

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



translating
the code of life



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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 City Government

Wen-Je Ko, Ph.D.
Mayor

*Office of the Mayor
Taipei, Taiwan, Republic of China*

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

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E-mail: kowj@mail.taipei.gov.tw Website: <http://www.taipei.gov.tw>

HUMAN PROTEOME ORGANIZATION (HUPO)



translating
the code of life

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

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(ex-officio)

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(2016)

VICE-PRESIDENT

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(2016-2017)

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(2014-2016)

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(2015-2016)

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(2015-2016)

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Hisashi Narimatsu

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Tesshi Yamada

Tadashi Yamamoto

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National Central University,
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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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GENERAL INFORMATION

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 throughout 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.

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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
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AWARDS

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HUPO AWARDS

Distinguished Achievement in Proteomic Sciences Award



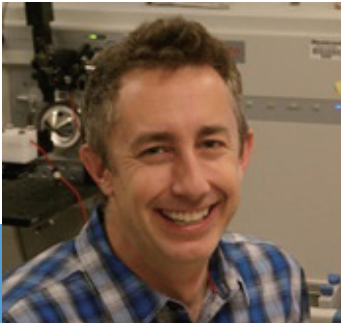
Ralph Bradshaw

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 ReEx, 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).

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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 Proteomics 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

Hiroimi 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

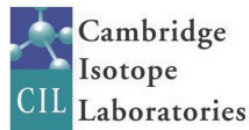
Bo Zhang, Sweden

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

Cambridge Isotope Laboratories Student Travel Award Winner

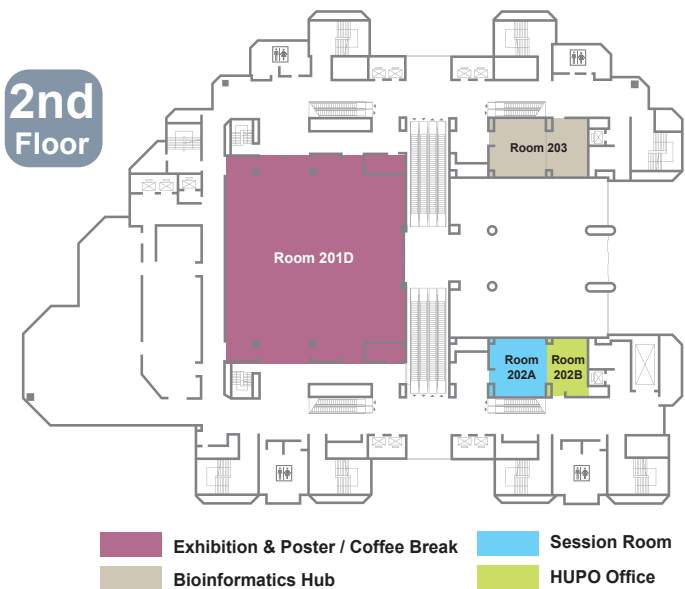
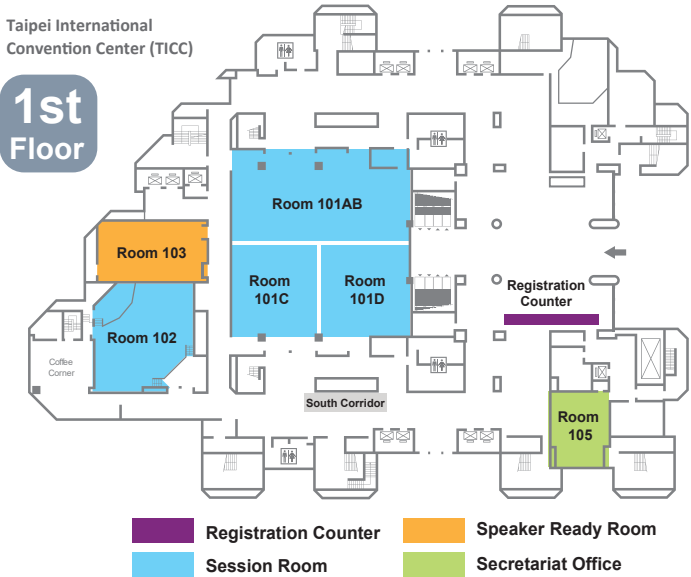
Yinghua Zhao, China

