



**HUPO**  **VANCOUVER**  
14TH HUMAN PROTEOME ORGANIZATION WORLD CONGRESS

SEPTEMBER 27 - 30  
**2015**

# CONGRESS PROGRAM BOOK



Translating Proteomics and  
Allied -Omics to the Clinic

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translating  
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- Receive our newsletter, the HUPOST, which highlights news and activities across the proteomics community
- Be eligible to receive a HUPO award
- Enjoy special HUPO-rates for Molecular & Cellular Proteomics (MCP) online

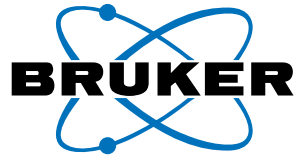
# CONGRESS SPONSORS

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## DISTINGUISHED ACHIEVEMENT AWARD



## TRANSLATIONAL PROTEOMICS AWARD



## TRAVEL AWARDS



BCProteomicsNetwork



CNPN



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# INDUSTRIAL ADVISORY BOARD

Created in 2006, the HUPO Industrial Advisory Board (IAB) facilitates communication and input from industry partners to support the proteomics community and to recognize these partners as HUPO affiliates. HUPO supports industry allies active in the development of innovative technologies and appropriate standards that are responsive to the constant changes in the scientific proteomics environment.

## The IAB Mission

To provide HUPO leadership (the Executive Committee) valuable input on technology and product innovation for the benefit of members and to identify industry trends that will position HUPO to meet the future challenges of its partners and organization.

## BENEFITS OF AN IAB MEMBERSHIP

- Two complimentary individual HUPO memberships available for company employees (value \$200).
- Involvement in Human Proteome Project (HPP) with regular updates from project leadership.
- Direct connection with HUPO Executive Committee and Congress Organizers via monthly IAB calls.
- IAB sponsored Science and Technology Award, established in 2011, awarded to an industrial scientist. IAB representatives solicit and vet nominees. Award recipient presents a talk on the project at the annual world congress.
- Selection of abstracts for the New Technological Advances in Proteomics presentations at the annual HUPO Congress.

The Human Proteome Organization wishes to thank the following IAB members for their participation this year!



Agilent Technologies



Interested in joining HUPO as an IAB member? Come and visit us in the Exhibit Hall or contact **Chelsea Prangnell (HUPO Office)** [chelsea@hupo.org](mailto:chelsea@hupo.org)



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## SECTION 3 PROGRAM SUNDAY, SEPTEMBER 27

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# HUPO 2015



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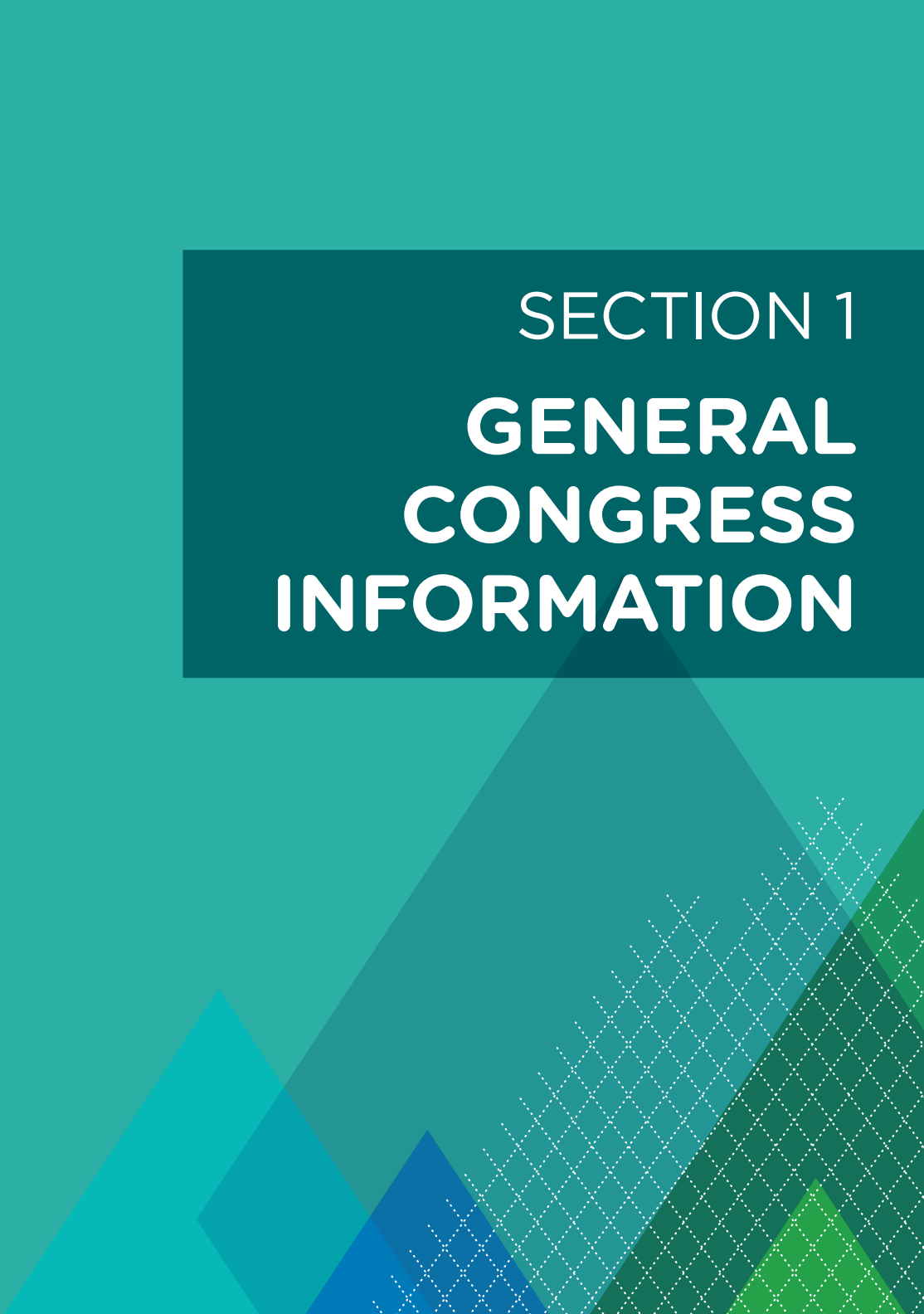
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 Human Proteome Organization  
(HUPO)

The background is a solid teal color. In the lower half, there are several overlapping geometric shapes: a large teal triangle pointing upwards, a smaller teal triangle pointing downwards, and a blue triangle pointing upwards. A white grid pattern of small squares is overlaid on the teal shapes in the bottom right corner.

SECTION 1

**GENERAL  
CONGRESS  
INFORMATION**

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## WELCOME MESSAGES

# Welcome Message from the Congress Chairs

Dear Friends and Colleagues,

On behalf of the **Human Proteome Organization (HUPO)**, the **Canadian National Proteomics Network (CNPN)** and the **British Columbia Proteomics Network (BCPN)**, we are pleased to welcome you to the **14<sup>th</sup> Human Proteome World Congress (HUPO 2015)**, taking place September 27–30, 2015 at the Vancouver Convention Centre, East Building in Vancouver, Canada.



**The Vancouver Congress will continue the extraordinary success of previous meetings in Boston, Yokohama and Madrid among other outstanding locations over the past years. Vancouver will hopefully provide a legacy and foundation for those to come in Taipei, Taiwan in 2016 and Dublin, Ireland in 2017. The theme of the 2015 meeting ‘Translating Proteomics and Allied -Omics to the Clinic’ will underpin the need for collaboration and cooperation of individuals from a wide range of professional backgrounds.**

Vancouver is an exceptional location for the Congress. It is renowned as one of the world’s outstanding convention cities, with the sparkling Pacific Ocean and towering Coast Mountains providing a unique and spectacular setting. The HUPO 2015 Congress will be held in the East Building of the Vancouver Convention Centre right under the famous sails and perched on the edge of the Pacific Ocean with wonderful space for both scientific presentations and commercial exhibition.

The social program highlighting our West Coast cuisine, unique culture and arts, combined with the breathtaking natural beauty and pre- and post congress meetings and tours will underscore the role of Vancouver as one of the world’s most popular tourist destinations.





The HUPO 2015 Congress will provide a wonderful forum for you to refresh your knowledge base and explore the innovations in proteomics and genomics. The Congress has striven to offer plenty of networking events, providing you with the opportunity to meet and interact with the leading scientists and researchers, friends and colleagues as well as sponsors and exhibitors.

We hope you will join us for a symphony of outstanding science over the next four days, and take a little extra time to enjoy the spectacular and unique beauty of this region.

With best wishes,



*Christoph Borchers*

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**Christoph Borchers**  
HUPO 2015  
Congress Co-Chair



*Pierre Thibault*

---

**Pierre Thibault**  
HUPO 2015  
Congress Co-Chair



*A Message from Premier Christy Clark*

As Premier of the Province of British Columbia, I am pleased to welcome everyone to the 14<sup>th</sup> Human Proteome Organization World Congress here in Vancouver, British Columbia.

Your meetings will be taking place in our world-class convention facilities, the Vancouver Convention Centre East Building, where experienced staff will help to ensure a successful gathering.

Thank you for coming to British Columbia and I wish you all the best in your important deliberations around new technologies, techniques and training relating to proteomics.

Sincerely,

A handwritten signature in black ink that reads "Christy Clark".

Christy Clark  
Premier

---

niʔ ct xatəmotaʔ, tə ʔnimət, tə tamax\* ʔiʔ tə kʷaʔkʷə ʔ \*  
We watch over the land and sea and in turn they watch over us.

September, 2015

## *A Message from the Mayor*

On behalf of the citizens of Vancouver, and my colleagues on City Council, I want to extend my warmest greetings to the delegates of the 14<sup>th</sup> Human Proteome Organization World Congress.

We are very proud of the reputation Vancouver enjoys as one of the world's most beautiful and unique meeting destinations. I hope that in addition to attending the conference you are able to experience the many cultural and recreational activities the City has to offer. I know everyone involved in organizing the conference will ensure your time with us is special.

Best wishes on a successful and productive conference.

Yours truly,



Gregor Robertson  
MAYOR

☎ 604.873.7621 📠 604.873.7685 📧 [gregor.robertson@vancouver.ca](mailto:gregor.robertson@vancouver.ca) 🌐 [vancouver.ca](http://vancouver.ca)

Office of the Mayor, City of Vancouver, 453 West 12th Avenue, Vancouver, British Columbia, Canada V5Y 1V4

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# CONGRESS SUMMARY OF EVENTS

ALL HUPO 2015 SESSIONS (EXCEPT FOR THE HPP WORKSHOP ON THURSDAY, OCTOBER 1) WILL TAKE PLACE AT THE **VANCOUVER CONVENTION CENTRE, EAST BUILDING, 999 CANADA PLACE, VANCOUVER, BC, V6C 3C1, CANADA**

## Onsite Registration Hours & Poster Pick Up

LOBBY,  
STREET/CONVENTION LEVEL

Saturday, September 26	16:00–20:00
Sunday, September 27	08:30–19:30
Monday, September 28	07:00–17:30
Tuesday, September 29	07:00–17:30
Wednesday, September 30	07:00–16:30

## Exhibit Hours

EXHIBIT HALL (HALL B),  
STREET/CONVENTION LEVEL

Sunday, September 27	19:30–21:00	Welcome Reception
Monday, September 28	10:00–17:30	
Tuesday, September 29	10:00–17:30	
Wednesday, September 30	10:00–16:30	

## Speaker Ready Room Hours

MEETING ROOM 7, LEVEL 1/MEETING LEVEL

Saturday, September 26	16:00–20:00	Monday, September 28	07:00–17:30
Sunday, September 27	08:30–19:30	Tuesday, September 29	07:00–17:30
		Wednesday, September 30	07:00–16:30





# OFFICIAL NETWORKING EVENTS

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## Welcome Reception

EXHIBIT HALL (HALL B),  
STREET/CONVENTION LEVEL

Sunday, September 27      19:30–21:00

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## Networking Breaks and Poster Viewing

EXHIBIT HALL (HALL B),  
STREET/CONVENTION LEVEL

Monday, September 28      10:00–11:10  
and 16:20–17:30

Tuesday, September 29      10:00–11:10  
and 16:20–17:30

Wednesday, September 30      10:00–11:10

---

## Congress Night 'Hockey Night in Canada'

EAST BALLROOMS,  
STREET/CONVENTION LEVEL

Tuesday, September 29      19:30–22:30



# HUMAN PROTEOME ORGANIZATION



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the code of life

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FAX +1 604 681 1049  
EMAIL OFFICE@HUPO.ORG

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's mission is:

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 PROTEOME ORGANIZATION

## HUPO GOVERNANCE - COUNCIL

## EXECUTIVE COMMITTEE 2015

## PRESIDENT

**Mark Baker**  
(ex-officio)

## PAST PRESIDENT

**Pierre Legrain**  
(2013-2015)

## VICE-PRESIDENT

**Mike Snyder**  
(2015-2017)

## TREASURER

**Bruno Domon**  
(2015-2017)

## SECRETARY GENERAL

**Gyorgy Marko-Varga**  
(2015-2016)

## MEMBER-AT-LARGE

**Yu-Ju Chen**  
(2015-2016)

## MEMBER-AT-LARGE

**Emma Lundberg**  
(2015-2016)

## COUNCIL MEMBERS 2015

Alexander Archakov

Mark Baker

Ana Paulina Barba

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Gyorgy Marko-Varga

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Visith Thongboonkerd

Takeshi Tomonaga

George Tsangaris

Mathias Uhlen

Marc Wilkins

Tadashi Yamamoto

Pengyuan Yang

# HUPO AWARDS



## Distinguished Achievement in Proteomic Sciences Award

### Amanda Paulovich

Fred Hutchinson Cancer Research Center,  
Seattle, Washington, USA

### HUPO AWARDS

WINNERS WILL BE AWARDED DURING THE CLOSING PLENARY SESSION ON WEDNESDAY, SEPTEMBER 30 IN THE PLENARY HALL (HALL A), VANCOUVER CONVENTION CENTRE, EAST BUILDING, STREET/CONVENTION LEVEL.

**Wednesday,  
September 30  
16:30-18:30**

Dr. Amanda Paulovich is awarded the HUPO Achievement Award 2015 for her significant impact in advancing the accuracy/precision of clinical proteomic mass spectrometry. She has been in the forefront of developing targeted proteomic assays based on Multiple Reaction Monitoring mass spectrometry technology, which can be multiplexed, standardized, reproduced, and shared across laboratories and instrument platforms.

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Journal of  
**proteome**  
research

# HUPO AWARDS

## Discovery in Proteomic Sciences Award



### **Bernhard Kuster**

Technical University of Munich,  
Chair of Proteomics and Bioanalytics,  
Freising, Germany



### **Akhilesh Pandey**

Institute of Genetic Medicine and  
Department of Biological Chemistry,  
Oncology and Pathology,  
John Hopkins University School of Medicine,  
Baltimore, Maryland, USA

Professors Bernhard Kuster and Akhilesh Pandey are jointly awarded the 2015 HUPO Discovery Award for their independent large-scale mass spectrometry-based studies of the human proteome. They investigated a wide range of tissues and cell lines with advanced instruments and made their results, published in Nature in May 2014, publicly available through ProteomeX-change for reanalysis by others throughout the proteomics community. Their data were rapidly incorporated into the ongoing Human Proteome Project of HUPO and stimulated renewed interest in confirmation and validation of protein identifications.

# HUPO AWARDS

## Science & Technology Award



### **Morteza Razavi**

Director of Lab Operations  
SISCAPA Assay Technologies  
Victoria, BC, Canada

### **Selena Larkin**

Vice President, Marketing and Sales  
SISCAPA Assay Technologies  
Victoria, BC, Canada

### **Leigh Anderson**

Chairman, CEO and Founder  
SISCAPA Assay Technologies, Inc.,  
Washington, DC, USA

## HUPO AWARDS

WINNERS WILL BE AWARDED DURING THE CLOSING PLENARY SESSION ON WEDNESDAY, SEPTEMBER 30 IN THE PLENARY HALL (HALL A), VANCOUVER CONVENTION CENTRE, EAST BUILDING, STREET/CONVENTION LEVEL.

**Wednesday,  
September 30  
16:30-18:30**

Leigh Anderson, Morteza Razavi and Selena Larkin are collectively awarded the HUPO Science and Technology Award 2015 for the development of the SISCAPA (Stable Isotope Standards and Capture by Anti-Peptide Antibodies) technology. The SISCAPA assays enable targeted quantitation of proteins and peptides from complex biological samples. The SISCAPA process involves up-front trypsin digestion of the sample followed by immunocapture enrichment of proteotypic peptides that are surrogates for the proteins of interest. Stable isotope labeled peptides are spiked into each sample for relative quantitation of the target molecules via quantitative mass spectrometry (MS).

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# HUPO AWARDS



## Translational Proteomics Award

### Jennifer van Eyk

Cedars Sinai Medical Center,  
Los Angeles, California, USA

Dr. Jennifer Van Eyk is awarded the HUPO Translational Proteomics Award 2015 for her substantial contributions in translational medicine applying proteomics technology. She was one of the first to validate the concept that disease-induced modified protein biomarkers can add specificity to disease status and discovered the disease induced modifications of cardiac troponin I that revolutionized our understanding of the complexity of heart disease and improved our ability to diagnosis heart attacks. Based on this information she developed assays for the quantification of disease induced modified forms of cardiac troponin I that revolutionized the diagnosis of heart attacks.

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## HUPO AWARDS



### Distinguished Service Award

**Catherine Costello,**

Center for Biomedical Mass Spectrometry,  
University School of Medicine,  
Boston, USA

#### HUPO AWARDS

WINNERS WILL BE AWARDED DURING THE CLOSING PLENARY SESSION ON WEDNESDAY, SEPTEMBER 30 IN THE PLENARY HALL (HALL A), VANCOUVER CONVENTION CENTRE, EAST BUILDING, STREET/CONVENTION LEVEL.

**Wednesday,  
September 30  
16:30-18:30**

Prof. Catherine Costello is awarded the Distinguished HUPO Service Award for her long-term dedication to promote HUPO and HUPO activities.

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# HUPO 2015 TRAVEL AWARDS

## **Anuli Uzozie, Switzerland**

P06.02 - Quantitative Mass Spectrometry Reveals Markers for Colorectal Tumors

## **Victor Llombart, Spain**

CS04.07 - Protein Profiling of Brain Ischemia by MALDI-Imaging-Mass-Spectrometry

## **Manja Wölter, Germany**

CS28.06 - Risk Assessment of Development Impairment in Preterm Babies by Cord Blood Proteome Profiling

## **Yelena Yefremova, Germany**

CS26.10 - Ion Mobility and Surface Topology Mapping Reveals the Cause of the Protein G-IgG Affinity Switch

## **Kondethimmanahalli Chandramouli, Saudi Arabia**

P11.03 - Proteomic Changes Associated with Reproductive Periods in Male Polychaetous Nearthes Arenaceodontata

## **Martin Frejno, United Kingdom**

CS22.03 - Kinome, Total Proteome and Phosphoproteome Analysis of the CRC64 Cell Line Panel

## **Sandra Goetze, Switzerland**

P06.06 - Development of a Risk Stratification Test to Discern Aggressive and Non-Aggressive Prostate Cancer

## **Maria Yakovleva, Sweden**

P06.07 - Large-Scale Analysis of Melanoma Tissue Samples

## **Linda Switzar, Netherlands**

P04.09 - Development of LC-Electrochemistry-MS for Disulfide Mapping: Application to Notch3 Protein Fragments

## **Asfa Alli Shaik, Singapore**

P15.06 - Quantitative Proteomics Analysis Unravels Functional Roles of Englerin A in Renal Cancer

## **Hongqiang Qin, China**

CS20.05 - Development of Methods for Site-Specific Analysis of N-Linked Protein Glycosylation

## **Aman Makaju, USA**

CS10.04 - Identification of Cofactors Influencing Smyd1's Histone Methyltransferase Activity via ChIP-MS

## **Sarah Hayes, Australia**

P06.15 - SWATH-MS Profiling of NSCLC Cell Lines: Defining Mechanisms of Erlotinib Resistance

## **Mathieu Lavallée-Adam, USA**

CS25.06 - MS3ID: A Novel MS3-Based Method Coupled to a Supervised Learning Algorithm for Top-Down Proteomics

## **Vincent Puard, United Kingdom**

CS16.06 - Detection of Biomarkers of Sepsis Using Affimer Microarrays

## **Evelyne Maes, Belgium**

P06.20 - Proteomic Analysis of Tumor-Associated Macrophages in an In Vivo Tumor Microenvironment

## **Barbara Cardinali, Italy**

P07.05 - Evaluation of New Biomarkers of Resistance to Trastuzumab in the Treatment of HER2+ Breast Cancer

## **Vincent Geoghegan, United Kingdom**

CS20.07 - Analysis of Arginine Methylation in Primary T Cells Reveals Roles in Cell Signalling and Fate

## **Christoph Krisp, Australia**

P06.26 - SWATH Quantitation Using Ion Libraries from Multiple Cancer Cell-Types Identifies Drug Resistance

## **David Greening, Australia**

P06.28 - YBX1 Induces Oncogenicity via Release of Angiogenic Factors into the Tumour Microenvironment

## **Ya-Ju Hsieh, Taiwan**

P04.16 - Systematic Exploration of Subcellular Redox Status by Methionine-Containing Peptide Enrichment

## **Verena Tinnfeld, Germany**

CS26.09 - Enrichment of Cross-Links from Complex Samples by Charge-Based Fractional Diagonal Chromatography

# HUPO 2015 TRAVEL AWARDS

**Elena Ponomarenko, Russia**

P13.06 - Gene-centric Knowledgebase as a Tool for Estimating Protein Species Number

**Frank Fleurbaaij, Netherlands**

P09.12 - CE-MS for the Detection of Carbapenemases in (Multi-)Drug-Resistant Gram-Negative Bacteria

**Michael Götze, Germany**

P01.09 - Efficient Identification of Cross-Linked Peptides with StavroX and MeroX in Structural Proteomics

**Zon Lai, Germany**

CS01.04 - Proteolytic Processing in the Progression of Low-Grade Astrocytomas to Glioblastoma Multiforme

**Teresa García-Berrocso, Spain**

CS07.04 - Plasmatic RBP4 and GFAP as Biomarkers to Differentiate Ischemic from Hemorrhagic Stroke

**Linnea Lagerstedt, Switzerland**

P07.13 - A Biomarker Panel to Rule-Out CT-Scan Lesions in Mild Traumatic Brain Injury

**Maria Pavlou, Switzerland**

CS21.07 - The *Listeria Monocytogenes* Prototype

**Anna Häggmark, Sweden**

P16.09 - Neuroproteomic Profiling of 277 Brain-Enriched Proteins in CSF and Plasma

**Latifa Latrous, Tunisia**

P11.12 - Gas Phase Interactions of Nucleosides with Organomercuric Compounds

**Jennifer Abelin, USA**

CS08.08 - Insights into Immune Responses to Commensal Bacteria through MHC Class II Antigen Quantification

**Claudia Corbo, Italy**

CS14.06 - Membrane Proteins of Leukocyte-Inspired Nanoparticles Improve Their Therapeutic Efficacy

**Sandra Anjo, Portugal**

P01.14 - Oxidative Stress Dependent Regulation of DJ-1: An Interatomic Point of View

