Speaker Ready Room

Speakers/Presenters may preview their presentation in the Speaker Ready Room at Room 103, during the service hours.

Sunday, September 18, 2016	07:30-19:30
Monday, September 19, 2016	07:30-17:30
Tuesday, September 20, 2016	08:00-17:30
Wednesday, September 21, 2016	08:00-16:00

Staff and Volunteers

Volunteers are present at the Taipei International Convention Center throughput the Congress and are happy to answer any question delegates may have regarding the Congress. Staffs are easily identified by their purple uniforms inside the Convention Center.

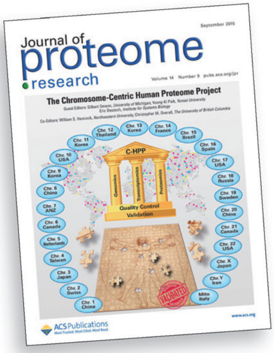
Supported by: ThermoFisher SCIENTIFIC

Tours

Optional Tours can be booked through the Tour Desk in the lobby on the 1st floor.

Venue

Taipei International Convention Center
Add : 1 Hsin-Yi Rd., Sec.5, Taipei 11049, Taiwan
Tel: +886-2-2725-5200
Fax: +886-2- 2723-2589

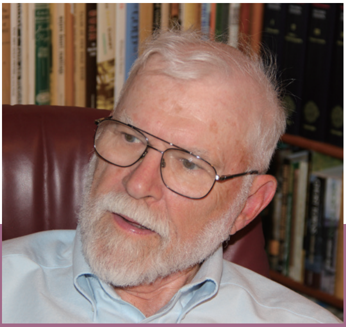

Journal of proteome research
The Chromosome-Centric Human Proteome Project

AWARDS

2016 TAIPEI
HUPO

HUPO AWARDS

Distinguished Achievement in Proteomic Sciences Award



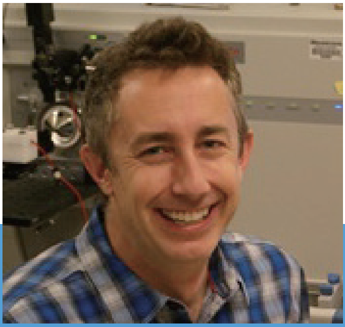
Ralph Bradshaw

College of Medicine, University of California, USA

Professor Ralph Bradshaw is awarded the HUPO Distinguished Achievement in Proteomic Sciences Award for his true dedication to promoting protein and proteomics science. He has been one of the strongest proponents of HUPO and protein science throughout his distinguished career. He has worked tirelessly with the US Government to support HUPO from the very beginning and has supported both HUPO and US-HUPO continuously through the years. Through his efforts as Associate Editor of the Journal of Biological Chemistry and Co-Editor of Molecular and Cellular Proteomics, he has guided protein and proteomics research to be published with the highest degree of confidence and has set standards to ensure results are properly analyzed and reported. His distinguished career in protein science has helped many within HUPO to achieve their best and he has been a mentor to so many scientists within proteomics.

Sponsored by the Journal of proteome research

Discovery in Proteomic Sciences Award



Michael MacCoss

School of Medicine, University of Washington, USA

Professor Michael MacCoss is awarded the HUPO Discovery in Proteomic Sciences Award for his developments in methodology and software for the quantitative analysis of complex protein mixtures. Prof. MacCoss and his research team have developed the software program Skyline, an application with a remarkable impact within the proteomics community, which has placed him as a leader in the field of quantitative proteomics. The focus of his lab is the development of high-throughput quantitative proteomic methods and their application to model organisms. During his post-doc he developed RelEx, one of the first tools to quantify proteins from stable isotope labeling experiments. His lab at the University of Washington has developed several widely used tools for quantitative proteomic analysis including Skyline, a free software package for the design and interpretation of targeted proteomics experiments.

Translational Proteomics Award

Joshua LaBaer

Biodesign Institute, Arizona State University, USA

Professor Joshua LaBaer is awarded the HUPO Translational Proteomics Award for his significant contribution to biomarker discovery and the use of clinical proteomics in personalized medicine. His group has developed novel protein microarray technologies, including the Nucleic Acid Programmable Protein Array (NAPPA) platform, which has been used extensively in biomedical research and biomarker discovery (e.g. breast cancer and diabetes).

Sponsored by ELSEVIER

Science and Technology Award

Bob Bateman and John Hoyes

Waters Corporation, Wilmslow, UK

The IAB felt the nomination of Bob Bateman and John Hoyes of Waters for the development of the Q-TOF mass spectrometer was outshining any other nomination for this year's HUPO Science and Technology Award. The history of the Q-TOF goes back to the mid 1990s, and Bateman and Hoyes played a key role in their development. The availability of a Q-TOF tandem MS instrument had tremendous influence on the development of proteomics in its early days, since this type of mass spectrometer coupled with a nanoLC provided unprecedented performance in analyzing a proteome. The Q-TOF design was subsequently adopted by other mass spectrometry companies and today a large variety of QTOF instruments exists.

Sponsored by the HUPO Industrial Advisory Board

STUDENT TRAVEL AWARDS

Bruker Corporation Student Travel Award Winners

(Alphabetical by Author's Last Name)

Sergi Clotet, Canada

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

Victoria Dardov, USA

WO08-004: Proteomic Analysis of Motor Neurons from Induced Pluripotent Stem Cells: ALS

Fei Fang, China

MO02-004: All MS/MS Ions Monitoring Acquired by Data-Dependent Acquisition without Dynamic Exclusion: A New Concept for In-Depth Protein Quantification

Humberto Gonczarowska-Jorge, Germany

MO08-003: Subtilisin for Large Scale (Phospho) Proteomics – The Beginning of a Wonderful Love Story?

Honggang Huang, Denmark

MP09-002: Quantitative Simultaneous Multiple Ptmomics Characterization of Arteries from Patients with Atherosclerosis and Type 2 Diabetes

Jiangming Huang, China

TP02-012: Simplified Cell Strategy for Large Scale Identification of Mucin-Type O-Glycoproteins

Emila Kurbasic, Sweden

TP01-041: Changes in Protein Expression between Primary Breast Tumour and Lymph Node or Distant Metastases

Hiromi Koh, Singapore

MP06-025: EBprotV2: Statistical Analysis of Labeling-Based Quantitative Proteomics Data with Applications to Clinical Data

Hiroshi Kusamoto, Japan

WP03-003: Thio-Tag Tip Method by Using Zinc (II)–Cyclen-Attached Agarose Beads for Enrichment of Cysteine-Containing Biomolecules

Chongyang Li, Canada

TP03-004: PIAS1-Mediated SUMOylation of BAF57 Is a Critical Regulator of Cell Growth and Drug Sensitivity in Ovarian Cancer Cells

Yang Li, China

TO06-003: A High-Content Functional Mycobacterium Tuberculosis Proteome Microarray and Its Applications

Parul Mittal, Australia

WP16-003: Lymph Node Metastasis of Primary Endometrial Cancers: Associated Proteins Revealed by Maldi Imaging

Dan Bi Park, South Korea

TP02-026: Glycomic Approach for Design of Humanized Mouse Model via Nano-LC/MS and LC/MS/MS

Gun Wook Park, South Korea

TP02-025: Integrated GlycoProteome Analyzer (I-GPA) for Automatic Identification and Quantitation of Site-Specific N-Glycosylation in Human Plasma

Cristian Piras, Italy

TO10-004: Adipose Tissue Pathways in Obesity: Iberian Pig as Large Animal Model of Metabolic Disorders

Priya Sivadasan, India
TP01-073: Salivary Proteins from Pre-Malignant and Malignant Lesions of the Oral Cavity and Their Translational Potential for Early Diagnosis

Zhiduan Su, Australia
WO03-004: Proteomic and Redox Proteomic Analyses Reveal a Dual ROS-Regulation of Glucose Uptake in Adipocytes

Chisato Takahashi, Japan
MP05-020: Phosphoproteomics-Based Prediction of Cellular Protein Kinome Profiles

Mathias Walzer, Germany
TO10-003: The HUPO-PSI Quality Control Working Group: Making QC More Accessible for Biological Mass Spectrometry

Xin Wang, Japan
WP12-010: Proteomic Analysis to Reveal the Calcium Function on Protein Glycosylation in Endoplasmic Reticulum of Soybean under Flooding and Drought Stresses

Churat Weeraphan, Thailand
TP01-088: Phosphoproteome Profiling of Isogenic Cholangiocarcinoma Exosomes Reveal Differential Expression of a Key Metastatic Factor

Ting Wu, Australia
MP07-022: Quantitative Shifts in the Influenza Immunopeptidome Reveal the Relative Contributions of Direct and Cross-Presentation to T Cell Mediated Immunity

Jeonghun Yeom, South Korea
WP01-011: Identification for Protein-level Evidence of Genomic Variants in Cancer Cells Using New Proteogenomic Approach

Kun-Hsing Yu, USA
TP01-096: Predicting Ovarian Cancer Patients' Clinical Response to Platinum-Based Chemotherapy by Their Tumor Proteomic Signatures

Bo Zhang, Sweden
MP06-051: Diffacto: A Robust and Accurate Quantification-Centered Proteomics Method for Large-Scale Differential Analysis

Cambridge Isotope Laboratories Student Travel Award Winner

Cambridge Isotope Laboratories CIL

Yinghua Zhao, China
WP15-016: Application of High Throughput Urinary Proteomic Strategy in the Diagnosis of Acute Appendicitis with Confusable Acute Abdomens

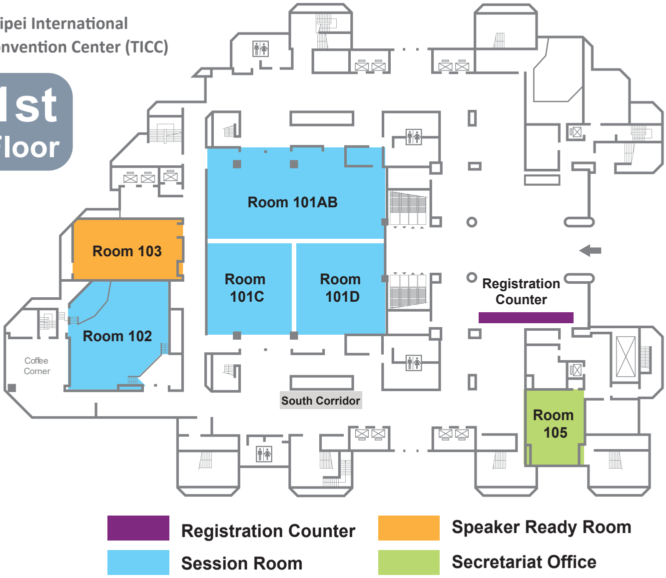
CONGRESS VENUE MAP

2016 TAIPEI HUPO

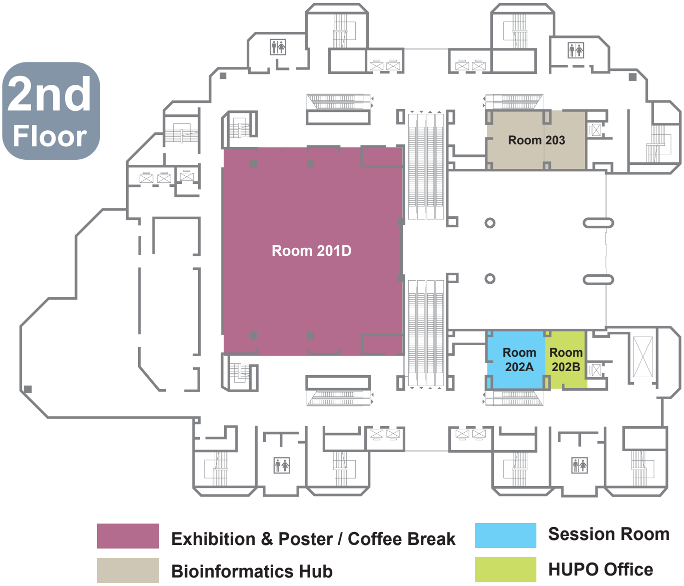
CONGRESS VENUE MAP

Taipei International
Convention Center (TICC)

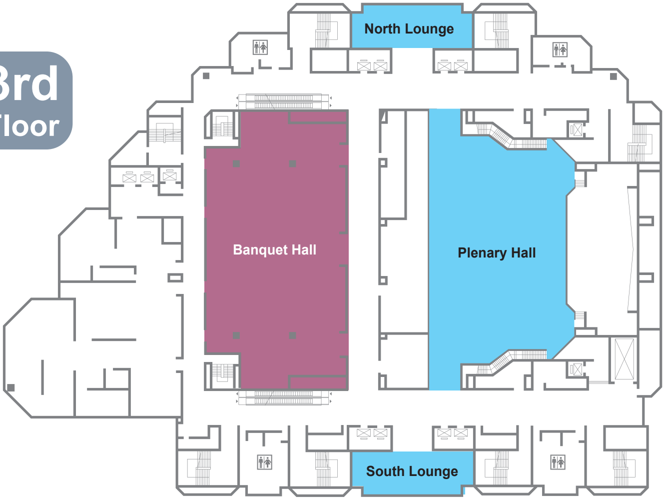
1st Floor



2nd Floor

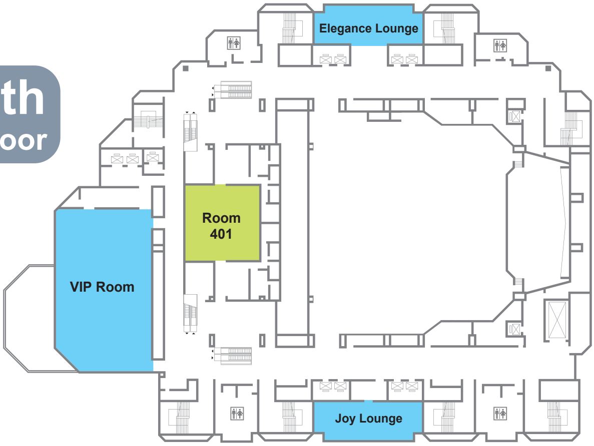


3rd Floor



🟪 **Exhibition & Poster / Coffee Break** 🟦 **Session Room**

4th Floor



🟦 **Session Room** 🟩 **HUPO Council Meeting**

EXHIBITION INFORMATION

2016 TAIPEI HUPO

EXHIBITION INFORMATION

During the HUPO 2016, all participants will have the opportunity to visit the industrial exhibition, which will feature the latest in technology and research. The exhibition is located at the Room 201 (2nd Floor) and Banquet Hall (3rd Floor). Coffee break will be served on the same floor along with the industrial exhibition.

Exhibition Hours

Sunday, September 18, 2016	20:00-21:30 (Welcome Reception)
Monday, September 19, 2016	09:30-17:30
Tuesday, September 20, 2016	09:30-17:30
Wednesday, September 21, 2016	09:30-15:30

Exhibitor Listing

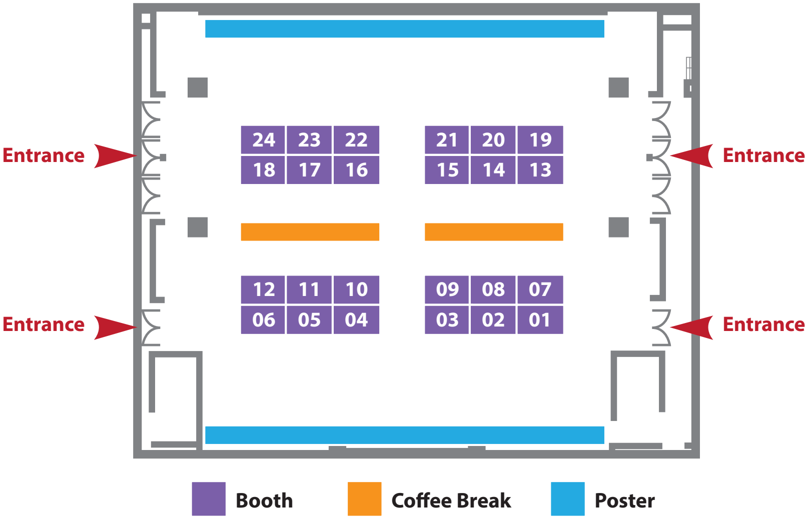
Alphabetical by Exhibitor

Company	Booth #
ACS Publications	22
Agilent Technologies, Inc.	1, 2
Bioinformatics Solutions Inc.	4
Biophysical Society of R.O.C. Human Personalized Omics Profiling Taiwan Proteomics Society	26
Bruker Corporation	18, 24
Cambridge Isotope Laboratories, Inc.	10
Cold Spring Biotech Corp.	32
Column Scientific	28
Denator AB	11
Elsevier Taiwan Bioinformatics Institute	34
Genmall Biotechnology Corporation, LTD	30
HUPO 2017	33
Matrix Science	23

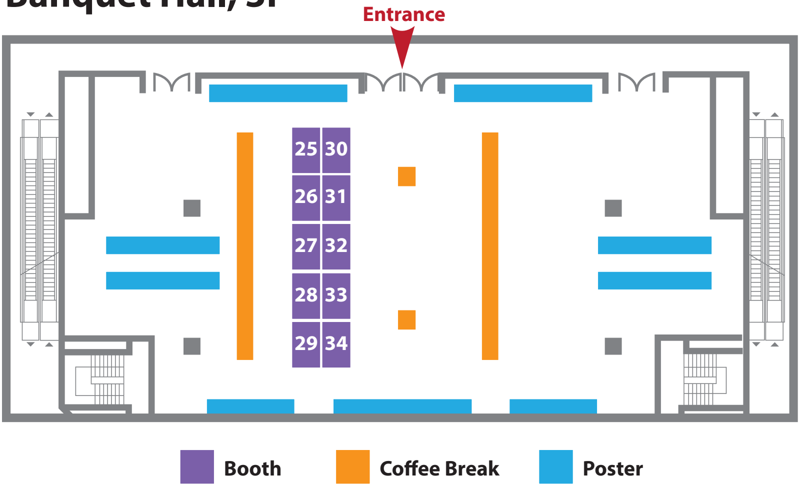
Company	Booth #
Merck Millipore and Sigma-Aldrich	16
Meridigen Biotech Co., Ltd.	9
Pressure BioSciences, Inc.	29
Promega Corporation	3
SCIEX	6, 12
SENGENICS	17
Shimadzu Scientific Instruments (TAIWAN) Co., Ltd.	27
Taiwan Protein Project Si2C	25
Taiwan Society for Mass Spectrometry The Taiwan Society for Biochemistry and Molecular Biology	31
Thermo Fisher Scientific	13-15 & 19-21
Veritomyx, Inc.	5
Waters Corporation	7, 8

Taipei International
Convention Center (TICC)

ROOM 201, 2F



Banquet Hall, 3F



Company Profiles

ACS Publications

ACS Publications, a world leader in scientific publishing, presents you with one of its prestigious publications—Journal of Proteome Research. It is the most cited and comprehensive journal in its field publishing impactful research on protein analysis and function. Visit our booth to learn how to publish with the Journal and enjoy unrivaled publication times and worldwide exposure among your peers in the scientific community.

Agilent Technologies, Inc.

Agilent is a leader in life sciences, diagnostics and applied chemical markets. The company provides laboratories worldwide with instruments, services, consumables, applications and expertise, enabling customers to gain the insights they seek. Agilent's expertise and trusted collaboration give them the highest confidence in our solutions.

Bioinformatics Solutions Inc.

BSI is well-known for their software, PEAKS Studio and recently PEAKS AB. Proteomics software, PEAKS Studio, includes *de novo* sequencing; database and PTM search; homology search, and quantification. Utilizing this development, BSI now provides PEAKS AB Service and Software to provide a solution for all antibody characterization and sequencing needs.

Biophysical Society of R.O.C.

The Biophysical Society of R.O.C., founded in 1995, by Academician Cheng-Wen Wu and a group of biophysics related experts in Taiwan, and it held its very first conference on May 5, 1995 at IBMS of Academia Sinica. The purpose of this society is to promote research and development in the biophysics field in Taiwan.

Bruker Corporation

Bruker is a global technology leader delivering innovative, integrated analytical instrumentation for use in the Food Safety, Environmental analysis, Life Science, Pharmaceutical, Forensic and Clinical Research markets. Bruker Daltonics, a division of the Bruker Corporation, provides cutting edge mass spectrometry solutions which include MALDI-TOF, UHR-QTOF, Ion Traps, FTMS as well as LC and GC systems to solve the most demanding analytical questions presented to these markets today.

Cambridge Isotope Laboratories, Inc.

Cambridge Isotope Laboratories, Inc. is the world leader in the manufacture of stable isotope-labeled (^{13}C, D, ^{15}N, ^{17}O, ^{18}O) compounds used for quantitative MS-based applications. CIL has many products for the proteomic community: PeptiQuant™ MRM Assay Kits, MouseExpress® feed/tissue, SILAC reagents, heavy labeled proteins, INLIGHT™ Glycan Tagging kit and others.

Cold Spring Biotech Corp.

The management team of Cold Spring Biotech Company has engaged in the biotech business for a history of 35 years. Our business started from selling consumables to sell large and accurate instruments and to become a company providing total solutions for the problems encountered by our customers.

Column Scientific

Column Scientific focus on micro/nanoflow liquid phase separation. We provide nanoLC columns to support high resolution, high selectivity and high throughput chromatography and biological discovery. The METER-long column, Separameter, provides extreme peak capacity for single dimensional separation, it is made to push the limit of single-shot proteomics. Our wide range product line includes reversed phase (C18, C8, C4), HILIC, Ion Exchange (SCX, SAX), size exclusion and graphitic columns and trap columns. We also do custom-packing to satisfy your unique needs.

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Heat stabilization is a revolutionary sample preservation technique that stops degradation and biological change immediately and permanently. It enables accurate analysis and quantification of unstable protein biomarkers such as phosphorylations, endogenous peptides and small molecules. It ensures quality and standardization of sample collection, ensuring more precise, reliable data from your proteomics research.

Elsevier

Elsevier is a world-leading provider of information solutions that help you make better decisions, deliver better care, and sometimes make groundbreaking discoveries in science, health, and technology. We provide web-based, digital solutions — among them ScienceDirect, Scopus, Evolve, Knovel, Reaxys and ClinicalKey — and publish over 2,500 journals and more than 33,000 book titles.

Genmall Biotechnology Corporation, LTD

Genmall Biotechnology Corporation, LTD was established in June, 2007. It leads by an outstanding company of Life Science, with experienced marketing sales and proficient supportive groups. It mainly focuses on basic research equipments, reagents, and software. Genmall products include full sets of Genomics, Proteomics, Centrifuge, Autoclave, Pipettes, and other instruments to provide "Total Solution" to our customers.

Human Personalized Omics Profiling

The hPOP (Human Personalized Omics Profiling) project is designed to study the variance of molecular markers across a large number of participants. Recent advances in high throughput technologies allow profiling of thousands of analytes within a single experiment.

HUPO 2017

BSPR and EuPA are delighted to welcome you to the 16th Annual World Congress of HUPO to be held in Dublin 17-20th September 2017.
We are looking forward to providing you with a superb environment in which to present, discuss and advance your proteomic research.
Please visit www.hupo2017.ie

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Get closer to your raw data with Mascot Distiller, giving direct access to all popular file formats for peak picking, de novo sequencing, quantitation, and more.

Merck Millipore and Sigma-Aldrich

Merck Millipore and Sigma-Aldrich have come together as the life science business of Merck KGaA, Darmstadt, Germany. With a portfolio spanning more than 300,000 products, our company is committed to solving the toughest problems in life science by collaborating with the global scientific community. For more information, visit www.merckmillipore.com and www.sigma-aldrich.com

Meridigen Biotech Co., Ltd.

Meridigen Biotech co. was founded in 2011. With sustainability being the core value, we are a company based in Taiwan yet aim for world-class. Committed to mesenchymal stem cells (MSCs) research and drug development, we strive to manufacture MSCs drugs that live up to PIC/S GMP standards. Meridigen focuses on stem cell drug development as well as diagnostic techniques and drug screening platform through partnerships.

Pressure BioSciences, Inc.

Pressure BioSciences, Inc. (“PBI”) (OTCQB: PBIO) focuses on the development and sale of proprietary laboratory instrumentation and consumables based on Pressure Cycling Technology (“PCT”). PCT is a patented enabling technology platform that uses cycles of hydrostatic pressure between ambient and ultra-high levels for biomarker discovery, enhanced protein digestion, and other research applications.

Promega Corporation

Promega is a global leader in providing innovative solutions and technical support to life scientists in academic, industrial and government settings. We are with a portfolio of more than 3,000 products covering the fields of genomics, protein analysis and expression, cellular analysis, drug discovery and genetic identity.

SCIEX

SCIEX is dedicated to placing the power of life-changing answers into the hands of those who care, everywhere. We provide integrated, reliable analytical tools to advance scientific understanding and safeguard health. SCIEX broad portfolio of scientific analytical tools includes innovative instrument systems, intuitive software, pre-packaged methods and chemistry reagents.

SENGENICS

Sengenics flagship technology is the patented Immunome™ auto-antibody profiling platform which was spun out from research that was commercialised as a joint collaboration between the University of Oxford and the University of Cambridge in 1996. The Immunome™ protein array can be used for understanding the role the immune system plays in cancer and autoimmune diseases. It can also be used to model human infections, response to drugs and external stresses.

Shimadzu Scientific Instruments (TAIWAN) Co., Ltd.