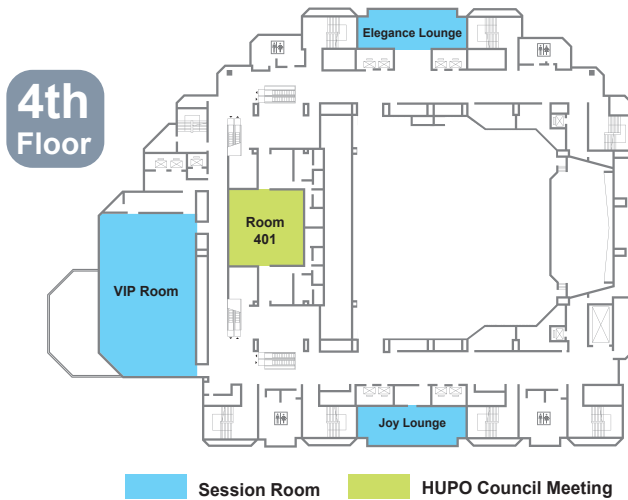
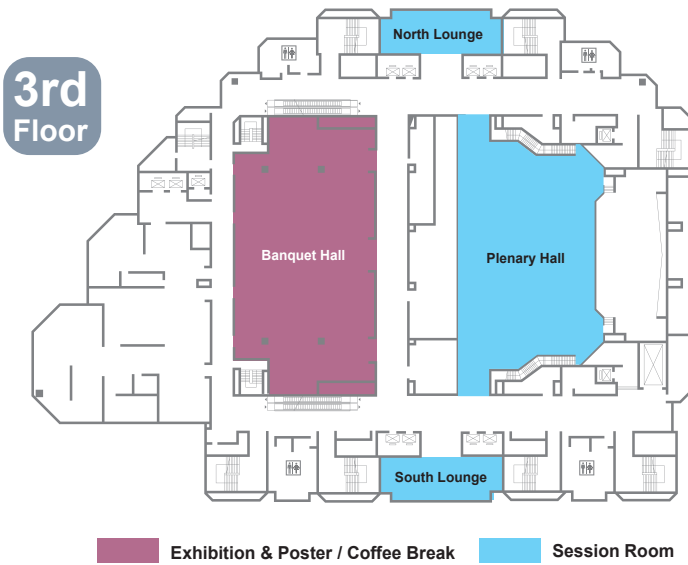
WP15-016: Application of High Throughput Urinary Proteomic Strategy in the Diagnosis of Acute Appendicitis with Confusable Acute Abdomens