**Shamim Mushtaq, Pakistan**

P14.01 - Expression & Association of CDK10 with ETS2 during Human Corneal Wound Healing

**Can Cenik, USA**

CS23.03 - Integrative Analysis of RNA, Translation and Protein Level Variation across Humans

**Cristian Piras, Italy**

P09.19 - Label Free Study for Control of *Listeria Monocytogenes* to Enhance Food Safety

**Pia Jensen, Denmark**

P15.20 - Identifying Novel Signaling Mechanisms Underlying Insulin Release from Glucose Stimulated Beta Cells

**Viviana Greco, Italy**

P09.23 - Proteomics Investigation of *Pseudomonas Fluorescens* Chromogenic Strains: Insight in Blue-Mozzarella

**Marina Rodchenkova, Russia**

P16.17 - Implementation of Mass Spectrometry for Detection Amyloid-? Peptides in Plasma

**Ruth Huttenhain, USA**

P09.24 - Investigating HIV-Mediated Dynamics of Cullin RING E3 Ligases by AP-MS and Proximity Biotinylation

**Andrea Matlock, USA**

CS13.05 - Pathological Variability of Motor Neuron Disorders in Patient-Derived iPSC Using SWATH-MS



# HUPO 2015 TRAVEL AWARDS



## BCPN Travel Award Winners

BCPNetwork

### Nicholas Brodie, Canada

P10.01 - A Structural Proteomics Study of Native Alpha-Synuclein in Solution

### Patrick Chan, Canada

P11.10 - Proteomic Profiling of the [PSI<sup>+</sup>] Yeast Prion Strain by Quantitative Mass Spectrometry

### Gillian Dornan, Canada

CS22.10 - The Molecular Mechanism of PI3K Mutations Implicated in Immunodeficiencies

### Nikolaus Fortelny, Canada

P19.01 - Truncated Protein Isoforms and Their Genesis in the Human Proteome

### Karen Lithgow, Canada

P09.31 - Proteomic Characterization of Vascular Adhesins from the Syphilis Spirochete, *Treponema Pallidum*

### Steven McArthur, Canada

P09.01 - Detecting and Quantifying Dengue Viral Proteins and Virus Maturation by MRM-MS

### Robert Popp, Canada

P06.14 - Immuno-MALDI for Quantifying Akt1 and Akt2 Phosphorylation in Colorectal Cancer

### Amrit Singh, Canada

P28.13 - Multi-Omic Blood Biomarker Signatures of the Late Phase Asthmatic Response

### Nestor Solis, Canada

CS08.09 - Multi-Omics to Examine Proteolytic Cleavage, Expression and Abundances in Macrophage Differentiation

### ChenXi Yang, Canada

P07.35 - Differential Expression of C3a and C5a in Allergic Asthma

### Yuzi Zheng, Canada

CS02.05 - Investigating TDP-43-Mediated Neurodegeneration by Mass Spectrometry

### Mang Zhu, Canada

P10.03 - A Feature Analysis of Lower Solubility Proteins in Unstressed and Heat-Shocked Yeast Cells

### Giada Marino, Canada

P11.27 - Pulmonary Fibrosis: TAILS N-Terminomics Unravels the Role of MMP12

### Claudia Gaither, Canada

CS21.10 - Proteomic Investigation of a Potential Type I Secretion System in the Syphilis Spirochete, *Treponema Pallidum*

### Theo Klein, Canada

HPPO3.04 - TMT10-TAILS Analysis of Lymphocytes to Unravel the Role of Proteolysis in B Cell Activation

### Nicholas Scott, Canada

P13.01 - Characterization of the Protein Complex Landscape of Murine Tissues

### Ameya Ranade, Canada

PQ2.14 - Methodology Development for Quantification of Tightly Adsorbed Proteins

# HUPO 2015 TRAVEL AWARDS

## CNPN Travel Award Winners



### Carolyn Kachuk, Canada

CS24.05 - Comparison of Acetone Precipitation and FASP II for Protein Identification through Bottom up MS

### James Knight, Canada

P13.10 - ProHits 2.0: A Bioinformatics Management and Analysis System Optimized for Interaction Studies

### Dimitrios Korbakis, Canada

PO4.27 - Immunoaffinity-MS Platform for Antibody Screening and Native Protein Analysis in Biological Fluids

### Nikunj Gevariya, Canada

PO6.56 - Omega-3 Fatty Acid-Enriched Diet Favors a Reduction of Murine TRAMP-C2 Prostate Tumor Growth Compared to Omega-6 Fatty Acid-Enriched Diet

### Theano D. Karakosta, Canada

P17.15 - Multiplexed SRM Assay for Measurement of Tissue Kallikrein-Related Peptidases in Biological Fluids

### Antoine Méant, Canada

PO6.35 - Characterization of the Interactome of RSK Isoforms to Decipher Their Roles in Cancer Cells

### Mario Navarrete, Canada

CS09.09 - Serine Hydrolase Activities in Urine from Patients Undergoing Cardiac Bypass Surgery

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# HUPO 2015 COMMITTEES

## HUPO 2015 LOCAL ORGANIZING COMMITTEE

### CONGRESS CHAIR

#### **Christoph Borchers**

University of Victoria  
Victoria, Canada

### CONGRESS CO-CHAIR

#### **Pierre Thibault**

University of Montreal  
Monreal, Canada

### COMMITTEE

#### **George Agnes**

Simon Fraser University  
Vancouver, Canada

#### **Yossef Av-gay**

University of  
British Columbia  
Vancouver, Canada

#### **Mari DeMarco**

University of  
British Columbia  
Vancouver, Canada

#### **Suzanne Gill**

Genome BC  
Vancouver, Canada

#### **Natalie Glavas**

BC Proteomics Network  
Vancouver, Canada

#### **Juergen Kast**

University of  
British Columbia  
Vancouver, Canada

#### **Paul Keown**

University of  
British Columbia  
Vancouver, Canada

#### **Thibault Mayor**

University of  
British Columbia  
Vancouver, Canada

#### **Bruce McManus**

University of  
British Columbia  
Vancouver, Canada

#### **Rob McMaster**

University of  
British Columbia  
Vancouver, Canada

#### **Susan Murch**

University of British  
Columbia Okanagan  
Kelowna, Canada

#### **Chris Overall**

University of  
British Columbia  
Vancouver, Canada

#### **Bingyun Sun**

Simon Fraser University  
Vancouver, Canada

#### **Scott Tebbutt**

University of  
British Columbia  
Vancouver, Canada

# HUPO 2015 COMMITTEES

## HUPO 2015

### SCIENTIFIC ORGANIZING COMMITTEE

**Mark Baker**

Australian School of  
Advanced Medicine,  
Macquarie University  
Sydney, Australia

**Christoph Borchers**

University of Victoria  
Victoria, Canada

**Maxey C.M. Chung**

National University  
of Singapore  
Singapore, Singapore

**Eric Deutsch**

Institute for Systems Biology  
Seattle, USA

**Oliver Fiehn**

UC Davis  
Davis, USA

**David Goodlett**

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Baltimore, USA

**Sam Hanash**

University of Texas MD  
Anderson Cancer Center  
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**Fuchu He**

Beijing Proteome  
Research Center  
Beijing, China

**Gil Omenn**

University of Michigan  
Ann Arbor, USA

**Young-Ki Paik**

Yonsei Proteome Research  
Center, Yonsei University  
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**Richard Smith**

Pacific Northwest National  
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Osaka, Japan

**Jennifer Van Eyk**

Cedars-Sinai Medical Center  
Los Angeles, USA

**David Wishart**

University of Alberta  
Edmonton, Canada

**Tadashi Yamamoto**

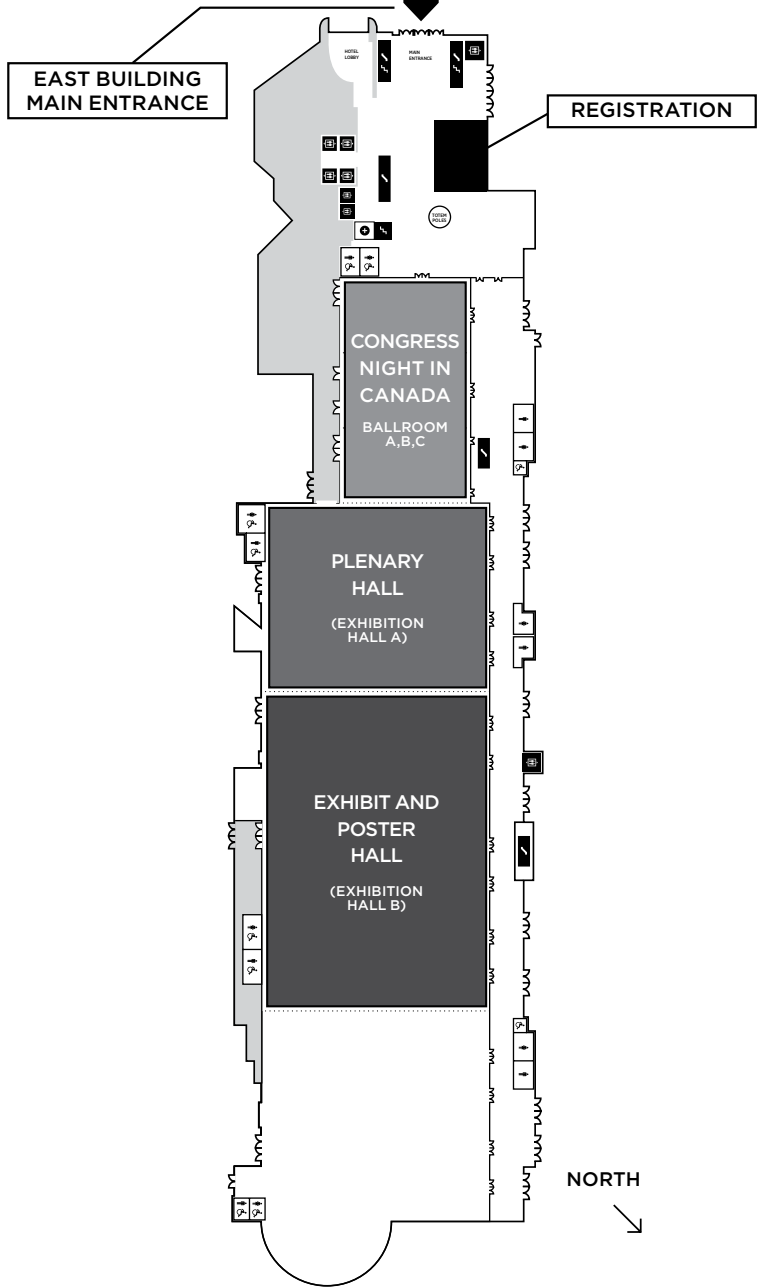
Niigata University  
Niigata, Japan

**John Yates**

The Scripps  
Research Institute  
LaJolla, USA

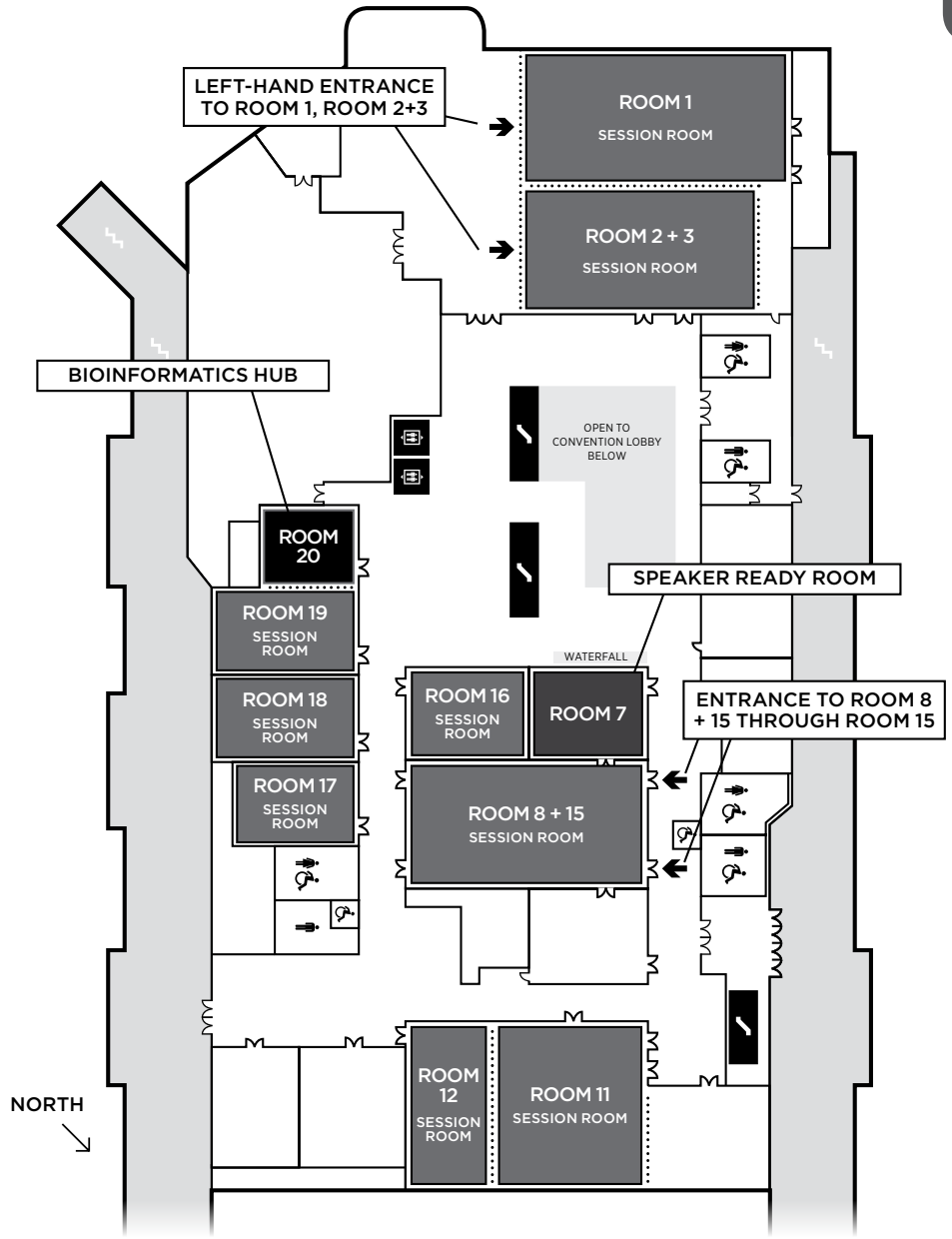
# CONVENTION CENTRE, EAST BUILDING

CONVENTION/STREET LEVEL



# CONVENTION CENTRE, EAST BUILDING

## MEETING LEVEL/LEVEL 1



# REGISTRATION

**Registration for all attendees (delegates, exhibitors) is located at the Vancouver Convention Centre, East Building Lobby, Street/Convention Level.**

## Hours of Operation

Saturday, September 26	16:00–20:00
Sunday, September 27	08:30–19:30
Monday, September 28	07:00–17:30
Tuesday, September 29	07:00–17:30
Wednesday, September 30	07:00–16:30

## REGISTRATION MATERIALS

### Registration Fees for full Congress includes:

Access to all scientific session except for the Clinical, Educational and Mentoring Day as well as the HPP Workshop on Thursday, October 1 (additional fees apply)

Access to Welcome Reception on Sunday, September 27

Access to Exhibit and Poster Hall

Access to all Networking Breaks and Poster Viewing Sessions

Delegate Bag with Congress materials

### Registration Fees for Single Day Registration includes:

Access to all scientific session on the day of attendance

Access to Exhibit and Poster Hall on day of attendance

Access to Networking Breaks and Poster Viewing Sessions on day of attendance

Delegate Bag with Congress materials

## NAME BADGES

Delegates and guests are requested to wear their name badge at all times in order to participate in the Scientific Sessions, Networking Events and Exhibition.

## LOST BADGE/NAME CHANGES

A 50 CAD fee applies for any reprints due to onsite name changes or lost badges.



# ONSITE SERVICES AND GENERAL INFORMATION

## HUPO 2015 Official Mobile App

Download the free HUPO 2015 mobile app for a convenient way to stay up-to-date via your phone or tablet. View the full scientific schedule, abstracts, exhibit information including floor plan and exhibitor biographies, and general Congress and venue information on our easy to use app!

The app is compatible with all iOS devices (iPhone, iTouch and iPad) and all Android mobile devices. Timely updates on program or room changes will be distributed through the mobile app via notification alerts.

## Join the Conversation

HUPO 2015 OFFICIAL SOCIAL MEDIA ACCOUNTS

Share your experience and images from HUPO 2015 with colleagues and friends via Facebook, LinkedIn and Twitter. Our official social media feeds throughout the Congress can be followed @hupo\_org. We encourage you to tag your posts with #HUPO2015.



@hupo\_org



/humanproteomeorg



Human Proteome  
Organization (HUPO)

## Delegate Services Information Desk

LOCATED IN THE ENTRANCE LOBBY OF THE  
VANCOUVER CONVENTION CENTRE EAST  
BUILDING, STREET/CONVENTION LEVEL

Sunday, September 27	08:00-16:00
Monday, September 28	08:00-16:00
Tuesday, September 29	08:00-16:00
Wednesday, September 30	08:00-16:00

Knowledgeable local staff will provide local information and assist with:

- Ground Transportation
- Airport Transfers
- Sightseeing Tours
- Pre- and Post Tours
- Restaurant recommendations and booking

# ONSITE SERVICES AND GENERAL INFORMATION

## ABSTRACTS

Abstracts selected for HUPO are presented in Oral, Mini Oral and Poster Sessions. All accepted and confirmed abstracts are available in the mobile app and are also collected in an online abstract book available on the Congress website at [www.hupo2015.com](http://www.hupo2015.com).

## AIRPORT TRANSFERS

For individual airport transfer bookings please see the Delegate Services Information Desk located in the entrance lobby of the Vancouver Convention Centre East Building, Street/Convention Level.

## ATTIRE

Business casual is appropriate. Room temperature can vary in session rooms. We encourage attendees to dress in layers for their personal comfort. Attire for the Congress Night on Tuesday, September 29 is casual.

## ATM

Two ATMs are located in the Lobby of the East Building behind the information desk.

## BAGGAGE CHECK

See Coat Check

## BUSINESS CENTRE

There is no business centre inside the Vancouver Convention Centre, East Building. Delegates may visit the FedEx Office Print & Ship Centre located at 779 W Pender St., Vancouver, BC, C6C 1H2, two blocks away from the Vancouver Convention Centre, East Building.

## CAMERAS AND CELL PHONES

No cameras or video cameras are allowed in any event during HUPO. As a courtesy to fellow attendees, please turn off cell phones during scientific sessions.

## CERTIFICATE OF ATTENDANCE

International attendees can request a 'Certificate of Attendance' by completing the Congress Evaluation Form available on the Congress website on Thursday, October 1, 2015. After completing the evaluation form you will be able to download your Certificate of Attendance.

## CHARGING STATIONS

A Charging Station area is located in the Exhibit Hall (Hall B) allowing delegates to power up their cell phones, iPads, laptops and other electronic devices for free. This station will be in high demand; therefore sessions are limited to 15 minutes.

CHARGING STATION  
SUPPORTED BY



# ONSITE SERVICES AND GENERAL INFORMATION

## CME ACCREDITATION AND CME CERTIFICATE

The Congress is not CME accredited.

## COAT CHECK

With all official Congress hotels being in walking distance to the Convention Centre, there will be no coat check.

## COFFEE BREAKS

See Networking Breaks

## DELEGATE BAG RETURN

If you do not want to take home your Delegate Bag, please return it to the Registration Desk.

## EMERGENCY SERVICES AND FIRST AID

### EMERGENCY NUMBER

In the event of a health, safety, or criminal emergency, dial 9-1-1.

You may also dial 7500 from any of the house phones or +1 604 647 7500 from your mobile phone.

The First Aid Office is located in the East Lobby next to the washrooms. Kindly note that the First Aid Office is not staffed. For access please call the above mentioned emergency numbers.

## EVALUATIONS

A Congress evaluation survey will be e-mailed to all delegates after the Congress. Please help us to improve the Congress by completing your survey.

## EXHIBITS

The exhibits are an integral part of the experience at HUPO and will feature the latest in technology and research. The exhibits are located in the Exhibit Hall (Hall B), Street/Convention Level at the Vancouver Convention Centre, East Building.

## HIGHLIGHT OF THE DAY EBLAST

Watch out for daily morning emails (Sunday-Wednesday) providing you with an update highlighting the best sessions and presentations as well as exciting things to do in Vancouver. The eNews will also include any speaker or room updates.

## HUPO



translating  
the code of life

Please visit the HUPO Booth (#401) for updates on membership, and general information.

## LANGUAGE

The official language of the HUPO 2015 Congress is English.

## LOST AND FOUND

Lost and Found items should be returned/claimed at the Registration Desk.

# ONSITE SERVICES AND GENERAL INFORMATION

## NETWORKING BREAKS

Networking Breaks will take place in the Exhibit Hall (Hall B), Street/Convention Level at the following times. Refreshments will be provided.

### Networking Break and Poster Viewing

#### EXHIBIT HALL (HALL B), STREET/CONVENTION LEVEL

Monday, September 28      10:00 – 11:10  
and 16:20 – 17:30

Tuesday, September 29      10:00 – 11:10  
and 16:20 – 17:30

Wednesday, September 30      10:00 – 11:10  
and 16:20 – 16:30

## PARKING

Parking is available in the Vancouver Convention Centre West and East Building.

#### VANCOUVER CONVENTION CENTRE EAST 999 CANADA PLACE

#### VINCI PARK

Enter at the foot of Howe Street, obtain ticket from dispenser and proceed to P1 or P2.

Use Convention Centre/Hotel elevators (not World Trade Centre elevators).

For Convention Level: press "G" for Registration, Ballrooms and Exhibits.

For Meeting Rooms: press "M".

## PUBLIC TRANSPORTATION

Vancouver is a walkable city and all Congress hotels are within a maximum of 15 minute walking distance.

## RESTAURANTS

There are plenty of restaurant choices in Vancouver. You may also want to try out one of the many food trucks around the Convention Centre and the downtown area. A food court is located right underneath the Fairmont Waterfront Hotel across from the Vancouver Convention Centre, East Building.

The staff at the Delegate Services Information Desk will be happy to assist with recommendations and bookings. Delegates may also seek assistance within Vancouver from the Vancouver Downtown Ambassadors. Staff are easily located by their blue uniforms outside the Convention Centre.

## SMOKING

It is against the law to smoke in any indoor public place or worksite, including pubs, bars, restaurants, and shopping centres. Designated smoking rooms are non-existent, and public transit, transit shelters, taxis and work vehicles are also smoke-free.

In addition, there is a 3 metre non-smoking "buffer zone" around public and work place doorways, opening windows and air intakes including apartments and condominiums.

# ONSITE SERVICES AND GENERAL INFORMATION

## SPEAKER READY ROOM

Meeting Room 7 located on Level 1/ Meeting Level is the designated Speaker Ready Room. All Presenters are required to submit and/or preview their slides at least 24 hours prior to their scheduled presentation to ensure compatibility with the Congress AV Equipment.

## HOURS OF OPERATION

Saturday, September 26	16:00–20:00
Sunday, September 27	08:30–19:30
Monday, September 28	07:00–17:30
Tuesday, September 29	07:00–17:30
Wednesday, September 30	07:00–16:30

## STAFF AND VOLUNTEERS

Volunteers are working throughout the Convention Centre and are happy to assist with any questions delegates may have regarding the Congress or the Convention Centre. Delegates can easily locate them by their staff/volunteer shirts.