Shimadzu, based on "Contributing to Society through Science and Technology", continues to develop all our businesses more than 140 years since 1875. We offer robust and high performance analytical and measuring instruments including UV-Vis, FTIR, TOC, Particle Sizer, Microchip Electrophoresis, LC, GC and Mass spectrometry, such as LC-Q/QQQ, GC-Q/QQQ, ICP-OES/MS, MALDI-TOF/TOF systems.

Si2C

Si2C is the only Taiwan government-funded accelerator for drug and medical device development from academia to commercialization. We provide milestone-based seed funding for academics and startups to facilitate the projects towards later stages with multi-function to add value to our projects, such as IP/regulatory strategy, business development and project management.

Taiwan Bioinformatics Institute

Bioinformatics Core Facility for Translational Medicine and Biotechnology Development (TMBD Bioinformatics Core) of TBI (Taiwan Bioinformatics Institute) supports biomedical research and translational medicine in Taiwan through providing state-of-the-art bioinformatics services including on-line bioinformatics tools and databases as well as customized data analysis services, especially in high throughput omics technology applications.

Taiwan Protein Project

Taiwan Protein Project (TPP), by supporting cutting edge research in academia, creating a bridge between academia and the industry, and supporting the building of protein research facilities, aims to create a sustainable and mutually beneficial platform for academia-industry collaboration, which in turn will lead Taiwan into the future.

Taiwan Proteomics Society

Taiwan Proteomics Society (TPS) was founded in 2003. The main goal of this society is to raise awareness and promote the importance of the protein research in Taiwan. At the same time, the society wishes to establish fundamental education in protein study at the university level.

Taiwan Society for Mass Spectrometry

The Taiwan Society for Mass Spectrometry (TSMS) has been established to promote and foster the developments in the mass spectrometry field in Taiwan. Mass spectrometry is an important scientific technique enabling identification of molecules in variety of samples, including biological, environmental, and industrial matrices.

The Taiwan Society for Biochemistry and Molecular Biology

The Taiwan Society for Biochemistry and Molecular Biology (TSBMB) was established in 1970, joint by IUBMB, FAOBMB, and major research investigators in Taiwan.
Annual TSBMB Autumn Camp happens every fall, for more information on TSBMB and to become a member, please visit http://www.tsbmb.org.tw/html.
TSBMB welcomes you to HUPO 2016 World Congress in the most beautiful island in Pacific Ocean, Formosa, Taiwan.

Thermo Fisher Scientific

Thermo Fisher Scientific is the world leader in serving science. Through our Thermo Scientific brand, we help customers accelerate innovation with solutions for the world's proteomics community. With applications that span mass spectrometry based proteomics and protein analysis– we provide a broad range of products and services supporting leading edge biological research from disease and biomarker discovery, drug development and clinical research.

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PeakInvestigator™ software deconvolves overlapped MS data, increasing MS resolution by 3-4X and revealing critical hidden information with large sensitivity and precision improvements. More accurate and complete information accelerates correct biomolecular IDs. PeakInvestigator works with profile data from Iontrap, TOF, Orbitrap and FTICR analyzers from 3,000-3,000,000+ resolution. See what you're missing!

Waters Corporation

Waters Corporation, the premium brand in the analytical instruments industry, creates business advantages for laboratory-dependent organizations by delivering practical and sustainable scientific innovation. Waters helps customers make profound discoveries, optimize laboratory operations, deliver product performance, and ensure regulatory compliance within the pharmaceutical, health sciences, food and beverage, environmental and chemical materials industries by providing the tools to improve the quality of today's science and explore the infinite possibilities of tomorrow's.

INFORMATION FOR INVITED SPEAKERS AND PRESENTERS

2016 TAIPEI
HUPO

INFORMATION FOR INVITED SPEAKERS AND PRESENTERS

Speaker Ready Room

An LCD projector and laptop for MS PowerPoint presentations are provided in all session rooms. All invited speakers as well as Oral Abstract Presenters are required to check, change and upload your presentation in **Room 103 on the 1st floor** at least **half day before the start of the session.** The speaker ready room will be available every day throughout the Congress during the following service hours. Congress staffs will be of assistance anytime.

Sunday, September 18, 2016	08:00-19:30
Monday, September 19, 2016	08:00-17:30
Tuesday, September 20, 2016	08:00-17:30
Wednesday, September 21, 2016	08:00-16:00

No File Submissions will be Accepted in the Session Rooms

Computers are available to preview and upload presentations. Presenters should make sure all fonts appear as expected and all sound/video clips are working properly. The final version must be submitted to the Speaker Ready Room, no presentation submission will be accepted in the Session Rooms.

Poster Sessions

Posters will be displayed for one full day only in the Room 201 and Banquet Hall. Each poster board is marked with the number assigned to each abstract, which can be found in the final program book. The time set for poster mounting and removal shall be considered. The presence of the authors on the given presentation date is a MUST for discussions and questions. All posters left beyond the given removal times will be disposed of without notifications.

Poster Presentation (Author Stand By Time)

Presentation Date	Poster #	Room	Mounting	Removal
September 19	MP04, 06 & PhD Abstract Competition Finalist	**Room 201 (2F)**	**08:15-09:30**	**16:30-17:00**
	MP01, 02, 03, 05, 07, 08, 09, 10, 11, 12	**Banquet Hall (3F)**		
September 20	TP03, 04, 05, 06, 08, 09 & PhD Abstract Competition Finalist	**Room 201 (2F)**	**08:15-09:30**	**16:30-17:00**
	TP01, 02, 07, 10	**Banquet Hall (3F)**		
September 21	WP01, 02, 03, 04, 05, 07 & PhD Abstract Competition Finalist	**Room 201 (2F)**	**08:15-09:30**	**15:00-15:30**
	WP06, 08, 09, 10, 11, 12, 13, 14, 15, 16	**Banquet Hall (3F)**		

Presentation Date	Presentation Time
September 19	EVEN Poster #: 09:30-10:30 ODD Poster #: 15:30-16:30
September 20	EVEN Poster #: 09:30-10:30 ODD Poster #: 15:30-16:30
September 21	EVEN Poster #: 09:30-10:30 ODD Poster #: 12:30-13:30

❗ PhD Abstract Competition Finalist Presentation Time: 15:30-16:30, Tuesday, September 20.

All Oral Presenters have been invited to prepare a Poster in addition to their Oral Presentations. Poster Presentations for Oral Presenters will be labeled with their Oral Presentation number (e.g. MO01-001)

SOCIAL PROGRAMS

2016 TAIPEI HUPO

SOCIAL PROGRAMS

All registered participants are cordially invited to the following programs.

Opening Plenary Session

Date: Sunday, September 18, 2016
Time: 18:00-20:00
Venue: Plenary Hall, 3F, TICC
Dress Code: Business Casual

Welcome Reception

Date: Sunday, September 18, 2016
Time: 20:00-21:30
Venue: Room 201, 2F, TICC
Banquet Hall, 3F, TICC
Dress Code: Business Casual

Supported by:
SCIEX

Invited Speaker Dinner (by invitation only)

Date: Monday, September 19, 2016
Time: 19:30-21:30
Venue: Taipei World Trade Center Club, 33rd Floor,
333 Keelung Rd, Sec. 1, Taipei City, Taiwan
(3 walking minutes from the conference venue)
Dress Code: Business Casual

Supported by:
ASPEC
advancing science

HUPO Congress Night – Formosa Night (ticket event)

Date: Tuesday, September 20, 2016
Time: 18:00-21:00
Venue: 14 Floor, Taipei New Horizon
Dress Code: Casual
Transportation: Shuttle Bus will be provided.
- Assembly Time: 17:30-17:40
- Assembly Place: Lobby, TICC
- Departure Time: 17:45

Supported by:
ThermoFisher
SCIENTIFIC

Closing Plenary Session with Award Lectures

Date: Wednesday, September 21, 2016
Time: 15:30-17:30
Venue: Plenary Hall, 3F, TICC
Dress Code: Business Casual

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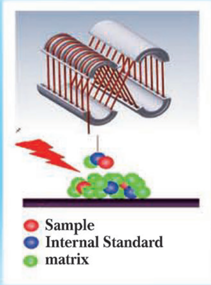

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SCIENTIFIC PROGRAMS

2016 TAIPEI HUPO

DAILY PROGRAM

SUNDAY, SEPTEMBER 18, 2016

07:30-19:30	**Registration (Lobby, 1F)**
07:30-19:30	**Speaker Ready Room (Room 103, 1F)**
08:00-15:30	HPP Investigator's Meeting (Room 101 B, 1F)
08:30-17:30	Bioinformatics Hub (Room 203, 2F)
09:00-15:00	Clinical Day* (Room 101 C, 1F)
09:00-15:30	Mentoring Day* (Room 101 D, 1F)
	Education Day* (Room 101 A, 1F)
09:00-15:30	Technology Day (Room 102, 1F)
10:20-12:30	C-HPP Session (Room 202 A, 2F)
13:20-15:20	Cancer Cluster Group (Room 101 B, 1F)
	IVTT Cluster Group (Room 202 A, 2F)
	Reproductive Disease (South Lounge, 3F)
15:45-17:45	HUPO Council Meeting (Room 401, 4F)
18:00-18:30	Opining Ceremony (Plenary Hall, 3F)
18:30-19:15	Plenary Session 1 (Plenary Hall, 3F)
19:15-20:00	Plenary Session 2 (Plenary Hall, 3F)
20:00-21:30	Welcome Reception (Room 201, 2F & Banquet Hall, 3F)

** Ticketed Session*

Registration Open	**07:30-19:30 @Lobby, 1F**
Speaker Ready Room Open	**07:30-19:30 @103, 1F**

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

Bioinformatics Hub

09:00-15:30 **Room 101 A (1F)**

Education Day - Refresher on Biology & Medicine (*Ticketed Session)*

MORNING COFFEE AND LUNCH PROVIDED

Chairs: **Garry Corthals,** Netherlands; **Tove Alm,** Sweden

9:00	**Intro to Precision Proteomics** *Garry Corthals, University of Amsterdam, Netherlands*
9:15	**Molecular Mechanisms / Mass Cytometry & Tissue Analysis** *Bernd Bodenmiller, University of Zurich, Switzerland*
9:45	**Protein & Peptide Arrays for Autoimmunity Profiling** *Arash Zandian, Scilifelab, KTH Royal Institute of Technology, Sweden*
10:15	**Affinity Proteomics** *Jochen Schwenk, Scilifelab, KTH Royal Institute of Technology, Sweden*
10:45	**Coffee Break**
11:00	**Food & Nutrition for Health Benefits** *Loïc Dayon, Nestlé Institute of Health Sciences SA, Switzerland*
11:30	**Precision Analysis by MS** *Pengyuan Yang, Fudan University, China*
12:00	**Food & Nutrition** *Paola Roncada, Istituto Sperimentale Italiano Lazzaro Spallanzani, Italy*
12:30	**Lunch Break**
13:30	**Glyco as Nutrient Sensor** *Gerald Hart, Johns Hopkins University, USA*
14:00	**Precision Analytics, Positional Proteomics Technologies** *Christopher Overall, University of British Columbia, Canada*
14:30	**Aging** *Richard Semba, Johns Hopkins University, USA*
15:00	**Recap, Question & Feedback**

08:00-15:30 HPP Investigator's Meeting (B/D HPP Session & C-HPP Session)

MORNING COFFEE AND LUNCH PROVIDED

08:00-10:00 HPP Plenary Session I — Room 101 B (1F)

Chairs: **Young-Ki Paik,** South Korea; **Fernando Corrales,** Spain

8:00 **HPP Overview**
C-HPP: *YK Paik, CM Overall, L Lane*
B/D-HPP: *JE van Eyk, FJ Corrales*
Resource Pillars: *EW Deutsch, E Lundberg, S Weintraub*

9:00 **HPP Plenary Lecture 1: Genomics for HPP**
Michael Snyder, Stanford University, USA

9:30 **HPP Plenary Lecture 2: Emerging Tech - Small ORF Analysis**
Alan Saghatelian, The Salk Institute for Biological Studies, USA

10:00 **Coffee Break**

10:20-12:30 B/D-HPP Session 1 — Room 101 B (1F)

10:20 **Extreme Conditions Proteomics**
Eugene Nikolaev, Russian Academy of Sciences, Russia

10:35 **Glycoproteomics**
Hisashi Narimatsu, National Institute of Advanced Industrial Science and Technology, Japan

10:50 **Brain Proteome Project**
Peter Nilsson, SciLifeLab, KTH Royal Institute of Technology, Sweden

11:05 **Cardiovascular Initiative**
Maggie Lam, University of California, Los Angeles, USA
PeiPei Ping, University of California, Los Angeles, USA

11:20 **Plasma Initiative**
Jochen Schwenk, SciLifeLab, KTH Royal Institute of Technology, Sweden

11:35 **Food and Nutrition Initiative**
Paola Roncada, Istituto Sperimentale Italiano Lazzaro Spallanzani, Italy

11:50 **Diabetes Initiative**
Loïc Dayon, Nestlé Institute of Health Sciences SA, Switzerland

12:05 **Mitochondria Initiative**
Mauro Fasano, University of Insubria, Italy

10:20-12:30 C-HPP Session 1 — Room 202 A (2F)

10:20 **The C-HPP Top 50 MP Marathon Challenge with Cluster Collaboration**
Christopher Overall, University British Columbia, Canada

10:50 **Progress Reports on Missing Proteins**

Chr 3 *Toshihide Nishimura, St. Marianna University, Kanagawa, Japan*
Chr 10 *Josh LaBaer, Arizona State University, USA*
Chr 15 *Gilberto Domont, Universidade Federal do Rio de Janeiro, Brazil*
Chr 18 *Stanislav Naryzhny, Institute of Biomedical Chemistry, Russia*
Chr 19 *Gyorgy Marko-Varga, Lund University, Sweden*
Chr 22 *Akihlesh Pandey, Johns Hopkins University, USA*
Chr X *Tadashi Yamamoto, Niigata University, Japan*
Chr Y *Ghasem Hosseini Salekdeh, Royan Institute, Iran*

12:30-15:20 HPP Plenary Session II - Joint Cluster Group Meeting for C-HPP and B/D-HPP **Room 101 B (1F)**

12:30 **Lunch Break**
13:10 **Introduction: What is "Cluster Collaboration?**
Young-Ki Paik, Yonsei University, South Korea
13:30 **Break-out Session (A, B, C Groups)**

13:30 **A. Cancer Cluster Group** **Room 101 B (1F)**
Led by Siqi Liu, Ed Nice & Hui Zhang
Moonshot Project & Int'l Cancer Proteomics Collaboration
Mark Baker (HUPO President), Phil Robinson (ProCan) and Jerry Lee (NCI Office)
Introduction of B/D-HPP Cancer/CPTAC initiative
Hui Zhang and Henry Rodriguez (Coordinators)
Discussion on the Strategic Points

13:30 **B. IVTT Cluster Group** **Room 202 A (2F)**
Led by Gyorgy Marko-Varga, Joshua LaBaer
Discussion on the Strategic Points

13:30 **C. Reproductive Disease** **South Lounge (3F)**
Led by Charles Pineau & Ghasem Hosseini Salekdeh
Discussion on the Strategic Points

09:00-15:00 **Room 101 C (1F)**

Clinical Day - Clinical Proteomics for Precision Medicine (Ticketed Session)
MORNING COFFEE AND LUNCH PROVIDED

Chairs: **Christoph Borchers,** Canada; **Josh LaBaer,** USA
9:00 **Chairs' Intro**
9:15 **Making Proteomics Ready for the Clinic - Multiplexed MRM-based Protein Quantitation in Human Plasma Using Two Different Stable Isotope Labeled Peptides for Calibration**
Christoph Borchers, University of Victoria- Genome BC Proteomics Centre, Canada

9:45	**Current and Future Applications of ImmunoMALDI MS in the Clinical Laboratory** *Michael Chen, McGill University, Canada*
10:15	**Preterm Versus New Born Plasma: Proteins as an Indicator for Organ Maturity** *Oliver Poetz, University of Tübingen, Germany*
10:45	**Coffee Break**
11:00	**Proteomics as Diagnostic Tool for Platelet Function** *Albert Sickmann, Leibniz-institut für Analytische Wissenschaften – ISAS – e.V., Germany*
11:30	**Cell Free Methods for Producing Protein Microarrays** *Josh LaBaer, Biodesign Institute, USA*
12:30	**Lunch Break**
13:30	**From Cancer Biomarker Discovery to Clinical Application: a Long and Winding Road** *Tesshi Yamada, National Cancer Center Research Institute, Japan*
14:00	**Taiwan Biobank for the Health of Next Generation** *Chen-Yang Shen, Academia Sinica, Taiwan*
14:30	**Lessons Learned at CPTAC NIH/NCI – A Perspective in Clinical Proteomics Research** *Henry Rodriguez, National Cancer Institute, National Institutes of Health, USA*

09:00-15:30 **Room 101 D (1F)**

Mentoring Day (Ticketed Session)

MORNING COFFEE AND LUNCH PROVIDED

Chairs: **Justyna Fert-Bober,** USA; **Burcu Ayoglu,** USA; **Ferdinando Cerciello,** Switzerland

9:00	**Opening: Self Introduction**
9:15	**"How Did I Start My Lab" Two Representatives – Typical Academia and Maybe Coming Back to Academia (20 min + 10 min Questions from Audience)** *Ruedi Aebersold, ETH Zurich, Switzerland*
9:45	**How to Cope with Various career Pressures that Might Affect the Quality of Your Science** *Paola Roncada, Istituto Sperimentale Italiano Lazzaro Spallanzani, Italy* *Peipei Ping, University of California, Los Angeles, USA*
10:45	**Coffee Break**
11:00	**How to Write a Grant Proposal?** *David Herrington, Wake Forest School of Medicine, USA*

11:30	**Building Relationship with Industrial Vendors**
	Michael MacCoss, University of Washington, USA
	John Yates, The Scripps Research Institute, USA
	Christine Miller, Agilent Technologies, USA
	Christine Hunter, Sciex, USA
	Ken Miller, Thermo Fisher Scientific, USA
12:00	**Elevator Speech- Power Point Presentation – Youtube Movie**
12:30	**Lunch Break**
13:30	**Conflict-Resolution Exercises:**
	The Attendants Will Train Their Interpersonal, Scientific, and Technical Skills Necessary to Address Various Issues in Scientific Rigor. Judge a Situation
	Panel Members:
	Ruedi Aebersold, Paola Roncada, Peipei Ping, David Herrington, Michael MacCoss, John Yates, Christine Miller, Jennifer Van Eyk

09:00-15:30 **Room 102 (1F)**

Technology Day - Emerging Technologies

MORNING COFFEE PROVIDED

Chairs:	**Robert Moritz,** USA**; Yu-Ju Chen,** Taiwan
9:00	**Chair's Introduction**
9:15	**New Approaches to Study Protein-Protein Interactions**
	John Yates, The Scripps Research Institute, USA
10:00	**Glycoanalysis: Are We There Yet?**
	Nicolle Packer, Macquarie University, Australia
10:45	**Coffee Break**
11:00	**The "Why", "How" and Future of Single Cell Proteomic Approaches**
	Bernd Bodenmiller, University of Zurich, Switzerland
11:40	**Towards the Structure and Function of the Modular Proteome**
	Ruedi Aebersold, ETH Zurich, Switzerland
12:30	**Lunch Break**
13:30	**Ultralong Hybrid Silica Monolithic Columns for Proteome Analysis**
	LiHua Zhang, Chinese Academy of Sciences, China
14:10	**Reinventing Hyphenated Tandem Mass Spectrometry: Building a Novel Tool for Characterization of Intact Proteins and Protein Complexes**
	Roman Zubarev, Karolinska Institutet, Sweden
14:50	**Instrumentation and Methods for the Identification and/or Sequence Analysis of Intact Proteins on a Chromatographic Time-Scale**
	Donald Hunt, University of Virginia, USA

15:45-17:45 **Room 401 (4F)**

HUPO Council Meeting

18:00-18:30 **Plenary Hall (3F)**

Opening Ceremony

18:30-19:15 **Plenary Hall (3F)**

Opening Plenary Session

Chair: **Mark Baker,** Australia

18:30 **PL 01**

Managing Health and Understanding Disease Using Big Data

Michael Snyder, Stanford University, USA

19:15-20:00 **Plenary Hall (3F)**

Opening Plenary Session

Chair: **Ming-Daw Tsai,** Taiwan

19:15 **PL 02**

Precision Lung Cancer Therapy: Current and Beyond

Pan-Chyr Yang, National Taiwan University, Taiwan

20:00-21:30 **Room 201 (2F) & Banquet Hall (3F)**

Welcome Reception

DAILY PROGRAM

MONDAY, SEPTEMBER 19, 2016

07:30-17:30	**Registration (Lobby, 1F)**
07:30-17:30	**Speaker Ready Room (Room 103, 1F)**
09:30-17:30	**Exhibition & Poster (Room 201, 2F and Banquet Hall, 3F)**
07:30-08:30	Neurodegenerative Disease Cluster Group (Room 102, 1F)
07:30-08:30	Membrane Proteome Cluster Group (Room 203, 2F)
08:30-09:15	Plenary Session 3 (Plenary Hall, 3F)
08:30-17:30	Bioinformatics Hub (Room 203, 2F)
09:30-10:30	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
10:30-12:15	[M01] Cancer & Translational Proteomics (Plenary Hall, 3F)
	[M02] Innovative MS Techniques for Global & Targeted Proteomics (Room 101 AB, 1F)
	[M03] Chemical Probes & Chemical Biology for Proteomics (Room 101 C, 1F)
	[M04] Metabolomics & Metabolic Disorders (Room 101 D, 1F)
	[M05] Brain & EyeOME: Connecting two images (Room 102, 1F)
12:30-13:30	Industry Seminar supported by SCIEX (Room 101 C, 1F)
	Industry Seminar supported by Waters Corporation (South Lounge, 3F)
	Industry Seminar supported by Thermo Fisher Scientific (North Lounge, 3F)
	Industry Seminar supported by Thermo Fisher Scientific (Joy Lounge, 4F)
	Industry Seminar supported by Agilent Technologies, Inc. (Elegance Lounge, 4F)
	Industry Seminar supported by Bruker Corporation (VIP Room, 4F)
13:45-15:30	[M06] Immunity, Inflammation & Infectious Diseases (Plenary Hall, 3F)
	[M07] BioInformatics & Computational Proteomics (Room 101 AB, 1F)
	[M08] PTM Crosstalks I - Phosphoproteomics, Kinome & OGlcNAc (Room 101 C, 1F)
	[M09] New Technological Advancements (Room 101 D, 1F)
	[M10] Diabetes and Cardiovascular Diseases: Energy Balance in Disease Phenotypes (Room 102, 1F)
15:30-16:30	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
16:45-17:30	Plenary Session 4 (Plenary Hall, 3F)
17:30-18:15	Plenary Session 5 (Plenary Hall, 3F)
18:15-19:15	HUPO General Assembly (Room 101 AB, 1F)
19:30-21:30	Invited Speaker Dinner* (Room A, 33F, Taipei World Trade Center Club)

** by Invitation Only*

Registration Open **07:30-17:30 @Lobby, 1F**
Speaker Ready Room Open **07:30-17:30 @103, 1F**

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

Neurodegenerative Disease Cluster Group, JS Yoo, A Urbani

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

Membrane Proteome Cluster Group, D Figeys, YJ Chen

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

Bioinformatics Hub

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

Plenary Session 3

Chair: **Robert Moritz,** USA

8:30 **PL 03**

The Proteome in Context

Ruedi Aebersold, ETH Zurich, Switzerland

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

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

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

M01: Cancer & Translational Proteomics

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

10:30 **MK-01**

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

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

10:55 **MK-02**

Verification of Oral Cancer Biomarkers and Their Translation to Clinical Settings

Jau-Song Yu, Chang Gung University, Taiwan

11:20 **MO01-001**

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

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

11:35 **MO01-002**

Proteomic Multimarker Panel Complements CA19-9 Insufficiency in the Diagnosis of Pancreatic Ductal Adenocarcinoma

Youngsoo Kim, Seoul National University, South Korea

11:50 **MO01-003**

Pathology-Driven Comprehensive Proteomic Profiling of the Prostate Cancer Tumor Microenvironment

Stephen Pennington, UCD Conway Institute of Biomolecular and Biomedical Research, Ireland

11:55 **MO01-004**

Tissue Derived Neo-Antigens for T Cell-Based Cancer Immunotherapy

Michal Bassani, UNIL/CHUV, Switzerland

12:00 **MO01-005**

LinkedOmics: Discovering Associations Between Genomic, Proteomic and Clinical Attributes in Human Cancer

Jing Wang, Vanderbilt University Medical Center, USA

10:30-12:15 **Room 101 AB (1F)**

M02: Innovative MS Techniques for Global & Targeted Proteomics

Chairs: **Jesper Olsen,** Denmark; **Michael MacCoss,** USA

10:30 **MK-03**

Comprehensive Analysis of Human Proteomes with Similar Depth as RNA-Seq

Jesper Olsen, University of Copenhagen, Denmark

10:55 **MK-04**

Comprehensive DIA with High Precursor Selectivity: How Can We Have Our Cake and Eat It Too?