CONGRESS VENUE MAP

CONGRESS VENUE MAP





EXHIBITION INFORMATION

2016 TAIPEI
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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

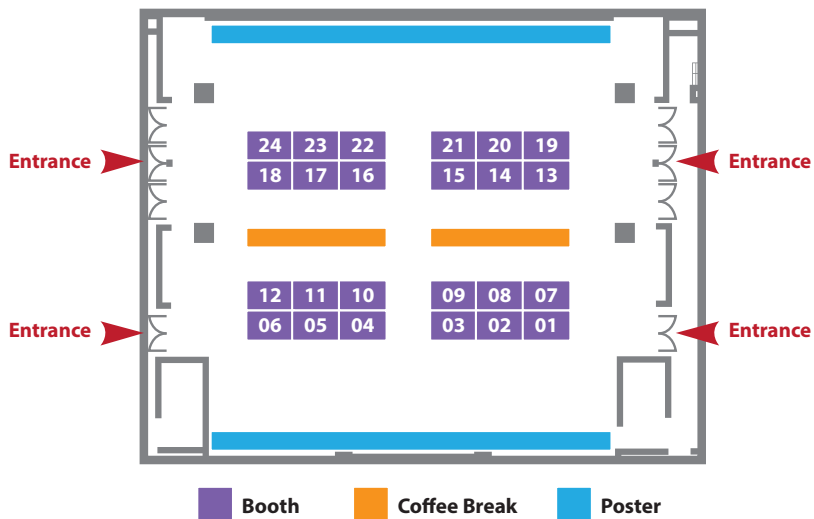
Sunday , September 18, 2016	20:00-21:30 (Welcome Reception)
Monday , September 19, 2016	09:30-17:30
Tuesday , September 20, 2016	09:30-17:30
Wednesday , September 21, 2016	09:30-15:30

Exhibitor Listing

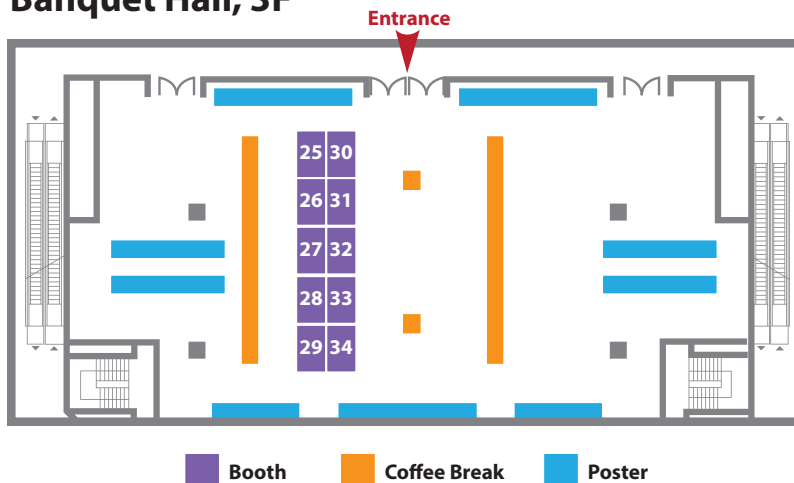
Alphabetical by Exhibitor

Company	Booth #	Company	Booth #
ACS Publications	22	Merck Millipore and Sigma-Aldrich	16
Agilent Technologies, Inc.	1, 2	Meridigen Biotech Co., Ltd.	9
Bioinformatics Solutions Inc.	4	Pressure BioSciences, Inc.	29
Biophysical Society of R.O.C.		Promega Corporation	3
Human Personalized Omics Profiling	26	SCIEX	6, 12
Taiwan Proteomics Society		SENGENICS	17
Bruker Corporation	18, 24	Shimadzu Scientific Instruments (TAIWAN) Co., Ltd.	27
Cambridge Isotope Laboratories, Inc.	10	Taiwan Protein Project	25
Cold Spring Biotech Corp.	32	Si2C	
Column Scientific	28	Taiwan Society for Mass Spectrometry	31
Denator AB	11	The Taiwan Society for Biochemistry and Molecular Biology	
Elsevier	34	Thermo Fisher Scientific	13-15 & 19-21
Taiwan Bioinformatics Institute		Veritomyx, Inc.	5
GenMall Biotechnology Corporation, LTD	30	Waters Corporation	7, 8
HUPO 2017	33		
Matrix Science	23		

ROOM 201, 2F



Banquet Hall, 3F





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.



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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.



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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.



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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.



Denator AB

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.



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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.

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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.



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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.



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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

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.



台灣質譜學會
Taiwan Society for Mass Spectrometry

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.



台灣生物化學及分子生物學學會

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.