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## DISCLAIMER

THE ORGANIZERS HAVE MADE EVERY ATTEMPT TO ENSURE THAT ALL INFORMATION IN THIS PUBLICATION IS CORRECT. THE ORGANIZERS TAKE NO RESPONSIBILITY FOR CHANGES TO THE PROGRAM OR ANY LOSS THAT MAY OCCUR AS A RESULT OF CHANGES TO THE PROGRAM. SOME OF THE INFORMATION PROVIDED IN THIS PUBLICATION HAS BEEN PROVIDED BY EXTERNAL SOURCES. ALTHOUGH EVERY EFFORT HAS BEEN MADE TO ENSURE THE ACCURACY, CURRENCY AND RELIABILITY OF THE CONTENT, THE ORGANIZERS ACCEPT NO RESPONSIBILITY IN THAT REGARD.

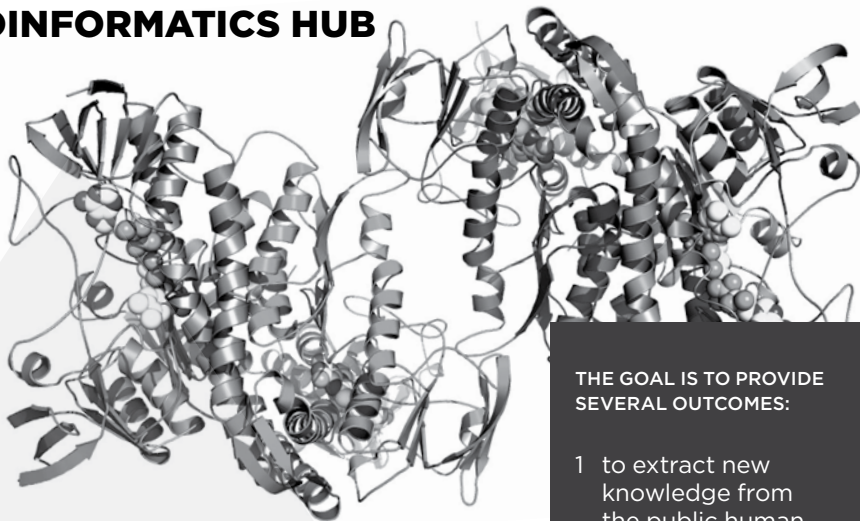
## WIRELESS INTERNET

HUPO is providing free Wi-Fi throughout the Vancouver Convention Centre. To ensure a positive Wi-Fi experience for all users please do not use your own wireless Hotspot device. These additional Wi-Fi devices create significant RF interference which can interfere with all Wi-Fi networks. Please turn these devices off and connect to the Wi-Fi network HUPO 2015 and open your web browser to connect to the Internet.

## NETWORK: HUPO 2015

**NO PASSWORD IS REQUIRED, BUT YOU WILL NEED TO OPEN YOUR BROWSER TO CONNECT.**

## BIOINFORMATICS HUB



**The Bioinformatics Hub at HUPO 2015 in Vancouver is organized by the Computational Mass Spectrometry initiative, a joint initiative of HUPO, ISCB and the Metabolomics Society.**

The objective of this hands-on meeting is to develop and execute original bioinformatics analyses on the publicly available human proteomics data during the Congress, facilitated by several leading proteomics informatics groups, and completely open for participation by any and all interested Congress attendees.

Moreover, the intent is to maximize constructive interactions between wet-lab researchers, mass spectrometry practitioners and bioinformaticians by organizing dedicated 'problem-busting' Ask-The-Experts sessions, where proteomics bioinformatics experts and the audience together provide and answer any hot topic questions in proteomics bioinformatics.

The Bioinformatics Hub will start on September 27, the day preceding the main Congress, and continue the work, the brainstorming, the problem-busting and interaction during the remainder of the Congress.

THE GOAL IS TO PROVIDE SEVERAL OUTCOMES:

- 1 to extract new knowledge from the public human proteomics data;
- 2 to come up with novel approaches and ideas to perform integrative proteomics data analysis and interpretation;
- 3 to discuss with participants about the possibilities and limitations of existing tools and data processing algorithms, fostering collaborative interactions between wet-lab researchers and bioinformaticians; and
- 4 to identify gaps in the existing proteomics bioinformatics tools, inspiring future work to fill these gaps.

# BIOINFORMATICS HUB

Ask-The-Experts sessions will be held every day between 10:00 and 11:00.

Just a few examples of highly interesting topics that can be explored include:

- The search for missing proteins
- The identification of splice isoforms and splice junction peptides, calculations of protein-level FDR based on across-experiment data
- The mapping of post-translational modifications on peptides and proteins.

## CONTRIBUTORS:

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CEA GRENOBLE, FRANCE

THE BIOINFORMATICS HUB AT  
HUPO 2015 IS SPONSORED BY





# INFORMATION FOR INVITED FACULTY AND ABSTRACT PRESENTERS

## Speaker Ready Room

All Invited Speakers as well as Oral and Mini Oral Abstract Presenters are required to report to the Speaker Ready Room at least 4 hours prior to their scheduled presentation in order to upload their presentation slides or to check their previously uploaded slides.

### **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 submissions will be accepted in the Session Rooms.

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#### **SPEAKER READY ROOM IS LOCATED IN MEETING ROOM 7, LEVEL 1/MEETING LEVEL**

Saturday, September 26	16:00-20:00
Sunday, September 27	08:30-19:30
Monday, September 28	07:00-17:30
Tuesday, September 29	07:00-17:30
Wednesday, September 30	07:00-16:30

## Oral Presentation with Poster Presentation

You will have a total of **15 minutes**; 12 minutes of presentation, followed by 3 minutes time for questions from the audience. Time limits will be strictly enforced.

Please be in room for your session 10 minutes before the start time of the session. The Session Chairs will start and end strictly on time.

You are asked to prepare a PPT Presentation with **max. 10 slides** (not including title and author slide).

You are required to submit your presentation slides to the Speaker Ready Room (onsite) at least 4 hours prior to your scheduled presentation.

In addition to your talk you will be given the opportunity to prepare a poster and have it displayed in the Exhibit Hall for the entire duration of the Congress. Please see Poster Presentation information below for further instructions.

## Mini Oral with Poster Presentation

You will have a total of **5 minutes** (no Q&A). Time Limits will be strictly enforced.

Please be in room for your session 10 minutes before the start time of

# INFORMATION FOR INVITED FACULTY AND ABSTRACT PRESENTERS

the session. The Session Chairs will start and end strictly on time.

You are asked to prepare a PPT Presentation with **max. 5 slides** (not including title and author slide).

You are required to submit your presentation slides to the Speaker Ready Room (onsite) at least 4 hours prior to your scheduled presentation.

In addition to your 5 minute oral talk you will be asked to prepare a poster. Please see Poster Presentation below for further instructions.

## Poster Presentation

**The maximum poster size is: 4' x 4'.** Poster Boards will be Velcro and Push Pin compatible.

All Posters will be displayed in the Exhibit Hall (Hall B) at the Vancouver Convention Centre, East Building.

All Posters will be on display for the entire duration of the Congress. However, poster presenters are asked to stand by their poster during the morning and afternoon networking breaks on the day of their Poster Session to informally answer questions from Congress Delegates.

## Author Stand By Times

### ODD POSTER NUMBERS

Monday, September 28	10:00-11:10 and 16:20-17:30
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### EVEN POSTER NUMBERS

Tuesday, September 29	10:00-11:10 and 16:20-17:30
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### SETUP HOURS

Sunday, September 27	19:30-21:00
OR	
Monday, September 28	07:30-10:00

### TAKE DOWN HOURS

Wednesday, September 30	16:30
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## Poster Pick Up Counter

### REGISTRATION DESK, STREET/CONVENTION LEVEL

Saturday, September 26	16:00-20:00
Sunday, September 27	08:30-19:30
Monday, September 28	07:00-17:30
Tuesday, September 29	07:00-17:30
Wednesday, September 30	07:00-16:30

# SOCIAL PROGRAM

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## Welcome Reception

Sunday,  
September 27, 2015

19:30-21:00

**VANCOUVER CONVENTION  
CENTRE, EAST BUILDING,  
EXHIBIT HALL (HALL B)**

The Welcome Reception is included in full registration. Additional tickets for guests can be purchased at the time of registration or onsite.

Additional tickets for friends and guests: 75 CAD

Following the Opening Ceremony, delegates are invited to the Exhibition Hall for the Welcome Reception and the chance to mix and mingle with exhibitors, friends and colleagues while enjoying local wines and exquisite canapés.

## SOCIAL PROGRAM

### Congress Night – Hockey Night in Canada



**Experience a Congress Night like no other with a truly Canadian Hockey Night in Canada!**

“HELLO OUT THERE, WE'RE ON THE AIR, IT'S 'HOCKEY NIGHT' TONIGHT.

TENSION GROWS, THE WHISTLE BLOWS, AND THE PUCK GOES DOWN THE ICE

THE GOALIE JUMPS, AND THE PLAYERS BUMP, AND THE FANS ALL GO INSANE

SOMEONE ROARS, “BOBBY SCORES!”, AT THE GOOD OL' HOCKEY GAME.

OH! THE GOOD OL' HOCKEY GAME, IS THE BEST GAME YOU CAN NAME

AND THE BEST GAME YOU CAN NAME, IS THE GOOD OL' HOCKEY GAME”

- Stompin' Tom Connors,  
The Good Old Hockey Game

#### Congress Night – Hockey Night In Canada

Tuesday,  
September 29, 2015

19:30–22:30

VANCOUVER CONVENTION  
CENTRE, EAST BUILDING,  
BALLROOMS A+B+C

Tickets are only 100 CAD,  
and includes skate rentals  
and commemorative photos  
with various hockey players.

Don't miss out and join us  
at the HUPO 2015 Congress  
Night, “Hockey Night in  
Canada” on September 29,  
2015!

Hockey is an incredibly important pastime that began in Canada in the 1880's and all Canadians, young and old, grew up watching hockey.

To pass on this important tradition to our guests and international delegates, we invite you, your family and friends to experience a once in a lifetime experience at the **HUPO 2015 Congress Night, “Hockey Night in Canada,” on Tuesday, September 29, 2015, from 19:30 to 22:30.**

As the Vancouver Convention Centre East Ballroom is magically transformed into a hockey ice rink, delegates will have the chance to skate and play hockey on the large synthetic ice rink, or dance along with our amazing cover band on the dance floor, or alternatively to sit back and relax while enjoying a casual Vancouver West Coast Style buffet dinner in the lounge area. There will be fun & exciting activities for everyone!

This will be a Congress Night like no other, and we encourage you to bring your families and friends to enjoy this special night with us.

# SOCIAL PROGRAM

## LOCAL SIGHTSEEING TOURS

### Local Sightseeing Tours

“VANCOUVER IS A CITY UNLIKE ANY OTHER. WHEREVER I LOOK, I SEE WATER OR MOUNTAINS — OR BOTH. AND EVERYONE LOOKS SO HEALTHY.”

— THE DAILY TELEGRAPH  
(UK)

Nestled between the Pacific Ocean and Coast Mountains, Vancouver is consistently ranked as one of the most livable cities.

Bring a camera to capture the breathtaking panoramic views while walking along the Seawall, relax in Stanley Park, take a boat ride to Granville Island, enjoy world-class shopping and our famous West Coast cuisine and join a guided sightseeing adventure.

HERE ARE THE MOST POPULAR TOURS:



### Vancouver City Tour



### Whistler and Shannon Falls



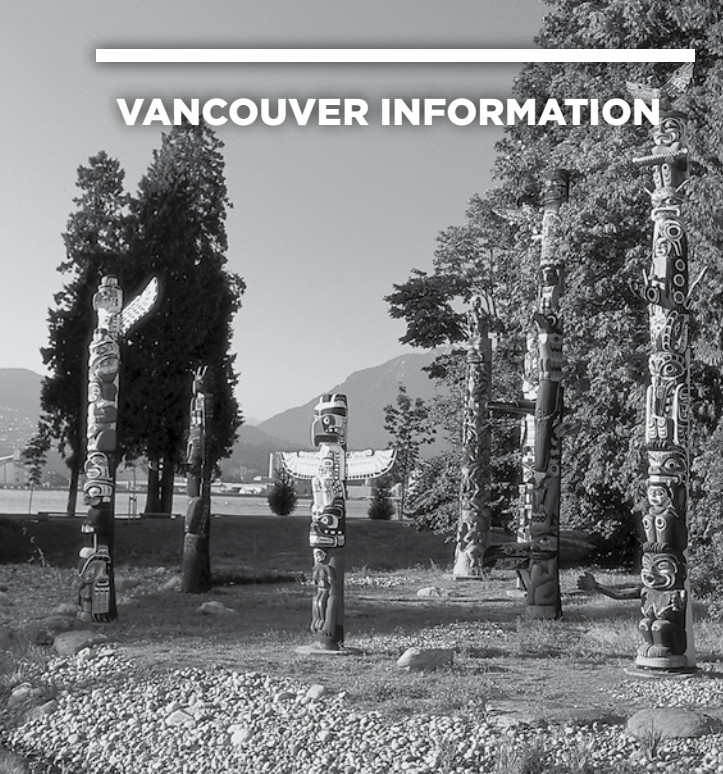
### Enchanting Victoria

FOR FURTHER INFORMATION AND RESERVATIONS

Please contact our partner Westcoast Sightseeing Tours at 1.887.451.1777 or 1.604.451.1600 or visit [www.vancouversightseeing.com](http://www.vancouversightseeing.com)



# VANCOUVER INFORMATION



## QUICK FACTS

The Vancouver Metropolitan Area has a population of 2.4 million as of 2010, which is approximately half of the entire population of British Columbia; the city of Vancouver proper has over 600,000 people (census data from 2011)

Vancouver was ranked as the third most livable city by the EIU in 2013 and fifth most livable city by the Mercer Quality of Life Survey

Vancouver boasts one of the most diverse multi-cultural populations in Canada—alongside English and Chinese, you may also hear Punjabi, German, Italian, French, Tagalog, Japanese, Korean, and Spanish as you walk around the city

Through various initiatives, Vancouver is on track to its goal of being the greenest city in the world by 2020—currently 93% of the electricity used in Vancouver is generated from sustainable sources such as hydroelectricity

Stanley Park, just northwest of downtown Vancouver, is one of the largest urban parks in North America

The City of Vancouver is a highly diverse and multicultural city with people from all around the world. As such, it is a popular tourist destination and has been regarded as one of the most outstanding convention cities in the world.

Vancouver has been ranked one of the most livable cities in the world for the past decade and was ranked as having the 4th highest quality of living in the world as of 2010, on par with cities such as Melbourne, Vienna, and Toronto. The city offers plenty of fine dining and shopping, but it is also an excellent place for more outdoor pursuits such as hiking, golfing, boating, and surfing.

Learn more about Vancouver's diverse marine life at the **Vancouver Aquarium**, or see unique artwork at numerous art galleries (including the **Vancouver Art Gallery**).

There is something to do for everybody!





# Join the conversation!



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#HUPO2015



**HUPO**

14TH HUMAN PROTEOME ORGANIZATION



**ANCOUVER**

WORLD CONGRESS

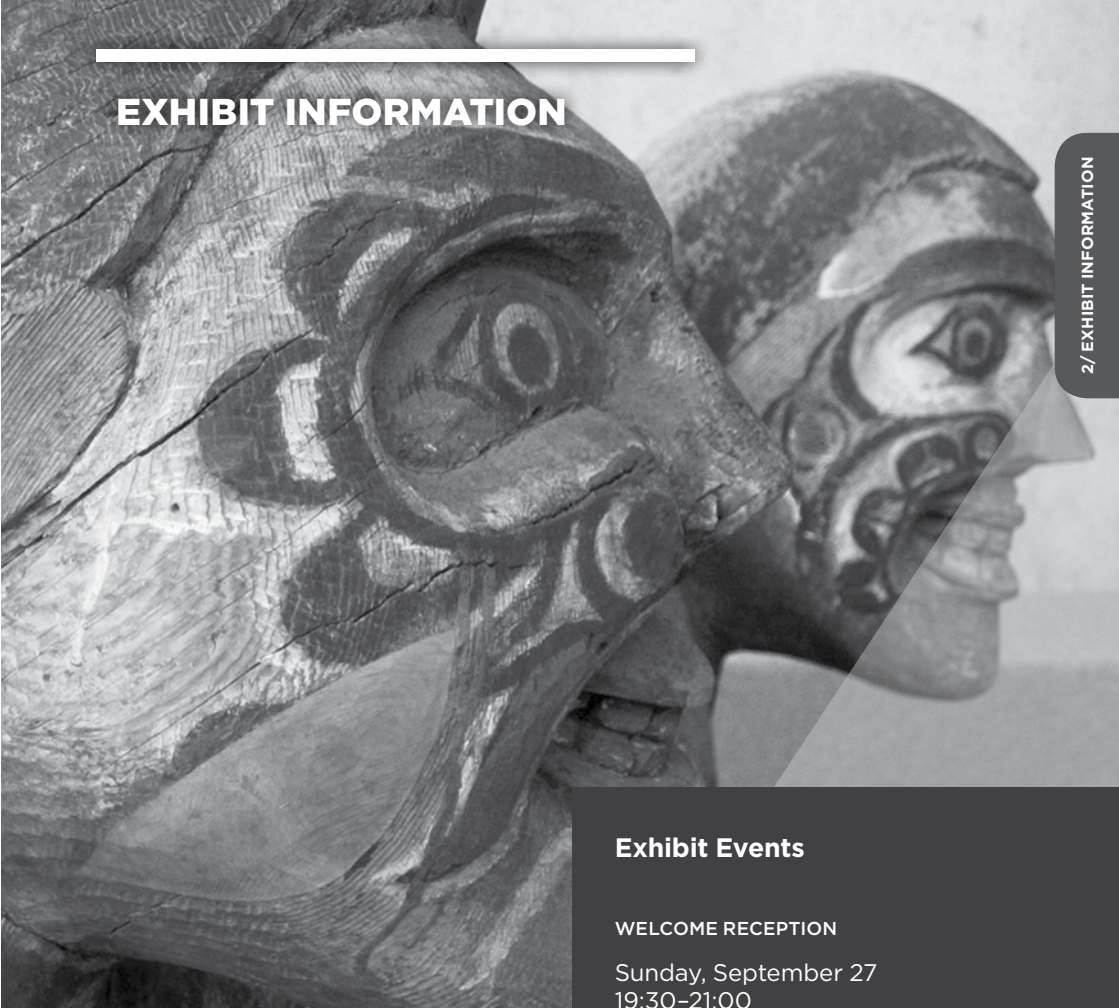
SEPTEMBER 27 - 30

**2015**

SECTION 2  
**EXHIBIT  
INFORMATION**



# EXHIBIT INFORMATION



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## Location

### EXHIBIT HALL (HALL B), STREET LEVEL

Sunday, September 27	19:30–21:00
Monday, September 28	10:00–17:30
Tuesday, September 29	10:00–17:30
Wednesday, September 30	10:00–16:30

## Exhibit Events

### WELCOME RECEPTION

Sunday, September 27  
19:30–21:00

### NETWORKING BREAKS

Monday and Tuesday  
10:00–11:10 and 16:20–17:30

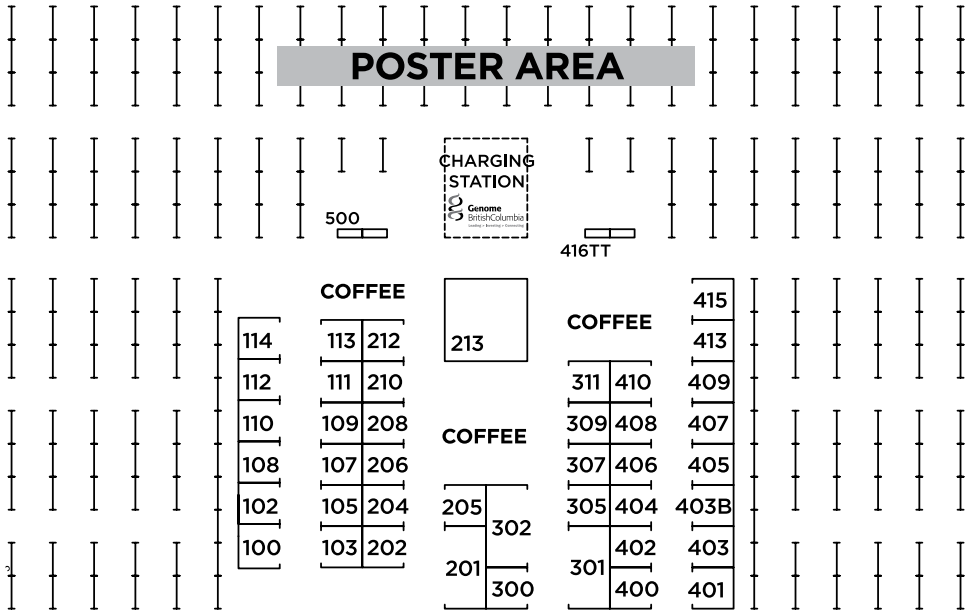
Wednesday  
10:00–11:10 and 16:20–16:30

### POSTER SESSIONS

Presenter Attendance during  
morning and afternoon  
Networking Breaks

# EXHIBIT INFORMATION

## FLOOR PLAN



## ENTRANCE

# EXHIBIT INFORMATION

## EXHIBITOR LISTING

### ALPHABETICAL BY EXHIBITOR

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### BY BOOTH #

BOOTH #	COMPANY
100	EMD Millipore Corporation
102	BC Proteomics Network / Canadian National Proteomics Network
103	Matrix Science
105	Optys Tech Corporation
107	Biotech Support Group LLC
108	Rapid Novor Inc
109	VICI Valco Instruments
110	SENGENICS
111	Proteintech Group, Inc.
112	Abcam
113	GE Healthcare
114	Wako Laboratory Chemicals
201	Waters Corporation
202	Cell Signaling Technology
204	Atlas Antibodies
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206	PEAKS Software (Bioinformatics Solutions Inc.)
208	Denator
210	Genome Canada
210	Genome BC
212	Cambridge Isotope Laboratories, Inc.
213	Bruker Daltonics
300	SCIEX
301	Thermo Scientific
302	Agilent Technologies
305	Proteome Software
307	JPT Peptide Technologies, GmbH
309	UVic Genome BC Proteomics Centre
311	Pressure BioSciences, Inc.
400	INTAVIS Bioanalytical Instruments
401	HUPO, Human Proteome Organization
402	IMSC 2016
403	HUPO 2016, Taipei
403B	HUPO 2017, Dublin
404	Protein Metrics Inc.
405	The Metabolomics Innovation Centre
406	Fluidigm Corporation
407	BIOCRATES Life Sciences AG
408	Elsevier
409	Silantes GmbH
410	Veritomyx
413	Molecular & Cellular Proteomics (ASBMB Journal)
415	ProteinSimple
416TT	PROOF Centre of Excellence

# EXHIBIT INFORMATION

## COMPANY PROFILES



### Abcam

Abcam plc is a provider of protein research tools and services, with an unrivaled range of products and expert technical support, enabling scientists to analyze living cells at the molecular level and improving the understanding of health and disease. To find out more, please visit [www.abcam.com](http://www.abcam.com)



### Agilent Technologies

### Agilent Technologies

Agilent manufactures and distributes a complete line of instrumentation serving the clinical, analytical, biotech, environmental, pharmaceutical, forensic science, food and flavor, academia, and all other laboratory markets that have needs for the best in quality, performance, and serviceability in the instruments they purchase.