Michael MacCoss, University of Washington, USA

11:20 **MO02-001**

MS1 Based Quantification Optimization on DIA Methods on a Quadrupole-Orbitrap Mass Spectrometer

Yue Xuan, Thermo Fisher Scientific, Germany

11:35 **MO02-002**

Digging Deeper into Large SWATH MS1 Windows Using Gas Phase Fractionation SWATH-MS

Mark Molloy, Australian Proteome Analysis Facility, Australia

11:50 **MO02-003**

iST: Sample Preparation for High Throughput Clinical Proteomics- A Novel, Fast, Sensitive and Reproducible Sample Preparation for MS-based proteomics-

Garwin Pichler, Preomics GmbH, Germany

11:55 **MO02-004**

All MS/MS ions Monitoring Acquired by Data-Dependent Acquisition without Dynamic Exclusion: A New Concept for In-Depth Protein Quantification

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

12:00 **MO02-005**

Analyses of Intact Proteins by LC-FT-ICR Mass Spectrometry at 21 Tesla

Lissa C. Anderson, National High Magnetic Field Laboratory, USA

10:30-12:15 **Room 101 C (1F)**

M03: Chemical Probes & Chemical Biology for Proteomics

Chairs: **Alice Y. Ting,** USA

10:30 **MK-05**

Spatially-Resolved Proteomic Mapping in Living Cells via Enzyme-Mediated Proximity Labeling

Alice Ting, Stanford University, USA

10:55 **MK-06**

Drug Resistance Assessed by Multi-Proteomics Approaches

Simone Lemeer, Utrecht University, Netherlands

11:20 **MO03-001**

Quantitative Activity-Based Profiling of Kinase Inhibitor Binding and Selectivity on Protein Microarrays Containing >300 Human Protein Kinases

Jonathan Blackburn, University of Cape Town, South Africa

11:35 **MO03-002**

Novel Hybrid Platform for Rapid, Highly Sensitive and Specific Quantification of Proteins and Their Post-Translational Modifications

Liqi Xie, Fudan University, China

11:45 **MO03-003**

A Highly Sensitive Probe for Fucosylated Glycans for Biomarker Discovery

Naoyuki Taniguchi, RIKEN, Japan

11:55 **MO03-004**

A Novel Set of Isobaric Peptide Labeling Eeagent Enabled Proteomic Quantification over 10 Different Samples

Yan Ren, BGI-Shenzhen, China

12:00 **MO03-005**

TMTcalibrator™ Enhances Biomarker Discovery in Peripheral Fluids

Hui-Chung Liang, Proteome Sciences Plc, United Kingdom

10:30-12:15 **Room 101 D (1F)**

M04: Metabolomics & Metabolic Disorders

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

10:30-12:15 **Room 102 (1F)**

M05: Brain & EyeOME: Connecting Two Images

Chairs:	**Peter Nilsson,** Sweden; **Richard Semba,** USA
10:30	**MK-09** **Neuroproteomic Profiling of Proteins and Autoantibody Repertoires in Plasma and CSF** *Peter Nilsson, SciLifeLab, KTH Royal Institute of Technology, Sweden*

10:55 **MK-10**

Proteomic Approaches to Understanding Age-Related Macular Degeneration

Richard Semba, Johns Hopkins University, USA

11:20 **MO05-001**

Proteomics Reveals Individual Patient Responses to Therapeutic Treatment for Dry Eye

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

11:35 **MO05-002**

A Comprehensive Inter-Grade Proteomic Analysis of Serum, CSF and Tissue in Glioma

Manubhai Kp, Indian Institute of Technology Bombay, India

11:50 **MO05-003**

Building a Comprehensive Chick Retinal Proteome Dataset by Liquid Chromatography (LC) Fractionation for Tandem MS and SWATH Analysis

Hu Xiao, Hong Kong Polytechnic University, China

11:55 **MO05-004**

Do Platelet-Derived Extracellular Vesicles Contain Specific Biomarkers Allowing for Early Diagnostics of Alzheimer's Disease?

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

12:00 **MO05-005**

Generating a Proteomic Profile of Neurogenesis, through a Quantitative Comparison of Neuroepithelial and Radial Glial Like Stem Cells

Shaun Garnett, University of Cape Town, South Africa

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

M06: Immunity, Inflammation & Infectious Diseases

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

13:45 **MK-11**

Proteomics in Viral Infectious Diseases: Global and Targeted Functional Insights into the Virus-Host Interface

Ileana Cristea, Princeton University, USA

14:10 **MK-12**

Immunotherapy of Cancer; An Overview and Recent Results

Donald Hunt, University of Virginia, USA

14:35 **MO06-001**

The Human Immunopeptidome: Can Big Data Improve the Precision of Immunotherapy?

Anthony Purcell, Monash University, Australia

14:50 **MO06-002**

Quantitative Host-Pathogen Protein Network Analysis Using Data-Independent Acquisition Mass Spectrometry Analysis

Johan Malmström, Lund University, Sweden

15:00 **MO06-003**

Proteomic of Host-Microbiome Interactions in a Pediatric Inflammatory Bowel Disease Inception Cohort to Identify Protein Biomarkers

Daniel Figeys, University of Ottawa, Canada

15:10 **MO06-004**

Challenges of Biomarker Discovery in Developing Countries: A Proteomics Investigation to Identify Unique Disease Signatures in Infectious Diseases

Sanjeeva Srivastava, Indian Institute of Technology Bombay, India

15:15 **MO06-005**

Robust Temporal Profiling of GRB2 Protein Complexes in Primary T Lymphocytes Using SWATH Mass Spectrometry

Etienne Caron, ETH Zurich, Switzerland

13:45-15:30 **Room 101 AB (1F)**

M07: BioInformatics & Computational Proteomics

Chairs: **Lennart Martens,** Belgium; **Nuno Bandeira,** USA

13:45 **MK-13**

More Power and More Depth: New Tools for Proteomics Data Processing

Lennart Martens, VIB UGhent, Belgium

14:10 **MK-14**

Exploring the Diversity in the Human Proteome

Nuno Bandeira, University of California, San Diego, USA

14:35 **MO07-001**

Investigating the Basic Assumptions in Protein Abundance Estimation Using SWATH-MS Data

Wenguang Shao, ETH Zurich, Switzerland

14:50 **MO07-002**

Reactome - Interactive Pathway Analysis for Proteomics

Henning Hermjakob, EMBL-EBI, United Kingdom

15:05 **MO07-003**

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

Andrew Webb, The Walter and Eliza Hall Institute, Australia

15:10 **MO07-004**

neXtProt in the Context of Human Proteomics Projects

Lydie Lane, Swiss Institute of Bioinformatics, Switzerland

15:15 **MO07-005**

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

Eu-Yu Lai, Academia Sinica, Taiwan

13:45-15:30 **Room 101 C (1F)**

M08: PTM Crosstalks I - Phosphoproteomics, Kinome & OGlcNAc

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

13:45 **MK-15**

Modulation of Multiple PTMs Upon Brief Cellular Stimulation

Martin Larsen, University of Southern Denmark, Denmark

14:10 **MK-16**

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

Gerald Hart, Johns Hopkins University, USA

14:35 **MO08-004**

Profiling Kinome Activities Using Kinase-Specific Substrate Peptides

Naoyuki Sugiyama, Kyoto University, Japan

14:50 **MO08-002**

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

Hsin-Yi Wu, Academia Sinica, Taiwan

15:05 **MO08-003**

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

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

15:10 **MO08-005**

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

Mats Borén, Denator, Sweden

13:45-15:30 **Room 101 D (1F)**

M09: New Technological Advancements

Chairs: **Neil Kelleher,** USA; **Kathryn Lilley,** United Kingdom

13:45 **MK-17**

Proteomics 2.0: Recent Advances in Top Down Proteomics

Neil Kelleher, Northwestern University, USA

14:10 **MK-18**

Capturing the Dynamic Spatial Proteome

Kathryn Lilley, University of Cambridge, United Kingdom

14:35 **MO09-001**

Structural Characterization of Protein Phosphorylation and Antibody Complexes by Top/Middle-Down Mass Spectrometry

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

14:50 **MO09-002**

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

Melvin Park, Bruker Daltonics, USA

15:05 **MO09-003**

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

Johannes Pc Vissers, Waters Corporation, United Kingdom

15:10 **MO09-004**

ProteusQC™: the Versatile Standard for Bottom-Up Proteomics

Andrew Percy, Cambridge Isotope Laboratories, USA

15:15 **MO09-005**

Sampling of Tissues for Proteomics by Soft Laser Ablation

Hartmut Schlueter, University Medical Center Hamburg-Eppendorf, Germany

13:45-15:30 **Room 102 (1F)**

M10: Diabetes and Cardiovascular Diseases: Energy Balance in Disease Phenotypes

Chairs: **Loïc Dayon,** Switzerland; **Maggie Lam,** USA

13:45 **MK-19**

Proteomic and Metabolic Health Phenotypes in Dietary Clinical Interventions

Loïc Dayon, Nestlé Institute of Health Sciences, Switzerland

14:00 **MK-20**

Proteome Homeostasis and Remodeling in the Stressed Myocardium

Maggie Lam, University of California, Los Angeles, USA

14:15 **MO10-001**

Changes in Protein Expression Patterns in Islets of Langerhans: Implications for Treatment of Children with Obesity and Type 2 Diabetes

Peter Bergsten, Uppsala University, Sweden

14:30 **MO10-002**

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

David Herrington, Wake Forest School of Medicine, USA

14:45 **MO10-003**

Proteomic Analysis of Membranes in Mouse and Human Cardiovascular Tissues

Anthony Gramolini, University of Toronto, Canada

15:00 **MO10-004**

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

Ferheen Baig, King's College London, United Kingdom

15:05 **MO10-005**

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

Kosaku Shinoda, University of California, San Francisco, USA

15:10 **MO10-006**

Protective Effects of GLP-1 Analogues Against Cellular Stress: An *in Vitro* Proteomic Study

Ali Tiss, Dasman Diabetes Institute, Kuwait

15:15 **MO10-007**

Poorly Controlled Diabetes Mellitus is Associated with Decreased Aspirin-Mediated Acetylation of Platelet Cyclooxygenase 1 (COX-1) at Serine 529

Jean-Charles Sanchez, Geneva University, Switzerland

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

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

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

Plenary Session 4

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

16:45 **PL 04**

Proteogenomic Analysis of Cancer: New Opportunities in Cancer Biology and Precision Medicine

Henry Rodriguez, National Cancer Institute, National Institutes of Health, USA

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

Plenary Session 5

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

17:30 **PL 05**

The Phoenix Center and CNHPP

Fuchu He, Beijing Proteome Research Center, China

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

HUPO General Assembly

DAILY PROGRAM

TUESDAY, SEPTEMBER 20, 2016

08:00-17:30	**Registration (Lobby, 1F)**
08:00-17:30	**Speaker Ready Room (Room 103, 1F)**
09:30-17:30	**Exhibition & Poster (Room 201, 2F and Banquet Hall, 3F)**
08:30-09:15	Plenary Session 5 (Plenary Hall, 3F)
08:30-17:30	Bioinformatics Hub (Room 203, 2F)
09:30-10:30	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
10:30-12:15	[T01] Interactomics & Protein Network (Plenary Hall, 3F)
	[T02] Glycoproteomics - Technical Limitations & Prospects (Room 101 AB, 1F)
	[T03] PTM Crosstalks II - Lysine & other Modificomics (Room 101 C, 1F)
	[T04] Imaging Mass Spectrometry (Room 101 D, 1F)
	[T05] Liver & Toxicoproteomics: Metabolism, Drug Transformation & Toxicity (Room 102, 1F)
12:30-13:30	Industry Seminar supported by Bruker Corporation (South Lounge, 3F)
	Industry Seminar supported by SCIEX (North Lounge 3F)
	Industry Seminar supported by Meridigen Biotech Co., Ltd. (Joy Lounge, 4F)
	Industry Seminar supported by Merck Millipore and Sigma-Aldrich (Elegance Lounge, 4F)
	Industry Seminar supported by Thermo Fisher Scientific (VIP Room, 4F)
13:45-15:30	[T06] Antibodies & Protein Arrays (Plenary Hall, 3F)
	[T07] Integrative Glyco(proteo)mics for Glycobiology & Diseases (Room 101 AB, 1F)
	[T08] Proteome Dynamics: Stability, Turnover & Degradomics (Room 101 C, 1F)
	[T09] Spatial & Single Cell Proteomics (Room 101 D, 1F)
	[T10] Protein Standards and Model Organisms: Expanding our Horizons (Room 102, 1F)
15:30-16:30	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
	PhD Abstract Competition (Room 201, 2F)
16:45-17:30	Plenary Session 6 (Plenary Hall, 3F)
18:00-21:00	HUPO Congress Night* (Taipei New Horizon, 14F)

** Ticket Event*

Registration Open **07:30-17:30 @Lobby, 1F**
Speaker Ready Room Open **07:30-17:30 @103, 1F**

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

Bioinformatics Hub

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

Plenary Session 6

Chair: **Gerald Hart,** USA

8:30 **PL 06**

Glycoproteomics – A genetic Approach to Deconstruction and Simplification of Protein Glycosylation

Henrik Clausen, University of Copenhagen, Denmark

09:30-10:30: Networking Break and Poster Viewing *(Even Poster Numbers)*

Room 201 (2F) and Banquet Hall (3F)

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

T01: Interactomics & Protein Network

Chairs: **Jun Qin,** China; **Junmin Peng,** USA

10:30 **TK-01**

Membrane Protein Complexes

Jun Qin, National Center for Protein Sciences, Beijing, China

10:55 **TK-02**

Multilayer Proteomics Approaches to Understanding Common Human Diseases

Junmin Peng, St. Jude Children's Research Hospital, USA

11:20 **TO01-001**

The Regulatory Role of Methylation and Methylation–Phosphorylation Crosstalk in Protein Interaction Networks

Marc Wilkins, University of New South Wales, Australia

11:35 **TO01-002**

Network Analysis Reveals a Dominant Role of Protein-Level Regulation in Coordinating Gene Functions

Bing Zhang, Vanderbilt University Medical Center, USA

11:50 **TO01-003**

Profiling the Phosphotyrosine Interactome of Receptor Tyrosine Kinases

Runsheng Zheng, Technische Universitaet Muenchen, Germany

11:55 **TO01-004**

Phylointeractomics Reconstructs Functional Evolution of Protein Binding

Dennis Kappei, Cancer Science Institute of Singapore, Singapore

12:00 **TO01-005**

Determining Network Topology, Distance Restraints and Activation Markers from Endogenous Protein Complexes

Marco Faini, ETH Zurich, Switzerland

10:30-12:15 **Room 101 AB (1F)**

T02: Glycoproteomics - Technical Limitations & Prospects

Chairs: **Katalin Medzihradszky,** Hungary; **Hui Zhang,** USA

10:30 **TK-03**

Extracellular Glycosylation: How to See the Forest Despite All the Trees

Katalin Medzihradszky, Biological Research Centre, Szeged, Hungary

10:55 **TK-04**

Comprehensive Analysis of N-Linked Protein Glycosylation Using NGAG and Mass Spectrometry

Hui Zhang, Johns Hopkins University, USA

11:20 **TO02-001**

In-Depth Analysis of Human Plasma Glycoproteins by a Combination of High-Resolution Native Mass Spectrometry and Middle-Down Proteomics

Vojtech Franc, University of Utrecht, Netherlands

11:35 **TO02-002**

Confident, Automated N-Glycoproteomics Profiling in Enriched and Unenriched Cell Samples

Scott Peterman, Thermo Fisher Scientific, USA

11:50 **TO02-003**

Identification of Intact Glycopeptides with In-Silico Deglycosylation Strategy for O-Glycoproteomics Analysis

Hongqiang Qin, Chinese Academy of Sciences, China

11:55 **TO02-004**

Glycoproteomic Analysis of Human Plasma Using SWATH-MS

Chi-Hung Lin, Macquarie University, Australia

12:00 **TO02-005**

A Suite of SWATH Glycoproteomic Approaches for Easy Global Glycoprotein Analysis

Ben Schulz, The University of Queensland, Australia

10:30-12:15 **Room 101 C (1F)**

T03: PTM Crosstalks II - Lysine & Other Modificomics

Chairs: **Chunaram Choudhary,** Denmark; **Yingming Zhao,** USA

10:30 **TK-05**

Systems-Wide Analysis of Properties and Functions of Lysine Acetylation and Ubiquitylation

Chunaram Choudhary, University of Copenhagen, Denmark

10:55 **TK-06**

Discovery and Initial Characterization of a Family of Lysine Acylation Pathways

Yingming Zhao, The University of Chicago, USA

11:20 **TO03-001**

Unravelling Crosstalks between SUMOylation and Other Protein Modifications in Human Cells Using Dynamic Proteomics

Frederic Lamoliatte, Universite de Montreal, Canada

11:35 **TO03-002**

Towards Comprehensive Analysis of Protein ADP-Ribosylation

Yonghao Yu, UT Southwstern Medical Center, USA

11:50 **TO03-003**

Acetylome Analysis Reveals Carbon Metabolism as a Key Factor Enhancing Thermogenesis in White Adipocytes

Hsin-Yi Chang, Kyoto University, Japan

11:55 **TO03-004**

Effects of Co-/Post-Translational Modifications on Protein Function

Hisashi Hirano, Yokohama City University, Japan

12:00 **TO03-005**

Efficient Enrichment of SUMOylated Peptides from Alpha-Lytic Protease Digest Using K- Ɛ -GG Remnant Immuno-Affinity Purification

Hongbo Gu, Cell Signaling Technology, USA

10:30-12:15 **Room 101 D (1F)**

T04: Imaging Mass Spectrometry

Chairs: **Peter Hoffmann,** Australia; **Per Andrén,** Sweden

10:30 **TK-07**

Peptide and Glycan Mass Spectrometry Imaging as Diagnostic Tool in Cancer Research

Peter Hoffmann, University of Adelaide, Australia

10:55 **TK-08**

Molecular Imaging of the Brain by Mass Spectrometry

Per Andrén, Uppsala University, Sweden

11:20 **TO04-001**

Molecular Imaging of Protein in Tissues Using Ambient Ionization Top-Down Mass Spectrometry

Cheng-Chih Hsu, National Taiwan University, Taiwan

11:35 **TO04-002**

3D MALDI Imaging Mass Spectrometry Using Next Generation Technologies - Reconstruction of a Molecular Imaged Epididymis

Charles Pineau, Protim - Inserm U1085, France

11:45 **TO04-003**

Localization and Identification of Peptides from Tissue Using High-Speed MALDI TOF/TOF Mass Spectrometry

Sabu Sahadevan, Bruker Daltonics, France

11:55 **TO04-004**

Monitoring ErbB1 and ErbB2 Interaction and Activation Using Engineered Cell Lines and Duolink Proximity Ligation Assay by High-Content Imaging

Tracy Adair-Kirk, MilliporeSigma, USA

12:00 **TO04-005**

Molecular Profile Discrimination and Mapping of Skeletal Muscle Regeneration in Rat Crush Model Using MALDI Imaging

Anne Denys, Université Paris 13, UMR CNRS 7244, France

10:30-12:15 **Room 102 (1F)**

T05: Liver & Toxicoproteomics: Metabolism, Drug Transformation & Toxicity

Chairs: **Fernando J. Corrales,** Spain; **Oliver Poetz,** Germany

10:30 **TK-09**

Systematic Analysis of One Carbon Metabolism by SRM. Implications in the Progression of Chronic Liver Disorders

Fernando Corrales, University of Navarra, Spain

10:55 **TK-10**

Drug-Drug Interaction – Analyses of CYP450 Enzymes and Transporters in Mice and Men

Oliver Poetz, University of Tübingen, Germany

11:20 **TO05-001**

Personalized Proteomic Characterization of Hepatitis B Virus-Associated Hepatocellular Carcinomas

Ying Jiang, National Center for Protein Science, Beijing, China

11:35 **TO05-002**

In Vitro Investigation Of An Adverse Outcome Pathway Of Cholestatic Liver Injury Using Quantitative Phosphoproteomics

René Zahedi, Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany

11:50 **TO05-003**

Differential Proteomic Analysis of Cholangiocarcinoma Cells and Cell-Derived Extracellular Vesicles by Label Free Mass Spectrometry

Felix Elortza, CIC bioGUNE, CIBERehd, ProteoRed-ISCIII, Spain

12:00 **TO05-004**

Proteome Analysis of Microdissected Tumor Cells Reveals Annexin A10 as Biomarker Candidate for Differentiation of ICC And Liver Metastases of PDAC

Thilo Bracht, Ruhr Universität Bochum, Germany

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

T06: Antibodies & Protein Arrays

Chairs: **Heng Zhu,** USA; **Mathias Uhlén,** Sweden

13:45 **TK-11**

Application of Protein Microarrays in Epigenetics and Biomarker Discovery

Heng Zhu, Johns Hopkins University, USA

14:10 **TK-12**

Validation of Antibodies to Study the Human Proteome

Mathias Uhlén, KTH Royal Institute of Technology, Sweden

14:35 **TO06-001**

Status of the Affinity Binder Knockdown Initiative

Tove Alm, Scilifelab, KTH Royal Institute of Technology, Sweden

14:50 **TO06-002**

Heterogeneous Ribonucleoprotein K (hnRNP K) Binds the 5' Terminal Sequence of the Hepatitis C Virus RNA and Mature miR-122

Chien-Sheng Chen, National Central University, Taiwan

15:05 **TO06-003**

A High-Content Functional Mycobacterium Tuberculosis Proteome Microarray and Its Applications

Yang Li, Shanghai Jiao Tong University, China

15:10 **TO06-004**

Utilizing Protein Microarray to Monitor Blood-Brain Barrier Disruption and Active Inflammation in Plasma Samples from Multiple Sclerosis Patients

Malene Moeller Joergensen, Aalborg University Hospital, Denmark

15:15 **TO06-005**

Mapping Transcription Factor Interactome Networks Using HaloTag Protein Arrays

Junshi Yazaki, Riken, Japan

13:45-15:30 **Room 101 AB (1F)**

T07: Integrative Glyco(proteo)mics for Glycobiology & Diseases

Chairs: **Nicolle Packer,** Australia; **Hisashi Narimatsu,** Japan

13:45 **TK-13**

Advances in Glycoproteomics Facilitate the Discovery of a New Class of Functionally Important Cancer and Inflammation-Centric Human Glycoproteins

Morten Thaysen-Andersen, Macquarie University, Australia

14:10 **TK-14**

Accurate Mass- and Glycan Composition-Based Assignment of Glycosylation Site-Specific Glycomes of Complex Glycoprotein Mixture

Hiroyuki Kaji, National Institute of Advanced Industrial Science & Technology (AIST), Japan

14:35 **TO07-001**

Identification of Intact Glycopeptides at a Proteome Scale

Mingqi Liu, Fudan University, China

14:50 **TO07-002**

Integrated Glycoproteomics Demonstrates Fucosylated Serum Paraoxonase 1 Alterations and functions in Lung Cancer

Je Yoel Cho, Seoul National University, South Korea

15:05 **TO07-003**

Decoding Site-Specific Alteration of Sialo-Glycoproteome in EGFR-Subtype of Non-Small Cell Lung Cancer

Yi-Ju Chen, Academia Sinica, Taiwan

15:10 **TO07-004**

Identifying Antibody and Lectin Recognition to HIV N-Glycans Through Native Mass Spectrometry and Glycoproteomic Analysis of Viral Envelope Spikes

Weston Struwe, University of Oxford, United Kingdom

15:15 **TO07-005**

Dynamic Mapping of Human Frontal Cortex According to the Developmental Stage via Neuroglycomic Approach

Jua Lee, Chungnam National University, South Korea

13:45-15:30 **Room 101 C (1F)**

T08: Proteome Dynamics: Stability, Turnover & Degradomics

Chairs: **Christopher Overall,** Canada; **Donald Kirkpatrick,** USA

13:45 **TK-15**

Positional Proteomics Technologies to Functionally Annotate Tissue Proteomes in Pathology: Mechanistic Analysis Linear Ubiquitination by LUBAC in Immunodeficiency Disease by TAILS

Christopher Overall, University of British Columbia, Canada

14:10 **TK-16**

Ubiquitin Proteomics – Revelations of a Master Manipulator

Donald Kirkpatrick, Genentech, USA

14:35 **TO08-001**

Copy Number Alteration Programmed Protein Turnover Quantified by pSILAC and SWATH Mass Spectrometry

Yansheng Liu, ETH Zurich, Zurich, Switzerland

14:50 **TO08-002**

High Resolution Mass Spectrometry Cellular Thermal Shift Assay (HR-MS-CETSA) - Post-Translational Modifications Impact on Protein Stability

*Radoslaw Sobota, Agency for Science, Technology and Research (A*STAR), Singapore*

15:05 **TO08-003**

A Dynamic Picture of the Proteome and Ibiquitinome Upon Proteasome Inactivation

Jeroen Demmers, Erasmus University Medical Center Rotterdam, Netherlands

15:10 **TO08-004**

Proteome Turnover Analysis Reveals Substrates and Physiological Role of Membrane Proteases

Ansgar Poetsch, IIB-CONICET-UNMdP Mar del Plata, Argentina

15:15 **TO08-005**

A Novel Function of CRL2 Ubiquitin Ligase in Protein Quality Control

Hsiu-Chuan Lin, Academia Sinica, Taiwan

13:45-15:30 **Room 101 D (1F)**

T09: Spatial & Single Cell Proteomics

Chairs: **Emma Lundberg,** Sweden; **Bernd Bodenmiller,** Switzerland

13:45 **TK-17**

The Human Cell Atlas

Emma Lundberg, Scilifelab, KTH Royal Institute of Technology, Sweden

14:10 **TK-18**

Analysis of Tumor Heterogeneity in Three Dimensions by Imaging Mass Cytometry

Bernd Bodenmiller, University of Zurich, Switzerland

14:35 **TO09-001**

Quantitative Proteome-Wide Profiling of the Retromer Cargo Landscape

Christina Bell, Harvard Medical School, USA

14:50 **TO09-002**

Refining the Details in the Tissue-Based Map of the Human Proteome

Cecilia Lindskog, Uppsala University, Sweden

15:05 **TO09-003**

Membrane Localization of Metabolic Enzymes and Metabolic Modulation in a Cell Division Mutant of *Escherichia Coli* Identified by Omics Approaches