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INFORMATION FOR INVITED SPEAKERS AND PRESENTERS

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
	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
	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

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:



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:



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:



Closing Plenary Session with Award Lectures

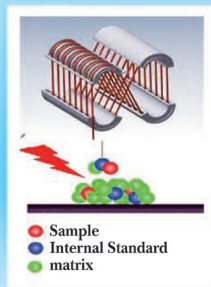
Date: Wednesday, September 21, 2016
Time: 15:30-17:30
Venue: Plenary Hall, 3F, TICC
Dress Code: Business Casual



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SCIENTIFIC PROGRAMS

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 & OGIcNAc (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 **Room 201, (2F) and**
(Even Poster Numbers) **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)

MO2: 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 Reagent 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 Likhov, 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 & O-GlcNAc

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 Kingdom13:45 **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, USA13:45 **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
(Odd Poster Numbers)** Room 201 (2F) and
Banquet Hall (3F)

**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 Room 201 (2F) and
(Even Poster Numbers) 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 Medzihradzsky, Hungary; Hui Zhang, USA**

- 10:30 **TK-03**
Extracellular Glycosylation: How to See the Forest Despite All the Trees
Katalin Medzihradzsky, 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 Modifications**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 Southwestern 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- ϵ -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

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*

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
(Even Poster Numbers) Banquet Hall (3F)

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

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-sulphydration 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 Stagljär**, 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 Stagljär, 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 **Room 201 (2F) and Banquet Hall (3F)**
(Odd Poster Numbers)

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 Breinholt Bekker-Jensen, University of Copenhagen, Denmark

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 FRRS11 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-GlcNAc Profiling of Brain Tissue in Alzheimer's Disease***Wei-Wei Chang, Academia Sinica, Taipei, Taiwan*

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
HUBO

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 Q1 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 Platform

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

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 Variants (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, BML, 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 P. 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 Therapeutics Using Mass Spectrometry-Based Methods

Ya-Fen Chen, Sun Jet Biotechnology Incorporation, Taiwan

MP03-004

Thermostable Plasma Proteome and Its Potential Applications in Biomarker Discovery

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

MP03-005**A New Method for Label Free Quantification in the Proteome Discoverer Framework**

Bernard Delanghe, Thermo Fisher Scientific, Germany

MP03-006**Studying Protein Phosphorylation with Ultra-High Temporal Resolution Using a Microfluidic Device**

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

MP03-007**Improving Proteome Coverage via Efficient, Complementary and Automated Digestion Using High Content Magnetically Immobilized Trypsin and Chymotrypsin**

Isak Gerber, Resyn Biosciences, South Africa

MP03-008**2D-SWATH® Mass Spectrometry was Applied in Quantitation of Membrane Proteome of Rat Brain Hippocampus**

Lihai Guo, Sciex, China

MP03-009**Systematic Exploration of Subcellular Redox Status by Methionine Containing Peptide Enrichment**

Ya-Ju Hsieh, Chang Gung University, Taiwan

MP03-010**Identification of Metal Species by ESI-MS/MS through Release of Free Metals from the Corresponding Metal-Ligand Complexes**

Yu-Chen Huang, Academia Sinica, Taiwan

MP03-011**Sensitive and Accurate Quantitation of Phosphopeptides Using TMT Isobaric Labeling Technique**

Xiaoyue Jiang, Thermo Fisher Scientific, 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 Biotechnology 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, Institute 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, Academia 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, Academia 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, Academia 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***Jaeyeon 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 Peptidofoms 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

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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

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

Anthony Purcell, Monash University, Australia

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

Johan Malmström, Lund University, Sweden

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

Daniel Figeys, University of Ottawa, Canada

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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

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

Etienne Caron, Eth Zurich, Switzerland

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

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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

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Direct Identification of Viral Epitopes from MHC I Molecules by Mass Spectrometry

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

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Defective Wound Healing as Observed through Clinical and Proteome Measurements