### ATLAS ANTIBODIES

### Atlas Antibodies

Based in Sweden, Atlas Antibodies manufactures and distributes advanced research reagents targeting all human proteins, among those the antibodies developed and validated in the prestigious Human Protein Atlas project. In 2014 the company launched a new product family of isotope labeled multipепptide Mass Spectrometry standards for absolute quantification, called QPREST.



### BCProteomicsNetwork

### BC Proteomics Network

The BC Proteomics Network is a network of research professionals from universities, research institutions and industry throughout British Columbia. The network's mandate is to leverage proteomics resources, promote awareness of proteomics, educate current and future researchers in proteomics, and harness the proficiency of BC scientists to perform cross-disciplinary research.

### BIOCRATES

LIFE SCIENCES

The Deep Phenotyping Company

### BIOCRATES Life Sciences AG

Biocrates Life Sciences, developer of targeted metabolic phenotyping solutions, supports the discovery and validation of biomarkers for complex multifactorial diseases in pre-clinical and clinical research. Biocrates kits and services analyze more than 630 endogenous metabolites under quality-controlled conditions and can be used with a wide range of species and matrices.



### BIOTECH SUPPORT GROUP

### Biotech Support Group LLC

Biotech Support Group serves the explosive growth in proteomic sample prep, with unique and proprietary surface chemistries. We are dedicated to create new methods and applications to drive efficient workflows and better data quality for all downstream proteomic and biomarker analyses.



# EXHIBIT INFORMATION

## COMPANY PROFILES



### **Bruker Daltonics**

Bruker is a leading provider of Chromatography and Mass Spectrometry instruments and solutions for the Analytical Sciences. Our innovative and easy-to-use product families (ESI-QTOF, Ion Trap, FTMS, MALDI-TOF, LC-Triple Quads and GC-Triple Quads) provide the highest performance, ruggedness and value for a wide range of applications in the food, environmental, forensic, industrial, pharmaceutical and life science research markets.



Cambridge Isotope  
Laboratories, Inc.  
**isotope.com**

### **Cambridge Isotope Laboratories, Inc.**

Cambridge Isotope Laboratories, Inc. (CIL) is the world leader in the manufacture of stable isotope-labeled ( $^{13}\text{C}$ ,  $\text{D}$ ,  $^{15}\text{N}$ ,  $^{17}\text{O}$ ,  $^{18}\text{O}$ ) compounds used for quantitative MS-based applications. CIL has many products to meet the needs of the proteomic community: MRM Proteomics kits, MouseExpress<sup>®</sup> mouse feed and tissue, SILAC reagents, and others.



### **Canadian National Proteomics Network**

CNPN is a not-for-profit, federally incorporated organization created to provide a co-operative mechanism for building the proteomics research infrastructure in Canada and to further a better understanding of proteomics in the Canadian life-sciences community. CNPN sponsors scientific conferences, seminars and forums to create a national focus for scientific collaboration and education.



Cell Signaling  
TECHNOLOGY<sup>®</sup>

### **Cell Signaling Technology**

Founded by research scientists, Cell Signaling Technology (CST) is a family-owned company focused on proteomic discovery especially in the cancer field. Our products and services support your proteomics research and because we believe you have the right to expect more reliable results, our scientists produce, validate and support all our antibodies in-house.



### **Denator**

Denator offers a superior sample preservation technology that eliminates molecular changes and degradation of biological samples. It enables accurate analysis and quantification of unstable protein biomarkers such as phosphorylations and endogenous peptides. It ensures quality and standardization of sample collection, ensuring more precise, reliable data from your clinical proteomics research.



ELSEVIER

### **Elsevier**

Discover Elsevier's leading scholarly publications and online solutions for proteomics. Our proteomics journals include Journal of Proteomics, BBA Proteins and Proteomics and the fully Open Access journals Translational Proteomics, EuPA Open Proteomics.

# EXHIBIT INFORMATION

## COMPANY PROFILES



### EMD Millipore Corporation

EMD Millipore is the Life Science division of Merck KGaA of Germany, supporting research, development and production of biotech and pharmaceutical drug therapies. We support our customers in physiologically predictive cellular analysis, multianalyte network elucidation and functional genomics with innovative platforms for protein detection, complemented by protein preparation technologies that enable fast, effective purification without sample loss.



### Fluidigm Corporation

Fluidigm partners with life science researchers and enterprises to provide simplified workflows for genomics and proteomics applications. Whether your quest is to understand the profiles and functions of single cells or to meet high-throughput data demands of a production-scale laboratory, you'll find a solution at [fluidigm.com](http://fluidigm.com).



### GE Healthcare

GE Healthcare Life Sciences provides expertise and tools for a wide range of applications, including basic research of cells and proteins, drug discovery research, and tools to support large-scale manufacturing of biopharmaceuticals. By combining our knowledge, talent, and resources, we deliver innovative products and solutions that help our customers achieve their goals.



### Genome BC

Genome BC is a catalyst for the life sciences cluster on Canada's West Coast and manages a cumulative portfolio of over \$660M in research projects and science and technology platforms. Working with governments, academia and industry, the organization's goal is to generate social and economic benefits for BC and Canada.



### Genome Canada

Genome Canada is a not-for-profit organization that acts as a catalyst for developing and applying genomics and genomic-based technologies across multiple sectors to create economic and social benefits for Canadians. For more information, visit [www.genomecanada.ca](http://www.genomecanada.ca).



### HUPO 2016, Taipei

HUPO 2016 will be held in Taipei, September 18-22, 2016. It is our intention to make the scientific program of HUPO 2016 a most vibrant and forward looking one by capturing the essence of current technical advances and future possibilities in all emerging fields of proteomic applications, from basic to translational sciences.

# EXHIBIT INFORMATION

## COMPANY PROFILES



### HUPO 2017, Dublin

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.

Please come & visit us at our stand to find out more about HUPO 2017 & to enter our competition to win a free registration.



translating  
the code of life

### HUPO, Human Proteome Organization

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 to better understand human disease. HUPO fosters international initiatives and encourages the formation of national and regional human proteome-related societies.



### IMSC 2016

The Canadian Society for Mass Spectrometry (CSMS) will host the 21st International Mass Spectrometry Conference (IMSC 2016) in Toronto, Canada. This is the first time the IMSC is being held in North America. The IMSC 2016 provides an excellent forum for scientists to discuss research related to mass spectrometry.



### INTAVIS Bioanalytical Instruments

INTAVIS Bioanalytical Instruments focuses on automation of complex scientific protocols. We concentrate on applications in proteomics, and functional genomics. The DigestPro MSi, is a dedicated platform for protein digestion and sample preparation in proteome research. It automates both in-gel and solution digest procedures for protein analysis by mass spectrometry.



Innovative Peptide Solutions

### JPT Peptide Technologies, GmbH

JPT is an ISO certified provider of innovative peptide products and services focused on proteomics, developing immune therapeutics & diagnostics and enzyme profiling. JPT has a large portfolio of proprietary products such as SpikeMix™ Peptide Pools & SpikeTides™ that provide access to low cost stable isotope labeled and/or quantified peptides.



### Matrix Science

Matrix Science develops and markets Mascot software, the benchmark for identification, characterization and quantitation of proteins using mass spectrometry data.

# EXHIBIT INFORMATION

## COMPANY PROFILES



### Molecular & Cellular Proteomics (ASBMB Journal)

Molecular & Cellular Proteomics (MCP) showcases contributions that describe the structural and functional properties of proteins and their expression. Emphasis is placed on determining how the presence or absence of proteins affect biological responses, and how the interaction of proteins with germane cellular partners allows them to function.



### Optys Tech Corporation

Pinnacle is Optys' revolutionary flagship software for proteomics and glycoproteomics. Available in a single software is: comprehensive quantitation of 10,000s of proteins across of 100s of samples using DIA, DDA, PRM or SRM with fully integrated statistics and biological interpretation; complete N-linked glycoprotein identification routine; in-depth analysis in protein characterization.



### PEAKS Software (Bioinformatics Solutions Inc.)

Bioinformatics Solutions Inc. is the creator of PEAKS Software: A Complete Proteomics Analysis Package. PEAKS provides a simple workflow for in-depth analysis of raw LC-MS/MS proteomic data. From de novo sequencing, database search, homology search to peptide feature extraction and LC-MS alignment, PEAKS provides tools for complete data analysis qualitatively and quantitatively at both the protein and peptide levels.



### Pressure BioSciences, Inc.

Pressure BioSciences, Inc. ("PBI") (OTCQB: PPIO) is focused 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 to control bio-molecular interactions for biomarker discovery, enhanced protein digestion, and other research applications.



### PROOF Centre of Excellence

PROOF Centre is a not-for-profit biomarker development engine focused on producing omics-derived laboratory tests to better predict, diagnose and prognose vital organ failure. We embrace a cross-disciplinary team representing academia, health care, government, industry, patients and the public, convened to improve health and reduce the burden of organ disease. [www.proofcentre.ca](http://www.proofcentre.ca)

# EXHIBIT INFORMATION

## COMPANY PROFILES



### Protein Metrics Inc.

Protein Metrics is a software company serving biopharmaceutical development and proteomics research. The company focuses on the analysis of mass spectrometry and LC-UV data and offers a software products that address peptide identification, rapid peptide mapping, quantitative comparisons, and sensitive analysis and reporting of variants and post-translational modifications.



### ProteinSimple

Our goal is to make protein analysis simpler, more quantitative and affordable. Our comprehensive portfolio of tools includes Simple Western systems that quantify protein expression and Biologics systems that probe the structure and purity of protein-based therapeutics.



### Proteintech Group, Inc.

Proteintech is the original manufacturer of over 11,000 antibodies validated in WB and IHC on primary tissues and cell lysates. Whole protein antigens produce antibodies w/unparalleled high quality working in more species and applications. Locations (US, Europe, China, Japan), all antibodies in stock, next-day delivery.



### Proteome Software

Proteome Software builds user-friendly bioinformatics tools for intuitive visualization and management of experimental results. Our Scaffold Suite validates, organizes, compares, and interprets mass spectrometry data, and has become the industry standard in sharing MS/MS proteomics data. Elements for Metabolomics brings many of these valued features to MS/MS based metabolomics analysis.



### Rapid Novor Inc

Rapid Novor offers Novor software for real-time peptide sequencing and variation (PTM and mutation) detection, FREE for academic research.



### SCIEX

SCIEX delivers advanced analytical technologies and software that contribute to the understanding and research of human disease. Innovative LC/MS, LC/MS/MS and CE solutions enable deeper analysis of complex biological systems by providing comprehensive quantitation and characterization required across proteomics, lipidomics and metabolomics — leading to advances in systems biology and biomarker discovery. [sciex.com](http://sciex.com)

# EXHIBIT INFORMATION

## COMPANY PROFILES



### SENGENICS

Sengenics core technology is the patented Immunome™ auto-antibody profiling platform. It is the only protein array platform in the world where EVERY protein is full-length, correctly folded and functionally validated. Applications include monitoring differential immune response to drugs or vaccines, modelling microbial infections and biomarker discovery for any disease where immune system dysfunction plays a role.



### Sigma-Aldrich Life Sciences

SIGMA® Life Science offers a wide portfolio of innovative technologies, products and services spanning cell biology, proteomics, protein biochemistry, genomics, functional genomics, biomolecules and epigenetics. Through continued investment in innovation and quality we are the leading destination for life science researchers to access deep biological information and market leading products that improve the quality of life.



### Silantes GmbH

Silantes activities are focused on the production and marketing of compounds labelled with stable isotopes (SI: 2H, 13C, 15N) used in NMR structural analysis and quantitative mass spectrometry. Silantes is specialized on SILAC/SILAM-products. NMR(SI): growth media & nucleotides; Proteomics(SI): amino acids; cell culture-kits & in vivo-13C-lys-labelling of SILA(C/M)-model organism



### The Metabolomics Innovation Centre

The Metabolomics Innovation Centre (TMIC) is Canada's national metabolomics laboratory. TMIC uses real-world proven technologies, in-house innovations, and years of analytical experience to provide cutting-edge metabolomic services and technologies. Our mission is to provide quantitative metabolomic analysis to a wide range of clients at the most reasonable prices.



### Thermo Scientific

Thermo Fisher Scientific Inc. is the world leader in serving science. Our mission is to enable our customers to make the world healthier, cleaner and safer. We help our customers accelerate life sciences research, solve complex analytical challenges, improve patient diagnostics and increase laboratory productivity. For more information, visit [www.thermoscientific.com](http://www.thermoscientific.com).

# EXHIBIT INFORMATION

## COMPANY PROFILES



### UVic Genome BC Proteomics Centre

The Proteomics Centre ([www.proteincentre.com](http://www.proteincentre.com)) is a Genome Canada-funded hub for proteomics research. We develop cutting-edge technologies that are translated into an expansive range of high-quality proteomics services. Services provided through UVic and UBC include specialized techniques for quantitative/clinical proteomics (in collaboration with McGill), structural and functional proteomics, and custom projects.



### Veritomyx

Veritomyx' advanced signal processing algorithms in PeakInvestigator™ mass-spectral analysis software reveal information hidden in overlapped peaks, increasing effective mass-analyzer resolution by 3-4x. This improves metabolomic and proteomic discovery and identification rates. Also, Veritomyx' next-generation PeptideSequencer™ software (alpha) outperforms current market leaders in de novo peptide identifications. See what you're missing!



### VICI Valco Instruments

A designer and manufacturer of standard and custom valves and fittings for precision analytical, bio-medical, and bio-compatible instrumentation. Products also include a variety of related products including pneumatic and electric actuators, tubing and sampling loops, heated enclosures, valve sequence and temperature controllers, gas purifiers, GC detectors, and digital interfaces.



### Wako Laboratory Chemicals

Wako Laboratory Chemicals, strives to supply unique laboratory reagents to scientists in all fields of research. Following nine decades of tradition, we supply high quality, high purity reagents for your life's research. Product lines consist of antibodies, enzymes, biochemicals, organic chemicals, analytical standards, HPLC columns and much more.



### Waters Corporation

Waters Corporation creates business advantages for laboratory-dependent organizations by delivering scientific innovation to enable customers to make significant advancements. Waters helps customers make profound discoveries, optimize laboratory operations, deliver product performance, and ensure regulatory compliance with a connected portfolio of separations and analytical science, laboratory informatics, mass spectrometry, as well as thermal analysis.

Visit us in  
**Booth  
301**

# Clarity in the Chaos

**NEW**

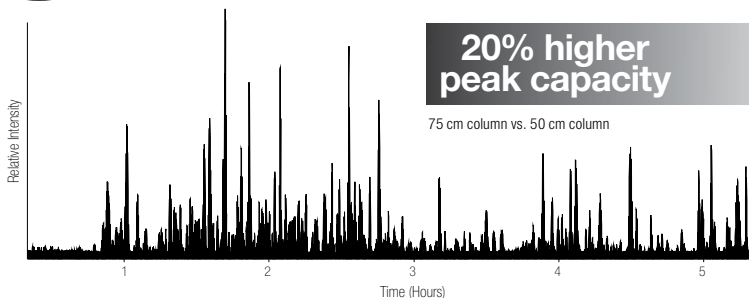
Thermo Scientific™  
Acclaim™ PepMap™  
75 cm nanoLC  
column

**More productivity in proteomics with  
ultra-high performance nano LC**

**NEW**



Thermo Scientific™  
EASY-nLC™ 1200 System



## **EASY-nLC 1200 System**

Enhanced pressure capabilities and improved system usability results in a unique customer experience

- 1200 bar backpressure
- Proprietary switching valves for maintenance free handling
- Fingertight nanoViper™ fittings of all high-pressure connections for easy, tool-free maintenance
- Well proven features, such as Intelligent Flow Control for fast column equilibration and sample loading

## **Acclaim PepMap Columns**

Experience higher analytical depth by exploiting the enhanced pressure capability of the EASY-nLC 1200 with a 75 cm column

- 1200 bar pressure rating
- Available with Acclaim PepMap 2  $\mu\text{m}$  100  $\text{\AA}$  C18 stationary phase
- Complete with nanoViper fitting for ease-of-use

**Come and see us during our Lunchtime Seminar**

**Tuesday, September 29 from 1:15-2:15 p.m.**

**Vancouver Convention Centre, East Building, Meeting Room 1**

**Pushing the Boundaries of Comprehensive Proteome Profiling**

*"How to Boost your nanoLC-MS Performance and Throughput in Proteomics"*

Dr. Paul Taylor, Senior Proteomics Specialist, SPARC BioCentre, Hospital for Sick Children, Toronto

For more information, visit: [www.thermoscientific.com/nanoLCMS](http://www.thermoscientific.com/nanoLCMS)

**Thermo**  
SCIENTIFIC

A Thermo Fisher Scientific Brand



SECTION 3  
PROGRAM  
**SUNDAY,**  
**SEPTEMBER 27**

The background features a series of overlapping triangles in various shades of blue and green. A prominent feature is a large, light blue triangle that contains a white grid pattern of small dots. The overall design is modern and geometric.

# PROGRAM

SATURDAY, SEPTEMBER 26 & SUNDAY, SEPTEMBER 27, 2015

SATURDAY, SEPTEMBER 26, 2015

Registration Open 16:00 – 20:00

Speaker Ready Room Open 16:00 – 20:00

SUNDAY, SEPTEMBER 27, 2015

Bioinformatics Hub 08:00 – 17:00

Registration Open 08:30 – 19:30

Speaker Ready Room Open 08:30 – 19:30

Exhibit Hall Open 19:30 – 21:00  
(Welcome Reception)

08:30 - 17:00 HPP General Investigators Meeting

CHAIR: GIL OMENN, USA  
ROOM 11

**i** FOR DETAILED SESSION INFORMATION  
PLEASE SEE PAGE 91 IN THIS PROGRAM  
BOOK.

09:00 - 15:30 Mentoring Day  
(Ticketed Session)

CHAIR: JENNIFER VAN EYK, USA  
ROOM 8+15



REFRESHMENTS AND LUNCH PROVIDED

09:00 **The HUPO Expedition**

Mark S. Baker, Macquarie University,  
Australia

09:15 **Value of proteOMICS for Science  
and Life**

Fred E. Regnier, Purdue University, USA

09:35 **Proteomics, Present and Future**

Ruedi Aebersold, ETH Zurich,  
Institute for Systems Biology,  
Switzerland

09:55 **Visualizing (Proteo) Omics:  
proteOMICS and Society**

Beth Anderson, Arkitek Scientific, USA

10:15 **Economical Contingency of (Prote)  
Omics**

Hanno Langen, F. Hoffmann-La  
Roche Ltd, Switzerland

Donna Edmonds, Immunarray Ltd, USA

10:35 **Coffee Break**

11:00 **How Do I Start and Conduct a (Big)  
Project: Idea, Collaborations,  
Collaborators, Grant (Concrete  
Example)**

Luigi Ferrucci, National Institute on  
Aging (NIA), USA

Catherine Costello, Boston University  
School of Medicine, USA

11:20 **Proteomics Academia/Industry:  
“Collaboration/Common Goals  
Academia and Industry”**

Henry Rodriguez, National Cancer  
Institute, USA

Jeff Chapman, SCIE X, USA

**11:45 Proteomics Industry: "How to Prepare a Career in Industry, What and When"**

Leigh Anderson, SISCAPA Assay Technologies, USA

Christie Hunter, SCIEX, USA

**12:10 Proteomics in 20 Years: "Challenges to Meet in the Future"**

John R. Yates III, The Scripps Research Institute, USA

**12:30 Lunch****14:00 Mentoring Day Part 3: Table Workshop Session****09:00 - 15:30 Technology Day: On Disruptive Technologies in Omics**CHAIR: CHRISTOPH BORCHERS, CANADA  
ROOM 12

REFRESHMENTS AND LUNCH PROVIDED

**MAIN SPONSORS:****SPEAKER SPONSOR:****09:00 Welcome****09:05 Nanomechanical Mass Spectrometry: Toward Native Single-Molecule Analysis**

Michael L. Roukes, California Institute of Technology, USA

**09:40 Disruption in the Protein Sciences**

John R. Yates III, The Scripps Research Institute, USA

**10:15 Coffee Break****10:30 Ultrahigh Resolution Mass Spectrometry: Extending the Size and Detail of Protein Structure Analysis**

Alan Marshall, Florida State University, USA

**11:05 Study of Cancer Cell Signalling and Drug Sensitivity Using CRISPR-CAS9 sgRNA Libraries**

Stephane Angers, University of Toronto, Canada

**11:40 Lunch****12:40 High Specificity Sequencing of Circulating Tumor DNA for Liquid Biopsy and Early Detection Applications**

Andre Marziali, Boreal Genomics, Canada

**13:15 Imaging Mass Cytometry - Technology and Progress in Multiparameter Assays**

Olga Ornatsky, Fluidigm Corp., Canada

**13:50 Coffee Break****14:05 Towards Genomic Medicine for Cancer Populations**

Marco Marra, Genome Sciences Centre, BC Cancer Agency, Canada

**14:40 After Revolutionizing Identification, Can MALDI-TOF be Used for Other Applications in the Microbiology Laboratory?**

Nathan Ledebouer, Medical College of Wisconsin, USA

09:00 - 15:30 Education Day  
(Ticketed Session)

CHAIR: GARRY CORTHALS, NETHERLANDS  
ROOM 17



REFRESHMENTS AND LUNCH PROVIDED

- 09:00** **Arrival and Welcome**
- 09:15** **PeptideAtlas - A Submitting to and Exploring PeptideAtlas**  
Luis Mendoza, Institute of Systems Biology, Seattle
- 10:00** **Coffee Break**
- 10:15** **PeptideAtlas - B Using SRMATlas to Design SRM Assays**  
Ulrike Kusebauch, Institute of Systems Biology, Seattle
- 11:00** **ProteinAtlas - How, When, and Why to Use the Protein Atlas Information and Antibodies**  
Cecilia Lindskog, Science for Life Laboratory, Sweden
- 11:45** **ProteinAtlas - Human Protein Atlas Antigens and Antibodies for Array-Based Profiling of Plasma and CSF**  
Peter Nilsson, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden
- 12:30** **Lunch**
- 13:00** **Characterization of PTMs in Proteomics**  
Martin Larsen, University of Southern Denmark, Denmark
- 14:30** **Coffee Break**
- 14:45** **Quantitative Targeted Proteomics Technologies (MRM, PRM, iMALDI, SISCAPA)**  
Dominik Domanski, Institute of Biophysics and Biochemistry PAS, Poland
- 15:30** **Quantitative Targeted Proteomics Clinical Applications (Blood, Dried Blood Spots, Urine, CSF, etc.)**  
Andrew Percy, University of Victoria, Canada

09:00 - 15:30 Clinical Day  
(Ticketed Session)

ROOM 2+3




REFRESHMENTS AND LUNCH PROVIDED

- 09:00 - 10:30** **Part 1: Omics Technologies Improving Patient Care**  
Chairs: Bruce McManus, Canada & Pei Pei Ping, USA
- 
- 09:00** **Next-Generation Sequencing Clinical Oncology Panel**  
Christina Lockwood, University of Washington, USA
- 09:25** **Alzheimer Disease Diagnostics**  
Mari DeMarco, University of British Columbia, Canada
- 09:50** **Proteomics & Informatics for Amyloid Typing**  
Surendra Dasari, Mayo Clinic, USA
- 10:15** **Moderated Discussion**
- 10:30** **Coffee Break**
- 
- 11:00 - 12:30** **Part 2: The Devil is in the Details: Developing Clinical-Grade Assays**  
Chairs: Emma Zheng, Canada & Leonard Foster, Canada
- 
- 11:00** **Validating Complex Diagnostics**  
Stephen Master, Weill Cornell Medical College, USA
- 11:25** **MALDI-TOF MS Clinical Assay Development**  
Michael X. Chen, Jewish General Hospital; McGill University, Canada
- 11:50** **Clinical Considerations for Tryptic Digestions**  
Irene Van den Broek, Cedars Sinai Medical Center, USA
- 12:15** **Moderated Discussion**
- 12:30** **Lunch**

**14:00 - 15:30 Part 3: Town-Hall Event  
- Balancing Innovation and  
Regulation of Laboratory Tests**

Chairs: Christina Lookwood, USA  
& Daniel Holmes, Canada

Panelists: Erick Koonick,  
University of Washington, USA,  
Daniel Chelsky, Caprion  
Proteome Inc., Canada, Ross  
Molinaro, Siemens, USA  
Victoria Zhang, University of  
Rochester, USA

**10:00 - 11:00  Bioinformatics Hub  
- Meet the Expert Session**

**Room 20**

**12:30 - 14:00 HUPO National Society  
President's Lunch  
(by invitation only)**

**Room 16**

**15:45 - 17:45 HUPO Council Meeting  
(by invitation only)**

Chairs: Mark Baker, HUPO  
President & Gyorgy Marko-  
Varga, HUPO Secretary  
General

**Room 1**

**18:00 - 19:35 PL 01: Opening Plenary  
Session**

**Chairs: Christoph Borchers,  
Canada & Pierre Thibault,  
Canada**

**Plenary Hall (Hall A)**

**18:00 Official Opening**

**18:05 Honourable Amrik Virk, Minister  
of Technology, Innovation and  
Citizens' Services, British Columbia,  
Canada**

**18:10 Cindy Bell, Interim President and  
CEO, Genome Canada**

**18:15 Population Proteomics: Embracing  
Genomic Variability**


Ruedi Aebersold, ETH Zurich,  
Institute for Systems Biology,  
Switzerland

**18:55 Opening Up New Areas of Drug  
Discovery with High Quality  
Research Tools**

Aled Edwards, University of Toronto,  
Canada

**19:35 - 21:00 Welcome Reception  
Exhibit Hall (Hall B)**

SECTION 4  
PROGRAM  
**MONDAY,**  
**SEPTEMBER 28**



# PROGRAM

MONDAY, SEPTEMBER 28, 2015

**Registration Open** 07:00 – 17:30

**Speaker Ready Room Open** 07:00 – 17:30

**Exhibit Hall Open** 10:00 – 17:30

**Bioinformatics Hub** 08:00 – 17:00

## 07:30 - 09:00 HPP 01: Cancer HPP

CHAIRS: HUI ZHANG, USA & CONNIE JIMENEZ, NETHERLANDS & EDWARD NICE, USA  
ROOM 1

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 92 IN THIS PROGRAM BOOK.