Yu-Ling Shih, Academia Sinica, Taiwan

15:10 **TO09-004**

Determining Post-Translational Modifications of Nuclear Proteins

Ryotaro Ban, Yokohama City University, Japan

15:15 **TO09-005**

Single-Cell Proteome Profiling: Innovations in Sample Preparation

Masaki Wakabayashi, Kyoto University, Japan

13:45-15:30 **Room 102 (1F)**

T10: Protein Standards and Model Organisms: Expanding Our Horizons

Chairs: Eric Deutsch, USA**; Joshua Heazlewood,** Australia

13:45 **TK-19**

Recent Progress and New Projects for the HUPO Proteomics Standards Initiative

Eric Deutsch, Institute for Systems Biology, USA

14:10 **TO10-001**

The ProteomeXchange Consortium: 2016 Update

Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, United Kingdom

14:25 **TO10-002**

proBAMconvert: Organizing MS Identifications in a Genome-Centric Fashion Enables Proteogenomics and Proteomics Integration

Gerben Menschaert, University of Ghent, Belgium

14:30 **TO10-003**

The HUPO-PSI Quality Control Working Group: Making QC More Accessible for Biological Mass Spectrometry

Mathias Walzer, University of Tuebingen, Germany

14:35 **TK-20**

The Golgi Localized UDP-GlcNAc Transporter is Required for the Maturation of Complex *N*-Glycans in Plants

Joshua Heazlewood, The University of Melbourne, Australia

14:50 **TO10-004**

Adipose Tissue Pathways in Obesity: Iberian Pig as Large Animal Model of Metabolic Disorders

Cristian Piras, University of Milan, Milan, Italy

15:05 **TO10-005**

Proteomics in Food Safety: Monitoring Competition between *Listeria Monocytogenes* and *Lactococcus Lactis* by Imaging Mass Spectrometry

Isabella Alloggio, Università degli studi di Milano, Italy

15:20 **TO10-006**

Proteome Alterations in the Porcine Endometrium during Embryo Implantation

Thomas Fröhlich, LMU-Munich, Germany

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

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

Plenary Session 7

Chair: **Catherine E. Costello,** USA

16:45 **PL 07**

Complementary Methods for Probing Protein Assemblies and Interactions

Albert Heck, Utrecht University, The Netherlands

DAILY PROGRAM

WEDNESDAY, SEPTEMBER 21, 2016

08:00-16:00	**Registration (Lobby, 1F)**
08:00-16:00	**Speaker Ready Room (Room 103, 1F)**
09:30-15:30	**Exhibition & Poster (Room 201, 2F and Banquet Hall, 3F)**
08:30-09:15	Plenary Session 7 (Plenary Hall, 3F)
08:30-17:30	Bioinformatics Hub (Room 203, 2F)
09:30-10:30	ECR Manuscript Competition (Room 102, 1F)
	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
10:30-12:15	[W01] Pharmacoproteomics & Drug Development (Plenary Hall, 3F)
	[W02] Proteogenomics & The Missing Proteins (Room 101 AB, 1F)
	[W03] Cysteine Modifications & Redoxomics (Room 101 C, 1F)
	[W04] Membrane & Extracellular Proteomics (Room 101 D, 1F)
	[W05] Food & Nutrition and Immuno- Peptidome: Focus on Food Allergies (Room 102, 1F)
12:30-13:30	Networking Break and Poster Viewing (Room 201, 2F and Banquet Hall, 3F)
13:45-15:30	[W06] Chemical Proteomics & Drug Profiling (Plenary Hall, 3F)
	[W07] Proteomics in the Era of Big Data (Room 101 AB, 1F)
	[W08] Neurological Disorders & Neuroproteomics (Room 101 C, 1F)
	[W09] Plant & Microbial Proteomics (Room 101 D, 1F)
	[W10] Kidney, Urine and Plasma: Opportunities for Early Diagnosis and Risk Assessment (Room 102, 1F)
15:30-17:30	Closing Plenary Session with Award Lectures (Plenary Hall, 3F)
18:00	Transfer to HPP Workshop Day Venue, Sun Moon Lake (Lobby, 1F)

Registration Open **08:00-16:30 @Lobby, 1F**
Speaker Ready Room Open **08:00-15:30 @103, 1F**

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

Bioinformatics Hub

10:30-15:30: Special Planned Topics: Glycoproteomics Informatics

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

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

Plenary Session 8

Chair: **Gilbert Omenn,** USA

8:30 **PL 08**
Precision Medicine: Proteomics in the Context of Health Assessment and Systems Biology
Jennifer Van Eyk, Cedars-Sinai Medical Center, USA

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

W01: Pharmacoproteomics & Drug Development

Chairs: **Yasushi Ishihama,** Japan; **Henrik Daub,** Germany

10:30 **WK-01**
Kinase-Centric Pharmacoproteomics for Molecular-Targeting Drug Discovery
Yasushi Ishihama, Kyoto University, Japan

10:55 **WK-02**
Quantitative Proteomics to Support the Discovery and Development of Targeted Drugs
Henrik Daub, Evotec (München) GmbH, Germany

11:20 **WO01-001**
Proteome-Wide Drug Dose-Response of Prostate Cancer Cell Lines Exposed to Androgen Receptor Antagonists by Microflow-LC SWATH MS Analysis
Christie Hunter, Sciex, USA

11:35 **WO01-002**
Profiling Changes in the Phosphoproteome of Hematopoietic Cells in Response to a Novel Class of Anti-Oncogenic Compounds
Peter Kubiniok, University of Montreal, Canada

11:50 **WO01-003**

Cancer Proteomics towards Precision Medicine by Molecular Targeting Drug

Zhiwei Qiao, National Cancer Center Research Institute, Japan

12:00 **WO01-004**

Drug Development by Linking Pathophysiology in Cancer to Proteomics

Marko-Varga György, University of Lund, Sweden

10:30-12:15 **Room 101 AB (1F)**

W02: Proteogenomics & The Missing Proteins

Chairs: **Akhilesh Pandey,** USA; **Daehee Hwang,** South Korea

10:30 **WK-03**

A Novel Data-Independent Acquisition (DIA) Mass Spectrometry Approach Integrated With RNA-Seq for Deep Proteogenomic Profiling

Akhilesh Pandey, Johns Hopkins University, USA

10:55 **WK-04**

A Proteogenomic Analysis of Early Onset Gastric Cancer

Daehee Hwang, DGIST, South Korea

11:20 **WO02-001**

A Proteogenomics Approach to Reveal Molecular Mechanisms of COPD

Peter Horvatovich, University of Groningen, Netherlands

11:35 **WO02-002**

Launch of MissingProteinPedia: Accelerating Discovery of the Human Proteome Project's "Missing Proteins"

Mark Baker, Macquarie University, Australia

11:50 **WO02-003**

Proteogenomics of Human Cancer Cell Lines: Coding Variants Identified by Shotgun Proteomics

Sergei Moshkovskii, Institute of Biomedical Chemistry, Russia

11:55 **WO02-004**

Proteogenomic Profiling of Neoantigens for Personalized Cancer Immunotherapy

Koji Ueda, Japanese Foundation for Cancer Research, Japan

12:00 **WO02-005**

Missing Genes and Supplementary Tissues in the Human Protein Atlas

Evelina Sjostedt, KTH Royal Institute of Technology, Sweden

10:30-12:15 **Room 101 C (1F)**

W03: Cysteine Modifications & Redoxomics

Chairs: **Stuart Cordwell,** Australia; **Kong-Joo Lee,** South Korea

10:30	**WK-05** **Proteomic-Scale Approaches for Identifying Reversible and Irreversible Cysteine Redox PTM in Myocardial Ischemia / Reperfusion** *Stuart Cordwell, The University of Sydney, Australia*
10:55	**WK-06** **ROSics: Principle of ROS in Oxidative Modifications and Structural Regulations** *Kong-Joo Lee, Ewha Womans University, South Korea*
11:20	**WO03-001** **Quantitative Proteomics Depicts the Landscape of Cysteine Redoxome for Nitric Oxide-Mediated Myocardial Protection against Ischemia-Reperfusion Injury** *Tzu-Ching Meng, Academia Sinica, Taiwan*
11:35	**WO03-002** **Proteomic Analysis of S-sulfhydration by Ultrafilter-Assisted Functional Supramolecular Polymer Capture** *Huiming Yuan, Chinese Academy of Sciences, China*
11:50	**WO03-003** **TRPC6-Dependent S-Nitrosylation in Duchenne Muscular Dystrophy** *Heaseung Sophia Chung, Johns Hopkins University, USA*
11:55	**WO03-004** **Proteomic and Redox Proteomic Analyses Reveal a Dual ROS-Regulation of Glucose Uptake in Adipocytes** *Zhiduan Su, The University of Sydney, Australia*
12:00	**WO03-005** **Identification of Protein Estrogenization as a Redox Post-Translational Modification by Shot-Gun Proteomics and Activity Probe with Dimethyl Labeling** *Shu-Hui Chen, National Cheng Kung University, Taiwan*

10:30-12:15 **Room 101 D (1F)**

W04: Membrane & Extracellular Proteomics

Chairs: **Bernd Wollscheid,** Switzerland; **Igor Stagljar,** Canada

10:30 **WK-07**

Decoding Ligand Receptor Interactions

Bernd Wollscheid, ETH Zurich, Switzerland

10:55 **WK-08**

Targeting Epidermal Growth Factor Receptor (EGFR) in Lung Cancer: Towards Interactome-Informed Medicine

Igor Stagljar, University of Toronto, Canada

11:20 **WO04-003**

Analysis of Proteoforms in Membrane Protein Complexes by CID/ETD Top-Down Proteomics

Hans Wessels, Radboudumc, Netherlands

11:35 **WO04-002**

Tumour-Dependent Fibroblast Activation: When a Good Neighbour Turns Bad

Wei Wu, Utrecht University, Netherlands

11:45 **WO04-004**

In Silico Characterization of the Human Lipid Raft Proteome

Michelle Hill, La Trobe University, Australia

11:55 **WO04-005**

Exosomal EphA2 Transmits Chemoresistance and Predicts Pancreatic Cancer Patient Responses to Therapy

Tony Hu, Cornell University, USA

12:00 **WO04-006**

Systemic Perturbation of Keratinocyte Homeostasis by Genetic Loss of the Extracellular Matrix Protein Collagen VII

Kerstin Thriene, University of Freiburg, Germany

10:30-12:15 **Room 102 (1F)**

W05: Food & Nutrition and Immuno- Peptidome: Focus on Food Allergies

Chairs: **Paola Roncada,** Italy; **Etienne Caron,** Switzerland

10:30 **WK-09**

Food and Nutrition Proteomics: Focus on Food Allergens and Allergies

Paola Roncada, Istituto Sperimentale Italiano L. Spallanzani, Italy

10:55 **WK-10**

The Human Immuno-Peptidome Project: A New Initiative of B/D-HPP Program

Etienne Caron, ETH Zurich, Switzerland

11:20 **WO05-001**

The Benefits of Hybrid Fragmentation Technologies (EThcD) for Analysing the Immunopeptidome

Albert Heck, Utrecht University, The Netherlands

11:35 **WO05-002**

Digestomics of Raw Peanut and Characterization of Gastric-Phase Released Peptides of Peanut Allergens

Tanja Cirkovic Velickovic, University of Belgrade, Serbia

11:50 **WO05-003**

Ultra-Fast Analysis of Allergens Using Capillary Electrophoresis Coupled to Mass Spectrometry and Ultraviolet Photodissociation

Daniel Lopez-Ferrer, Thermo Fisher Scientific, USA

11:55 **WO05-004**

Characterisation of Specificity of Different Commercial Proteases for Food Hydrolysates

Cristian De Gobba, University of Copenhagen, Denmark

12:00 **WO05-005**

Characterization and Modulation of Fish Allergens

Pedro Rodrigues, Universidade do Algarve, Portugal

12:30-13:30: Networking Break and Poster Viewing *(Odd Poster Numbers)* — **Room 201 (2F) and Banquet Hall (3F)**

13:45-15:30 — **Plenary Hall (3F)**

W06: Chemical Proteomics & Drug Profiling

Chair: **Ho Jeong Kwon,** South Korea

13:45 **WK-11**

Genetically Encoded Protein Photocrosslinker for Comparative Proteomics

Peng Chen, Peking University, China

14:10 **WK-12**

Thermal Proteome Profiling for Drug Discovery

Mikhail Savitski, EMBL, Germany

14:35 **WO06-001**

Target Identification in Living Cells via Mass Spectrometry-Based Chemical Proteomics

*Xuezhi Bi, Agency for Science, Technology and Research (A*STAR), Singapore*

14:50 **WO06-002**

Comprehensive Mass Spectrometry Analysis Identifies a Novel Therapeutic Target in the Wnt Signaling Pathway

Tesshi Yamada, National Cancer Center Research Institute, Japan

15:05	**WO06-003** **The Phosphoproteome of the NCI-60 Cell Line Panel Reveals Markers of Drug Sensitivity** *Chen Meng, Technische Universitat Muenchen, Germany*
15:10	**WO06-004** **Targeted Proteomic Profiling of Enzymes that Activate the Prodrug PR-104A in Human Leukaemias** *Yongchuan Gu, University of Auckland, New Zealand*
15:15	**WO06-005** **Identification of TIFA as a Novel Therapeutic Target in Acute Myeloid Leukemia** *Tong-You Wei, Academia Sinica, Taiwan*

13:45-15:30 **Room 101 AB (1F)**

W07: Proteomics in the Era of Big Data

Chairs:	**Pengyuan Yang,** China; **Weimin Zhu,** China
13:45	**WK-13** **Precision Analysis of Proteome by HPLC-ESI-MS** *Pengyuan Yang, Fudan University, China*
14:10	**WK-14** **Big Data infrastructure for Chinese Human Proteome Project** *Weimin Zhu, National Institute for Protein Sciences – Beijing, China*
14:35	**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*
14:50	**WO07-002** **HUPO Human Proteome Project Metrics for 2016** *Gilbert Omenn, University of Michigan, USA*
15:00	**WO07-003** **Quantitation and Evaluation of Candidate Biomarkers of Pancreatic Cancer in Plasma Using Multiple Reaction of Monitoring Method** *Weimin Zheng, Fudan University, China*
15:10	**WO07-004** **ProDiGy: A Proteome Knowledge Discovery Gateway** *Dong Li, Beijing Proteome Research Center, China*
15:15	**WO07-005** **Comprehensive Draft of the HeLa Proteome to a Depth of More than 13,000 Proteins.** *Dorte Breinholdt Bekker-Jensen, University of Copenhagen, Denmark*

13:45-15:30	Room 101 C (1F)

W08: Neurological Disorders & Neuroproteomics

Chairs:	**Daniel Martins-de-Souza,** Brazil; **Andrea Urbani,** Italy
13:45	**WK-15** **Employing Neuroproteomics to Understand the Molecular Basis of Schizophrenia** *Daniel Martins-de-Souza, University of Campinas, Brazil*
14:10	**WK-16** **Exploring the Role of Hydrogen Sulfide in Neurodegenerative Disorders** *Andrea Urbani, Catholic University of the Sacred Heart, Italy*
14:35	**WO08-001** **Gene Expression and Proteomic Analysis of Cognitive Dysfunction in People with Remitted Major Depression** *Klaus Oliver Schubert, The University of Adelaide, Australia*
14:50	**WO08-002** **Proteomic Dissection of AMPA Receptor Complexes Identifies FRRS1l as a Determinant for Receptor Biogenesis Mutated in Severe Intellectual Disability** *Uwe Schulte, University of Freiburg, Germany*
15:05	**WO08-003** **Autoantibody Response in Meningioma Patients Reveals Aberrations in Signalling Pathways** *Shabarni Gupta, Indian Institute of Technology Bombay, India*
15:10	**WO08-004** **Proteomic Analysis of Motor Neurons from Induced Pluripotent Stem Cells: ALS** *Victoria Dardov, Cedars Sinai Medical Center, USA*
15:15	**WO08-005** **Analysis of the *O*-GlcNAcomic Profiling of Brain Tissue in Alzheimer's Disease** *Wei-Wei Chang, Academia Sinica, Taipei, Taiwan*

13:45-15:30 **Room 101 D (1F)**

W09: Plant & Microbial Proteomics

Chairs: **Weiguo Andy Tao,** USA; **Michael R. Sussman,** USA

13:45 **WK-17**

Using Proteomic Tools to Reveal New Facets of Plant Signaling

Weiguo Andy Tao, Purdue University, USA

14:10 **WK-18**

Application of Mass Spectrometric Technology for Quantifying Changes in Plasma Membrane Receptor-Mediated Signaling in Arabidopsis Thaliana

Michael Sussman, University of Wisconsin-Madison, USA

14:35 **WO09-001**

Quantitative Proteomic Analysis of Flooding and Its Recovery in Soybean Exposed to Aluminum Oxide Nanoparticles

Setsuko Komatsu, National Institute of Crop Science, Japan

14:50 **WO09-002**

Single-Species Proteomics, Multi-Species Metaproteomics, Trends and Opportunities to Read-Across in Environmental Assessment

Susana Cristobal, Linköping University, Sweden

15:05 **WO09-003**

Gastric Bypass Surgery Clearly Perturbs the Community Structure and the Functional Composition of the Intestinal Microbiota

Nico Jehmlich, Helmholtz-centre for Environmental Research - UFZ, Germany

15:10 **WO09-004**

Integrated Extracellular Matrix Proteome and Organ Specific Transcriptome Decipher Cell Wall Mediated Immunity in Plant

Kanika Narula, National Institute of Plant Genome Research, India

15:15 **WO09-005**

Phosphoproteomic Analysis of Abscisic Acid Signaling Components in Arabidopsis Seed

Anna Amagai, Tokyo University of Agriculture and Technology, Japan

13:45-15:30 **Room 102 (1F)**

W10: Kidney, Urine and Plasma: Opportunities for Early Diagnosis and Risk Assessment

Chairs: **Tadashi Yamamoto,** Japan; **Jochen Schwenk,** Sweden

13:45 **WK-19**

Social Implementation Vision of All-In-One Urine Test for Health Checkups

Tadashi Yamamoto, Niigata University, Japan

14:10 **WK-20**

Affinity Proteomics with Plasma Biobanks - From Discovery to Validation

Jochen Schwenk, Scilifelab, KTH Royal Institute of Technology, Sweden

14:35 **WO10-001**

Comparative Proteomic Analysis of Kidney Distal Convoluted Tubule and Cortical Collecting Duct Cells Following Long-Term Hormonal Stimulation

Qi Wu, Aarhus University, Denmark

14:50 **WO10-002**

Targeted MS-based Assay of Circulating Proteoforms Related to Aging in Human Plasma

Pingbo Zhang, Johns Hopkins University, USA

15:05 **WO10-003**

Can Proteomics Contribute to Solving the Riddle of Diabetic Nephropathy?

Leena Liljedahl, Lund University, Sweden

15:10 **WO10-004**

Quantification of Angiotensin II-Regulated Proteins in Urine of Patients with Polycystic and Chronic Kidney Diseases by Selected Reaction Monitoring

Ana Konvalinka, University of Toronto, Toronto, Canada

15:15 **WO10-005**

Analysis of the HDL Proteome - Myths and Legends and Reality

Manfred Raida, National University of Singapore, Singapore

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

Award Lectures & Closing Ceremony

DAILY PROGRAM

THURSDAY, SEPTEMBER 22, 2016

HPP Post-Congress Day
Venue: Fleur de Chine Hotel, Sun Moon Lake, Nantou

08:30-16:00 HPP Post-Congress Day — Cosmos Cloud B (3F)

Moderator:	**Gilbert Omenn,** USA
8:30	**Highlights from Congress and discussions of B/D, C-HPP, Resource Pillars** *Moderators: Gil Omenn, Young-Ki Paik, Jennifer van Eyk*
9:00	**Bioinformatics Hub, JPR Special Issue 2016 and Future, Experience with HPP MS Guidelines v2.1.** *Eric Deutsch, ISB, USA and Christopher Overall, Univ. British Columbia, Canada*
9:30	**Open Discussion about Recent Strategic Successes and Strategic Planning for Next Year and for 5 Years: Aims, Directions, Changes, Deliverables**
10:00	**Coffee Break**
10:20	**HPP Plenary Lecture 3: Lung Cancer Genomics** *Sung-Liang Yu, National Taiwan University, Taiwan*
10:50	**Reports on the Cluster Meeting (C- & B/D-HPP+CPTAC)** (1) Cancer (2) In Vitro Transcription/Translation Platform (3) Reproductive Biology (4) Membrane Proteins (5) Neurodegenerative Disease
12:30	**Lunch**
13:30	**HPP Strategy Session** Strategic Evaluation by members of HPP SAB, led by Cathy Costello, Naoyuki Taniguchi, Mathias Uhlen, John Yates
14:30	**Communications, Publications, Resources** Publications, including assessment of 2016 JPR special issue and plans for 2017, HPP Operations & Communication matters (C. Pineau, C. Borchers), HPP Resources and Funding, Upcoming Workshops and Meetings: Brazil, 10-12 Dec 2016; joint C-HPP Workshop with EuPA (June, 2018, Spain)

16:00-18:00 Boad Tour

INDUSTRY SESSIONS

2016 TAIPEI HUPO

INDUSTRY SESSIONS

MONDAY, SEPTEMBER 19, 2016

12:30-13:30 **Room 101C (1F)**

SCIEX

Applications of Industrialized Quantitative Proteomics to Advance Precision Medicine

Chair: Mark Cafazzo, SCIEX, USA

Enabling Precision Medicine: High Throughput Proteomics for Accelerated Biomarker Translation

Jenny Van Eyk, Cedars Sinai Medical Center, USA

Building an Industrialized Proteomics Platform: Implications for Delivering on the Promise of Precision Medicine

Phil Robinson, CMRI, Australia

12:30-13:30 **South Lounge (3F)**

Waters Corporation

Novel DIA and Processing Strategies for Quantitative Proteomics

SONAR- Advanced Data Independent Analysis for Complex Proteome Profiling

James Langridge, Waters Corporation, United Kingdom

Progenesis QI for Proteomics and Proteolabels – Delivering High-Performance Quantitation for Stable Isotope Labeled Proteomes

Andrew Collins, University of Liverpool, United Kingdom

12:30-13:30 **North Lounge (3F)**

Thermo Fisher Scientific

High-Throughput Multiplexed Quantitative Proteomics for Personalized Medicine Applications

Clinical-Scale Discovery Proteomics in Human Body Fluids

Loic Dayon, Nestle Institute of Health Sciences, Switzerland

Zurich-Cancer-Maps: Turning Clinical Biopsies into Searchable Digital Biobanks

Bernd Wollscheid, ETH Zurich, Switzerland

12:30-13:30 **Joy Lounge (4F)**

Thermo Fisher Scientific

Sweet Revolution: Analytical Tools for the Characterization of Glycans and Glycoproteins

Simple Cell Glycoproteomics: Discovery and Applications

Sergey Vakhrushev, University of Copenhagen, Denmark

Unlocking the Low Mass Range with Trap-HCD for Glycan Analysis

Christopher Ashwood, Macquarie University, Australia

12:30-13:30 **Elegance Lounge (4F)**

Agilent Technologies, Inc.

Advances in Proteomics from Agilent Technologies

Innovations for Proteomics Research

Christine Miller, Agilent Technologies, Inc., USA

Developing Peptide Quantification for (Human Disease) Biomarker Measurement

Steve Pennington, University College Dublin, Ireland

12:30-13:30 **VIP Room (4F)**

Bruker Corporation

Uncompromised Performance: Exploiting the Potential of UHR-Q-TOF for Discovery Proteomics

Identifying Disease Biomarkers Using Peptide Based Classification

Andrew Webb, Walter and Eliza Hall Institute of Medical Research, Australia

Towards More Effective Glycopeptide Characterization on A UHR-Q-TOF Platfrom

Gary Kruppa, Bruker Daltonics, USA

INDUSTRY SESSIONS

TUESDAY, SEPTEMBER 20, 2016

12:30-13:30 **South Lounge (3F)**

Bruker Corporation

Answering the Proteoforms Challenge: Alternative Approaches for Biomarker Discovery

Intact Protein Profiling by LC-Q TOF MS/MS

Hans Wessels, Radboud Universiteit Nijmegen, Netherlands

Tissue Typing: Merging MS and Clinical Expertise for More Efficient Biomarker Discover

Rohan A. Thakur, Bruker Daltonics, USA

12:30-13:30 **North Lounge (3F)**

SCIEX

Innovations in Industrializing Quantitative Proteomics

Chair: Gavin Fisher, SCIEX, USA

Industrializing SWATH™ Acquisition Workflows with Automated Sample Preparation and Microflow LC

Christie Hunter, SCIEX, USA

From Large Data Sets to Biological Answers: A Robust Cloud-Based Analysis Pipeline for Quantitative SWATH Proteomics

Stephen Tate, SCIEX, Canada

12:30-13:30 **Joy Lounge (4F)**

Meridigen Biotech Co., Ltd.