James Broadbent, Queensland University of Technology, Australia

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Identifying the Endomembrane System and Organelle Proteomic Analysis in Protozoan Parasite, *Trichomonas Vaginalis*

Chien-Hsin Chu, Academia Sinica, Taiwan

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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

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Proteomic Study of Monocyte Chemoattractant Protein-1 Induced polarisation

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

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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

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Proteomic Analysis of Human Saliva Samples Obtained from Caries-Free and Caries-Susceptible People

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

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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

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

Manalisha Nayak, Indian Institute of Technology Bombay, India

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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

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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

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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 Peptidome 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*

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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

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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

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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

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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

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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

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

Ali Tiss, Dasman Diabetes Institute, Kuwait

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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

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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

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Quantitative Simultaneous Multiple PTMomics Characterization of Arteries from Patients with Atherosclerosis and Type 2 Diabetes

Honggang Huang, University of Southern Denmark, Denmark

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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

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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

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Proteome Identification of Human Beta-Defensins in Male Reproductive System, and Induced Expression by Epigenetic Regulation

Yang Liu, Fudan University, China

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Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update

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

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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

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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

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

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

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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)

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From SNP to Glycosylation: A Comprehensive Geno-Glycomic Approach to Discover New Lung Disease Glycobiomarkers

Andras Guttman, Sciex, USA

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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

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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

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

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

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

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

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

Michal Bassani, Unil/chuv, Switzerland

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

Jing Wang, Vanderbilt University Medical Center, USA

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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

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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

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Clinically-Actionable Proteomic Biosignatures of Colorectal Cancer

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

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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

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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

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

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

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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

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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

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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

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

Yi-Ting Chen, Chang Gung University, Taiwan

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Functional Re-Activation of Mitochondria in the TGF- β 1 Induced EMT of Lung Cancer A549 Cells

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

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Quantitative Profiling of Plasma Proteome in Kawasaki Disease

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

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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

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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

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

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

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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

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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

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

Lylia Drici, University of Southern Denmark, Denmark

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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

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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

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

Sai Ge, Beijing Proteome Research Center, China

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

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

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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*

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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*

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Verification of Prostate Cancer Genomics Biomarker Candidates at Protein Level Using SRM-MS*Jacob Kagan, National Cancer Institute, USA*

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Proteomics Identified the Proteins Associated with Tumor Invasion in Myxofibrosarcoma*Kazutaka Kikuta, Division of Rare Cancer Research, National Cancer Center Research Institute, Japan*

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Development for Lung Cancer Diagnostic Meta-Markers Using Multiple Reaction Monitoring*Yong-In Kim, Seoul National University, South Korea*

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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*

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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*

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Changes in Protein Expression between Primary Breast Tumour and Lymph Node or Distant Metastases*Emila Kurbasic, Lund University, Sweden*

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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*

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Anchorage-Independancy 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*

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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*

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Identification of Hypoxia-Induced Splicing Variants in Cancer Cells Using Proteomics Approach*Chia-Hung Li, National Taiwan Ocean University, Taiwan*

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Quantitative Analysis of HER2 Protein Expression in Multiple Cancer Indications*Wei-Li Liao, Nantomics, USA*

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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*

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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*

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Using SWATH to Analysis Peripheral Blood Mononuclear Cells of Pancreatic Cancer

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

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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

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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

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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

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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

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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

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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

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

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

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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

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Proteomic Analysis of TGF- β -Induced Cancer Metastasis

Akiko Okayama, Yokohama City University, Japan

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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 University, 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 Sivasadan, Institute of Bioinformatics, International Tech Park, Bangalore, India***TP01-074****Quantitative Analytical Method for Measuring the Levels of PIVKAI1 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*

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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

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

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

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

Stoyan Stoychev, CSIR, South Africa

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

Hsiang-Chun Su, Academia Sinica, Taiwan

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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