## 07:30 - 09:00 HPP 02: HPPP (Plasma)

CHAIRS: JOCHEN SCHWENK, CANADA & ERIC DEUTSCH, USA  
ROOM 2+3

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 93 IN THIS PROGRAM BOOK.

## 07:30 - 09:00 HPP 03: Cardiovascular Initiative Workshop

CHAIR: POTHUR SRINIVAS, USA  
ROOM 8+15

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 94 IN THIS PROGRAM BOOK.

## 07:30 - 09:00 HPP 04: HDPP - Diabetes

CHAIRS: PETER BERGSTEN, SWEDEN & JEAN-CHARLES SANCHEZ, SWITZERLAND  
ROOM 11

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 95 IN THIS PROGRAM BOOK.

## 07:30 - 09:00 HPP 05: Human Antibody Initiative

CHAIRS: MATHIAS UHLEN, SWEDEN & TOVE ALM, SWEDEN & EMMA LUNDBERG, SWEDEN  
ROOM 12

**X** BREAKFAST WILL BE PROVIDED DURING THIS SESSION.

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 96 IN THIS PROGRAM BOOK.

## 07:30 - 09:00 HPP 06: EyeOME - Proteomics: Towards Understanding Biological Pathways in the Eye

CHAIRS: RICHARD SEMBA, USA & MARIUS UEFFING, GERMANY & HYEWON CHUNG, KOREA  
ROOM 19

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 97 IN THIS PROGRAM BOOK.

**07:30 - 09:00 BioBank Workshop**

CHAIRS: GYORGY MARKO-VARGA,  
SWEDEN

ROOM 18

**07:30 Biobanking in Practice**

Beatrix Knudsen, Cedars Sinai  
Hospital & Medical Center, USA

**07:35 The Centralized Biobank in Southern  
Swedish Healthcare**

Johan Malm, Lund University, Sweden

**07:40 Utilising Biobank Resources to  
Discover Proteins Impact in Disease**

Carol L. Nilsson, University of Texas  
Medical Branch, USA

**07:45 Truly Sustainable Biobanking -  
A Call to Action**

Erik Steinfeld, ESBB President,  
The Netherlands

**07:50 Pharma Biobanking**

Thomas Fehniger, Lund University,  
Sweden

**07:55 TBA**

Brent Schachter, ISBER, Canada

**09:15 - 10:00 PL 02: Plenary Session  
Chair: Leigh Anderson, USA**

**Plenary Hall (Hall A)**


**Quantitative Proteomics in Biology,  
Chemistry and Medicine**

Steven A. Carr, Broad Institute, USA

**10:00 - 11:10  Networking Break and  
Poster Viewing**

**(Even Poster Numbers)**

**Exhibit Hall (Hall B)**

**10:00 - 11:00  Bioinformatics Hub  
- Meet the Expert Session**

**Room 20**

**11:10 - 13:00 CS 01: Cancer Proteomics**

CHAIRS: SCOTT GERBER, USA & MARTIN  
LARSEN, DENMARK

ROOM 1

**11:10 CS01.01: Chromosome Instability,  
Protein Homeostasis and  
Mechanisms of Drug Resistance in  
Cancer**

Scott A. Gerber, Geisel School of  
Medicine at Dartmouth, USA

**11:35 CS01.02: Cancer Biomarkers -  
Searching for the Needle in the  
Haystack**

Martin Larsen, University of Southern  
Denmark, Denmark

**12:00 CS01.03: Proteomic  
Characterization of Pancreatic  
Ductal Adenocarcinoma**

Sheng Pan, University of Washington,  
USA

**12:15 CS01.04: Proteolytic Processing  
in the Progression of Low-Grade  
Astrocytomas to Glioblastoma  
Multiforme**

Zon Lai, Institute of Molecular  
Medicine and Cell Research, Germany

**12:30 CS01.05: Autoantibody Profiling  
of Glioma Serum Samples Using  
Human Proteome Arrays**

Sanjeeva Srivastava, IIT Bombay,  
India

**12:35 CS01.06: Large-Scale Proteomic  
Characterization of Ovarian High-  
Grade Serous Carcinoma**

Zhen Zhang, Johns Hopkins  
University, USA



**12:40 CS01.07: Coupling an EML4-ALK Centric Interactome with RNAi Screen to Identify Sensitizers to ALK Inhibitors**

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

**12:45 CS01.08: MicroRNAs Upregulated in Colorectal Cancer Metastasis Target Multiple Overlapping Proteins**

Ignacio Casal, Centro de Investigaciones Biológicas, Spain

**12:50 CS01.09: Identification of Cancer-Associated HLA Antigens as Targets for Soluble TCR-Based Immunotherapy**

Geert PM Mommen, Immunocore, UK

**12:55 CS01.10: Protein Expression Profiling of the Chemoresistant AML Proteome**

Elise Aasebø, University of Bergen, Norway

**11:10 - 13:00 CS 02: Neurological Disorders**CHAIRS: BRADFORD GIBSON, USA & DANIEL MARTINS-DE-SOUZA, BRAZIL  
ROOM 2+3**11:10 CS02.01: Proteomic Analysis of Synaptosomes Isolated from a Huntington Mouse Model: A Cautionary Tale**

Bradford Gibson, Buck Institute for Research on Aging, USA

**11:35 CS02.02: Employing Proteomics to Unravel the Molecular Underpinnings of Schizophrenia**

Daniel Martins-De-Souza, University of Campinas, Brazil

**12:00 CS02.03: Aggregation of Physiological and Parkinson-Synucleins Revealed by Ion Mobility-MS and HDX- MS**

Michael Przybylski, Steinbeis Centre for Biopolymer Analysis and Biomedical Mass Spectrometry, Germany

**12:15 CS02.04: CSF Proteome Resource (CSF-PR) as a Tool for Proteomics Biomarker Discovery in Multiple Sclerosis**

Astrid Gulbrandsen, University of Bergen, Norway

**12:30 CS02.05: Investigating TDP-43-Mediated Neurodegeneration by Mass Spectrometry**

Yuzi Zheng, University of British Columbia, Canada

**12:35 CS02.06: Mitochondrial Networks Reveals Novel Components Associated with Neurological Disorders**

Mohan Babu, University of Regina, Canada

**12:40 CS02.07: Quantitative Proteomics Analysis of Human Autoptic Pineal Glands to Study Autism Spectrum Disorders**

Mariette Matondo, Institut Pasteur, France

**12:45 CS02.08: Development of Cerebrospinal Fluid Signatures of Lewy Bodies and Neuronal Loss**

Vladislav A. Petyuk, Pacific Northwest National Laboratory, USA

**12:50 CS02.09: Analyzing Laser Microdissected Neuromelanin Granules from Human Post Mortem Substantia Nigra**

Katrin Marcus, Ruhr-University Bochum, Germany

**12:55 CS02.10: Q&A****11:10 - 13:00 CS 03: Glycomics in Biology and Diseases**CHAIRS: NICOLLE H. PACKER, AUSTRALIA & CATHERINE COSTELLO, USA  
ROOM 8+15**11:10 CS03.01: Glycomics-Assisted Glycoproteomics: Deciphering the Complexity**

Nicolle H. Packer, Macquarie University, Australia

**11:35 CS03.02: Evolving Approaches for Separation and Tandem MS of Disease-related Glycans and Glycoconjugates**

Catherine E. Costello, Boston Univ. School of Medicine, USA

**12:00 CS03.03: N-Acetylglucosaminyl-transferrase III (GnT-III) Is a Novel Drug Target for Alzheimer's Disease**

Naoyuki Taniguchi, RIKEN, Japan

**12:15 CS03.04: N- and O-Glycomics on Formalin-Fixed Paraffin-Embedded (FFPE) Clinical Specimens by PGC-LC ESI-MS/MS**

Daniel Kolarich, Max Planck Institute of Colloids and Interfaces, Germany

**12:30 CS03.05: Identification of Biomarkers from Oral Cancer Patient Serum by Glycoproteomic Approaches**

Chuan-Fa Chang, National Cheng Kung University, Taiwan

**12:35 CS03.06: MALDI Imaging Mass Spectrometry of Glycans on Formalin-Fixed Paraffin-Embedded Ovarian Tumours**

Matthew T. Briggs, The University of Adelaide, Australia

**12:40 CS03.07: Lectin RCA-I Specifically Binds to Metastasis-Associated Cell Surface Glycans in TNBC**

Sheng-ce Tao, Shanghai Jiao Tong University, China

**12:45 CS03.08: Glycan Analyses of Murine Plasma and Lung Membrane to Find Biomarker Candidate for COPD**

Miyako Nakano, Hiroshima University, Japan

**12:50 CS03.09: Confident, Automated and Quantitative N-Glycoproteomics Analysis in Exosome Samples**

Scott Peterman, Thermo Scientific, USA

**12:55 CS03.10: Development of a Method for Large-Scale Analysis of the Site-Specific Glycomes of Glycoproteins**

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

**11:10 - 13:00 CS 04: Imaging Mass Spectrometry**

CHAIRS: RON HEEREN, NETHERLANDS & RICHARD CAPRIOLI, USA

ROOM 11

**11:10 CS04.01: Types of Tumors: Imaging the Difference**

Ron Heeren, Maastricht University, Netherlands

**11:35 CS04.02: Imaging Mass Spectrometry: Molecular Microscopy for Biological and Clinical Research**

Richard Caprioli, Vanderbilt University School of Medicine, USA

**12:00 CS04.03: Phospholipid MALDI Imaging MS Stratification of Colorectal Cancer Liver Metastasis Clinical Biopsies**

Pierre Chaurand, Université de Montréal, Canada

**12:15 CS04.04: Optimizing MALDI-MS Based Virtual 2D Gel Method for Protein Characterization**

Kate Liu, UCLA, USA

**12:30 CS04.05: Peptide and Glycan Tissue Imaging Mass Spectrometry on Tissue Micro Arrays for Cancer Diagnostics**

Peter Hoffmann, The University of Adelaide, Australia

**12:35 CS04.06: MSI and Proteomic Studies of Rat Spinal Cord Injury: Caudal Segment for Possible Therapy Target**

Stéphanie Devaux, INSERM U1192 Laboratoire PRISM, France

**12:40 CS04.07: Protein Profiling of Brain Ischemia by MALDI-Imaging-Mass-Spectrometry**

Victor Lombart, Vall Hebron Institute of Research, Spain

**12:45 CS04.08: Multiplexed Imaging of Biomolecules in Tissues by MALDI-MS**

Christoph H. Borchers, University of Victoria, Canada

**12:50 CS04.09: Applying Mass Spectrometry Imaging for the Acceleration of Drug Discovery and Development**

Kenichi Watanabe, Lund University, Sweden

**12:55 CS04.10: MALDI - MS Imaging Reveals Calreticulin Overexpression in Penile Cancer**

Elisângela J. Silva, AC Camargo Cancer Center, Brazil

**11:10 - 13:00 CS 05: Proteomics at Pharma**

CHAIRS: HANNO LANGEN, SWITZERLAND & TASSO MILLIOTIS, SWEDEN  
ROOM 12

**11:10 CS05.01: Application of Proteomics Technologies in the Pharmaceutical Industry**

Hanno Langen, F. Hoffmann-La Roche Ltd, Switzerland

**11:35 CS05.02: Automated MRM - Applied to Quantification of Circulating Proteins Associated with Insulin Sensitivity Improvement following Bariatric Surgery**

Tasso Miliotis, AstraZeneca R&D, Sweden

**12:00 CS05.03: Screening of Drug-Induced Protein Expression - Quantifying Cytochrome P450 Enzymes and Transporter**

Oliver Poetz, NMI Natural and Medical Sciences Institute at the University of Tuebingen, Germany

**12:15 CS05.04: Development of a Protease Inhibition Assay Based on Targeted Top down Quantitation**

Phillip Chu, Genentech, USA

**12:30 CS05.05: The Proteome of Human Cells Is Altered by Toxins of Clostridium Dificile**

Andreas Pich, Hannover Medical School, Germany

**12:35 CS05.06: ISDetect: Rapid, Semi-Automated Protein Terminal Characterization by Mass Spectrometry**

Corey E. Bakalarski, Genentech, Inc., USA

**12:40 CS05.07: Label-Free Method for Profiling Human Liver Enzymes: Validation with QconCAT**

Brahim Achour, University of Manchester, UK

**12:45 CS05.08: Phosphoproteomics in Drug Discovery - Application to Cancer Drug Resistance**

Hans Voshol, Novartis Institutes for BioMedical Research, Switzerland

**12:50 CS05.09: Monkey, Dog, Rat and Men - Safety Biomarker across Species**

Oliver Poetz, NMI Natural and Medical Sciences Institute at the University of Tuebingen, Germany

**13:15 - 14:15 HPP 07: HPP Bioinformatic Session**

CHAIR: ERIC DEUTSCH, USA  
ROOM 12



FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 98 IN THIS PROGRAM BOOK.

**13:15 - 14:15**    **EDRN Workshop:  
Proteomic Biomarkers  
for Cancer Detection and  
Diagnosis in Precision  
Medicine**

**Chairs: Sam Hanash, USA &  
Sudhir Srivastava, USA**

**Room 18**

The development of new biomarkers for early cancer detection that can change clinical practice and ultimately have an impact on overall survival and mortality from the disease is a lengthy process that begins with the discovery of promising candidate biomarkers, rigorous validation, and implementation in the clinic. The success of this process requires a complex, dedicated infrastructure that facilitates the coordination, management and collaboration among many institutions, both from academia and industry, with the involvement of scientists and clinicians with diverse expertise. Since its inception, the main focus of the EDRN has been to bring new biomarkers to clinical validation. Early on, EDRN investigators recognized that the biomarker field was quite nascent, and consequently took on the responsibility to establishing guidelines for a phase-based biomarker development, as well as study design criteria for rigorous clinical validation. These have now been well accepted and adopted by the biomarker research community at large.

Over the past five years, EDRN investigators invested significant efforts for enriching the proteomic biomarker development pipeline to address significant unmet clinical needs in the early detection of cancer. The proposed session will highlight the proteomics in early cancer detection and its implication for precision medicine.

**13:15**    **Onco-proteomics and its  
Implications for Precision Detection  
and Diagnosis**

Jacob Kagan, National Cancer  
Institute, USA, Sudhir Srivastava,  
National Cancer Institute, USA

**13:30**    **The Search for Cancer Biomarkers  
Using Proteomics - What Have We  
Learned?**

Sam Hanash, The University of Texas  
MD Anderson Cancer Center, USA

**13:45**    **Proteomics of Proximal  
Biospecimens for Discovery of  
Early Detection Ovarian Cancer  
Biomarkers**

Steven Skates, Massachusetts  
General Hospital, USA

**14:00**    **From Shotgun Proteomics to  
Molecular Imaging for the Early  
Detection of Lung Cancer**

Pierre Massion, Vanderbilt University  
Medical Center, USA

**13:15 - 14:15**    **Thermo Scientific:  
From Markers to Assays:  
Accelerating Translation  
Proteomics**

**Room 1**

**i** For further information,  
please visit the Industry  
Session pages in this  
program book

**13:15 - 14:15**    **Bruker Daltonics:  
New Solutions in LC/MS  
Based Proteomics**

**Room 2+3**

**i** For further information,  
please visit the Industry  
Session pages in this  
program book


**13:15 - 14:15**    **Waters Corporation:  
Improving Multi-omic  
Workflows for the Discovery  
and Development of Novel  
Biomarkers**

**Room 8+15**

**i** For further information,  
please visit the Industry  
Session pages in this  
program book

**13:15 – 14:15** **Agilent Technologies:  
Multi-omic Analysis for  
Integrated Biology**

**Room 11**

 For further information,  
please visit the Industry  
Session pages in this  
program book

**14:30 – 16:20** **CS 06: New Technological  
Advances in Proteomics**

CHAIRS: BERND BODENMILLER,  
SWITZERLAND & RICHARD D. SMITH, USA  
ROOM 1

**SESSION GENEROUSLY SUPPORTED BY**



Cambridge Isotope  
Laboratories, Inc.  
[isotope.com](http://isotope.com)

**14:30** **CS06.01: Imaging Mass Cytometry:  
A Novel Imaging Modality to  
Visualize Dozens of Biomarkers in a  
Targeted and Simultaneous Manner  
in Tumor Samples**

Bernd Bodenmiller, University of  
Zurich, Switzerland

**14:55** **CS06.02: Advances in Proteomics  
Based upon Ion Mobility in  
Structures for Lossless Ion  
Manipulations**

Richard D. Smith, Pacific Northwest  
National Laboratory, USA

**15:20** **CS06.03: Methods to Increase  
Reproducibility of a Multi-Analyte  
MRM MS Assay for Analysis of  
Plasma Samples**

Xiao-jun Li, Integrated Diagnostics  
Inc., USA

**15:35** **CS06.04: PALM (Pulse  
Azidohomoalanine Labeling in  
Mammals): Tissue Analysis of  
Newly-Synthesized Proteins**

Dan McClatchy, The Scripps Research  
Institute, USA

**15:50** **CS06.05: Extending the Reach of  
Data Independent Acquisition**

Christie Hunter, SCIEX, USA

**15:55** **CS06.06: Rapid and Automated  
Quantitation of Candidate Disease  
Biomarkers in Mouse Plasma and  
Tissues**

Sarah Michaud, MRM Proteomics, Inc.,  
Canada

**16:00** **CS06.07: It's Easy: Ultra-High  
Resolution Separations for the  
Complete Analysis of the Yeast  
Proteome**

Barbara Dunn, Stanford University,  
USA

**16:05** **CS06.08: Enhanced Trypsin  
Digestion for Improved  
Biomarker Sensitivity and Peptide  
Identification**

Kevin Meyer, Perfinity Biosciences,  
USA

**14:30 – 16:20** **CS 07: Translational  
Proteomics**

CHAIRS: JEAN-CHARLES SANCHEZ,  
SWITZERLAND & HENRY RODRIGUEZ, USA  
ROOM 2+3

**SESSION GENEROUSLY SUPPORTED BY**



ELSEVIER

**14:30** **CS07.01: Discovery of Brain  
Biomarkers and Their Translation to  
Clinical Settings**

Jean-Charles Sanchez, University of  
Geneva, Switzerland

**14:55** **CS07.02: CPTAC Omics Data  
Combined with TCGA Omics Data  
Produces a Unified Snapshot of  
Tumors**

Henry Rodriguez, National Cancer  
Institute, USA

- 15:20 CS07.03: Serum Diagnostic Glycoprotein Biomarkers for Esophageal Adenocarcinoma**  
Michelle M. Hill, The University of Queensland, Australia
- 15:35 CS07.04: Plasmatic RBP4 and GFAP as Biomarkers to Differentiate Ischemic from Hemorrhagic Stroke**  
Teresa García-Berrococo, Vall Hebron Institute of Research, Spain
- 15:50 CS07.05: Neutrophil Extracellular Traps in Ulcerative Colitis - A Proteome Analysis of Intestinal Biopsies**  
Tue B. Bennike, Aalborg University, Denmark
- 15:55 CS07.06: Targeted Discovery of Subtype-Differentiating Biomarkers for Early Diagnosis of Breast Cancer**  
David Juncker, McGill University, Canada
- 16:00 CS07.07: Quantitative Proteomic Analysis of Microdissected Oral Epithelium for Cancer Progression**  
Hua Xiao, Shanghai Jiao Tong University, China
- 16:05 CS07.08: Method Comparison of an Immuno-MALDI Plasma Renin Activity (PRA) Assay with Two Clinical Methods**  
Michael X. Chen, Jewish General Hospital, Canada
- 16:10 CS07.09: Targeted Quantitation of Human Gastric Fluid Proteins for Gastric Cancer Detection**  
Siok Yuen Kam, National University of Singapore, Singapore
- 16:15 CS07.10: Correlation of Gene and Protein Tissue Expression for Treatment Decisions in Early Stage Lung Cancer**  
Ferdinando Cerchiello, James Thoracic Center, James Cancer Center, The Ohio State University Medical Center, USA