Discover the Future Applications of Mesenchymal Stem Cell

Multi-Omic Analysis for Mesenchymal Stem Cell

Chih-Wei Chien, Meridigen Biotech Co., Ltd, Taiwan

High-throughput Dynamics Omics System

Shu-Han Yu, Meridigen Biotech Co., Ltd, Taiwan

12:30-13:30 **Elegance Lounge (4F)**

Merck Millipore and Sigma-Aldrich

Verify the Protein Interactome with Visual Confirmation

Chair: Jeffrey L. Turner, Merck KGaA Darmstadt Germany, USA

Uncovering the Interactome: Probing Biology Beyond Protein Quantitation

Jeffrey L. Turner, Merck KGaA Darmstadt Germany, USA

Advanced Molecular Tools for Parallel Analyses and Imaging of Proteins

Masood Kamali-Moghaddam, Uppsala University, Sweden

12:30-13:30 **VIP Room (4F)**

Thermo Fisher Scientific

Defining Biological Phenotypes by Quantifying Small Molecular Changes

Maximizing S-nitrosylation Detection: Quantifying Pathological Diversity

Jenny Van Eyk, Cedars Sinai Medical Center, USA

Personalized 'Omics Profiling' of S. Cerevisiae Strains Isolated from Differing Environments

Daniel Lopez-Ferrer, Thermo Fisher Scientific, USA

POSTERS

2016 TAIPEI HUPO

POSTERS

POSTER WILL BE DISPLAYED FOR THE ENTIRE DURATION OF THE CONGRESS

Monday, September 19, 2016

MP04, 06	**Room 201 (2F)**
MP01, 02, 03, 05, 07, 08, 09, 10, 11, 12	**Banquet Hall (3F)**
Presentation Time:	Poster Viewing Time (09:30-10:30 & 15:30-16:30)
Poster Mounting:	08:15-09:30
Poster Removal:	16:30-17:00

Tuesday, September 20, 2016

TP03, 04, 05, 06, 08, 09	**Room 201 (2F)**
TP01, 02, 07, 10	**Banquet Hall (3F)**
Presentation Time:	Poster Viewing Time (09:30-10:30 & 15:30-16:30)
Poster Mounting:	08:15-09:30
Poster Removal:	16:30-17:00

Wednesday, September 21, 2016

WP01, 02, 03, 04, 05, 07	**Room 201 (2F)**
WP06, 08, 09, 10, 11, 12, 13, 14, 15, 16	**Banquet Hall (3F)**
Presentation Time:	Poster Viewing Time (09:30-10:30 & 12:30-13:30)
Poster Mounting:	08:15-09:30
Poster Removal:	15:00-15:30

Presenting Author Stand By Time

Time in which poster presenters must be at their poster board and available to discuss their research personally with interested delegates.

***EVEN POSTER NUMBER:**	**09:30-10:30, September 19-21**
***ODD POSTER NUMBER:**	**15:30-16:30, September 19-20; 12:30-13:30, September 21**

All Oral Presenters have been invited to prepare a Poster in addition to their Oral Presentations. Poster Presentations for Oral Presenters will be labeled with their Oral Presentation number (e.g. MO01-001).

MP01	**Innovative Fractionation and Enrichment Techniques**
MP02	**Innovative Mass Spectrometry Techniques**
MP03	**New Technological Advancements**
MP04	**Chemical Probes and Chemical Biology For Proteomics**
MP05	**Phosphoproteomics, Kinome and Ptm Crosstalks**
MP06	**Bioinformatics and Computational Proteomics**
MP07	**Immunity, Inflammation and Infectious Diseases**
MP08	**Brain and Eyeome: Connecting Two Images**
MP09	**Diabetes and Cardiovascular Diseases: Energy Balance in Disease Phenotypes**
MP10	**Missing Proteins-Identification, Validation and Functional Characterization (CHPP)**
MP11	**Functional Roles of Alternative Splicing Varients (CHPP)**
MP12	**Snps And Ptms (Identification, Validation and Functional Consequences) (CHPP)**
TP01	**Cancer, Clinical and Translational Proteomics**
TP02	**Glycoproteomics, Glycomics and Glycosylation In Diseases**
TP03	**Lysine Modifications and PTM Crosstalks**
TP04	**Other PTMomics and Crosstalks**
TP05	**Proteome Dynamics: Turnover and Degradomics**
TP06	**Interactomics and Protein Network**

TP07	Protein Complexes and Structural Proteomics
TP08	Antibodies and Protein Arrays
TP09	Liver and Toxicoproteomics: Metabolism, Drug Transformation and Toxicity
TP10	Protein Standards and Model Organisms: Expanding Our Horizons
WP01	Proteogenomics
WP02	Multiomics for Precision Medicine and Systems Biology
WP03	Cysteine Modifications and Redoxomics
WP04	Imaging Mass Spectrometry
WP05	Subcellular, Spatial and Single Cell Proteomics
WP06	Membrane and Extracellular Proteomics
WP07	Stem Cell Proteomics
WP08	Neurological Disorders and Neuroproteomics
WP09	Pharmacoproteomics and Drug Development
WP10	Chemical Proteomics and Drug Profiling
WP11	Metabolomics and Metabolic Disorders
WP12	Plant Proteomics
WP13	Microbial Proteomics
WP14	Food and Nutrition and Immuno-Peptidome: Focus on Food Allergies
WP15	Kidney, Urine and Plasma: Opportunities for Early Diagnosis and Risk Assessment
WP16	Late Breaking Abstracts

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, USA

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™ Using Dynabeads™ 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, USA

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, USA

MP02-001

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

Catherine Costello, Boston Univ School of Medicine, USA

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, USA

MP02-005

Comparison of SWATH and iTRAQ in Clinical Study with Multiple Small Protein Samples

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

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, United Kingdom

MP03 - New Technological Advancements

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, USA

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, USA

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 Terapeutics 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, USA

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, USA

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, USA

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, USA

MP03-025

Advanced Peak Detection, Deconvolution, And Centroiding Algorithms Improve MS/MS Spectral Quality And Peptide Identification

Jeff Peterson, Veritomyx, Inc., USA

MP03-026

Higher Multiplexing with NeuCode SILAC Metabolic Labeling

John Rogers, Thermo Fisher Scientific, USA

MP03-027

Urine Protein Preparation Workflow for Urine Proteomics

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

MP03-033

The SOMAscan® Assay and SOMAmer® Reagents: Translatable Tools from High-Throughput Biomarker Discovery to Targeted

Sheri Wilcox, Somalogic, Inc., USA

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, USA

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

MK-06

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, USA

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, USA

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, 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, USA

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, USA

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, USA

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, USA

MP06-010

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

Devin Drew, Thermo Fisher Scientific, USA

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, USA

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, 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, USA

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, USA

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

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

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 Sureus*

Alessio Soggiu, Department of Veterinary Medicine , University of 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 Diabetes

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, USA

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, USA

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, 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 Dysfunction

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, 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 Glycobiomarkers

Andras Guttman, Sciex, USA

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

TP01 - Cancer, Clinical and Translational Proteomics

MO01-001

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

Takeshi Tomonaga, Laboratory of Proteome Research, National Institutes of Biomedical Innovation, Health and Nutrition, Japan

MO01-002

Proteomic Multimarker Panel Complements CA19-9 Insufficiency in the Diagnosis of Pancreatic Ductal Adenocarcinoma

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

MO01-003

Pathology-Driven Comprehensive Proteomic Profiling of the Prostate Cancer Tumor Micro environment

Stephen Pennington, UCD Conway Institute of Biomolecular and Biomedical Research, Ireland

MO01-004

Tissue Derived Neo-Antigens for T Cell-Based Cancer Immunotherapy

Michal Bassani, Unil/chuv, Switzerland

MO01-005

LinkedOmics: Discovering Associations between Genomic, Proteomic and Clinical Attributes in Human Cancer

Jing Wang, Vanderbilt University Medical Center, USA

TO05-004

Proteome Analysis of Microdissected Tumor Cells Reveals Annexin A10 as Biomarker Candidate for Differentiation of ICC and Liver Metastases of PDAC

Thilo Bracht, Medizinisches Proteom Center, Ruhr Universität Bochum, Germany

WO07-003

Quantitation and Evaluation of Candidate Biomarkers of Pancreatic Cancer in Plasma Using Multiple Reaction of Monitoring Method

Weimin Zheng, Department of Chemistry, Fudan University, China

TP01-001

Clinically-Actionable Proteomic Biosignatures of Colorectal Cancer

Seong Beom Ahn, Department of Biomedical Sciences, Macquarie University, Australia

TP01-002

Integrative Analysis for the Discovery of Non-Small Cell Lung Cancer Serological Markers and Validation by MRM-MS and ELISA

Hee-Sung Ahn, Department of Biological Chemistry, Korea University of Science and Technology, South Korea

TP01-003

Paradigm Shift in Accurate Assessment of HER-2 in Breast Cancer Patients by Expression Proteomics: Precision Medicine and Cost Saving Implications

Ayodele Alaiya, Proteomics Unit, King Faisal Specialist Hospital and Research Center, Saudi Arabia

TP01-004

Identification of New Biomarkers for Castration Resistant Prostate Cancer by Secretome Analysis

Noriaki Arakawa, Graduate School of Medical Life Science, Yokohama City University, Japan

TP01-005

Muscadine Grape Skin Extract Induces an Unfolded Protein Response Mediated Autophagy in Prostate Cancer Cells

Nawal Boukli, Center for Cancer Research and Therapeutic Development, Dept Biological Sciences, Clark Atlanta Uni, USA

TP01-006

Biomarkers of Colorectal Carcinoma Liver metastasis in Urine

Meng Cai, National Cancer Center/cancer Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, China

TP01-007

Targeted Proteomics Based Clinical Investigation of Serum Early Detection Biomarkers for Malignant Pleural Mesothelioma Cancer

Ferdinando Cerciello, James Thoracic Center, James Cancer Center, The Ohio State University Medical Center, USA

TP01-008

Development of a Multiplexed LC-MRM MS Method of Salivary Proteins for Evaluation of Oral Cancer Biomarkers

Yi-Ting Chen, Chang Gung University, Taiwan

TP01-009

Functional Re-Activation of Mitochondria in the TGF-β1 Induced EMT of Lung Cancer A549 Cells

Zhipeng Chen, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

TP01-010

Quantitative Profiling of Plasma Proteome in Kawasaki Disease

Yi-Hung Chen, Taipei Medical University/master Program for Clinical Pharmacogenomics and Pharmacoproteomics, Taiwan

TP01-011

Evaluation of Biofluid Biopsies by Targeted Proteome Analysis for Oral Cancer Biomarker Discovery and Verification

Lang-Ming Chi, Clinical Proteomics Core Laboratory, Chang Gung Memorial Hospital, Taiwan

TP01-012

Identification of Salivary Biomarkers for Detecting Oral Cavity Squamous Cell Carcinoma by Quantitative Proteomics

Hao-Wei Chu, Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan

TP01-013

Variabilities of Potential Protein Biomarkers Level in Saliva Samples from Healthy Donor

Lichieh Chu, Molecular Medicine Research Center, Chang Gung University, Taiwan

TP01-014

Discovery and Verification of Blood Biomarker for a Diagnosis of Acute Graft-Versus-Host Disease Based on Mass Spectrometry and Proteomics Technology

Kisoon Dan, Proteomics Core Facility, Biomedical Research Institute, Seoul National University Hospital, South Korea

TP01-015

In-Depth Proteomic Analysis of Pancreatic Cyst Fluid in Intraductal Papillary Mucinous Neoplasm Dysplasia of the Pancreas

Misol Do, Department of Biomedical Sciences, Seoul National University College of Medicine, South Korea

TP01-016

Identification of Protein and PTMs Changes in Gastric Cancer Patients from Before to After Surgery

Lylia Drici, University of Southern Denmark, Denmark

TP01-017

Immuno-MALDI for Quantifying PI3K/AKT/mTOR Signaling Pathway Activity in Breast and Colorectal Cancer Tumors

Björn Fröhlich, University of Victoria - Genome BC Proteomics Centre, Canada

TP01-018

Proteomic Analysis Identified Heat Shock Protein 72 as a Possible Target of Combination Therapy with Histone Deacetylase Inhibitor

Kazuyasu Fujii, Department of Dermatology, Kagoshima University Graduate School of Medical and Dental Sciences, Japan

TP01-019

Multi-Dimensional Proteomics Reveals a Role of UHRF2 in the Regulation of Epithelial-Mesenchymal Transition (EMT)

Sai Ge, Beijing Proteome Research Center, China

TP01-020

A Set of Mass Spectrometry-Derived Prognostic Biomarkers for Prostate Cancer Survival Prediction

Sandra Goetze, Swiss Federal Institute of Technology Zurich (ETH), Switzerland

TP01-021

Novel Risk Models for Early Detection and Screening of Ovarian Cancer

Robert.L.J. Graham, Stoller Biomarker Discovery Centre, Institute of Cancer Sciences, University of Manchester, United Kingdom

TP01-022

Systems-Wide Analysis of Protein Expression in Formalin-Fixed Paraffin-Embedded Secretory Breast Carcinoma Tissues

Dohyun Han, Biomedical Research Institute, Seoul National University Hospital, South Korea

TP01-023

An In-Depth Proteomics Investigation of the Perturbed Mechanisms Underlying Pemetrexed and Paclitaxel Treatments in Non-Small-Cell Lung Cancer

Chia-Li Han, Mastor Program for Clinical Pharmacogenomics and Pharmacoproteomics, Taipei Medical University, Taiwan

TP01-024

Understanding Male Infertility after SCI through Quantitative Proteomics

Dominic Helm, Human Reproduction Section, Division of Urology, Department of Surgery, São Paulo Federal University, Brazil

TP01-025

Clinical Application of Plasma Biomarkers for Early Detection of Pancreatic Cancer Identified from Proteomic Profile

Kazufumi Honda, National Cancer Center Research Institute, Japan

TP01-026

Integration of SWATH and MRM for Biomarker Discovery of Esophageal Squamous Cell Carcinoma

Guixue Hou, BGI-SHENZHEN, China

TP01-027

Quantitative Analysis of Wild-Type and V600E Mutant BRAF Proteins in Colorectal Carcinoma Using Immunoenrichment and Targeted Mass Spectrometry

Yung-Chin Hsiao, Molecular Medicine Research Center, Chang Gung University, Taiwan

TP01-028

Quantitative Tissue Proteomics Analysis of Primary Lung Adenocarcinoma for Potential Biomarker Discovery

Chiung-Hung Hsu, Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan

TP01-029

Identification of Potential Biomarker Related to EGFR Mutation by Functional Proteome Profiling in Primary Non-Small Lung Cancer

Yuan-Ling Hsu, National Taiwan University, Taiwan

TP01-030

Proteomic Study on Pancreatic Cancer Patients with Long and Short Survivals with Samples from the South Swedish Biobank

Dingyuan Hu, Department of Surgery, Clinical Sciences Lund, Lund University, Sweden

TP01-031

Verification of New Blood Protein Biomarkers for Breast Cancer

Yen-Chun Huang, Proteomics Research Center, National Yang-Ming University, Taiwan

TP01-032

Novel Circulating Peptide Biomarkers for Esophageal Squamous Cell Carcinoma Revealed by a Magnetic Bead-Based MALDI-TOFMS Assay

Kun Jia, National Cancer Center/cancer Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, China

TP01-033

Investigating the Platelet-Derived Growth Factor B regulation Network in Gastric Cancer with a Label Free Quantitative Proteomics Approach

Wenguo Jiang, Binzhou Medical University, China

TP01-034

Proteomic Analysis of Novel Targets Associated with Simvastatin-Induced Cell Death in DU145 Human Prostate Cancer Cells

Eun Joo Jung, Department of Biochemistry, Gyeongsang National University School of Medicine, South Korea

TP01-035

Verification of Prostate Cancer Genomics Biomarker Candidates at Protein Level Using SRM-MS

Jacob Kagan, National Cancer Institute, USA

TP01-036

Proteomics Identified the Proteins Associated with Tumor Invasion in Myxofibrosarcoma

Kazutaka Kikuta, Division of Rare Cancer Research, National Cancer Center Research Inutitute, Japan

TP01-037

Development for Lung Cancer Diagnostic Meta-Markers Using Multiple Reaction Monitoring

Yong-In Kim, Seoul National University, South Korea

TP01-038

Phosphoproteomic Analysis Aimed at Elucidating the Mechanisms Underlying the High Malignancy of Ovarian Clear Cell Carcinoma

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

TP01-039

Potential Diagnostic Value of Protein Biomarkers in Albumin-Depleted Pleural Effusions for Detection of NSCLC Malignancy and EGFR Mutation Status

*Yee Jiun Kok, Bioprocessing Technology Institute, Agency for Science, Technology and Research (A*STAR), Singapore*

TP01-040

Identification of Cerebrospinal Fluid Markers for Recurrent Malignant Brain Tumor by Quantitative Proteomics

Tomohiro Kouhata, Kumamoto University, Japan

TP01-041

Changes in Protein Expression between Primary Breast Tumour and Lymph Node or Distant Metastases

Emila Kurbasic, Lund University, Sweden

TP01-042

2D Proteomic Profile Following Agrimonia Pilosa Ledeb Roots Extract Treatment in Oral Squamous Cell Carcinoma

Yeon Ju Kwak, Department of Dental Pharmacology and Biophysics, School of Dentistry and Research Institute for Oral Biotechnology, Yangsan Campus of Pusan National University, South Korea

TP01-043

Anchorage-Independency Altered Tubular Phenotype of Melanoma Tumors through Downregulation in ANPEP/SDC1/beta4-integrin Axis

Shaochen Lee, Proteomics Laboratory, Cathay Medical Research Institute, Cathay General Hospital, Taiwan

TP01-044

The Roles of AKR1C1 and AKR1C2 in Ethyl-3, 4-Dihydroxybenzoateinduced Esophageal Squamous Cell Carcinoma Cell Death

Wei Li, National Cancer Center/cancer Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, China

TP01-045

Identification of Hypoxia-Induced Splicing Variants in Cancer Cells Using Proteomics Approach

Chia-Hung Li, National Taiwan Ocean University, Taiwan

TP01-046

Quantitative Analysis of HER2 Protein Expression in Multiple Cancer Indications

Wei-Li Liao, Nantomics, USA

TP01-047

Iron Deprivation Perturbs Ribosome Biogenesis on Protein Synthesis and Cell Growth in MCF-7 Human Breast Cancer Cells

Yih-Fong Liew, Department of Nutrition Science, Fu Jen Catholic University, Taiwan

TP01-048

Quantitative Proteomics Investigation of Frataxin Over-Expression in Colorectal Cancer Cells

Justin Lim, Department of Biological Sciences, Faculty of Science, National University of Singapore, Singapore

TP01-049

Using SWATH to Analysis Peripheral Blood Mononuclear Cells of Pancreatic Cancer

Xiaohui Liu, Institute of Biomedical Science, Fudan University, China

TP01-050

Quantitative Proteomics Analysis of a Primary Bladder Cell Line Treated with Ketamine, a Narcotics and Anesthesia Medicine

Juo Chuan Liu, Graduate Institute of Biomedical Sciences,Chang Gung University, Taiwan

TP01-051

Discovery of Potential Colorectal Cancer Serum Biomarkers through Quantitative Proteomics of the Tissue Interstitial Fluids from Two Mouse Models

Xiaomin Lou, Beijing Institute of Genomics, Chinese Academy of Sciences, China

TP01-052

Targeted Quantification of N-1-(Carboxymethyl) Valine and N-1-(Carboxyethyl) Valine Peptides of β-Hemoglobin for Better Diagnostics in Diabetes

Jagadeeshaprasad M.G, Department of Diabetes and Endocrine Research, Chellaram Diabetes Institute, India

TP01-053

Multicentric Study of the Effect of Pre-Analytical Variables in the Quality of Plasma Samples Stored in Biobanks by Complementary Proteomic Methods

Nieves Domenech, Plataforma de Proteómica. Instituto de Investigación Biomédica (INIBIC), Spain

TP01-054

Tissue Proteomic Analysis to Validate Differentially Expressed Markers Associated with Meningioma Pathobiology

Shuvolina Mukherjee, Department of Biosciences and Bioengineering, Indian Institute of Technology Bombay, India

TP01-055

Serum Proteomic Biomarkers of Hepatocellular Carcinoma Associated with Nonalcoholic Fatty Liver Diseases in Pigs

Naohiko Nakamura, Department of Surgery, Graduate School of Medicine, Kyoto University, Japan

TP01-056

A Novel Model System and Approach for Identification of Biomarkers of Response to Heat Shock Protein 90 Inhibitors in Prostate Cancer

Elizabeth Vi Nguyen, Monash University, Australia

TP01-057

Protein Panel for Monitoring the Progression of Keratoconus- Clinical Application of Mass Spectrometry

Krishnatej Nishtala, GROW Research Laboratory, Narayana Nethralaya Foundation, India

TP01-058

Proteomic Profiling of Serum Exosomes to Identify Novel Early Detection Biomarkers for Gastric Cancer

Naomi Ohnishi, Cancer Proteomics Group, Genome Center, Japanese Foundation for Cancer Research, Japan

TP01-059

Proteomic Analysis of TGF-β–Induced Cancer Metastasis

Akiko Okayama, Yokohama City University, Japan

TP01-060

Comparison of Protein Expression Profiles between Human Crown and Root Dentins by Label-Free Quantitative Proteomics Analysis

Pei-Jing Pai, Graduate Institute of Medicine, Kaohsiung Medical University, Taiwan

TP01-061

Data Independent Acquisition-Based Targeted Proteomics for Plasma Analysis – In the Context of Cancer Biomarker Detection

Sheng Pan, University of Washington, USA

TP01-062

Ubiquitin Specific Protease 19 Involved in Transcriptional Repression of Retinoic Acid Receptor

Jung-Hyun Park, Department of Biomedical Science, Cha Universtiy, South Korea

TP01-063

Proteomic and Bioinformatic Analysis of Overactive Bladder in a Rat Model

Edmond Changkyun Park, Drug & Disease Target Team, Korea Basic Science Institute, South Korea

TP01-064

The Surveillance and Early Diagnosis of Hepatocellular Carcinoma Using multiple Reaction Monitoring

Ji Young Park, Seoul National University College of Medicine, South Korea

TP01-065

Characterization of the Discoid Lateral Meniscus Tissues Using Mass Spectrometry-Based Proteomics

Jisook Park, Samsung Medical Center, South Korea

TP01-066

Bioactive Dietary Compounds (BDCs)-Mediated Anti-Cancer Effects on Colorectal Cancer Cells

Jung Eun Park, Nanyang Technological University, Singapore

TP01-067

Quantitative Analysis of AKT/mTOR Pathway Using Multiplex-Immunoprecipitation and Targeted Mass Spectrometry

Bhavin Patel, Thermo Fisher Scientific, USA

TP01-068

A Serum Based Combinatorial Proteomic Biomarker Assay is Unaffected by the Density of Breast Tissue

David Reese, Provista Diagnostics, USA

TP01-069

Proteomic Study of Thyroid Cancer Metastasis Using 3D Culture System

Kittirat Saharat, Applied Biological Sciences, Chulabhorn Graduate Institute, Thailand

TP01-070

Plasticizer Induced Tumor Migration by Regulating of Sialyltransferase Expression in Colon Cancer Cells

Pei-Chun Shih, Institute of Basic Medical Science, Taiwan

TP01-071

Proteomic Analysis of the Oral Squamous Cell Carcinoma

Shuichiro Shimada, Biofluid Biomarker Center, Institute for Social Innovation and Promotion, Niigata University, Japan

TP01-072

Proteomic Analysis of Metastatic Colorectal Cancer Cell and Verification by SRM/MRM Analysis

Takashi Shiromizu, Laboratory of Proteome Research, National Institutes of Biomedical Innovation, Health and Nutrition, Japan

TP01-073

Salivary Proteins from Pre-Malignant and Malignant Lesions of the Oral Cavity and Their Translational Potential for Early Diagnosis

Priya Sivadasan, Institute of Bioinformatics , International Tech Park , Bangalore, India

TP01-074

Quantitative Analytical Method for Measuring the Levels of PIVKAII in Human Serum Using Multiple Reaction Monitoring-Mass Spectrometry

Areum Sohn, Department of Biomedical Engineering, Seoul National University College of Medicine, South Korea

TP01-075

Method Validation of the Protein Biomarkers Approved by FDA and LDT Following CPTAC Assay Development Guidelines Using Multiple Reaction Monitoring

Minsoo Son, Departments of Biomedical Engineering, Seoul National University College of Medicine, South Korea

TP01-076

Serum Biomarker Panels for the Early Detection of Pancreatic Cancer

Jin Song, Department of Pathology, Johns Hopkins Medical Institutions, USA

TP01-077

Study on Sputum Cell Proteomics for Screening Early Detection Biomarkers of Lung Cancer

Jie Song, State Key Laboratory of Molecular Oncology, Cancer Institute and Hospital, Chinese Academy of Medical Sciences, China

TP01-078

Effects of Apigenin on Growth Inhibition and Apoptosis Induction of Human Cholangiocarcinoma Cell Line

Chantragan Srisomsap, Laboratory of Biochemistry, Chulabhorn Research Institute, Thailand

TP01-079

Discovery of ARV Induced Kidney-Injury Related Protein Biomarkers in Urine Using SWATH-MS

Stoyan Stoychev, CSIR, South Africa

TP01-080

MDC1-SDTD Repeats as a Potential Target to Block DDR and Promote Radiosensitization in Cancer Cells

Hsiang-Chun Su, Academia Sinica, Taiwan

TP01-081

Novel Hypoxia-Driven Oncogenic Pathways are Revealed by Tandem Quantitation of the Tumor Cell Proteome, Chromatome, and Secretome

Siu Kwan Sze, Nanyang Technological University, Singapore

TP01-082

Analysis of Human High-Grade Serous Ovarian Carcinoma by Mass Spectrometry Using Data-Dependent and Data-Independent Acquisition

Stefani Thomas, Department of Pathology, Johns Hopkins University School of Medicine, USA