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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 Biomolecular 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 Neuroglycomics 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 University, 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-MS²/MS³ 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 Southwestern 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, Academia 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 α 1) 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 Bomgardner, 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 Aquaporin 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 Biomedical 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 Flight***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 Tumorigenesis 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 Sciences, 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 FRRS11 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-GlcNAc 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***Omegan 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, Sciox, 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

Pharmacoproteomics 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 chinensis*, 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 Universität 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 Uozzie, 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**

Pa-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

WP12-002**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

WP12-004**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

WP12-005**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

WP12-006**Proteomic Analysis of Bee Pollen from a Natural Forest in Central Taiwan**

Ya-Jin Jheng, Genomics Research Center, Academia Sinica, Taiwan

WP12-007**Quantitative Proteomics of *Phaeodactylum tricornutum* in Acidified Environment**

Tai-Yi Jiang, National Taiwan Ocean University, Taiwan

WP12-008**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

WP12-009**Quantitative Proteomics of *Phaeodactylum tricornutum* in Phosphate Limited Environment**

Shiang-Yu Tsai, National Taiwan Ocean University, Taiwan

WP12-010**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

WP12-011**Proteomic and Transcriptomic Analyses to Reveal the Tolerance Mechanism in Soybean at Initial Flooding Stress**

Xiaojuan 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

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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

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Cristian De Gobba, University of Copenhagen, Denmark

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Rene Lametsch, University of Copenhagen, Denmark

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Pingbo Zhang, Wilmer Eye Institute, Johns Hopkins University School of Medicine, USA

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Leena Kerstin Maria Liljedahl, Immunotechnology, Lund University, Sweden

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Ana Konvalinka, Division of Nephrology, University Health Network, University of Toronto, Canada

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Manfred Raida, National University of Singapore, Microbiology and Immunology, Singapore

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Emily Chen, Herbert Irving Comprehensive Cancer Center at Columbia University Medical Center, USA

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Amr Elguoshy, Niigata University, Japan

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Youhe Gao, Beijing Normal University, China

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Frank Witzmann, Indiana University School of Medicine, USA

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Bo Xu, Niigata University Biofluid Biomaker Center (BB-C), Japan

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Keiko Yamamoto, Biofluid Biomarker Center/ Niigata University, Japan

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Yinghua Zhao, National Center for Protein Sciences · Beijing, China

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Yi-Chen Lin, Department of Medical Laboratory Science and Biotechnology, College of Medicine, National Cheng Kung University, Taiwan

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Gilberto B Domont, Federal University of Rio de Janeiro, Brazil

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Parul Mittal, The University of Adelaide, Australia

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Ulrike Kusebauch, Institute for Systems Biology, Seattle, USA

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**Low Microgram Amount Protein Samples
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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*

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**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).**

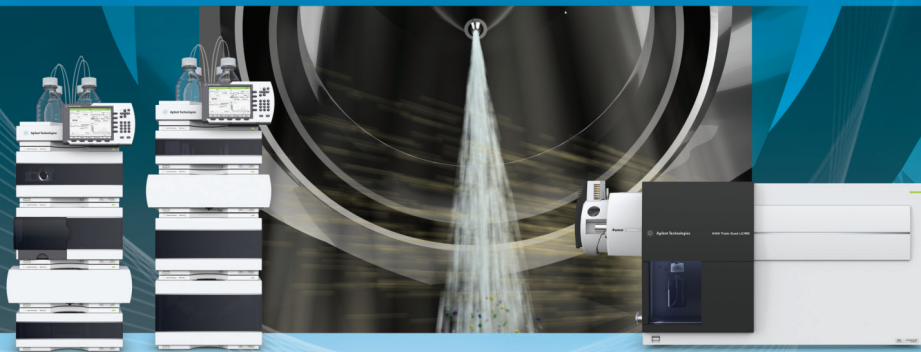
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 Harper, J Wade
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5th April 2017
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31st May 2017
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14th June 2017
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End of Regular Registration



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