**14:30 - 16:20 CS 08: Proteomics and Cell Immunity**

CHAIRS: CHRISTOPHER OVERALL, CANADA & ANTHONY PURCELL, AUSTRALIA  
ROOM 8+15

- 14:30 CS08.01: Proteolytic Events by the Paraacaspase MALT1 Integrate NFkB Signaling in Lymphocytes Revealed by TAILS N-Terminomics**  
Christopher Overall, Centre for Blood Research, Canada
- 14:55 CS08.02: Heterogeneity in the Immunoepitidome Impacts on the Outcome of Human Disease**  
Anthony W. Purcell, Monash University, Australia
- 15:20 CS08.03: Global Proteogenomics Analysis of Polymorphic Human MHC Class I-Associated Peptides**  
Diana Paola Granados, Université de Montreal, Canada
- 15:35 CS08.04: Characterization of Regulatory T Lymphocytes Using Label-Free Quantitative Proteomics**  
Anne Gonzalez De Peredo, CNRS Université de Toulouse, France
- 15:50 CS08.05: Proteomic Characterization of the Antigen-Specific Antibody Repertoire Elicited by Vaccination**  
Daniel Boutz, University of Texas at Austin, USA
- 15:55 CS08.06: HLA Ligandomics Drives Immunotherapies Based on High Affinity Soluble TCRs**  
Ricardo J. Carreira, Immunocore Ltd, UK
- 16:00 CS08.07: An Open-Source Computational and Data Resource to Analyze Digital Maps of Immunoepitidomes**  
Etienne Caron, ETH Zurich, Switzerland

**16:05 CS08.08: Insights into Immune Responses to Commensal Bacteria through MHC Class II Antigen Quantification**

Jennifer Abelin, Broad Institute of MIT and Harvard, USA

**16:10 CS08.09: Multi-Omics to Examine Proteolytic Cleavage, Expression and Abundances in Macrophage Differentiation**

Nestor Solis, University of British Columbia, Canada

**16:15 CS08.10: Proteomics Analysis of Tumor Associated Macrophages-Derived Exosomes**

Yinghui Zhu, Beijing Institute of Genomics, Chinese Academy of Sciences, China

**14:30 - 16:20 CS 09: Chemical Proteomics and Drug Discovery**

CHAIRS: HO JEONG KWON, KOREA & KAREN WANG, USA  
ROOM 11

**14:30 CS09.01: Chemical Proteomics Based Target Identification of Small Molecule towards Translational Studies**

Ho Jeong Kwon, Yonsei University, Korea, Republic of

**14:55 CS09.02: An Integrated Proteomics Strategy for Drug-Proteins Interactions and Compound Mode of Action**

Markus Schirle, Novartis Institutes for BioMedical Research, USA

**15:20 CS09.03: Target Selectivity of Clinical JAK Inhibitors in Peripheral Blood Monocytes**

Hans Christian Eberl, Cellzome GmbH, a GSK Company, Germany

**15:35 CS09.04: Proteomics Tools to Predict Nanoparticles Targeting and Uptake Capability**

Susana Cristobal, Linköping University, Sweden

**15:50 CS09.05: Selectivity Profiling of 200 Clinical Kinase Inhibitors Using Chemical Proteomics**

Susan Klaeger, Technical University of Munich, Germany

**15:55 CS09.06: High-Throughput Detection of Endogenous Protein Targets Bound by Bioactive Small Molecules**

Hui Peng, University of Toronto, Canada

**16:00 CS09.07: An R Package for the Analysis of Thermal Proteome Profiling Experiments**

Holger Franken, Cellzome GmbH, a GSK Company, Germany

**16:05 CS09.08: Chemical Proteomics for Development NDPKA/Nm23-H1 Activator**

Jae-Jin Lee, EWHA Womans University, Korea, Republic of

**16:10 CS09.09: Serine Hydrolase Activities in Urine from Patients Undergoing Cardiac Bypass Surgery**

Mario A. Navarrete, Manitoba Centre for Proteomics & Systems Biology, Canada

**16:15 CS09.10: MALDI-MSI Analysis of a Small Molecule and Its Target Protein Interaction on Tissues**

Yonghyo Kim, Chemical genomics National Research Laboratory, Yonsei University, Korea, Republic of



**14:30 - 16:20 CS 10: Epigenetics and Histone Landscape**

CHAIRS: BENJAMIN A. GARCIA, USA & MICHAEL FREITAS, USA  
ROOM 12

**14:30 CS10.01: Towards Understanding Cellular Signaling into Chromatin**

Benjamin A. Garcia, University of Pennsylvania School of Medicine, USA

**14:55 CS10.02: Interrogation of the Dynamic Role of Linker Histone Modifications in Cancer**

Michael Freitas, The Ohio State University Medical Center, USA

**15:20 CS10.03: Accelerating Epigenetic Cancer Drug Discovery Using a High Throughput Histone Analysis Platform**

Kan Zhu, Novartis Institute for BioMedical Research, USA

**15:35 CS10.04: Identification of Cofactors Influencing Smyd1's Histone Methyltransferase Activity via ChIP-MS**

Aman Makaju, University of Utah, USA

**15:50 CS10.05: Modification-Specific Chromatin Proteomics: Phosphorylated RNA Polymerase II Associated Proteins**

Andrey Tvardovskiy, University of Southern Denmark, Denmark

**15:55 CS10.06: In Gel Derivatization for Histone PTMs Analysis in Arabidopsis Thaliana**

Jiajia Chen, Fudan University, China

**16:00 CS10.07: Iron Induces Histone Deacetylation in the Human Pathogen Trichomonas Vaginalis**

Jung-Hsiang Tai, Institute of Biomedical Sciences, Academia Sinica, Taiwan

**16:05 CS10.08: AP-MS and BioID Generates Comprehensive Interactome for Chromatin-Associated Protein Complexes**

Brett Larsen, LTRI, Canada

**16:10 CS10.09: Comparison and Combination of Search Engines to Discover and Characterize Identifications and PTM Signatures in Biology**

Xiaoyue Jiang, Thermo Fisher Scientific, USA

**16:15 CS10.10: Monitoring Histone PTM Dynamics in Anti-Cancer Drug Resistant Cells Using MRM**

Byoung-Kyu Cho, Seoul National University, Korea, Republic Of

16:20 - 17:30



Networking Break and Poster Viewing

(Even Poster Numbers)

Exhibit Hall (Hall B)

**17:30 - 18:15 PL 03: Plenary Session**

Chair: Pierre Legrain, France

Plenary Hall (Hall A)

**A New Chapter in Liver Physiology & Pathology Is Being Written with Big Data**

Fuchu He, The Academy of Military Medicine Science, China



SECTION 5  
PROGRAM  
**TUESDAY,  
SEPTEMBER 29**

# PROGRAM

TUESDAY, SEPTEMBER 29, 2015

**Registration Open** 07:00 – 17:30

**Speaker Ready Room Open** 07:00 – 17:30

**Exhibit Hall Open** 10:00 – 17:30

**Bioinformatics Hub** 08:00 – 17:00

**07:30 - 09:00 HPP 08: CPTAC HPP - CPTAC Data, Tools, and Assays for Cancer Biology**

CHAIR: HENRY RODRIGUEZ, USA  
ROOM 1

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 99 IN THIS PROGRAM BOOK.

**07:30 - 09:00 HPP 09: Proteomics Standards Initiative and ProteomeXchange Consortium**

CHAIRS: ERIC DEUTSCH, USA & HENNING HERMJAKOB, UK  
ROOM 2+3

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 100 IN THIS PROGRAM BOOK.

**07:30 - 09:00 HPP 10: B/D-GPP (Biology/Disease-driven Glycoproteome Project)**

CHAIR: HISASHI NARIMATSU, JAPAN  
ROOM 8+15

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 101 IN THIS PROGRAM BOOK.

**07:30 - 09:00 HPP 11: Toxicoproteomics**

CHAIRS: LEKHA SLENO, CANADA & OLIVER POETZ, GERMANY  
ROOM 11

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 102 IN THIS PROGRAM BOOK.

**07:30 - 09:00 HPP 12: HBPP - Brain**

CHAIR: HELMUT E. MEYER, GERMANY  
ROOM 12

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 103 IN THIS PROGRAM BOOK.

**07:30 - 09:00 HPP 13: PediOme - Paediatrics and Proteomics: Back to the Beginning**

CHAIR: VERA IGNJATOVIC, AUSTRALIA  
ROOM 19

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 104 IN THIS PROGRAM BOOK.

**07:30 - 09:00 Affinity - Mass Spectrometry Workshop**

**CHAIRS: CHRISTOPH BORCHERS, CANADA & MICHAEL O. GLOCKER, GERMANY & MICHAEL PRZYBYLSKI, GERMANY**

**ROOM 18**

This workshop focuses on research activities and methodology development of affinity isolation and determination strategies combined with mass spectrometry. Pre-fractionation methods are the key issue when it comes to addressing the complexity of biological samples and when analyzing low abundant analytes from biological/clinical material. Many applications of affinity-based separation methods have been used and are continuously developed to increase the selectivity and sensitivity in mass spectrometry-based proteomics; now spreading out into many scientific and medical application areas.

Lately, immuno-affinity approaches which make use of defined sets of specific capture molecules such as antibodies have enabled the rapid and unequivocal identification of binding structures and surfaces (e.g. epitopes) by mass spectrometry, particularly by new developments of online MS approaches. With novel state-of-the-art "wet-lab" as well as "dry-lab" developments quantitative and functional analyses in model studies and even in patient samples can be tackled using affinity-MS procedures, thereby opening the field of structure- /function correlations with broad application potentials in cutting-edge research areas.

**07:30 Welcome and Introduction to the Workshop as well as a Brief Overview about Affinity-MS Developments**

Michael O. Glocker, University Medicine Rostock, Germany

**07:35 Rostock Risk Assessment of Preterm Newborns by Affinity Mass Spectrometry**

Michael O. Glocker, University Medicine Rostock, Germany

**07:45 A Novel Mass Spectrometry-Based Approach in Immuno-Diagnostics**

Petr Novak, Charles University, Czech Republic

**07:55 Computational Tools for Storing, Scoring and Showing Affinity Proteomics Data**

Anne-Claude Gingras, Lunenfeld-Tanenbaum Research Institute, Canada

**08:05 Discussion**

Christoph H. Borchers, University of Victoria, Canada

**08:15 iMALDI for Quantifying Akt1 and Akt2 Expression and Phosphorylation in Colorectal Cancer**

Christoph H. Borchers, University of Victoria, Canada

**08:25 Studying Protein-Small Molecule Affinities by Quantitative Proteomics**

Hans Christian Eberl, Cellzome GmbH, a GSK company, Germany

**08:35 Multiplexed Protein Quantification Using Peptide Group-Specific Capture Molecules and Mass Spectrometry**

Oliver Poetz, NMI Natural and Medical Sciences Institute at the University of Tuebingen, Germany

**08:45 Online Biosensor-Mass Spectrometry Combination: Principles and Application to Elucidation of Antibody Epitopes**

Michael Przybylski, Steinbeis Centre for Biopolymer Analysis and Biomedical Mass Spectrometry, Germany

**08:55 Final Discussion and Farewell**

Michael Przybylski, Steinbeis Centre for Biopolymer Analysis and Biomedical Mass Spectrometry, Germany

**07:30 - 09:00 Workshop: Proteomics in Food and Nutrition**

**CHAIR: PAOLA RONCADA, ITALY  
ROOM 17**

The central role of food proteins in nutritional science are indisputable, the well known affirmation that ‘we are what we eat’ and that food can be our medicine is not just philosophy but a true story. In fact it is clear that the food after ingestion is transformed and also contains proteins that our body uses, in a complex direct relationship. Study of the proteome of a given food makes us aware that, once it has been ingested and transformed by the human organism, it can change the structure of the proteins in the latter. Furthermore, every nutritional process involves huge number of proteins that are expressed at different levels, from cell to whole organism. Moreover, the global composition of diet, from microbiome to nutrient, including life style, can affect every step from gene expression to protein synthesis until degradation, lead to modulation of metabolic function in a multi-factorial way. Proteomics can help personalized medicine and nutrition, play important role in solving major nutrition problem in human and animals, on the verge of one health approach, including obesity, metabolic and cardiovascular disease, cancer, ageing, allergy and fetal health and development, also in relation to gut microbiome. Profiling food, microbiome, and biomarkers of nutritional status and disease from proteomics point of view lead to a new pillar of personalized medicine. This include also a special focus to food safety issues, providing new insights relate to safety aspects, from microbioma and consortia, food authenticity, detection of animal species in the food, until identification of food allergens.

**07:30 Introduction - Proteomics in Food and Nutrition: A Matter of Public Health**

Paola Roncada, Istituto Sperimentale Italiano L. Spallanzani, Italy

**07:40 The Proteomics of What We Eat**

Mark S. Baker, Macquarie University, Australia

**08:00 Metaproteomics Data Analysis: Charting War and Peace in a Microbiome**

Lennart Martens, Faculty of Medicine, Belgium

**08:20 MS-Based Proteomic Biomarker Discovery in 1,000 Human Plasma Samples Reveals Candidates for Personalized Nutrition**

Loïc Dayon, Nestlé Institute of Health Sciences SA, Switzerland

**08:40 Table Round New Initiatives, Discussion and Closing Remarks**

Paola Roncada, Istituto Sperimentale Italiano L. Spallanzani, Italy

**07:30 - 09:00 Workshop: Translating Proteomics in Diabetes and Metabolic Diseases**

**CHAIRS: PETER BERGSTEN, SWEDEN & SALVATORE SECHI, USA  
ROOM 16**



**BREAKFAST PROVIDED**

The aim of the workshop is to present some novel aspects on diabetes and metabolic diseases and their complications thus stimulating discussions between people addressing these topics by using different approaches. The format of the workshop will be six short presentations followed by a general discussion. The presentations will cover omics, cellular and patient data giving new aspects of pathophysiology and biomarkers of diabetes and metabolic disease. The translational approach of the workshop prompted the involvement of the HUPO journal “Translational Proteomics” that will publish a special issue to be entitled “Diabetes and Metabolic Disease”.

**07:30 Serum Proteomes Distinguish Children Developing Type-1 Diabetes**

Young Ah Goo, University of Maryland, USA


**07:45 Translating Integrative Personalized Omics Profiling in Type II Diabetes and other Metabolic Diseases**


Christine Y. Yeh, Stanford University, USA

- 08:00 Identifying Novel Signaling Mechanisms Underlying Insulin Release from Glucose Stimulated Beta Cells**  
Pia Jensen, University of Southern Denmark, Denmark
- 08:15 Heterogeneity in the Immunopeptidome Impacts on the Outcome of Human Disease**  
Anthony W. Purcell, Monash University, Australia
- 08:30 Multi-Omics Characterization of a Human Thyrotoxicosis Model – Towards the Identification of New Biomarkers of Hyperthyroidism**  
Uwe Voelker, University Medicine Greifswald, Germany
- 08:45 Factors and Mechanisms of Pancreatic  $\beta$ -cell Proliferation Revealed by Quantitative Proteomics and Phosphoproteomics**  
David G. Camp, PNNL, USA

**09:15 - 10:00 PL 04: Plenary Session**  
**Chair: David Wishart, Canada**  
**Plenary Hall (Hall A)**

**Metabolomics - An Important Piece in the 'Omics Puzzle**  
Ute Roessner, The University of Melbourne, Australia

**10:00 - 11:10**  **Networking Break and Poster Viewing**  
**(Odd Poster Numbers)**  
**Exhibit Hall (Hall B)**

**10:00 - 11:00**  **Bioinformatics Hub – Meet the Expert Session**  
**Room 20**

**11:10 - 13:00 CS 11: Hot Topics**

CHAIRS: ANDREW EMILI, CANADA  
ROOM 1

- 11:10 CS11.01: Exploring Mitosis Dynamics by Combining Data Dependent and Data Independent Strategies**  
Angela Bachi, IFOM, the FIRC Institute of Molecular Oncology, Italy
- 11:35 CS11.02: Sportomics: Building a New Concept in Metabolic Studies and Exercise Science**  
L. C. Cameron, Federal University of State of Rio de Janeiro, Brazil
- 12:00 CS11.03: How to Unravel the Brain Proteome**  
Evelina Sjöstedt, Royal Institute of Technology (KTH), Sweden
- 12:15 CS11.04: High-Throughput Detection of Protein Targets Bound by Bioactive Small Molecules**  
Andrew Emili, University of Toronto, Canada
- 12:30 CS11.05: CPTAC Assay Portal: A Public Repository for Well-Characterized Quantitative Targeted Assays**  
Jeff Whiteaker, Fred Hutchinson Cancer Research Center, USA
- 12:35 CS11.06: BatMass: A Software Platform for Visualization and Analysis of Raw MS Data and Processed Results**  
Dmitry Avtonomov, University of Michigan, USA
- 12:40 CS11.07: Visual and Intuitive Access to Repository Data**  
Grant M. Fujimoto, Pacific Northwest National Laboratory, USA
- 12:45 CS11.08: SuperQuant: A Data Pre-Processing Algorithm for Increasing Quantitative Proteome Coverage**  
Vladimir Gorshkov, University of Southern Denmark, Denmark

**12:50 CS11.09: New Functionality for the Trans-Proteomic Pipeline: Tools for the Analysis of Proteomics Data**

Luis Mendoza, Institute for Systems Biology, USA

**12:55 CS11.10: Q&A**

**11:10 - 13:00 CS 12: Metabolomics and Metabolomic Diseases**

CHAIRS: OLIVER FIEHN, USA & DAVID WISHART, CANADA

ROOM 12

**SESSION GENEROUSLY SUPPORTED BY**



Cambridge Isotope Laboratories, Inc.  
**isotope.com**

**11:10 CS12.01: How Metabolomics is Changing our Understanding of Human Disease**

David Wishart, University of Alberta, Canada

**11:35 CS12.02: Using Metabolomics to Investigate Pulmonary Diseases in Human Cohorts and Animal Models**

Oliver Fiehn, West Coast Metabolomics Center, USA

**12:00 CS12.03: The Unanticipated Complexity of Bile Acid Pools in Human and Mouse**

Jun Han, University of Victoria - Genome BC Proteomics Centre, Canada

**12:15 CS12.04: Digestomics: A New Paradigm for Investigating Pathogenic Diseases in Humans**

Ian A. Lewis, University of Calgary, Canada

**12:30 CS12.05: Exploring S-(1,2-Dichlorovinyl)-L-Cysteine (DCVC) Nephrotoxicity in the Rat Using UPLC-MS**

Nicola Gray, Imperial College London, UK

**12:35 CS12.06: A Lipidomic Analysis of Cancer Cells**

Ling Lin, Fudan University, China

**12:40 CS12.07: Plasma Metabolomic Profiling of Diabetic Retinopathy**

Lei Zhou, Singapore Eye Research Institute, Singapore

**12:45 CS12.08: LC-MS/MS Quantitation of Malondialdehyde (MDA) as a Biomarker of Oxidative Stress in Human Plasma**

Constance A. Sobsey, University of Victoria, Canada

**12:50 Q&A**

**11:10 - 13:00 CS 13: Regenerative Medicine and Stem Cells**

CHAIRS: BONGHEE LEE, KOREA & JEROEN KRIJGSVELD, GERMANY

ROOM 8+15

**11:10 CS13.01: Proteome Meets Genome: Dynamics of Chromatin Organization in Embryonic Stem Cells**

Jeroen Krijgsveld, European Molecular Biology Laboratory (EMBL), Germany

**11:35 CS13.02: Direct Conversion of Stem Cells Cells by Changing Protein Dynamics**

Bonghee Lee, Gachon University, Korea, Republic of

**12:00 CS13.03: Identifying Key Stem Cell-Associated Proteins in Normal Blood Development and Leukemia**

Erwin M. Schoof, University Health Network, Canada

**12:15 CS13.04: Super-SILAC Mix for Quantitative Proteomics of Bone Marrow-Derived Mesenchymal Stem Cells**

Virginia Sanchez-Quiles, University Of Southern Denmark, Denmark

**12:30 CS13.05: Pathological Variability of Motor Neuron Disorders in Patient-Derived iPSC Using SWATH-MS**

Andrea Matlock, Cedars-Sinai Medical Center, USA



**12:35 CS13.06: Identification of Novel Protein Signatures for Subtypes of Breast Cancer Stem/Progenitor Cells**

Ayodele Alaiya, King Faisal Specialist Hospital and Research Centre, Saudi Arabia

**12:40 CS13.07: Systematic Identification of Single Amino Acid Variants in Glioma Stem Cell Lines**

Ekaterina Mostovenko, University of Texas Medical Branch, USA

**12:45 CS13.08: Extracellular Matrix Quantification: Defining the Scaffolding of Regenerative Medicine and Disease**

Ryan C. Hill, University of Colorado-Denver, Anschutz Medical Campus, USA

**12:50 CS13.09: Proteome-Scale Analysis of Transcription Factors in Liver Regeneration**

Chen Ding, Beijing Proteome Research Center, China

**12:55 CS13.10: Q&A**

**12:15 CS14.04: A  $\beta$ -Induced Protein Phosphorylation Changes in the Mouse Synaptosome**

Hwan-Ching Tai, National Taiwan University, Taiwan

**12:30 CS14.05: Accurate Determination of Cellular Membrane Protein Copy Numbers**

Ansgar Poetsch, Ruhr University Bochum, Germany

**12:35 CS14.06: Membrane Proteins of Leukocyte-Inspired Nanoparticles Improve Their Therapeutic Efficacy**

Claudia Corbo, Fondazione IRCCS SDN, Italy

**12:40 CS14.07: Comparison of Membrane Enrichment Coupled Proteomics Methods for Immune Target Discovery**

Deniz Baycin Hizal, MedImmune, USA

**12:45 CS14.08: Analysis of Membrane Proteins - Opening the Treasure Chest Protected by the Phospholipid Bilayer**

Jiri Petrak, First Medical Faculty, Charles University in Prague, Czech Republic

**12:50 CS14.09: TGF $\beta$ 1 Induces Membrane Proteome Changes in Colorectal Cancer Cells**

Harish R. Cheruku, Macquarie University, Australia

**12:55 CS14.10: Q&A**

**11:10 - 13:00 CS 14: Membrane Proteomics**

CHAIRS: YU-JU CHEN, TAIWAN & IGOR STAGLJAR, CANADA

ROOM 11

**11:10 CS14.01: Exploring Plasma Membrane Proteome by Metal-Directed Glycoproteomic Approach**

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

**11:35 CS14.02: Membrane Protein Interactomes in Health & Disease: Application to Lung Cancer**

Igor Stagljjar, University of Toronto, Canada

**12:00 CS14.03: Membrane Proteome Profiling to Discover Therapeutic Targets for HTLV-1 Associated Myelopathy**

Makoto Ishihara, University of Tokyo, Japan

**11:10 - 13:00 CS 15: Cardiovascular and Haematological Proteomics**

CHAIRS: PEIPEI PING, USA & JENNIFER VAN EYK, USA

ROOM 2+3

**11:10 CS15.01: Complications of Life**

Jennifer van Eyk, Cedars Sinai Medical Center, USA

**11:35 CS15.02: Dynamics of Life**

Peipei Ping, NIH BD2K Center of Excellence at UCLA, USA

- 12:00 CS15.03: Antibody Proteomics in Plasma for Diseases Affecting the Cardiovascular System**  
 Jochen M. Schwenk, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden
- 12:15 CS15.04: Cardiac Recovery: Targeting Novel Cell Type and Chamber Specific Markers**  
 Rebekah L. Gundry, Medical College of Wisconsin, USA
- 12:30 CS15.05: Label-Free Quantification of Hypoxia-Induced Changes of the Cardiac Fibroblast Secreted Proteome**  
 Jake Cosme, University of Toronto, Canada
- 12:35 CS15.06: Source Specific cGMP Activates Distinct PKG Signaling Pathways in Cardiac Myocytes**  
 Ronald J. Holewinski, Cedars Sinai Medical Center, USA
- 12:40 CS15.07: Studying the Functional Role of Reactive Oxygen Species in Atherosclerosis by Redox Proteomics**  
 Juergen Kast, University of British Columbia, Canada
- 12:45 CS15.08: iTRAQ Comparison of Human Plasma Proteins in HCM and Selected Cardiovascular Disorders**  
 Alena Fucikova, Faculty of Military Health Sciences, UoD, Czech Republic
- 12:50 CS15.09: Discovery of Cardiovascular Disease Biomarkers in Human Plasma Using MRM-MS**  
 Gabriela Cohen Freue, University of British Columbia, Canada
- 12:55 CS15.10: Q&A**