TP01-083

Quantitative Proteomics of Transgenic Prostate Cancer Mice Reveals that PDGF-B Regulatory Network Plays a Key Role in Prostate Cancer Progression

Geng Tian, Binzhou Medical University, China

TP01-084

Global Proteome Analysis of Carcinoma Associated Fibroblasts and Dystrophic Epidermolysis Bullosa Fibroblasts in 3D Cell Culture

Regine Tölle, Department of Dermatology, University Medical Center, Germany

TP01-085

Integration of Urine and Tissue Proteomes for Biomarker Verification of Bladder Cancer Using Targeted Proteomics

Cheng-Han Tsai, Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan

TP01-086

The Effects of Dietary Polyunsaturated Fatty Acids on Prostate Cancer: Unbiased Proteomic and Phosphoproteomic Studies

Mu Wang, Indiana University, USA

TP01-087

Proteomic Analysis of Cell Response to Photon and Particle Irradiation

Uwe Warnken, German Cancer Research Center (DKFZ), Germany

TP01-088

Phosphoproteome Profiling of Isogenic Cholangiocarcinoma Exosomes Reveal Differential Expression of a Key Metastatic Factor

Churat Weeraphan, Center for Genomics and Bioinformatics Research, Faculty of Science, Prince of Songkla University, Thailand

TP01-089

GLP-1 was Identified as a Potential Therapy Target for Colorectal Cancer through Label-Free Quantitative Proteomic Analysis

Xiaodan Wei, Binzhou Medical University, China

TP01-090

Development of Phage Display-Based Platform for Discovery of Cancer Biomarkers and Targeting Ligands

Chien-Hsun Wu, Institute of Cellular and Organismic Biology, Academia Sinica, Taiwan

TP01-091

Comprehensive Proteome Analysis of Fine Needle Aspiration Cystic Fluid and Cancer Cell Secretome for Papillary Thyroid Cancer Biomarker Discovery

Chia-Chun Wu, Graduate Institute of Biomedical Sciences, College of Medicine, Chang Gung University, Taiwan

TP01-092

Uncovering the Molecular Mechanism of Inhibitory Activity of Taiwan Local Pomegranate Against Urinary Bladder Urothelial Carcinoma Cell

Ting-Feng Wu, Department of Biotechnology Southern Taiwan University of Science and Technology, Taiwan

TP01-093

Searching Tumor-Associated Proteins for Urinary Bladder Urothelial Carcinoma in Southwestern Taiwan Using Gel-based Proteomics

Chia Cheng Su, Department of Biotechnology Southern Taiwan University of Science and Technology, Taiwan

TP01-094

Salivary Proteome and Extracellular Vesicles for the Detection of Cancer

Hua Xiao, Shanghai Jiao Tong University, China

TP01-095

Metastatic Colorectal Cancer Cell-Derived Exosomes Directionally Promote the Translation and Protein Degradation of Macrophages

Lijuan Yang, Institute of Life and Health Engineering, Jinan University, China

TP01-096

Predicting Ovarian Cancer Patients' Clinical Response to Platinum-Based Chemotherapy by their Tumor Proteomic Signatures

Kun-Hsing Yu, Stanford University, USA

TP01-097

Targeted Quantitative Screening of Chromosome 18 Encoded Proteome in Plasma Samples of Astronaut Candidates

Victor Zgoda, Institute of Biomedical Chemistry, Russia

TP01-098

Multiple Post-Translational Modifications Proteomes (PTMomes) Associated with TKIs in Non Small Cell Lung Cancer

Guolin Zhang, H.Lee Moffitt Cancer Center & Research Institute, USA

TP01-099

EBP50 Suppresses the Metastasis of Breast Cancer and Hela Cells by Inhibiting Matrix Metalloproteinase-2 Activity

Junfang Zheng, Capital Medical University, China

TP01-100

Osteoporosis Risk Protein Biomarkers Suggested by a Proteome Study in Chinese Males

Xu Zhou, School of Public Health, Soochow University, China

TP02 - Glycoproteomics, Glycomics and Glycosylation In Diseases

TO02-001

In-Depth Analysis of Human Plasma Glycoproteins by a Combination of High-Resolution Native Mass Spectrometry and Middle-Down Proteomics

Vojtech Franc, Biomolecular Mass Spectrometry and Proteomics, University of Utrecht, Netherlands

TO02-002

Confident, Automated N-Glycoproteomics Profiling in Enriched and Unenriched Cell Samples

Scott Peterman, Optys Tech Corporation, USA

TO02-003

Identification of Intact Glycopeptides with In-Silico Deglycosylation Strategy for O-Glycoproteomics Analysis

Hongqiang Qin, Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China

TO02-004

Glycoproteomic Analysis of Human Plasma Using SWATH-MS

Chi-Hung Lin, Department of Chemistry and Bimolecular Sciences, Macquarie University, Australia

TO02-005

A Suite of SWATH Glycoproteomic Approaches for Easy Global Glycoprotein Analysis

Ben Schulz, The University of Queensland, Australia

TO07-001

Identification of Intact Glycopeptides at a Proteome Scale

Mingqi Liu, Institute of Biomedical Sciences, Fudan University, China

TO07-002

Integrated Glycoproteomics Demonstrates Fucosylated Serum Paraoxonase 1 Alterations and Functions In Lung Cancer

Je Yoel Cho, Seoul National University, South Korea

TO07-003

Decoding Site-Specific Alteration of Sialo-Glycoproteome In EGFR-Subtype of Non-Small Cell Lung Cancer

Yi-Ju Chen, Institute of Chemistry, Academia Sinica, Taiwan

TO07-004

Identifying Antibody and Lectin Recognition to HIV N-glycans through Native Mass Spectrometry and Glycoproteomic Analysis of Viral Envelope Spikes

Weston Struwe, University of Oxford, United Kingdom

TO07-005

Dynamic Mapping of Human Frontal Cortex According to the Developmental Stage via Neuroglycomic Approach

Jua Lee, Asia Glycomics Reference Site, Chungnam National University, South Korea

TP02-001

In-Depth LC-MS/MS Mapping of Sulfo-sialo-glycoproteome in B-chronic Lymphocytic Leukemia (CLL)

Merrina Anugraham, Institute of Biological Chemistry, Academia Sinica, Taiwan

TP02-002

Improving Confidence in Glycan Structure Characterisation Using Alternative CID Fragmentation

Christopher Ashwood, ARC Centre of Excellence in Nanoscale Biophotonics (CNBP), Macquarie University, Australia

TP02-003

Highly Selective Enrichment of Glycopeptides Based on Zwitterionically Functionalized Soluble Nanopolymers

Weiqian Cao, Institutes of Biomedical Sciences, Fudan Unversity, China

TP02-004

Glycoproteomic Analysis of O-Glcnac-Modified Proteins in Colorectal Cancer

Voraratt Champattanachai, Chulabhorn Research Institute, Thailand

TP02-005

Glycoproteomic Analysis of Serum Proteins for Oral Cancer

Shu-Chieh Chang, National Cheng Kung University, Taiwan

TP02-006

One-Fraction nanoLC-MS^2/MS^3 Analysis for High Throughput Glycome-Wide Precision Mapping of Glycotopes

Yen-Ying Chen, Institute of Biological Chemistry, Academia Sinica, Taiwan

TP02-007

Lectin Microarray: A Powerful Tool for Glycan-Based Biomarker Discovery

Li Cheng, Shanghai Jiao Tong University, China

TP02-008

Uncovering Target Glycoprotein Biosignatures Using a One-Pot Dual Nanoprobe Mass Spectrometry Assay

Mira Anne Dela Rosa, Department of Chemistry, National Taiwan University, Taiwan

TP02-009

Integrated Proteomic and N-glycoproteomic Analyses of Alzheimer's Disease Mouse Brain Reveal the Precise Alterations in Protein N-glycosylation

Pan Fang, Institutes of Biomedical Sciences, Fudan University, China

TP02-010

Increased Confidence for the Identification of N-linked Glycopeptides Using an Optimised Collision Energy Workflow

Lee Gethings, Academia Sinica, Taiwan

TP02-011

Glycoproteomics Reveals Decorin Peptides with Anti-Myostatin Activity in Human Atrial Fibrillation

Eloi Haudebourg, King's College London, United Kingdom

TP02-012

Simplified Cell Strategy for Large Scale Identification of Mucin-Type O-Glycoproteins

Jiangming Huang, Department of Chemistry, Fudan University, China

TP02-013

Influence of Sialylation on Intracellular Signalling Pathways of Hela Cells

María Ibañez-Vea, University of Southern Denmark, Denmark

TP02-014

Glycomic Profiling of Targeted Serum Haptoglobin for Gastric Cancer Using Nano LC/MS and LC/MS/MS

Seunghyup Jeong, Graduate School of Analytical Science and Technology, Chungnam National University, South Korea

TP02-015

Comparative Study of Fucosylation between Liver and Non-Liver Secreted N-Glycoproteins in Liver Cancer Plasma

Eun Sun Ji, Biomedical Omics Group, Korea Basic Science Institute, South Korea

TP02-016

In-Depth N-glycoproteome Analysis of Human Metastatic Hepatocellular Carcinoma Cell Lines

Biyun Jiang, Institutes of Biomedical Sciences, Fudan University, China

TP02-017

Direct Mapping of Additional Modifications on Phosphorylated O-glycans of α-Dystroglycan by Mass Spectrometry Analysis

Chu-Wei Kuo, Academia Sinica, Taiwan

TP02-018

Identification and Quantitation of Site-Specific N-glycoforms in Biopharmaceutical Glycoproteins Using LC-MS/MS with Glycoproteomic Database Search

Hyun Kyoung Lee, Korea Basic Science Institute, South Korea

TP02-019

Characterization of Site-Specific N-glycopeptides of Alpha-1-Acid Glycoprotein from Human Plasma by an Interlaboratory Study Using LC-MS/MS

Ju Yeon Lee, Korea Basic Science Institute, South Korea

TP02-020

Smart Polymer for Saccharide Discrimination and Glycopeptide Enrichment

Xiuling Li, Dalian Institute of Chemical Physics, chinese Academy of Sciences, China

TP02-021

Investigating the Roles of Glycosylation in Plasticizer Induced Tumor Migration in Colon Cancer Cells

Tsung-Hsien Lin, National Cheng Kung University, Taiwan

TP02-022

Glycoproteome-Wide Identifications of Novel *GALNT14* Substrates Using Tandem Mass Spectrometry

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

TP02-023

Salivary Glycomic Approach for the Distinction of Human Constitutions

Hantae Moon, Graduate School of Analytical Science and Technology, Chungnam National University, South Korea

TP02-024

Neural Glycomics and Epigenetic Regulation

Miyako Nakano, Graduate School of Advanced Sciences of Matter, Hiroshima University, Japan

TP02-025

Integrated GlycoProteome Analyzer (I-GPA) for Automatic Identification and Quantitation of Site-Specific N-Glycosylation in Human Plasma

Gun Wook Park, Biomedical Omics Group, Korea Basic Science Institute, South Korea

TP02-026

Glycomic Approach for Design of Humanized Mouse Model via Nano-LC/MS and LC/MS/MS

Dan Bi Park, Chungnam National University, South Korea

TP02-027

Building a High Confidence, Quantitative O-glycopeptide Profile for IgA

Amol Prakash, Optys Tech Corporation, USA

TP02-028

Performance Evaluation of First and Second Generation Quadrupole Dual Cell Linear Ion Trap Orbitrap Hybrid MS for Glycopeptide Analysis

Julian Saba, Thermo Fisher Scientific, Canada

TP02-029

Role of CD52 Glycosylation in Immunosuppression

Abdulrahman Shathili, Macquarie University, Australia

TP02-030

Ligand-Independence of the Colony Stimulating Factor 3 Receptor (CSF3R) Results from Loss of Sialylation which Leads to Increased Oncogenesis

David Spiciarich, Departments of Chemistry, University of California, USA

TP02-031

Glycoproteomic Alterations in Drug-resistance Lung Cancer Cell Lines Revealed by Lectin Magnetic Nanoprobe-based Affinity Mass Spectrometry

Juanilita Waniwan, Institute of Chemistry, Academia Sinica, Taiwan

TP02-032

Preference of the Universal Enrichment Methods for N-Glycopeptides with Particular Glycoforms

Yu Xue, Institute of Chemistry, Fudan University, China

TP02-033

Integrating Glycoproteomics in the Multi-Omics Analysis of Type II Diabetes Onset

Christine Yiwen Yeh, Stanford University School of Medicine, USA

TP02-034

Ion Mobility and High-Resolution Native Mass Spectrometry Reveals Glycan-Specific Modulation of Glycoprotein Stability

Hsin-Yung Yen, Department of Chemistry, Oxford University, United Kingdom

TP02-035

Preparative Purification of N-linked Glycopeptides by Using Two-Dimensional Chromatography for the Structural Characterization

Long Yu, Dalian Institute of Chemical Physics, China

TP02-036

New Glycoproteomic Tools to Study N-Glycosylation and to Uncover Novel Glycophenotypes in Human Diseases

Lucia Zacchi, The University of Queensland, Australia

TP03 - Lysine Modifications and PTM Crosstalks

TO03-001

Unravelling Crosstalks between SUMOylation and Other Protein Modifications in Human Cells Using Dynamic Proteomics

Frederic Lamoliatte, Institute for Research in Immunology and Cancer, Universite de Montreal, Canada

TO03-002

Towards Comprehensive Analysis of Protein ADP-Ribosylation

Yonghao Yu, Ut Southwstern Medical Center, USA

TO03-003

Acetylome Analysis Reveals Carbon Metabolism as a Key Factor Enhancing Thermogenesis in White Adipocytes

Hsin-Yi Chang, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

TO03-005

Efficient Enrichment of SUMOylated Peptides from Alpha-Lytic Protease Digest Using K- ε -GG Remnant Immuno-affinity Purification

Hongbo Gu, Cell Signaling Technology, USA

TP03-001

Apoptotic Protein Bax is Regulated by Multiple Deubiquitinating Enzymes in Response to DNA Damage

Kwang-Hyun Baek, CHA University, South Korea

TP03-002

Investigating the Significance of Methyltransferase-like (METTL)-Family Lysine Methylation Enzymes on Heat Shock Proteins and Their Role in Cancer

Byron Baron, Centre for Molecular Medicine and Biobanking, Faculty of Medicine and Surgery, University of Malta, Malta

TP03-003

Lysine Propionylation is a Widespread Post-Translational Modification Involved in Regulation of Photosynthesis and Metabolism in Cyanobacteria

Feng Ge, Institute of Hydrobiology, Chinese Academy of Sciences, China

TP03-004

PIAS1-Mediated SUMOylation of BAF57 is a Critical Regulator of Cell Growth and Drug Sensitivity in Ovarian Cancer Cells

Chongyang Li, Institute for Research in Immunology and Cancer, Canada

TP03-005

A Novel Post-Translational Modification: Lysine Propionylation was Identified in Bacterial Species

Hiroki Okanishi, Kumamoto University, Japan

TP03-006

Acetyl Proteomics Using a Novel Enrichment Strategy for Lysine Acetylated Peptides

Kazuya Tsumagari, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

TP03-007

Comprehensive Analysis of Proteome and Lysine Acetylome in Human Esophageal Carcinoma Cells

Kai Zhang, Tianjin Key Laboratory of Medical Epigenetics, Tianjin Medical University, China

TP04 - Other PTMomics and Crosstalks

TO03-004

Effects of Co-/Post-Translational Modifications on Protein Function

Hisashi Hirano, Yokohama City University, Japan

TP04-001

Quantification of ADP-Ribosylated Peptides during Oxidative Stress Using a Label-Free PRM Approach

Vera Bilan, Department of Molecular Mechanisms of Disease, University of Zurich, Switzerland

TP04-002

Characterization of Ribosomal Protein Modifications in Response to Glucose Starvation

Hsin-Lian Lin, Institute of Biochemistry and Molecular Biology, NYMU, Taiwan

TP04-003

Identification of Glycosylphosphatidylinositol-Anchored Proteins Profile in Organs

Yusuke Masuishi, Graduate School of Medical Life Science, Yokohama City University, Japan

TP04-004

A HPLC Coupled Mass Spectrometry Approach to Analyze Modified Ribonucleosides from RNA

Selene Swanson, Stowers Institute for Medical Research, USA

TP04-005

Rapid Identification and Quantification of Amino Acid Isomers Occurring in Peptides under Physiological Conditions: A Targeted Proteomics Approach

Atsuhiko Toyama, Shimadzu Corporation Mass Spectrometry Business Unit, Japan

TP04-006

Global Identification of Free Protein N-termini and Protease Substrates by Chemical Modification of N-Termini

Hao Zhang, Xi'an Jiaotong-Liverpool University (XJTLU), China

TP05 - Proteome Dynamics: Turnover and Degradomics

TO08-001

Copy Number Alteration Programmed Protein Turnover Quantified by pSILAC and SWATH Mass Spectrometry

Yansheng Liu, Department of Biology, Institute of Molecular Systems Biology, ETH Zurich, Switzerland

TO08-002

High Resolution Mass Spectrometry Cellular Thermal Shift Assay (HR-MS-CETSA) - Post-Translational Modifications Impact on Protein Stability

*Radoslaw Sobota, Institute of Molecular and Cell Biology, Agency for Science, Technology and Research (A*STAR), Singapore*

TO08-003

A Dynamic Picture of the Proteome and Ubiquitinome upon Proteasome Inactivation

Jeroen Demmers, Erasmus University Medical Center Rotterdam, Netherlands

TO08-004

Proteome Turnover Analysis Reveals Substrates and Physiological Role of Membrane Proteases

Ansgar Poetsch, IIB-CONICET-UNMdP Mar del Plata, Argentina

TO08-005

A Novel Function of CRL2 Ubiquitin Ligase in Protein Quality Control

Hsiu-Chuan Lin, Institute of Molecular Biology, Academia Sinica, Taiwan

TP05-001

Identification of HTRA1 Substrates in the Context of Age-Related Macular Degeneration

Chia-Yi Chen, Institute of Molecular Medicine and Cell Research, University of Freiburg, Germany

TP05-002

Old-Age Proteins Asymmetrically Inherited in Mother Cells of Budding Yeast

Keiji Kito, School of Agriculture, Meiji University, Japan

TP05-003

A Novel Ubiquitin Ligase Complex Regulates Gastric Cancer Proliferation by Modulating Biosynthesis of Guanine Nucleotides

J. Eugene Lee, Korea Research Institute of Standards and Science, South Korea

TP05-004

Proteome-Wide Analysis of Protein Stability in *E. Coli* Using Pulse Proteolysis

Liang Zhao, Max Planck Institute of Biochemistry, Germany

TP06- Interactomics and Protein Network

TO01-001

The Regulatory Role of Methylation and Methylation–Phosphorylation Crosstalk in Protein Interaction Networks

Marc Wilkins, University of New South Wales, Australia

TO01-002

Network Analysis Reveals a Dominant Role of Protein-Level Regulation in Coordinating Gene Functions

Bing Zhang, Vanderbilt University Medical Center, USA

TO01-003

Profiling the Phosphotyrosine Interactome of Receptor Tyrosine Kinases

Runsheng Zheng, Chair of Proteomics and Bioanalytics,Technische Universitaet Muenchen, Germany

TO01-004

Phylointeractomics Reconstructs Functional Evolution of Protein Binding

Dennis Kappei, Cancer Science Institute of Singapore, Singapore

TP06-001

Systematic Protein Interactome Analysis of Glycosaminoglycans Revealed YcbS as a Novel Bacterial Virulence Factor

Shih-Hsiang Hsiao, Department of Biomedical Science and Engineering, National Central University, Taiwan

TP06-002

Metastatic Hepatocellular Carcinoma Cells Enrich Translation Regulatory Proteins in Exosomes

Zhang Jing, Jinan University, China

TP06-003

Unraveling the Dynamic Signaling Network Capacity of HBx in HBV Host Infection

Emanuela Milani, Institute of Molecular Systems Biology, Dep. of Health Sciences and Technology, ETH Zürich, Switzerland

TP06-004

Tête-à-TET: Elucidating the Interactome of Tet1 and Tet3

Andrea Kuenzel, Ludwig-Maximilians Universität München, Germany

TP06-005

Identification of HAX1 Interacting Proteins by BioID System

Byoung Chul Park, KRIBB, South Korea

TP06-006

Discovery of Parasite-Host Interaction Contributing Changing of Host-Lipid Metabolism for Malaria Liver Stage Development

Supachai Topanurak, Dept. of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Thailand

TP06-007

Characterization of the EGFR Interactome in Non-Small Cell Lung Cancer Cells

Pei-Shan Wu, Institute of Chemistry, Acadamia Sinica, Taiwan

TP06-008

Proteomic Analysis Reveals a Role for PKM2 in Modulating DNA Damage Response

Li Xia, Shanghai Jiao Tong University School of Medicine, China

TP06-009

Interactome Analysis Reveals a Critical Role of DDX3-hnRNPK Interaction in the hnRNPK-Mediated Apoptosis

Jen-Hao Yang, Department of Life Sciences and Institute of Genome Sciences, National Yang-Ming University, Taiwan

TP06-010

PTPLAD1 Suppresses Colorectal Cancer Metastasis through Interacting with PHB

Jie Yang, Key Laboratory of Functional Protein Research of Guangdong Higher Education Institutes, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

TP06-011

Proteomic Exploration of Invasiveness-Associated KPNA2 (importin α1) Interactome and Its Upstream Signaling in Lung Cancer

Chia-Jung Yu, Molecular Medicine Research Center, Chang Gung University, Taiwan

TP06-012

Unfolded Protein and Preeclampsia: A Proteomics Investigation

Wanling Zhang, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

TP07- Protein Complexes and Structural Proteomics

TO01-005

Determining Network Topology, Distance Restraints and Activation Markers from Endogenous Protein Complexes

Marco Faini, ETH Zurich, Switzerland

TP07-001

Optimization of Crosslinked Peptide Analysis on an Orbitrap Fusion Lumos Mass Spectrometer

Ryan Bomgarden, Thermo Fisher Scientific, USA

TP07-002

Characterization of EV71 Replicative Mechanisms Targeted by Anti-EV71 Cocktail Therapy

Yen Chiu Chang, Department of Biotechnology and Laboratory Science in Medicine, National Yang-Ming University, Taiwan

TP07-003

Examination of Aptamer-Protein Complex Structure by Mass Spectrometry

Guo-Ming Hung, National Taiwan Ocean University, Taiwan

TP07-004

Interactome Analysis Identified the Specific Interaction of TCTP and EF1A2 in Neurofibromatosis Type 1 (NF1)-Associated Tumors

Daiki Kobayashi, Graduate School of Medical Sciences, Kumamoto University, Japan

TP07-005

Establishment of an APEX-Based Procedure that Effectively Helps Analyze Protein Quaternary Structures

Li-Hua Li, Department of Pathology and Laboratory Medicine, Taipei Veterans General Hospital, Taiwan

TP07-006

Effect of Different Lipid Membranes on the Structural Dynamics of Aquoporin Z

Qingsong Lin, Department of Biological Sciences, National University of Singapore, Singapore

TP07-007

Characterizing Folding and Misfolding Properties of Human Serum Amyloid A1

Jin-Lin Wu, Ph.D. Program for Cancer Biology and Drug Discovery, China Medical University and Academia Sinica, Taiwan

TP08- Antibodies and Protein Arrays

TO06-001

Status of the Affinity Binder Knockdown Initiative

Tove Alm, Science for Life Laboratory, KTH Royal Institute of Technology, Sweden

TO06-002

Heterogeneous Ribonucleoprotein K (hnRNP K) Binds the 5' Terminal Sequence of the Hepatitis C Virus RNA and Mature miR-122

Chien-Sheng Chen, Department of Biomedial Science and Engineering, National Central University, Taiwan

TO06-003

A High-Content Functional Mycobacterium Tuberculosis Proteome Microarray and Its Applications

Yang Li, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University, China

TO06-004

Utilizing Protein Microarray to Monitor Blood-Brain Barrier Disruption and Active Inflammation in Plasma Samples from Multiple Sclerosis Patients

Malene Moeller Joergensen, Department of Clinical Immunology, Aalborg University Hospital, Denmark

TO06-005

Mapping Transcription Factor Interactome Networks using HaloTag Protein Arrays

Junshi Yazaki, Riken, Japan

TP08-001

Molecular Design of scFv Antibodies for Site-Specific Photochemistry-Based Applications in Affinity Proteomics

Mattias Brofelth, Dept. of Immunotechnology, Lund University, Sweden

TP08-002

Deciphering Systemic Lupus Erythematosus Associated Serum Biomarkers Reflecting Apoptosis and Disease Activity

Payam Delfani, Dept. of Immunotechnology and CREATE Health, Lund University, Medicon Village, Lund, Sweden

TP08-003

Quantitative Analysis of Acetylated Protein and Its Modification Level Based on UCNPs

Fan Huizhi, Fudan University, China

TP08-004

Development of Lung Cancer Diagnostic Method Using Exosomal Protein DDOST

Jisu Lee, Department of Bioengineering, College of Engineering, Hanyang Univ., South Korea

TP08-005

Development of Humanized Antibody Against EpCAM for Cancer and Cancer Stem Cell Theranostics

Ruei-Min Lu, Institute of Cellular and Organismic Biology, Academia Sinica, Taiwan

TP08-006

Subpopulations of Hepatocellular Carcinoma with High MAPK and mTOR Signaling Activity Revealed by Reverse-Phase Protein Array Analysis