**13:15 - 14:15 HPP 14: C-HPP PIC Meeting**


**CHAIR: YOUNG-KI PAIK, KOREA ROOM 12**

 **BREAKFAST PROVIDED**

 **FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 104 IN THIS PROGRAM BOOK**


**13:15 - 14:15 Thermo Scientific: Pushing the Boundaries of Comprehensive Proteome Profiling**

**Room 1**

 **For further information, please visit the Industry Session pages in this program book**


**13:15 - 14:15 Wako Laboratory Chemicals: A Versatile Protein Tagging System for Recombinant Protein Production, Isolation, and Detection in Mammalian Cells**

**Room 2+3**

 **For further information, please visit the Industry Session pages in this program book**

**13:15 - 14:15 SCIEX: Testimonials in OneOmics™: Next Generation Proteomics at Work**

**Room 8+15**

 **For further information, please visit the Industry Session pages in this program book**

**14:30 - 16:20 CS 16: New Advances in Biomarker Discovery**

CHAIRS: MAXEY C.M. CHUNG, SINGAPORE & BRUCE MCMANUS, CANADA

ROOM 1

**14:30 CS16.01: Sieving through the Secretome of Colorectal Cancer Cells**

Maxeey C.M. Chung, National University of Singapore, Singapore

**14:55 CS16.02: Multi-Omic Signatures for Monitoring Patients with Limb-Girdle Muscular Dystrophy**

Bruce M. McManus, PROOF Centre of Excellence, Canada

**15:20 CS16.03: The Potential Clinical Impact of the Human Protein Atlas**

Cecilia Lindskog, Immunology, Genetics and Pathology, Sweden

**15:35 CS16.04: Equalizer- and TMT-Based Detection of Cellular Proteins in Clinical Peritoneal Dialysis Effluents**

Klaus Kratochwill, Medical University of Vienna, Austria

**15:50 CS16.05: Proteomic Alterations in Human Renal Epithelial Cells Exposed to Nephrotoxins**

Laxmikanth Kollipara, Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany

**15:55 CS16.06: Detection of Biomarkers of Sepsis Using Affimer Microarrays**

Vincent Puard, Avacta Life Sciences, UK

**16:00 CS16.07: Proteomic Biomarker Discovery in 1'000 Plasma Samples for Personalized Nutritional Intervention**

Loïc Dayon, Nestlé Institute of Health Sciences SA, Switzerland

**16:05 CS16.08: Identifying Exosome Biomarkers for Radiation Exposure Using a DDA and DIA Combined Workflow**

Emily I. Chen, Columbia University Medical Center, USA

**16:10 CS16.09: Large Scale Metabolic Exploration of Human CSF Proteins Using SILAV**

Nicolai Bache, Bruker daltonics, Denmark

**16:15 CS16.10: A SWATH-MS Approach for a Comprehensive Characterization of the Secretome under Oxidative Stress**

Sandra Anjo, Center for Neuroscience and Cell Biology - University of Coimbra, Portugal

**14:30 - 16:20 CS 17: Protein Networks and Computational Biology**

CHAIRS: ANNE-CLAUDE GINGRAS, CANADA & ALEXEY NESVIZHSHKII, USA ROOM 8+15

**14:30 CS17.01: Keynote Presentation**

Anne-Claude Gingras, Mount Sinai Hospital, Canada

**14:55 CS17.02: Computational Advancements and Challenges in MS-Based Proteomics**

Alexey Nesvizhskii, University of Michigan-Ann Arbor, USA

**15:20 CS17.03: Using SRM-MS to Uncover Signaling Networks Regulating Mammalian Cell Differentiation**

Mary N. Teruel, Stanford University, USA

**15:35 CS17.04: Sensitive Peptide Identification in Data-Independent Acquisition by Spectral Library Search**

Nuno Bandeira, University of California, USA

**15:50 CS17.05: The Interaction Proteome of the Human Kinome: Biochemical and Biomedical Implications**

Matthias Gstaiger, Institute of Molecular Systems Biology, Switzerland

**15:55 CS17.06: Construction of the Methylproteome Network Reveals a Novel Regulatory System in the Cell**

Gene O. Hart-Smith, UNSW, Australia

**16:00 CS17.07: Mapping Dynamic Protein Interaction Landscapes Using a Novel Whole Network Enrichment Approach**

Benjamin D. Stein, The Scripps Research Institute, USA

**16:05 CS17.08: Identifying Novel Sequences in the PRIDE Archive through Spectrum Clustering**

Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, UK

**16:10 CS17.09: Predicting Mutations Impact in Protein Interaction Networks in Cancer**

Mohamed Helmy, University of Toronto, Canada

**16:15 CS17.10: Small and Big Data in Proteomics: Reprocess Public Data to Design Better Experiments**

Marc Vaudel, University of Bergen, Norway

**14:30 - 16:20 CS 18: Subcellular Proteomics**

CHAIRS: KOJI UEDA, JAPAN & LEONARD J. FOSTER, CANADA  
ROOM 12

**14:30 CS18.01: Tumor Liquid Biopsy by Circulating Extracellular Vesicles**

Koji Ueda, Japanese Foundation for Cancer Research, Japan

**14:55 CS18.02: The Mitochondrial Interactome and Its Response to Apoptosis**

Leonard J. Foster, University of British Columbia, Canada

**15:20 CS18.03: High Throughput Structure-Function Analysis of the Centriole-Cilia Interface**

Etienne Coyaud, UHN - Princess Margaret Cancer Centre, Canada

**15:35 CS18.04: A Protein Marker-Based Physical Map of a Human Cell**

Christopher Go, Mount Sinai Hospital, Canada

**15:50 CS18.05: Plasma Membrane Proteomic Study of HIV Latent Infection**

Lijun Zhang, Shanghai Public Health Clinical Center, China

**15:55 CS18.06: Novel Components of Rods and Rings - A Subcellular Structure with Unknown Function**

Marie Skogs, Science for Life Laboratory, Sweden

**16:00 CS18.07: Pathogenic E. Coli Infection Alters the Mitochondrial Proteome and Mitochondrial Proteolysis**

Natalie C. Marshall, University of British Columbia, Canada

**16:05 CS18.08: Cancer-Associated Lipid Raft Function Revealed by Subcellular Proteomics and Computational Analysis**

Michelle M. Hill, The University of Queensland, Australia

**16:10 CS18.09: Abundance and Turnover of Synaptic Proteins by Mass Spectrometry and Super-Resolution Microscopy**

Sunit Mandad, Max Planck Institute for Biophysical Chemistry, Germany

**16:15 CS18.10: A Dynamic Picture of the Ubiquitinome upon Proteasome Inactivation**

Jeroen AA Demmers, Erasmus MC, Netherlands

**14:30 - 16:20 CS 19: Human Proteome Project**

CHAIRS: GILBERT S. OMENN, USA & YOUNG-KI PAIK, KOREA

ROOM 11

**14:30 CS19.01: The Progress and Challenges of the HUPO Human Proteome Project**

Gilbert S. Omenn, University of Michigan, USA

**14:55 CS19.02: Strategic Points for Dealing with Missing Protein Mapping in the C-HPP**

Young-Ki Paik, Yonsei University, Korea, Republic Of

**15:20 CS19.03: Controlling False Discovery Rates (FDRs) in Genome-Wide Proteomics Datasets**

Juergen Cox, Max Planck Institute for Biochemistry, Germany

**15:35 CS19.04: How Does an Extra Chromosome 21 Modulate the Quantitative Human Proteome?**

Yansheng Liu, ETH Zurich, Switzerland

**15:50 CS19.05: Mining Missing Proteins Base on the Transcriptomics and Proteomics to the Individual Testis Tissues**

Qidan Li, Beijing Institute of Genomics, Chinese Academic of Sciences, China

**15:55 CS19.06: Call for a Testis-Epididymis Proteome Project**

Charles Pineau, Inserm U1085 - Irset, France

**16:00 CS19.07: Refining the Human Proteome: Analyzing Human Tissues by RNA-Seq, Proteomics and Antibodies**

Hannes Hahne, Technische Universität München, Germany

**16:05 CS19.08: Urinary Proteins Originating Uniquely from Each Nephron Segment**

Tadashi Yamamoto, Niigata University, Japan

**16:10 CS19.09: Detection of Chromosome 16 Missing Proteins - Spanish HPP**

Concha Gil, Universidad Complutense de Madrid, Spain

**16:15 CS19.10: Q&A**

**14:30 - 16:20 CS 20: Protein Modifications (Other than Phosphoproteins)**

CHAIRS: THIBAUT MAYOR, CANADA & BRIAN RAUGHT, CANADA

ROOM 2+3

**14:30 CS20.01: Ubiquitin and the Kiss of Death under Stress Conditions**

Thibault Mayor, The University of British Columbia, Canada

**14:55 CS20.02: Keynote Presentation**

Brian Raught, UHN - Princess Margaret Cancer Centre, Canada

**15:20 CS20.03: Using the Ubiquitin-Modified Proteome to Monitor Protein Homeostasis Function**

Eric Bennett, UCSD, USA

**15:35 CS20.04: An Effective Method to Site-Specifically Analyze N-Sialoglycosylated Proteome on the Cell Surface**

Ronghu Wu, Georgia Institute of Technology, USA

**15:50 CS20.05: Development of Methods for Site-Specific Analysis of N-Linked Protein Glycosylation**

Hongqiang Qin, Dalian Institute of Chemical Physics, China, China

**15:55 CS20.06: A Chemical Proteomics Approach for Lysine Monomethylome Profiling**

Minjia Tan, Shanghai Institute of Materia Medica, Chinese Academy of Sciences, China

**16:00 CS20.07: Analysis of Arginine Methylation in Primary T Cells Reveals Roles in Cell Signalling and Fate**

Vincent Geoghegan, Lancaster University, UK


**16:05 CS20.08: Protein Citrullination - Novel Insight into Triggers of Autoimmune Diseases**

Allan Stensballe, Aalborg University, Denmark

**16:10 CS20.09: Lysine Succinylome Analysis of the Model Cyanobacterium Synechococcus sp. PCC 7002**

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

**16:15 CS20.10: Q&A**

**16:20 – 17:30**  **Networking Break and Poster Viewing**  
(Odd Poster Numbers)  
Exhibit Hall (Hall B)

**17:30 – 18:15 PL 05: Plenary Session**  
Chairs: **Joshua LaBaer, USA**  
Plenary Hall (Hall A)

**17:30** **Using Mass Spectrometry to Understand Cystic Fibrosis as a Protein Misfolding Disease**  
John R. Yates, The Scripps Research Institute, USA

**18:30 – 19:30 HUPO General Assembly**  
Room 1  
**This is the official General Assembly Meeting of the Members of HUPO. All active HUPO members are welcome and encouraged to attend.**  
Chairs: **Mark Baker, HUPO President & Gyorgy Marko-Varga, HUPO Secretary General**

**19:30 – 22:30 HUPO Congress Night: Hockey Night in Canada**  
(Ticketed Event)  
East Ballrooms A+B+C



Join us for a

**HOCKEY  
NIGHT**

*in  
Canada*

The Vancouver Convention Centre East Ballroom will be magically transformed into a hockey ice rink! Dance along with our amazing cover band and enjoy a casual Vancouver West Coast Style buffet dinner.

**Tuesday, September 29, 2015**  
**20:00-23:00**

Vancouver Convention Centre,  
East Building, Ballrooms A+B+C

**TICKETS 100CAD**

Includes skate rentals and  
commemorative photos  
with various hockey players!





SECTION 6

PROGRAM

**WEDNESDAY,  
SEPTEMBER 30**

**THURSDAY,  
OCTOBER 1**

# PROGRAM

WEDNESDAY, SEPTEMBER 30, 2015

**Registration Open** 07:00 – 16:30

**Speaker Ready Room Open** 07:00 – 16:30

**Exhibit Hall Open** 10:00 – 16:30

**Bioinformatics Hub** 08:00 – 17:00

**07:30 - 09:00 HPP 15: mtHPP (mitochondria)**

CHAIR: MAURO FASANO, ITALY  
ROOM 1

**i** FOR DETAILED SESSION INFORMATION  
PLEASE SEE PAGE 105 IN THIS PROGRAM  
BOOK.

**07:30 - 09:00 HPP 16: Human Liver  
Proteome Initiative**

CHAIRS: FERNANDO CORRALES, SPAIN &  
PUMIN ZHANG, USA  
ROOM 2+3

**i** FOR DETAILED SESSION INFORMATION  
PLEASE SEE PAGE 106 IN THIS PROGRAM  
BOOK.

**07:30 - 09:00 HPP 17: iMOP  
(Multi Organism Proteomes)**

CHAIR: EMOKE BENDIXEN, DENMARK  
ROOM 8+15

**i** FOR DETAILED SESSION INFORMATION  
PLEASE SEE PAGE 107 IN THIS PROGRAM  
BOOK.

**07:30 - 08:15 HPP 18a: Human Proteomics  
at Extreme Conditions**

CHAIRS: EVEGENIY NILOLAEV, RUSSIAN  
FEDERATION & IRINA LARINA, RUSSIAN  
FEDERATION  
ROOM 11

**i** FOR DETAILED SESSION INFORMATION  
PLEASE SEE PAGE 108 IN THIS PROGRAM  
BOOK.

**08:15 - 09:00 HPP 18b: Skeletal Muscle  
Proteome**

CHAIRS: LUIGI FERRUCCI, USA & KURT  
HOJLUND, DENMARK  
ROOM 11

**i** FOR DETAILED SESSION INFORMATION  
PLEASE SEE PAGE 109 IN THIS PROGRAM  
BOOK.

**07:30 - 09:00 HPP 19: Infectious Diseases  
(HID)-BD-HPP**

CHAIRS: CONCHA GIL, SPAIN & ILEANA  
M. CRISTEA, USA  
ROOM 12

**i** FOR DETAILED SESSION INFORMATION  
PLEASE SEE PAGE 110 IN THIS PROGRAM  
BOOK.

**07:30 - 09:00 HPP 20: Proteomics of Protein Misfolding and Aggregation Diseases**

CHAIRS: MELINDA REZELI, SWEDEN & PAOLA PICOTTI, SWITZERLAND  
ROOM 19

**i** FOR DETAILED SESSION INFORMATION PLEASE SEE PAGE 111 IN THIS PROGRAM BOOK.


**09:15 - 10:00 PL 06: Plenary Session**


**Chair: Bruno Domon, Luxembourg**

**Plenary Hall (Hall A)**

**Deciphering Functional Proteomes in the Human Protein Atlas - Organelles, Substructures and the Cell Cycle**

Emma Lundberg, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

**10:00 - 11:10**  **Networking Break and Poster Viewing**  
(Even and Odd Poster Numbers)  
**Exhibit Hall (Hall B)**

**10:00 - 11:00**  **Bioinformatics Hub - Meet the Expert Session**

**Room 20**

**10:15 - 11:00 Early Career Manuscript Competition - Presentations of Award Finalists**

**Room 1**

Burcu Ayoglu, KTH-Royal Institute of Technology, Sweden

Justyna Fert-Bober, Cedars Sinai, Heart Institute, USA

Olga Schubert, HHMI / UCLA, USA

**11:10 - 13:00 CS 21: Proteomics of Microbes and Infectious Diseases**

CHAIRS: STUART CORDWELL, AUSTRALIA & JULIAN HISCOX, UK  
ROOM 1

**11:10 CS21.01: The N-linked Glycosylation System of Campylobacter Jejuni: A Functional Proteomics Approach**

Stuart Cordwell, The University of Sydney, Australia

**11:35 CS21.02: High Resolution Analysis of Ebola Virus Biology: from Patient to Cell**

Julian Hiscox, University of Liverpool, UK

**12:00 CS21.03: Pathogenic E. Coli Manipulate Global Proteolysis within Human Intestinal Cells during Infection**

Natalie C. Marshall, University of British Columbia, Canada

**12:15 CS21.04: A Proteomics Approach for Characterization of the Human Adaptive Immune Response to S. Aureus**

Frank Schmidt, University Medicine Greifswald, Germany

- 12:30 CS21.05: A Novel Proline Specific Protease from C. Difficile Involved in Adhesion**  
Paul J. Hensbergen, Leiden University Medical Center, Netherlands
- 12:35 CS21.06: Quantitative Mass Spectrometry Meets Molecular Epidemiology and Vaccinology: Factor H Binding Protein (fHbp) from Neisseria Meningitidis**  
Massimiliano Biagini, GSK Vaccine, Italy
- 12:40 CS21.07: The Listeria Monocytogenes Proteotype**  
Maria Pavlou, ETH, Switzerland
- 12:45 CS21.08: A DIA-MS Approach for the Investigation of S. Aureus Specific In Vivo Host-Pathogen Interactions**  
Stephan Michalik, University Medicine Greifswald, Germany
- 12:50 CS21.09: Phosphorylation and Thiol-Redox Modifications as Molecular Switches in Host-Microbe Interactions**  
Falko Hochgräfe, University of Greifswald, Germany
- 12:55 CS21.10: Proteomic Investigation of a Potential Type I Secretion System in the Syphilis Spirochete, Treponema Pallidum**  
Claudia Gaither, University of Victoria, Canada

**11:10 - 13:00 CS 22: Phosphoproteomics and Cell Signaling**

- CHAIRS: JESPER OLSEN, DENMARK & DANIEL FIGEYS, CANADA**  
ROOM 2+3
- 11:10 CS22.01: Multi-Layered Proteomics Reveals Molecular Switches Dictating Biased Ligand-Dependent EGFR Signaling**  
Jesper V. Olsen, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Denmark
- 11:35 CS22.02: The Chronoproteome of the Brain**  
Daniel Figeys, Ottawa Institute of Systems Biology, Canada
- 12:00 CS22.03: Kinome, Total Proteome and Phosphoproteome Analysis of the CRC64 Cell Line Panel**  
Martin Frejno, University of Oxford, UK
- 12:15 CS22.04: Integrated Proteomic and Phosphoproteomic Analysis of TCGA Ovarian Tumors**  
Karin D. Rodland, Pacific Northwest National Laboratory, USA
- 12:30 CS22.05: Selective Enrichment of Phosphotyrosine Peptides Using Plastic Antibodies**  
Silje B. Torsetnes, University of Southern Denmark, Denmark
- 12:35 CS22.06: Profiling Protein Expression, Modifications and Interactions with Antibody Microarrays**  
Steven Pelech, Kinexus Bioinformatics Corporation, Canada
- 12:40 CS22.07: Mapping Signalling Network Intersection Downstream of Major Cell Surface Receptors**  
Emily S. Humphrey, Max Planck Institute for Biochemistry, Germany
- 12:45 CS22.08: Phosphoproteome Analysis Identifies Oncogenic Kinases in Hepatocellular Carcinoma**  
Ying Jiang, Beijing Proteome Research Center, China

**12:50 CS22.09: In-Depth Phosphoproteomic Analysis of Immune Signaling Pathways in Response to Salmonella Infection**

Alexander Schmidt, University of Basel, Switzerland

**12:55 CS22.10: The Molecular Mechanism of PI3K Mutations Implicated in Immunodeficiencies**

Gillian L. Dornan, University of Victoria, Canada

### 11:10 - 13:00 CS 23: Integrated OMICS

CHAIRS: ROBERT MORITZ, USA & MATHIAS UHLEN, SWEDEN  
ROOM 8+15

**11:10 CS23.01: Integrated Omics to Study the Human Proteome**

Mathias Uhlen, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

**11:35 CS23.02: Keynote**

Robert Moritz, Institute for Systems Biology, USA

**12:00 CS23.03: Integrative Analysis of RNA, Translation and Protein Level Variation across Humans**

Can Cenik, Stanford University, USA

**12:15 CS23.04: A Multi-Omics Perspective of a Population-Based Cohort - A Molecular Epidemiology Approach**

Uwe Voelker, University Medicine Greifswald, Germany

**12:30 CS23.05: Multi-Omics to Study the Effects of Diclofenac on Wild Type and Hepatic Reductase Null (HRN) Mice**

Nicola Gray, Imperial College London, UK

**12:35 CS23.06: Omic Analysis of Lung Cancer Reveals Proteome Signatures with Prognostic Impact**

Michael F. Moran, University of Toronto, Canada

**12:40 CS23.07: Serum Proteomes Distinguish Children Developing Type-1 Diabetes**

Dave Goodlett, University of Maryland Baltimore, USA

**12:45 CS23.08: Multilayered Genetic and Omics Dissection - A New Age for Biomedical Researches**

Yibo Wu, ETH Zurich, Switzerland

**12:50 CS23.09: Impact of THS 2.2 and Conventional Cigarette Smoke on the Lung Proteome of ApoE-/- Mice**

Catherine Nury, Philip Morris International, Switzerland

**12:55 CS23.10: Utilizing Proteomic and Genetic Methodologies to Discover Pathways Affecting Cytokines**

Janel Beckley, Vanderbilt University, USA

### 11:10 - 13:00 CS 24: Sample Preparation for Proteomics

CHAIRS: JOSHUA LABAER, USA & PIERRE CHAURAND, CANADA  
ROOM 11

**11:10 CS24.01: High-Throughput Protein Microarrays for Personalized Diagnostics**

Joshua LaBaer, The Biodesign Institute at Arizona State University, USA

**11:35 CS24.02: Sample Collection Method Bias Effects in Quantitative Phosphoproteomics**

Evgeny Kanshin, Institute for Research in Immunology and Cancer, University of Montreal, Canada