Mari Masuda, National Cancer Center Research Institute, Japan

TP08-007

Autoantibody Profiling in Healthy Heavy Smokers at Risk for COPD

Maria Mikus, Affinity proteomics, SciLifeLab, KTH-Royal Institute of Technology, Sweden

TP08-008

Generation and Purification of Highly Phosphorylated Site specific Antibodies for Human N1ICD

Yunshan Ning, Biotherapy Institute, School of Biotechnology, Southern Medical University, China

TP08-009

Autoimmunity Screening and Antibody Validation Using High-Density Protein Microarrays

Ulrika Qundos, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

TP08-010

PEAKS AB – A Software Tool for Monoclonal Antibody Sequencing and Characterization with LC-MS

Baozhen Shan, Bioinformatics Solutions Inc, Canada

TP08-011

Harnessing Translational Research with Protein Microarrays

Xiaobo Yu, Beijing Proteome Research Center, China

TP08-012

Autoantibody Profiling Using Ultra-Dense Peptide Microarrays

Arash Zandian, SciLifeLab - KTH (Royal Institute of Technology), Sweden

TP09- Liver and Toxicoproteomics: Metabolism, Drug Transformation and Toxicity

TO05-001

Personalized Proteomic Characterization of Hepatitis B Virus-Associated Hepatocellular Carcinomas

Ying Jiang, National Center for Protein Science . Beijing, China

TO05-002

In Vitro Investigation of an Adverse Outcome Pathway of Cholestatic Liver Injury Using Quantitative Phosphoproteomics

René Zahedi, ISAS, Germany

TO05-003

Differential Proteomic Analysis of Cholangiocarcinoma Cells and Cell-Derived Extracellular Vesicles by Label Free Mass Spectrometry

Felix Elortza, CIC bioGUNE, Proteomics Platform, CIBERehd, ProteoRed-ISCIII, Spain

TP09-001

Relative Quantitation for Expression Evaluation of Drug Metabolizing Enzymes Using Surrogate Peptide Approach by Quadrupole Time of Fight

Christine Miller, Agilent Technologies, India

TP09-002

Hepatic Proteome Analysis of Dioxin-Sensitive and -Resistant Mice Exposed to 2,3,7,8-Tetrabromodibenzo-*p*-Dioxin

Thanh Hoa Nguyen, Center for Marine Environmental Studies (CMES), Ehime University, Japan

TP09-003

Simultaneous Quantification of Drug Transporters, CYP Enzymes, and UGTs in Human Liver Microsomes by High-Microflow LC-MS/MS

Sumio Ohtsuki, Faculty of Life Sciences, Kumamoto University, Japan

TP10- Protein Standards and Model Organisms: Expanding Our Horizons

TO10-001

The ProteomeXchange Consortium: 2016 Update

Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, United Kingdom

TO10-002

proBAMconvert: Organizing MS Identifications in a Genome-Centric Fashion Enables Proteogenomics and Proteomics Integration

Gerben Menschaert, University of Ghent, Belgium

TO10-004

Adipose Tissue Pathways in Obesity: Iberian Pig as Large Animal Model of Metabolic Disorders

Cristian Piras, DIMEVET - Department of Veterinary Medicine, University of Milan, Italy

TO10-006

Proteome Alterations in the Porcine Endometrium during Embryo Implantation

Thomas Fröhlich, Laboratory for Functional Genome Analysis, Gene Center, LMU-Munich, Germany

TP10-001

A QPrEST Resource for Targeted Plasma Analysis

Fredrik Edfors, Science For Life Laboratory, Sweden

TP10-003

High-Throughput Production of Heavy Isotope-Labeled Protein Epitope Signature Tags to Use as Internal Standards in Mass Spectrometry

Anne-Sophie Svensson, Human Protein Atlas, Sweden

TP10-004

Development of an All-Recombinant Intact Protein Standard for LC MS Application Development and System Suitability Testing

Rosa I Viner, Thermo Fisher Scientific, USA

WP01- Proteogenomics

WO02-001

A Proteogenomics Approach to Reveal Molecular Mechanisms of COPD

Peter Horvatovich, University of Groningen, UMCG, Department of Pathology and Medical Biology, Netherlands

WO02-002

Launch of MissingProteinPedia: Accelerating Discovery of the Human Proteome Project's "Missing Proteins"

Mark S Baker, Macquarie University, Australia

WO02-003

Proteogenomics of Human Cancer Cell Lines: Coding Variants Identified by Shotgun Proteomics

Sergei Moshkovskii, Institute of Biomedical Chemistry, Russia

WO02-004

Proteogenomic Profiling of Neoantigens for Personalized Cancer Immunotherapy

Koji Ueda, Japanese Foundation for Cancer Research, Japan

WO02-005

Missing Genes and Supplementary Tissues in the Human Protein Atlas

Evelina Sjostedt, Kth - Royal Institute of Technology, Sweden

WP01-001

Identification of Proteomic and Proteogenomic Biomarkers of Prostate Cancer in Seminal Plasma

Andrei Drabovich, Department of Laboratory Medicine and Pathobiology, University of Toronto, Canada

WP01-002

Search Pipeline of Single Amino Acid Variants Using neXtProt Database

Heeyoun Hwang, Biomedical Omics Group, Korea Basic Science Institute, South Korea

WP01-003

Proteogenomic Approaches to Discovery of Alternatively Spliced Proteins in Hepatocellular Carcinoma Cell Lines

Seul-Ki Jeong, Yonsei Proteome Research Center, South Korea

WP01-004

Multiplexed Mass Spectrometric Screening of EGFR Mutation in Non-Small-Cell Lung Cancer

Chi-Ting Lai, Institute of Chemistry, Academia Sinica, Taiwan

WP01-005

Protein Expression Landscape of Mouse Embryos during Pre-Implantation Development

Lujian Liao, East China Normal University (ECNU), China

WP01-006

Have Small Proteins Been Overlooked? A Proteogenomics Approach Using Ribosome Profiling, MS and Bioinformatics

Volodimir Olexiouk, University of Ghent, Belgium

WP01-007

A Comprehensive Proteogenomic Workflow Reveals Novel Insights into Leukemogenesis

Jarrod Sandow, The Walter & Eliza Hall Institute, Australia

WP01-008

Proteogenomic Monitoring and Assessment of Increased Thermogenesis In response to β-Adrenergic Signaling in Ahnak Deficiency

Jawon Seo, Seoul National University, South Korea

WP01-009

proBAMsuite: A Bioinformatics Framework for Genome-Based Representation and Analysis of Proteomics Data

Xiaojing Wang, Vanderbilt University Medical Center, USA

WP01-010

GAPP: A Proteogenomic Software for Genome Annotation and Global Profiling of Posttranslational Modifications in Prokaryotes

Ming-Kun Yang, Institute of Hydrobiology, Chinese Academy of Sciences, China

WP01-011

Identification for Protein-Level Evidence of Genomic Variants in Cancer Cells Using New Proteogenomic Approach

Jeonghun Yeom, Department of Biological Chemistry, Korea University of Science and Technology, South Korea

WP01-012

Proteogenomic Monitoring and Assessment of Increased Thermogenesis In response to β-Adrenergic Signaling in Ahnak Deficiency

Junehyeong Yim, Department of Biochemistry, College of Veterinary Medicine, Research Institute for Veterinary Scienc, South Korea

WP01-013

A Rigorous Proteogenomics Workflow to Discover Functional Novel-Coding Loci and Single Amino Acid Variants

Yafeng Zhu, Karolinska Institutet, Sweden

WP02- Multiomics for Precision Medicine and Systems Biology

WP02-001

Human Personal Omics Profiling (hPOP)

Sara Ahadi, Stanford University, USA

WP02-002

Monitoring Oxidative Stress and Progression to Cell Death: From Secretome to Blood Diagnosis

Sandra I. Anjo, CNC - Center for Neuroscience and Cell Biology – University of Coimbra, Portugal

WP02-003

Meta-Analysis of Omics Profiling to Reveal Translational Regulation of Chronic Hypoxia Stress in Colon Cancer Cells

Jeng-Ting Chen, Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan

WP02-004

Extracellular Vesicles - A Novel Class of Biomarkers

Fouzi El Magraoui, Leibniz-Institut Für Analytische Wissenschaften – ISAS - e.V., Germany

WP02-005

Integrative Multi-Omic Analysis of a Single Immune Cell Type

Min-Sik Kim, Kyung Hee University, South Korea

WP02-006

The Dynamic Responses of Gene Expression in Meiosis I prophase of Mouse Spermatocytes

Qidan Li, BGI-SHENZHEN, China

WP02-007

Towards an In-Depth Overview about Increasing Arginine Production in C. *Glutamicum* by Rational Strain Design Using Metabolomics and Proteomics

Moon Liao, Bruker Daltonics, Taiwan

WP02-008

Quantitative Proteomics and Whole Transcriptomics Sequencing of Progeria-Derived Cells Point to a Key Role of IGF Signaling Pathway in Premature Aging

Jesús Mateos, Cell Therapy and Reg Med Group, INIBIC- SERGAS. Medicine Dept UDC, A Coruña, Spain

WP02-009

Transcriptomic and Proteomic Verification of Predicted Scheme of ATRA-Induced HL60 Cell Line Differentiation

Svetlana Novikova, Institute of Biomedical Chemistry, Russia

WP02-010

The Relationship between Urine Peptidome and Protein Misfolding During Preeclamsia

Igor Popov, Moscow Institute of Physics and Technology, Russia

WP02-011

Diversity of HNF4A Function in Regulating Growth and Invasion of HCC

Zhao-Yu Qin, Fudan University, China

WP02-012

Towards Spatially Resolved, Multiplexed (Up to 800 plex) Digital Characterization of Protein and mRNA Abundance in Tissue

Niroshan Ramachandran, Nanostring Technologies, USA

WP02-013

Proteomics E-Learning and Outreach Initiatives: An Effort from Indian Proteomics Community

Panga Jaipal Reddy, Indian Institute of Technology Bombay, India

WP02-014

Proteome and Transcriptome Analysis of Retinoic Acid-Induced Differentiation of Human Leukemia HL-60 C

Olga Tikhonova, Institute of Biomedical Chemistry, Russia

WP02-015

A Systems Biology Approach to Dissect Acetylation-dependent Cancer Vulnerabilities

Dijana Vitko, CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria

WP02-016

Lipidomic Analysis of Risk Factors for Chronic Total Occlusions after Percutaneous Coronary Intervention

Zhenxin Wang, Institute of Biomedical Science, Fudan University, China

WP02-017

Systematic Identification of Arsenic-Binding Proteins Reveals that Hexokinase-2 is Inhibited by Arsenic

Hainan Zhang, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University, China

WP02-018

Integrative Systems Biology Investigation of Fabry Disease

Marco Fernandes, Institute of Cardiovascular and Medical Sciences, University of Glasgow, United Kingdom

WP03- Cysteine Modifications and Redoxomics

WO03-001

Quantitative Proteomics Depicts the Landscape of Cysteine Redoxome for Nitric Oxide-Mediated Myocardial Protection Against Ischemia-Reperfusion Injury

Tzu-Ching Meng, Institute of Biological Chemistry, Academia Sinica, Taiwan

WO03-002

Proteomic Analysis of S-Sulfhydration by Ultrafilter-Assisted Functional Supramolecular Polymer Capture

Huiming Yuan, Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China

WO03-003

TRPC6-Dependent S-Nitrosylation in Duchenne Muscular Dystrophy

Heaseung Sophia Chung, The Johns Hopkins Medical Institutions, USA

WO03-004

Proteomic and Redox Proteomic Analyses Reveal a Dual ROS-Regulation of Glucose Uptake in Adipocytes

Zhiduan Su, The University of Sydney, Australia

WO03-005

Identification of Protein Estrogenization as a Redox Post-Translational Modification by Shot-Gun Proteomics and Activity Probe with Dimethyl Labeling

Shu-Hui Chen, National Cheng Kung University, Taiwan

WP03-001

Multiplexed Isobaric IodoTMT-Switch Approach to Identify and Quantify the Changes in the Cardiac Redox-Environment

Yi-Yun Chen, Institute of Biological Chemistry, Academia Sinica, Taiwan

WP03-002

Identification of Carbonylated Proteins Caused from Oxidative Stress in Hepatocyte Line: Preliminary Study on Pathology of Fatty Liver Disease

Peerut Chienwichai, Dept. of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University, Thailand

WP03-003

Thio-Tag Tip Method by Using Zinc(II)–Cyclen-Attached Agarose Beads for Enrichment of Cysteine-Containing Biomolecules

Hiroshi Kusamoto, Hiroshima University, Japan

WP03-004

Characterization of Total Thiol Redox Status in Human Fibroblasts Using MS-Based Quantitative Approach iodoTMT

Kristyna Pimkova, Biomedical Research Center University Hospital Hradec Kralove, Czech Republic

WP04- Imaging Mass Spectrometry

TO04-001

Molecular Imaging of Protein in Tissues Using Ambient Ionization Top-Down Mass Spectrometry

Cheng-Chih Hsu, Department of Chemistry, National Taiwan University, Taiwan

TO04-002

3D MALDI Imaging Mass Spectrometry Using Next Generation Technologies - Reconstruction of a Molecular Imaged Epididymis

Charles Pineau, Protim - Inserm U1085 - Irset, 35042 Rennes, France

TO04-003

Localization and Identification of Peptides from Tissue Using High-Speed MALDI TOF/TOF Mass Spectrometry

Sabu Sahadevan, Bruker Daltonics, France

TO04-004

Monitoring ErbB1 and ErbB2 Interaction and Activation Using Engineered Cell Lines and Duolink Proximity Ligation Assay by High-Content Imaging

Tracy Adair-Kirk, MilliporeSigma, USA

TO04-005

Molecular Profile Discrimination and Mapping of Skeletal Muscle Regeneration in Rat Crush Model Using MALDI Imaging

Anne Denys, Université Paris 13; Sorbonne-Paris-Cité, UMR CNRS 7244, Bobigny, France

WP04-001

Identification Algorithm of Proteins in 2DE gel image Basing on Matlab Development Environment

Lijie Wu, Tongji University, China

WP04-002

A New Mass Spectrometry Imaging Method for Evaluation of Drug Distribution in the Central Nervous System

Kenichi Watanabe, Department of Biomedical Engineering, Clinical Protein Science & Imaging, Lund University, Sweden

WP05- Subcellular, Spatial and Single Cell Proteomics

TO09-001

Quantitative Proteome-Wide Profiling of the Retromer Cargo Landscape

Christina Bell, Department of Cell Biology, Harvard Medical School, USA

TO09-002

Refining the Details in the Tissue-Based Map of the Human Proteome

Cecilia Lindskog, Science for Life Laboratory, Dept. of Immunology Genetics and Pathology, Uppsala University, Sweden

TO09-003

Membrane Localization of Metabolic Enzymes and Metabolic Modulation in a Cell Division Mutant of *Escherichia Coli* Identified by Omics Approaches

Yu-Ling Shih, Academia Sinica, Taiwan

TO09-004

Determining Post-Translational Modifications of Nuclear Proteins

Ryotaro Ban, Graduate School of Medical Life Science, Yokohama City University, Japan

TO09-005

Single-Cell Proteome Profiling: Innovations in Sample Preparation

Masaki Wakabayashi, Kyoto University, Japan

WP05-001

Standardization of Mitochondrial Preparations for the Human Proteome Project

Mauro Fasano, University of Insubria, Italy

WP05-002

A Mouse Tissue Transcription Factors Atlas

Mingwei Liu, National Center for Protein Sciences, Beijing, China

WP05-003

Subcellular Look at Asthenozoospermia: Proteomic Analysis of Human Sperm Tail in Asthenozoospermic Patients

Tohid Rezaei Tobraggaleh, Department of Embryology, Reproductive Biomedicine Research Center, Royan Institute, ACECR, Iran

WP05-004

Major Mitochondrial Machineries are Integral Part of Cell Architecture Comprising Cytoskeleton and Nuclear Matrix

Cheng Hsien Yang, Institute of Biochemistry & Molecular Biology, National Yang-Ming University, Taiwan

WP06- Membrane and Extracellular Proteomics

WO04-001

Analysis of Plasma Membrane Proteomes of Gastric Cancer Cells Reveals that ASCT2 is Involved in Cancer Metastasis by Targeting WNT/b-Catenin Signaling

Feng Liu, Department of Medical Systems Biology, Fudan University, China

WO04-002

Tumour-Dependent Fibroblast Activation: When a Good Neighbour Turns Bad

Wei Wu, Utrecht University, Netherlands

WO04-003

Analysis of Proteoforms in Membrane Protein Complexes by CID/ETD Top-Down Proteomics

Hans Wessels, Radboudumc, Netherlands

WO04-004

In silico characterization of the human lipid raft proteome

Michelle Hill, The University of Queensland, Australia

WO04-005

Exosomal EphA2 Transmits Chemoresistance and Predicts Pancreatic Cancer Patient Responses to Therapy

Tony Hu, Houston Methodist Research Institute/ weill Cornell Medical College of Cornell University, USA

WO04-006

Systemic Perturbation of Keratinocyte Homeostasis by Genetic Loss of the Extracellular Matrix Protein Collagen VII

Kerstin Thriene, Department of Dermatology, Medical Center - University of Freiburg, Germany

WP06-001

Bio-Inspired Nanoparticles Derived from Immune Cells: Design, Characterization, and Understanding Their Cellular Fate by Proteomic Tools

Claudia Corbo, Houston Methodist Research Institute, Houston, TX, USA

WP06-002

Label-Free Proteomic Analysis of Exosomes Secreted by HBV-Inducible HepAD38 Cell Line

Xiaofang Jia, Shanghai Public Health Clinical Center, Fudan University, Shanghai 201508, China, China

WP06-003

Mining Biomarkers for Gastric Cancer Diagnosis by Personalized Membrane Proteomics and Multiple Reaction Monitoring Mass Spectrometry

Tai-Du Lin, Institute of Chemistry, Academia Sinica, Taipei, Taiwan, Taiwan

WP06-004

Comprehensive Membrane Proteome Analysis for Discovery of Novel Potential Therapeutic Targets Against HTLV-1 Associated Disease

Satoshi Muraoka, Cancer Proteomics Group, Genome Center, Japanese Foundation for Cancer Research, Tokyo, Japan

WP06-005

A Novel *TP53* Pathway Influences the Colorectal Cancer Tumor Microenvironment via Exosomes

Yulin Sun, National Cancer Center/cancer Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, China

WP06-006

Inflammatory Signaling-Derived Exosome Activate Immune Response in Macrophages

Jian Wang, National Center for Protein Sciences (beijing), Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, China

WP06-007

Quantitative Proteomics of Fresh Tissue-Derived Secretome Reveal the Molecular Mechanisms of Hepatocellular Carcinoma Tumorignesis and Development

Xiaohua Xing, Mengchao Hepatobiliary Hospital of Fujian Medical University, China

WP07- Stem Cell Proteomics

WP07-001

Functional Integrated Proteomics Identified "Glyco-Niche" Signalings as a Regulator of the Maintenance and Differentiation of Cancer Stem Cells

Norie Araki, Graduate School of Medical Siences, Kumamoto University, Japan

WP07-002

Proteomic Analysis of Low Folate-Induced Onco Spheroid Formations in Human Colonic Adenocarcinoma Cells

Wen-Yu Lan, Department of Nutritional Science, Fu Jen Catholic University, Taiwan

WP07-003

A Study on Effects of sRAGE Secreting Human UCB-MSC in Parkinson's Disease Model

Jaesuk Lee, Lee Gil Ya Cancer and Diabetes Center, Gachon University, South Korea

WP07-004

Comprehensive N-Glycoproteomics of Neural Stem Cell Differentiation

Da Kyeong Park, Korea Basic Science Institute, South Korea

WP07-005

Proteomics Identifies Cell Surface Marker for Isolation of Cardiac Progenitors for Cell-Based Therapy in Cardiac Infarction

Ghasem Hosseini Salekdeh, Royan Institute for Stem Cell Biology and Technology, ACECR, Iran

WP07-006

Integrative Omics Reveals N-Glycoproteome-Wide Alterations and Their Functional Network in Induced Pluripotent Stem Cells

Putty-Reddy Sudhir, Genomics Research Center, Academia Sinica, Taiwan

WP08- Neurological Disorders and Neuroproteomics

WO08-001

Gene Expression and Proteomic Analysis Of Cognitive Dysfunction in People with Remitted Major Depression

Klaus Oliver Schubert, The University of Adelaide, Australia

WO08-002

Proteomic Dissection of AMPA Receptor Complexes Identifies FRRS1l as a Determinant for Receptor Biogenesis Mutated in Severe Intellectual Disability

Uwe Schulte, University of Freiburg, Institute for Physiology, Germany

WO08-003

Autoantibody Response in Meningioma Patients Reveals Aberrations in Signalling Pathways

Shabarni Gupta, Indian Institute of Technology Bombay, India

WO08-004

Proteomic Analysis of Motor Neurons from Induced Pluripotent Stem Cells: ALS

Victoria Dardov, Cedars Sinai Medical Center, USA

WO08-005

Analysis of the *O*-GlcNAcomic Profiling of Brain Tissue in Alzheimer's Disease

Wei-Wei Chang, Genomics Research Center, Academia Sinica, Taiwan

WP08-001

Proteomics Biomarkers from Human Cerebral Cortex for Molecular Diagnostic and Prognostic Management of Epilepsy Patients

Zakia Zhinwari, King Faisal Specialist Hospital and Research Centre, Saudi Arabia

WP08-002

Full-Length TDP-43 Forms Toxic Amyloid Oligomers in Frontotemporal Lobar Dementia-TDP Patients and Disturbs Amyloid-β Fibrillization

Yun-Ru (Ruby) Chen, Genomics Research Center, Academia Sinica, Taiwan

WP08-003

SCN Phosphoproteomic Analysis Reveals GRK2 as an Important Modulator of Neuronal Structure and Cytoskeleton Organization

Cheng-Kang Chiang, Ottawa Institute of Systems Biology, University of Ottawa, Canada

WP08-004

Quantitative Proteomics of the Cytosolic Fraction from Orbitofrontal Cortex of Patients with Schizophrenia

Gilberto Domont, Federal University of Rio De Janeiro, Brazil

WP08-005

CSF Analysis for Protein Biomarkers Identificatin in Patients with CNS Lymphoma

Manuel Fuentes, Cancer Research Center. University of Salamanca-csic, Spain

WP08-006

Proteomic Analysis of Vitamin D-Regulated Proteins in Primary Cultured OLGs

Jifang Gao, Institution of Biochemistry and Molecular Biology, School of Medicine, Shandong University, China

WP08-007

Proteomic Investigation of Glioblastoma Multiforme on the Basis of Svz Involvement

Saicharan Ghantasala, Indian Institute of Technology Bombay, India

WP08-008

An Innovative HPLC Quantitative Method Coupled with Proteomics Analysis to Investigate Hydrogen Sulphide Forms in Cerebrospinal Fluid

Viviana Greco, Santa Lucia Foundation, Italy

WP08-009

Chronic Low-Dose Rate Ionising Radiation Affects the Hippocampal Phosphoproteome in an ApoE$^{-/-}$-Alzheimer Mouse Model

Stefan J. Kempf, Institute of Radiation Biology, Helmholtz Zentrum München, Munich, Germany

WP08-010

Proteomic Analysis Reveals Metabolic Alteration of Substantia Nigra in Schizophrenic Patients

Ayesha Khan, University of Karachi, Pakistan

WP08-011

Mapping of Gangliosides from Nine Regions of Mouse Brain by Negative Ion Mode Nano LC/MS

Sumin Kim, Chungnam National University, South Korea

WP08-012

Chronic Exposure to Low Dose Methylmercury Induces Various Proteome Changes in Different Regions of Rat'S Brain

Hang-Kin Kong, The Hong Kong Polytechnic University, Hong Kong, China

WP08-013

Differential Proteome Changes in the Brains of Arctic Ringed Seal Induced by Bioaccumulation of Methylmercury

Samuel Chun-Lap Lo , The Hong Kong Polytechnic University, Hong Kong, China

WP08-014

A Peptidomic Profile of Transgenic Rat Model for Tatuopathy:LC-MALDI/MS Analysis of Cerebrospinal Fluid

Andrej Kovac, Institute of Neuroimmunology, Slovak Academy of Sciences, Slovakia

WP08-015

The Mechanism Research on GSN Remission of MS/EAE: A Proteome Analysis

Shilian Liu, Institute of Biochemistry and Molecular Biology, School of Medicine, Shandong University, China

WP08-016

Human Platelet Lysate (HPL) Proteome Analysis by NanoLC-MS/MS Mass Spectrometry: New Insights to Understand HPL Neuroprotective Properties

Didier Lutomski, Université Paris 13; Sorbonne-Paris-Cité; UMR CNRS 7244, Bobigny, France

WP08-017

Estrogen Partially Reverses Proteomic Changes Induced by Excessive Stretching of Brain Endothelial Cells

Abidali Mohamedali, Macquarie University, Australia

WP08-018

A Glimpse into the Proteomic Profile of Rasmussen's Encephalitis

Omesan Nair, Division of Chemical & Systems Biology, IIDMM, University of Cape Town, South Africa

WP08-019

Toxicoproteomics Highlights the Role of Vimentin In Neurotoxicity Induced by Fipronil

N. Monique Paricharttanakul, Environmental Toxicology, Chulabhorn Graduate Institute, Thailand

WP08-020

Amyloid Beta Activated Human Microglial Cells through Er-Resident Proteins

Young Mok Park, Institute for Basic Science, South Korea

WP08-021

Differential Protein Expression in the Cortex of Mice Exposed to the Antipsychotic Drugs Haloperidol and Clozapine

Cátia Santa, Center for Neuroscience and Cell Biology, Portugal

WP08-022

Proteomic Analysis of Maturation Dependent Adverse Effects of Paraquat Exposure in 3D Rat Brain Cell Cultures

Domitille Schvartz, University of Geneva, Switzerland

WP08-023

Beta-Amyloid Induces Pathology-Related Patterns of Tau Hyperphosphorylation at Synaptic Terminals via CDK5 Activation

Hwan-Ching Tai, Department of Chemistry, National Taiwan University, Taiwan

WP08-024

Investigation the Roles of TDP-43 Oligomers in Neurodegenerative Diseases

Tzu-Yu Weng, Academia Sinica, Taiwan

WP08-025

Chronic Exposure to Low Doses of Methylmercury Induced Proteome Changes on Polar Bear Brains

Yee-Man Melody Wong, The Hong Kong Polytechnic University, Hong Kong, China

WP08-026

Imaging Mass Spectrometry (IMS) for the Proteomic Studies of Experimental Autoimmune Encephalomyelitis (EAE) Mouse

Hiroki Yamashita, Doshisha University, Japan

WP09- Pharmacoproteomics and Drug Development

WO01-001

Proteome-Wide Drug Dose-Response of Prostate Cancer Cell Lines Exposed to Androgen Receptor Antagonists by microflow-LC SWATH MS Analysis

Christie Hunter, Sciex, USA

WO01-002

Profiling Changes in the Phosphoproteome of Hematopoietic Cells in Response to a Novel Class of Anti-Oncogenic Compounds

Peter Kubiniok, Department of Chemistry, University of Montreal, Canada

WO01-003

Cancer Proteomics towards Precision Medicine by Molecular Targeting Drug

Zhiwei Qiao, Division of Rare Cancer Research, National Cancer Center Research Institute, Japan

WO01-004

Drug Development by Linking Pathophysiology in Cancer to Proteomics

Marko-Varga György, Clinical Protein Science & Imaging Group, BioMedical Center, University of Lund, Lund, Sweden ; Dept. of Surgery, Tokyo Medical University, Tokyo, Japan, Sweden, Japan

WP09-001

A Study on the Intestinal Absorption and Functions of bioactive Peptide

Jing Chen, Shanghai Jiaotong University, China

WP09-002

Phamacoproteomics Reveals the Pan-Aurora Kinase Inhibitor Tozasertib as a Potential Therapeutic Drug for *Mycn*-Amplified Neuroblastoma

Chiao-Hui Hsieh, Institute of Molecular and Cellular Biology, National Taiwan University, Taiwan

WP09-003

The Discovery and Potential Application of Bioactive Peptides from Fermented Milk and Probiotics

Wanru Li, Shanghai Jiao Tong University, China

WP09-004

Corosolic Acid, the Active Principle of *Actinide chinensi*, Inhibits Hepatocellular Carcinoma by Targeting the VEGFR2/Src/FAK Pathway

Hsuan-Yuan Lin, National Taiwan Normal University, Taiwan

WP09-005

Deciphering the Molecular Insights of Phytoagent Deoxyelephantopin Against Triple Negative Breast Cancer Using LC-MS Based Quantitative Proteomics

Jeng-Yuan Shiau, Agricultural Biotechnology Research Center, Academia Sinica, Taiwan

WP09-006

Identification of Novel HLA-A2 Restricted Phosphopeptide for Cancer Vaccine Development

Wang-Chou Sung, National Institute of Infectious Diseases and Vaccinology, NHRI, Taiwan

WP09-007

Cellular Thermal Shift Assay (CETSA) Enables Identification of Drug Targets of Natural Products

Peng Yu, Chair of Proteomics and Bioanalytics, Technische Universität München, Germany

WP10- Chemical Proteomics and Drug Profiling

WO06-001

Target Identification in Living Cells via Mass Spectrometry-Based Chemical Proteomics

*Xuezhi Bi, Bioprocessing Technology Institute, Agency for Science, Technology and Research (A*STAR), Singapore*

WO06-002

Comprehensive Mass Spectrometry Analysis Identifies a Novel Therapeutic Target in the Wnt Signaling Pathway

Tesshi Yamada, National Cancer Center Research Institute, Japan

WO06-003

The Phosphoproteome of the NCI-60 Cell Line Panel Reveals Markers of Drug Sensitivity

Chen Meng, Lehrstuhl Für Proteomik Und Bioanalytik, Technische Universitat Muenchen, Germany

WO06-004

Targeted Proteomic Profiling of Enzymes that Activate the Prodrug PR-104A in Human Leukaemias

Yongchuan Gu, University of Auckland, New Zealand

WO06-005

Identification of TIFA as a Novel Therapeutic Target in Acute Myeloid Leukemia

Tong-You Wei, Academia Sinica, Taiwan

WP10-001

Drug Target Identification in Multiple Myeloma by Chemical Proteomics

Matthias Bach, University of Würzburg, Rudolf-Virchow-Center, Germany

WP10-002

Matrix Assisted Laser Desorption Ionization-Mass Spectrometry Imaging Based Analysis of Distribution of Anti-Tumor Agents on Tissue

Sungmin Cho, Chemical Genomics Global Research Laboratory, Department of Biotechnology, College of Life Science & Biotechnology, Yonsei University, South Korea

WP10-003

Comparative Proteomic Analysis Reveals the Molecular Mechanisms of Mandibular Glands in Two Lines of Honeybees (*Apis mellifera ligustica*)

Yue Hao, Institute of Apicultural Research, Chinese Academy of Agricultural Sciences, China

WP10-004

Anti-Cancer Gold(III) Porphyrins Target Mitochondrial Chaperone Hsp60

Di Hu, State Key Laboratory of Synthetic Chemistry, Chemical Biology Center, The University of Hong Kong, Hong Kong, China

WP10-005

A Novel Platform for Target Identification of a Natural Small Molecule and Its Target Protein Interaction on Tissues Using MALDI-MSI Analysis

Yonghyo Kim, Chemical Genomics Global Research Laboratory, Department of Biotechnology, College of Life Science & Biotechnology, Yonsei University, South Korea

WP11- Metabolomics and Metabolic Disorders

MO04-001

Global Data Standardization Algorithm for Applied Metabolomics

Petr Lokhov, Institute of Biomedical Chemistry, Russia

MO04-002

Systemic Proteomic and Metabolomic Analyses Identify Crucial Roles of the Polyol Pathway in Tumorigenesis

Anuli Uzozie, Institute of Molecular Systems Biology, Switzerland

MO04-003

Urine Proteomics for Evaluation of Taking Nano-Mist Sauna Effects on the Health

Yoshitoshi Hirao, Biofluid Biomarker Center, Niigata University, Japan

MO04-004

Mass Spectrometry-Based Proteomic and Metabolic Analysis of Different Cell Lines after Perturbation of Cellular Cholesterol Regulation

Peter Blattmann, ETH Zurich, Switzerland

MO04-005

imCorrect: New UHRMS Signal Handling Approach for More Accurate Elemental Composition Determination

Wei-Hung Chang, Academia Sinica, Taiwan

WP11-001

Investigations into the Effect of Fish Oil on Enzymes of Lipid Metabolism: A Proteomics Approach

Kk Asha, Icar-cift, India

WP11-002

Study the Regulation of Bioactive Compounds and Metabolome of *W. Chinensis* under Different Plant Hormone and Stress Treatment

Chih-Wei Chang, Academia Sinica, Taiwan

WP11-003

Monitoring Phosphatidylcholine and Sphingomyelin for Concentration Normalization in Cellular Lipidomics Studies Using FIA-ESI-MS/MS

Hsi-Chun Chao, School of Pharmacy, National Taiwan University, Taiwan

WP11-004

Development of the Absolute Quantification Method for Amino Acids

Ya-Wen Chou, Academia Sinica, Taiwan

WP11-005

Epigenetic Mechanism Investigation in Recessive Neurometabolic Disorder Mice

Jun Gao, Department of Chemistry & Institutes of Biomedical Sciences, Fudan University, China

WP11-006

IMS-DIA-MS Characterisation and IMS-MRM QconCAT Quantitation of the Lipidome and Apolipoprotein Complements of Obesity and Diabetes Cohorts

David Heywood, Waters, United Kingdom

WP11-007

Metabolomics Profiling of Paired OSCC Using Chemical Isotope Labeling LC-MS

Chia-Wei Hsu, Molecular Medicine Research Center, Chang Gung University, Taiwan

WP11-008

Quantitative Metabolome Analysis of Pleural Effusion with High-Performance Chemical Isotope-Labeling Liquid Chromatography-Mass Spectrometry

Pei-Chun Hsueh, Graduate Institute of Medical Biotechnology and Laboratory Science, Chang Gung University, Taiwan

WP11-009

Metabolomic Profiling of Subgrouping Ischemic Stroke

Tai-Ming Ko, Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan

WP11-010

Monte Carlo Simulation Reveals Reliable Molecular Formula Annotation of Metabolomic Data Obtained by Accurate Mass Spectrometry

Melody M. T. Lam, Proteomics Core, Faculty of Health Sciences, University of Macau, Macau, China

WP11-011

Urinary Exposure Marker Discovery for Toxicants Using UPLC-LTQ-Orbitrap and Three Untargeted Metabolomics Approaches

Pal-Chi Liao, Department of Environmental and Occupational Health, National Cheng Kung University, Taiwan

WP11-012

Discovery of Early-Stage Biomarkers for Diabetic Nephropathy Using LC/MS-Based Metabolomics

Yu-Ning Lin, Proteomics Core Laboratory, Department of Medical Research, China Medical University, Taiwan

WP11-013

Defining the Aberrant Molecular Profiles in Liver and Adipose Tissues of Ovariectomized Rat Model with Different n-3 Fatty Acid Interventions

Ming-Hsuan Lin, Master program for clinical pharmacogenomics and pharmacoproteomics, Taipei Medical University, Taiwan

WP11-014

Metabolomics Investigation of Voriconazole-Induced Hepatotoxicity

Shin-Lun Wu, School of Pharmacy, National Taiwan University, Taiwan

WP11-015

Using a Targeted Metabolomic Approach to Investigate Plasma Metabolites Associated With Risk of Diabetes Mellitus

Yi-Hao Wu, School of Pharmacy, College of Medicine, National Taiwan University, Taiwan

WP11-016

Fragmentation Analysis of Amino acids by High Resolution Tandem MS and High-Energy Collision Dissociation

Pengwei Zhang, Pilot Laboratory, Faculty of Health Sciences, University of Macau, Macau, China

WP12- Plant Proteomics

WO09-001

Quantitative Proteomic Analysis of Flooding and Its Recovery in Soybean Exposed to Aluminum Oxide Nanoparticles

Setsuko Komatsu, National Institute of Crop Science, Japan

WO09-004

Integrated Extracellular Matrix proteome and Organ Specific Transcriptome Decipher Cell Wall Mediated Immunity in Plant

Kanika Narula, National Institute of Plant Genome Research, India

WO09-005

Phosphoproteomic Analysis of Abscisic Acid Signaling Components in Arabidopsis Seed

Anna Amagai, BASE, Tokyo University of Agriculture and Technology, Japan

WP12-001

Quantitation of Tonoplast Proteins Simultaneously Regulating Inorganic Phosphate(Pi) Influx-Efflux during Varying Pi Levels

Debayan Bose, Academia Sinica, Taiwan

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The CAP Secretory Pathway is Required for CAPE Peptide Production for the Induction of SAR

Ying-Lan Chen, Agricultural Biotechnology Research Center, Academia Sinica, Taiwan

WP12-003

Studying of Plant Novel Systemic Signaling and RNA Trafficking Proteins under Pi Deficiency Using Proteomics Approach

Yet-Ran Chen, Academia Sinica, Taiwan

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Proteomic Analysis of "Oriental Beauty" Oolong Tea Leaves with Different Degrees of Leafhopper Infestation

Han-Ju Chien, Institute of Molecular Biology, National Chung Hsing University, Taiwan

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Proteometabolomic Study Illustrates Dual Role of Oxalic Acid in Anti-Nutrient Signaling and Non-Host Resistance

Sudip Ghosh, National Institute of Plant Genome Research, India

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Proteomic Analysis of Bee Pollen from a Natural Forest in Central Taiwan

Ya-Jin Jheng, Genomics Research Center, Academia Sinica, Taiwan

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Quantitative Proteomics of Phaeodactylum tricornutum in Acidified Environment

Tai-Yi Jiang, National Taiwan Ocean University, Taiwan

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Comparative Proteomics of Chlorella sp. FC2 IITG during Nitrogen-starvation Using iTRAQ and MRM Based Mass Spectrometry

Vineeta Rai, Indian Institute of Technology Bombay, India

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Quantitative Proteomics of *Phaeodactylum tricornutum* in Phosphate Limited Environment

Shiang-Yu Tsai, National Taiwan Ocean University, Taiwan

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Proteomic Analysis to Reveal the Calcium Function on Protein Glycosylation in Endoplasmic Reticulum of Soybean under Flooding and Drought Stresses

Xin Wang, University of Tsukuba, Japan

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Proteomic and Transcriptomic Analyses to Reveal the Tolerance Mechanism in Soybean at Initial Flooding Stress

Xiaojian Yin, University of Tsukuba, Japan

WP12-012

Comparative Phosphoproteomic Analysis of Dormant and After-Ripened Seeds of Barley

Shinnosuke Ishikawa, Tokyo University of Agriculture and Technology, Japan

WP13- Microbial Proteomics

TO10-005

Proteomics in Food Safety: Monitoring Competition between *Listeria Monocytogenes* and *Lactococcus Lactis* by Imaging Mass Spectrometry

Isabella Alloggio, Dipartimento di Medicina Veterinaria, Università degli studi di Milano, Italy

WO09-002

Single-Species Proteomics, Multi-Species Metaproteomics, Trends and Opportunities to Read-Across in Environmental Assessment

Susana Cristobal, Linköping University, Sweden

WO09-003

Gastric Bypass Surgery Clearly Perturbs the Community Structure and the Functional Composition of the Intestinal Microbiota

Nico Jehmlich, Helmholtz-centre for Environmental Research - Ufz, Germany

WP13-001

The Virulence Mechanism Mediated by a Metalloprotein in Streptococcus Pneumoniae

Kun Cao, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

WP13-002

Comparative Proteomic Analysis of Virulence Variations in Xanthomonas Campestris pv. Campestris Strain 17, 11A and P20H

Tao-Shan Chang, Institute of Molecular Biology College of Life Science, National Chung Hsing University, Taiwan

WP13-003

Biodegradation of Crude Oil and Diesel by Novel Microorganism, *Arthrobacter* sp. MWB-30

Young-Ho Chung, Korea Basic Science Institute, South Korea

WP13-004

Isobaric Tagging-Based MS Quantification of HIV-1/gp120/tat in Astrocytoma: Implications for HIV-Associated Neurodegeneration

Luis Cubano, Biomedical Proteomics Facility, Dept of Microbiology and Immunology, Universidad Central del Caribe, USA

WP13-005

Novel Characteristics of Highly Virulent Ribotype 027 - Quantitative and Qualitative Proteomic Analysis of C. Difficile Clinically Relevant Ribotypes

Jiri Dresler, Military Health Institute, Czech Republic

WP13-006

iTRAQ-Based Proteomics Revealed the Formation Mechanism of Drug-Resistant Bacteria

Gao Fei Du, Functional Protein Research of Guangdong Higher Education Institutes, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

WP13-007

A Comprehensive Proteomics Analysis for *Streptococcus Equi* Subspecies *Equi* Se071780 to Antigen Discovery and Vaccine Development

Hayoung Lee, Drug & Disease Target Team, Korea Basic Science Institute, South Korea

WP13-008

Using Multiple Data Analytical Approaches to Determine the Metaproteome of the Human Gut

Andrew Nel, University of Cape Town, South Africa

WP13-009

Alkaline Protease Activity and Alk Protein Level in Clinical Isolates of *A.flavus*

Mohammed Razeeth Shait Mohammed, Proteomics Department, Aravind Medical Research Foundation, Dr. G. Venkataswamy EyeResearch Institute, India

WP13-010

Metalloproteome Study on the Iron Transportation Mechanism in Bacteria

Xiaoyan Yang, Jinan University, China

WP13-011

iTRAQ-Based Proteomics Revealed the Bactericidal Mechanism of Sodium New Houttuyfonate (SNH) against *Streptococcus pneumoniae*

Xiao-Yan Yang, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

WP13-012

In-Depth Metaproteomic Studies of Human and Mouse Gut Microbiota

Xu Zhang, University of Ottawa, Canada

WP14- Food and Nutrition and Immuno-Peptidome: Focus on Food Allergies

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The Benefits of Hybrid Fragmentation Technologies (EThcD) for Analysing the Immunopeptidome

Albert J Heck, Utrecht University and Netherlands Proteomics Centre, Netherlands

WO05-002

Digestomics of Raw Peanut and Characterization of Gastric-Phase Released Peptides of Peanut Allergens

Tanja Cirkovic Velickovic, University of Belgrade - Faculty of Chemistry, Serbia

WO05-003

Ultra-Fast Analysis of Allergens Using Capillary Electrophoresis Coupled to Mass Spectrometry and Ultraviolet Photodissociation

Daniel Lopez-Ferrer, Thermo Fisher Scientific, USA

WO05-004

Characterisation of Specificity of Different Commercial Proteases for Food Hydrolysates

Cristian De Gobba, University of Copenhagen, Denmark

WO05-005

Characterization and Modulation of Fish Allergens

Pedro Rodrigues, Universidade do Algarve, Campus de Gambelas, Ed. 7, 8005-139 Faro, Portugal

WP14-001

Identification of 2-Oxohistidine Interacting Proteins Using E. Coli Proteome Chips

Yun-Huan Chen, Department of Chemistry, National Taiwan University, Taiwan

WP14-002

Quantitative Phosphoproteomic Characterization of the Effect of RN/HAL Genotypes on Post-Mortem Energy Metabolism in Pigs

Rene Lametsch, University of Copenhagen, Denmark

WP14-003

Proteomic Analysis of Antique Glue on a Stradivari Violin

Guo-Chien Li, Department of Chemistry, National Taiwan University, Taiwan

WP14-004

Rapid and Simultaneous Determination of γ-oryzanol, Vitamin E Isomers in Brown Rice Sample by Ultra-Performance Liquid Chromatography Mass

Hung-Yu Lin, Institute of Molecular Biology College of Life Science, National Chung Hsing University, Taiwan

WP15- Kidney, Urine and Plasma: Opportunities for Early Diagnosis and Risk Assessment

WO10-001

Comparative Proteomic Analysis of Kidney Distal Convoluted Tubule and Cortical Collecting Duct Cells Following Long-Term Hormonal Stimulation

Qi Wu, InterPrET Center, Department of Biomedicine, Aarhus University, Denmark

WO10-002

Targeted MS-Based Assay of Circulating Proteoforms Related to Aging in Human Plasma

Pingbo Zhang, Wilmer Eye Institute, Johns Hopkins University School of Medicine, USA

WO10-003

Can Proteomics Contribute to Solving the Riddle of Diabetic Nephropathy?

Leena Kerstin Maria Liljedahl, Immunotechnology, Lund University, Sweden

WO10-004

Quantification of Angiotensin II-Regulated Proteins in Urine of Patients with Polycystic and Chronic Kidney Diseases by Selected Reaction Monitoring

Ana Konvalinka, Division of Nephrology, University Health Network, University of Toronto, Canada

WO10-005

Analysis of the HDL Proteome - Myths and Legends and Reality

Manfred Raida, National University of Singapore, Microbiology and Immunology, Singapore

WP15-001

Proteomic Insight Reveals Elevated Levels of Albumin in Circulating Immune Complexes in Diabetic Plasma

Shweta Bhat, Proteomics Facility, Division of Biochemical Sciences, CSIR-National Chemical Laboratory, India

WP15-002

Profiling of Plasma for Proteomic Signatures of Mammographic Density

Sanna Byström, Science for Life Laboratory, School of Biotechnology, KTH – Royal Institute of Technology, Sweden

WP15-003

Novel Proteomics-Based Pipeline for Identifying Predictive Biomarkers of Chemotherapy-Induced Toxicity

Emily Chen, Herbert Irving Comprehensive Cancer Center at Columbia University Medical Center, USA

WP15-004

Human Native Peptidome Database for Peptidomics Studies

Amr Elguoshy, Niigata University, Japan

WP15-005

Urimem, A Membrane that Can Store Urinary Proteins Simply And Economically, Makes the Large-Scale Storage of Clinical Samples Possible

Youhe Gao, Beijing Normal University, China

WP15-006

Rapid and High-Throughput Identification of Acute Hepatic Porphyria by SALDI-TOF MS Analysis

Han-Chih Ke, Institute of Molecular Biology, National Chung Hsing University, Taiwan

WP15-007

Developing a Strategy to Identify Low-Abundance Native Peptides in Plasma

Yoshio Kodera, Center for Disease Proteomics, Kitasato University School of Science, Japan

WP15-008

Preliminary Study into the Quantitative Impact of Long-Duration Space Travel on the Cosmonaut Plasma Proteome

Irina Larina, Institution for Biomedical Problems, RAS, Moscow, Russia

WP15-009

Proteomics Analysis of Rat Kidney Under Maleic Acid Treatment by SWATH-MS Technology

Chao-Yi Lee, Institute of Molecular Biology, National Chung Hsing University, Taiwan

WP15-010

The Discovery of HDL-Associated Protein Biomarkers to Predict Stroke

Hsin-Yi Liao, College of Medicine, China Medical University, Taiwan

WP15-011

Evaluation of Cardiovascular System State by Urine Proteome after Manned Space Flight

Liudmila Pastushkova, Institute for Biomedical Problems – Russian Federation State Scientific Research Center RAS, Russia

WP15-012

Human Plasma Proteome Analysis Using Meter-Long Monolithic Silica Columns with Match-Between-Runs

Yi-Ting Wang, Center for Genomic Medicine, Kyoto University, Japan

WP15-013

Comparative Proteomic Analysis of Human Calcium Oxalate and Calcium Phosphate Kidney Stone Matrices

Frank Witzmann, Indiana University School of Medicine, USA

WP15-014

Proteomics of Urine from Healthy Volunteers by SWATH-MS

Bo Xu, Niigata University Biofluid Biomaker Center (BB-C), Japan

WP15-015

Proteomics of Diabetic Nephropathy Glomerulus

Keiko Yamamoto, Biofluid Biomarker Center/ Niigata University, Japan

WP15-016

Application of High Throughput Urinary Proteomic Strategy in the Diagnosis of Acute Appendicitis with Confusable Acute Abdomens

Yinghua Zhao, National Center for Protein Sciences · Beijing, China

WP16- Late Breaking Abstracts

WP16-001

Biological Characteristic of Human Enterovirus Species A in Human Nucleolin Transgenic Mice

Yi-Chen Lin, Department of Medical Laboratory Science and Biotechnology, College of Medicine, National Cheng Kung University, Taiwan

WP16-002

Zika Virus is not Alone: Proteomics Associates A Bovine-Like Viral Diarrhea Virus to Microcephaly

Gilberto B Domont, Federal University of Rio de Janeiro, Brazil

WP16-003

Lymph Node Metastasis of Primary Endometrial Cancers: Associated Proteins Revealed by Maldi Imaging

Parul Mittal, The University of Adelaide, Australia

WP16-004

Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome

Ulrike Kusebauch, Institute for Systems Biology, Seattle, USA

WP16-005

Low Microgram Amount Protein Samples Coupled with Novel Polymers for TAILS Terminomics Yield Efficient Enrichments Utilizing Precipitation with Organic Solvents

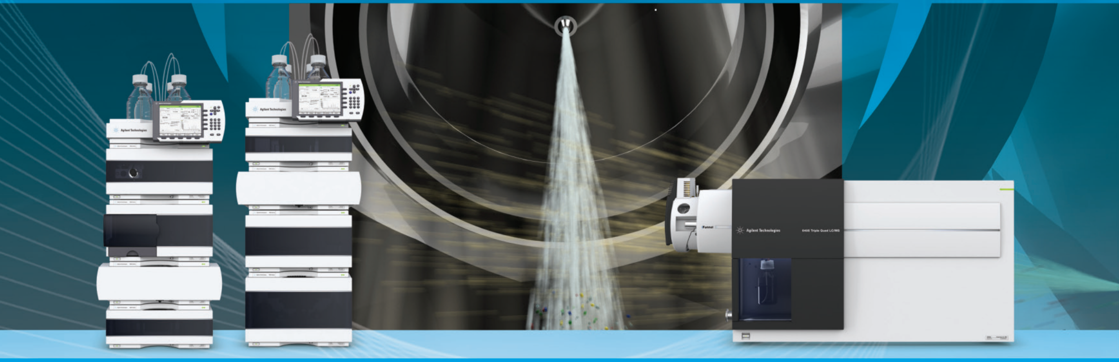
Nestor Solis, Centre for Blood Research, 2350 Health Sciences Mall Life Sciences Centre, University of British Columbia, Canada

WP16-006

Identification of Cofilin-1 Induces G0/G1 Arrest and Autophagy in Angiotensin-(1-7)-treated Human Aortic Endothelial Cells from iTRAQ Quantitative Proteomics

Wan-Yu Lo, Cardiovascular & Translational Medicine Laboratory, Department of Biotechnology, Hung Kuang University

All Oral Presenters have been invited to prepare a Poster in addition to their Oral Presentations. Poster Presentations for Oral Presenters will be labeled with their Oral Presentation number (e.g. MO01-001).



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5th April 2017
Close of Abstracts

31st May 2017
Notifications of Acceptance

14th June 2017
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16th August 2017
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