**12:00 CS24.03: Targeted Quantification of 97 Proteins in Dried Blood Spots**

Jingxi Pan, University of Victoria, Canada

**12:15 CS24.04: An Integrated Sample Preparation System for Targeted Proteomics**

Fred E. Regnier, Purdue University, USA

**12:30 CS24.05: Comparison of Acetone Precipitation and FASP II for Protein Identification through Bottom up MS**

Carolyn Kachuk, Dalhousie University, Canada

**12:35 CS24.06: Solvent-Based Protein Precipitation as a Tool for Detergent Removal Ahead of LC/MS**

Alan A. Doucette, Dalhousie University, Canada

**12:40 CS24.07: A Simple Affinity Proteomics System for Fast, Sensitive, Quantitative Analysis of Proteins in Plasma**

John P. O'Grady, Perfinity Biosciences, USA

**12:45 CS24.08: Isolation and Identification of Human Cell Line Proteins Using Acid-Labile Detergents on LC-ESI-TOF**

Robert May, Labor Dr. Spranger und Partner, Germany

**12:50 CS24.09: Automated Sample Preparation Solutions for MS-Based Proteomics**

Previn Naicker, Council for Scientific and Industrial Research, South Africa

**12:55 CS24.10: Optimized Clinical Use of RNALater and FFPE Samples for Quantitative Proteomics**

Kenneth Kastaniegaard, Aalborg University, Denmark

**11:10 - 13:00 CS 25: Top Down Proteomics and Macromolecular Complexes**

CHAIRS: LJILJANA PASA TOLIC, USA & NEIL L. KELLEHER, USA

ROOM 12

**11:10 CS25.01: Top-Down Mass Spectrometry: What Does the Future Hold?**

Ljiljana Pasa-Tolic, Pacific Northwest National Laboratory (PNNL), USA

**11:35 CS25.02: Native and Top Down MS – Revisited**

Neil L. Kelleher, Northwestern University, USA

**12:00 CS25.03: Top-Down, High-Throughput Proteomics of Allergens Using Complementary MS/MS Fragmentation Strategies**

Daniel Lopez-Ferrer, Thermo Fisher Scientific, USA

**12:15 CS25.04: Applying a Proteoform Profiling Method for Neurological Disorder Biomarker Discovery**

Michael B. Andersen, Bruker Daltonics, Denmark

**12:30 CS25.05: Top-Down Structural Analysis of Intact Antibodies Using H/D Exchange and ETD on an Orbitrap-MS**

Suping Zhang, MRM Proteomics Inc., Canada

**12:35 CS25.06: MS3ID: A Novel MS3-Based Method Coupled to a Supervised Learning Algorithm for Top-Down Proteomics**

Mathieu Lavallée-Adam, The Scripps Research Institute, USA

**12:40 CS25.07: Intact Protein Signatures in Substantia Nigra Associated with Lewy Bodies and Neuronal Loss**

Paul D. Piehowski, Pacific Northwest National Laboratory, USA

**12:45 CS25.08: Comprehensive Glycosylation Characterization of Therapeutic mAbs by Top- and Middle-Down MS**

Young Ah Goo, University of Maryland, USA

**14:30 - 16:20 CS 26: Structural Proteomics**

CHAIRS: ANDREA SINZ, GERMANY & EVGENY V. PETROCHENKO, CANADA  
ROOM 8+15

**14:30 CS26.01: The Advancement of Cross-Linking/Mass Spectrometry in Structural Proteomics**

Andrea Sinz, Martin Luther University Halle-Wittenberg, Germany

**14:55 CS26.02: Towards Solving Protein Structures by Structural Proteomics**

Evgeny V. Petrotchenko, University of Victoria, Canada

**15:20 CS26.03: Investigating the Basis of Nav1.5 Fast Inactivation Using a Crosslinking Unnatural Amino Acid and MS**

Christopher Murray, University of British Columbia, Canada

**15:35 CS26.04: Large-Scale Detection of Unstructured Protein Regions by Pulsed Proteolysis**

Roman Körner, MPI of Biochemistry, Germany

**15:50 CS26.05: Global Analysis of Protein Structural Changes in Complex Proteomes**

Yuehan Feng, ETH Zurich, Switzerland

**15:55 CS26.06: Investigation of Protein-RNA Interactions by UV Induced Cross-Linking and Mass Spectrometry**

Kundan Sharma, Max Planck Institute for Biophysical Chemistry, Germany

**16:00 CS26.07: Protein-RNA and Protein-DNA Cross-Link Identification Pipeline Integrated in Proteome Discoverer 2.0**

Oliver Kohlbacher, University of Tübingen, Germany

**16:05 CS26.08: Role of Drosophila Memory Related Fatty Acid Binding Protein on Transporting Fatty Acids**

Yi-Yun Cheng, National Tsing Hua University/National Health Research Institute, Taiwan, ROC, Taiwan

**16:10 CS26.09: Enrichment of Cross-Links from Complex Samples by Charge-Based Fractional Diagonal Chromatography**

Verena Tinnfeld, Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany

**16:15 CS26.10: Ion Mobility and Surface Topology Mapping Reveals the Cause of the Protein G-IgG Affinity Switch**

Yelena Yefremova, Proteome Center Rostock, Germany

**14:30 - 16:20 CS 27: CNPN**

CHAIRS: PIERRE THIBAUT, CANADA & JUERGEN KAST, CANADA  
ROOM 2+3

**SESSION GENEROUSLY SUPPORTED BY**



**14:30 CS27.01: From Edman Sequencing to Tandem Mass Spectrometry: 25 Years of Protein Research to Understand the Role of PARPs in Cell Death, Cancer Biology and Therapy**

Guy G. Poirier, Laval University, Canada

**14:55 CS27.02: Prognostic Significance of Head and Neck Cancer Biomarkers: Translation into Oral Surgery Clinics**

K.W. Michael Siu, University of Windsor, Canada

**15:20 CS27.03: Diagnosis of Urological Disorders with Protein Biomarkers Measured in Seminal Plasma**

Andrei P. Drabovich, University of Toronto, Canada

**15:35 CS27.04: Proteomic Analyses of Macrophage Response to Mycobacterium Tuberculosis Infection**

Yossef Av-Gay, University of British Columbia, Canada

**15:50 CS27.05: Using TAILS N-Terminomics to Identify Missing Proteins and Study Inflammatory Gingival Diseases**

Ulrich Eckhard, Centre for Blood Research, Canada

**15:55 CS27.06: Antibody Colocalization Microarray Quantifies 108 Proteins in 35  $\mu$ L of Serum at fM Concentration**

David Juncker, McGill University, Canada

**16:00 CS27.07: Quantifying the Active Kinases in Ovarian Cancer Cell Lines to Explore Cisplatin Resistance**

Brett Larsen, Mount Sinai Hospital, Canada

**16:05 CS27.08: Investigation of the CK2-Dependent Phosphoproteome Using Mass Spectrometry**

Adam J. Rabalski, Western University, Canada

**16:10 CS27.09: Negative Phosphoregulation of Protein Interaction Domains by Tyrosine Kinase Receptors**

Ugo Dionne, University Laval, CHU de Québec, Canada

**16:15 CS27.10: Assessment of SUMO/ Ubi Kinetic in Human Cells Using an Optimized Peptide Immunopurification**

Frederic Lamoliatte, Institute for Research in Immunology and Cancer, Canada

**14:30 - 16:20 CS 28: Personalized Medicine**

CHAIRS: MICHAEL SNYDER, USA & TADASHI KONDO, JAPAN

ROOM 1

**14:30 CS28.01: Integrative Personal Omics Profiling During Periods of Disease, Weight Gain and Loss**

Michael Snyder, Stanford University School of Medicine, USA

**14:55 CS28.02: Cancer Proteomics in the Era of Precision Medicine**

Tadashi Kondo, National Cancer Center Research Institute, Japan

**15:20 CS28.03: Identification of Tumor Antigens for Personalized Immunotherapy by Analysis of the HLA Peptidome**

Arie Admon, Technion - Israel Inst. of Technology, Israel

**15:35 CS28.04: Immune Response Proteins Predict HCV Treatment Outcome**

Daniel Chelsky, Caprion Proteome, Inc., Canada

**15:50 CS28.05: Substrate and Chaperone Binding Sites in  $\alpha$ -Galactosidase Identified by Proteolytic Affinity MS**

Michael Przybylski, Steinbeis Centre for Biopolymer Analysis and Biomedical Mass Spectrometry, Germany

**15:55 CS28.06: Risk Assessment of Development Impairment in Preterm Babies by Cord Blood Proteome Profiling**

Manja Wölter, University Medicine Rostock, Germany

**16:00 CS28.07: Urine Proteome Analysis for Differential Diagnostics of Respiratory Tract Pathologies in Newborns**

I. A. Popov, Moscow Institute of Physics and Technology, Russian Federation



**16:05 CS28.08: Prediction of Mortality in Acute Respiratory Distress Syndrome**

Maneesh Bhargava, University of Minnesota, USA

**16:10 CS28.09: Serological Epithelial Component Proteins Identify Intestinal Complications in Crohn's Disease**

Yunki Y. Yau, Concord Repatriation General Hospital, Australia

**16:15 CS28.10: Tear Proteome Correlates with Better Clinical Signs and Symptoms in Glaucoma Patients**

Roger Beuerman, University of Tampere, Finland

**15:55 CS29.06: Impact of Individual Single Nucleotide Variants on Signal Transduction Networks in Cancer Cell Lines**

Karsten Krug, University of Tuebingen, Germany

**16:00 CS29.07: Proteome-Scale Discovery of Protein Isoforms, including Those Predicted from RNA-Seq Analysis**

Gene O. Hart-Smith, UNSW, Australia

**16:05 CS29.08: Dynamic Linking of Public Proteomics Data in Ensembl Using TrackHubs**

Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, UK

**14:30 - 16:20 CS 29: Proteogenomics**

CHAIRS: VINEET BAFNA, USA & AKILESH PANDEY, USA

ROOM 11

**14:30 CS29.01: Keynote Presentation**

Akilesh Pandey, Johns Hopkins, USA

**14:55 CS29.02: Proteogenomics to Identify Ig Proteins**

Vineet Bafna, University California San Diego, USA

**15:20 CS29.03: Towards Improving the Genome Annotation of the Honey Bee (*Apis mellifera*)**

Alison McAfee, University of British Columbia, Canada

**15:35 CS29.04: Deep Proteogenomic Profiling of 55 Breast Cancer Cell Lines Reveals Novel Insights in Cancer Biology**

Arzu Umar, Erasmus MC Cancer Institute, Netherlands

**15:50 CS29.05: Peppy 2.0: New Software Addressing the Sensitivity Problem in Proteogenomics**

Mohamed Helmy, University of Toronto, Canada

**14:30 - 16:20 CS 30: Standardization in Proteomics**

CHAIRS: FERNANDO J. CORRALES, SPAIN & ALBERT SICKMANN, GERMANY

ROOM 12

**14:30 CS30.01: A Multi-Centric Study to Evaluate the Use of Relative Retention Times in Targeted Proteomics**

Fernando J. Corrales, Center for Applied Medical Research, Spain

**14:55 CS30.02: Keynote Presentation**

Albert Sickmann, Leibniz-Institut fuer Analytische Wissenschaften, Germany


**15:20 CS30.03: Multi-Site Assessment of Quantitative and Qualitative Performance of SWATH Mass Spectrometry**

Yansheng Liu, ETH Zurich, Switzerland

**15:35 CS30.04: Can Certified Reference Materials Support the Validation of Biomarkers?**

Amalia Muñoz, Joint Research Centre - IRMM, Belgium

- 15:50 CS30.05: Affinity Binder Knock-Down Initiative**  
Tove L. Alm, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden
- 15:55 CS30.06: DIGESTIF: A Universal Quality Standard for the Control of Bottom-Up Proteomics Experiments**  
Virginie Brun, CEA/INSERM/UGA, France
- 16:00 CS30.07: Comparison of iTRAQ Data Processing Approaches with Respect to Analytical and Biological Variability**  
Li Chen, Johns Hopkins University, USA
- 16:05 CS30.08: Harmonization of Proteomics Analyses: A Simple Method to Assess System Suitability**  
A. Bourmaud, L.I.H., Luxembourg
- 16:10 CS30.09: Glycome Profiling of Mouse Tissues Using a Standardized Method Combined LMD and Lectin Microarray**  
Xia Zou, Glycomedicine Technology Research Center, National Institute of Advanced Industrial Science and Technology (AIST), Japan

**16:20 - 16:30**  **Networking Break and Poster Viewing**  
(Even and Odd Poster Numbers)  
Exhibit Hall (Hall B)

**16:30 - 18:30 PL 07: Closing Plenary Session with Award Lectures**

**Chairs: Christoph Borchers, Canada & Pierre Thibault, Canada & Mark Baker, Australia & Martin Larsen, Denmark & Gyorgy Marko-Varga, Sweden**

**Plenary Hall (Hall A)**

- 16:30 Welcome**  
Martin Larsen, University of Southern Denmark, Denmark
- 16:35 Presentation of CNPN Award**
- 16:40 Poster and Travel Award Presentations**
- 16:50 Keynote Talk: Distinguished Achievement in Proteomics Sciences Award - Amanda Paulovich**  
Amanda Paulovich, Fred Hutchinson Cancer Research Center, USA
- 17:10 Keynote Talk: Discovery in Proteomic Sciences Award - Bernhard Kuster**  
Bernhard Kuster, Technische Universität München, Germany
- 17:20 Keynote Talk: Discovery in Proteomic Sciences Award - Akhilesh Pandey**  
Akhilesh Pandey, Johns Hopkins, USA
- 17:30 Keynote Talk: Science & Technology Award - Leigh Anderson, Morteza Razavi & Terry Pearson**
- 17:50 Keynote Talk: Translational Proteomics Award - Jennifer van Eyk**  
Jennifer Van Eyk, Cedars Sinai Medical Center, USA
- 18:10 Distinguished Service Award Presentation - Catherine Costello**
- 18:15 Comments and Reflections**  
Alan Winter, President and CEO, Genome BC
- 18:20 Comments and Reflections**  
Christoph Borchers, University of Victoria, Canada & Pierre Thibault, Université de Montréal, Canada
- 18:25 Invitation to HUPO 2016, Taiwan**
- 18:30 Formal Close/See You in Taiwan**  
Mark S. Baker, Macquarie University, Australia

# PROGRAM

THURSDAY, OCTOBER 1, 2015

08:30 - 17:45 Post-Congress HPP  
Workshop Day  
(Ticketed Session)

CHAIR: GIL OMENN, USA  
SFU HARBOUR CENTRE, JOSEPH AND  
ROSALIE SEAGAL CENTRE, 515 WEST  
HASTINGS STREET



REGISTRATION FEE: 50 CAD



LIGHT REFRESHMENTS AND LUNCH  
INCLUDED



FOR DETAILED SESSION INFORMATION  
PLEASE SEE PAGE 112 IN THIS PROGRAM  
BOOK.



SECTION 7  
**HPP**  
**SESSIONS**

# HPP SESSIONS

SUNDAY, SEPTEMBER 27, 2015

## 08:30 - 17:00 HPP General Investigators Meeting

CHAIR: GIL OMENN, USA

ROOM 11

**An opportunity to review all aspects of the HPP prior to the congress start.  
Participation in this meeting is included in registration.**

**08:30 Gathering/Coffee/Interactions within Groups & SSAB**

**09:00 HPP.01: Progress of the Human Proteome Project - Overview and Metrics**

Gilbert S. Omenn, University of Michigan, USA

**09:20 HPP.02: C-HPP Highlights**

Young-Ki Paik, Yonsei University, Korea, Republic of

**09:40 HPP.03: B/D-HPP Highlights**

Jennifer Van Eyk, Cedars Sinai Medical Center, USA

**10:00 HPP.04: neXtProt & PeptideAtlas 2015 Updates**

Eric W. Deutsch, Institute for Systems Biology, USA  
Lydie Lane, Swiss Institute of Bioinformatics, Switzerland

**10:20 HPP.05: Human Protein Atlas 2015**

Emma Lundberg, KTH - Royal Institute of Technology, Sweden  
Mathias Uhlen, KTH - Royal Institute of Technology, Sweden

**10:40 HPP.06: Highlights of the JPR C- HPP 2015 Special Issue**

Gilbert S. Omenn, University of Michigan, USA

**11:30 Lunch and Breakouts**

Breakout 1 (Room 18): C-HPP Working Session – Young-Ki Paik, Korea  
Breakout 2 (Room 19): B/D-HPP Working Session – Jennifer van Eyk, USA & Fernando Corrales, USA

**13:30 HPP.07: Project on Plasma Proteome Variation**

Michael Snyder, Stanford University School of Medicine, USA

**14:00 HPP.08: Panel on the Testis Proteome: Highly Enriched for Missing Proteins**

Charles Pineau, France & Siqi Liu, China & Ghasem Salekdeh, Iran & Cecilia Lindskog, Sweden

**15:00 HPP.09: Panel on Membrane Proteins: Special Challenges**

Lead Discussant: Alexey Nesvizhskii, University of Michigan-Ann Arbor, USA  
Yu-Ju Chen, Taiwan & Takeshi Tomonaga, Japan & Akhilesh Pandey, USA & Mathias Uhlen, Sweden

**16:00 HPP.10: Reports from Breakout Sessions**

Fernando Corrales, Cedars Sinai Medical Center, USA & Jennifer van Eyk, Cedars Sinai Medical Center, USA & Young-Ki Paik, Yonsei University, Korea

**16:30 HPP.11: Discussion of Plan of HPP Activities for the Week**

## 12:00 - 13:00 HPP Working Group on Cross-linking plus mass spectrometry to analyze protein complexes (XL-MS)

CHAIR: JURI RAPPSILBER, UK

ROOM 11

# HPP SESSIONS

MONDAY, SEPTEMBER 28, 2015

07:30 - 09:00 HPP 01: Cancer HPP

CHAIRS: HUI ZHANG, USA & CONNIE JIMENEZ, NETHERLANDS & EDWARD NICE, USA  
ROOM 1

Understanding the proteomic differences in multiple human tumor types is the current requisite and central theme of the cancer human proteome project (Cancer-HPP) with the ultimate goal of defining expression and interactions of these proteins. This will greatly increase our knowledge of human cancer biology and disease progression. Overall, the Cancer-HPP attempts to characterize different cancer proteomes, determine the correlation of transcriptome and proteome, identify the high priority proteins for each tumor type and generate and disseminate assays and resources to support the analysis of complex biological networks or clinical specimens underlying different disease processes. The use of immunoassays and protein assays as well as the emerging mass spectrometry (MS)-based platforms such as selected reaction monitoring (SRM), Parallel reaction monitoring (PRM), and targeted data extraction for candidate proteins from SWATH-MS data have become reliable popular methods for quantitative analysis of high priority target proteins. Data from multiple laboratories studying different cancer types has confirmed the supremacy of these technologies over conventional assays. Therefore, we propose an international cancer proteomic effort similar to The Cancer Genome Atlas (TCGA) project to identify and validate cancer proteins for different cancer types. Data deposition, quality control, and public availability are always a priority for the key proteomics journals and some funded programs such as CPTAC and EDNR, and they are the key components of the Cancer-HPP. We will further support and propose an open discussion on procedures how to accrue/share data for a list of target proteins from each cancer type, the strategy for assay development, quality control, and procedure and materials needed for disseminate the established assays to cancer biology or clinical laboratories. Toward this goal, it will be essential to involve the whole cancer community including not only proteomics but also genomics and cancer biologists and clinical oncologists in Cancer-HPP.

**07:30 HPP01.01: Integrative Analysis of the Colorectal Cancer Proteome and Its Subtypes with Differential Prognosis**

Connie R. Jimenez, VU University Medical Center, Netherlands

**07:40 HPP01.02: Translation of Membrane Proteome Interactions into Novel Colorectal Cancer Tissue Biomarkers**

Mark S. Baker, Macquarie University, Australia

**07:55 HPP01.03: The First Glimpse of the Proteomic Landscape of Cancer from CNHPP**

Jun Qin, Beijing Proteome Research Center, China

**08:10 HPP01.04: Advances in Breast Cancer Proteomics: Paving the Way towards the Clinic**

Arzu Umar, Erasmus MC Cancer Institute, Netherlands

**08:25 HPP01.05: Glycomics Approaches for the Identification of Cancer Biomarkers Using Targeted Glycoproteomic, Glycomic, and Functional Analyses to Identify a Unique N-Linked Glycan Structure Prevalent in Ovarian Cancer**

Karen Abbott, University of Arkansas for Medical Sciences, USA

**08:40 HPP01.06: Individualized Phosphoproteomics-Guided Screening of Tissue Signatures in Non-Small Cell Lung Cancer**

Yu-Ju Chen, Academia Sinica, Taiwan

# HPP SESSIONS

MONDAY, SEPTEMBER 28, 2015

07:30 - 09:00 HPP 02: HPPP (Plasma)

CHAIRS: JOCHEN SCHWENK, SWEDEN & ERIC DEUTSCH, USA  
ROOM 2+3

Due to its circulation throughout the human body and ease of acquisition, blood provides a unique window into human health and disease. However, analyzing blood plasma or serum still poses one of the major challenges for proteomics in terms of sensitivity and analytical depth. With growing numbers of plasma samples being systematically collected, stored, and made available through biobanks, proteomic methods and technologies advancing, and the remaining need for novel clinical markers to determine and monitor health and disease, the effort to understand the plasma proteome is becoming an increasingly active area of research. This HPPP session will host a selection of short talks on recent advances in plasma protein analysis that cover different technologies, diseases, and concepts. We bring together different contributions to the field in mass spectrometry and affinity-based assays. The presentations will demonstrate success stories, technological possibilities, viewpoints and perspectives on how plasma proteomics has and will continue to advance. The invited speakers will cover topics from the field of biomarker research to their translation into clinical use.

**07:30 HPP02.01: Welcome and Introduction**

Jochen M. Schwenk, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

**07:40 HPP02.02: Sensitive Biomarker Discovery in Plasma for Myocardial Injury**

Hasmik Keshishian, Broad Institute, USA

**07:50 HPP02.03: Quantitative Variability of Plasma Proteins Post-Translational Modifications in a Human Twin Population**

George Rosenberger, ETH Zurich, Switzerland

**08:00 HPP02.04: A Novel Proteomic Method for Plasma Biomarker Quantification**

Michal Harel, Tel Aviv University, Israel

**08:10 HPP02.05: Antibody Microarrays for Plasma Proteomics**

David Juncker, McGill University, Canada

**08:20 HPP02.06: Liaison of Immunocapture MS with Affinity Arrays**

Claudia Fredolini, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

**08:30 HPP02.07: Towards Clinical Measurement by iMALDI**

Robert Popp, University of Victoria, Canada

**08:40 HPP02.08: PeptideAtlas**

Eric W. Deutsch, Institute for Systems Biology, USA

**08:50 HPP02.09: Summary and End of Session**

Eric W. Deutsch, Institute for Systems Biology, USA

# HPP SESSIONS

MONDAY, SEPTEMBER 28, 2015

07:30 - 09:00 HPP 03: Cardiovascular Initiative Workshop

CHAIR: POTHUR SRINIVAS, USA

ROOM 8+15

The HUPO Cardiovascular Initiative Workshop updates cardiovascular researchers and general biological scientists with progresses in the Cardiovascular Human Proteome Project (HPP), whose goal is to understand proteome regulations in cardiovascular diseases and promote the translation of proteome technologies. The Cardiovascular Workshop this year will take place on Monday, September 28th 7:30 am to 9:00 am in Vancouver, Canada ([hupo2015.com](http://hupo2015.com)). The Workshop will feature the work of multiple young investigators from around the world. Selected topics will include advances in redox modifications, their regulations, and their particular importance in the diagnosis and prognosis of cardiovascular diseases; proteomics toolsets to elucidate context-dependent disease pathways in aortic aneurysm; novel quantification workflow using TMT10-TAIL; data science methods to expedite the translation of targeted quantification assays for cardiovascular-centric proteins; and others. Dr. Pothur Srinivas from NHLBI will begin the Workshop session with an overview on the current achievements and future directions of cardiovascular proteomics. A panel discussion period will be dedicated for open discussion to promote interactions with our panelists on the growth of cardiovascular proteomics.

**07:30 HPP03.01: Current Achievements and Future Directions of Cardiovascular Proteomics**

Pothur Srinivas, National Heart, Lung, and Blood Institute, USA

**07:35 HPP03.02: Optimizing a Proteomic Toolset to Elucidate Context-Dependent Disease Pathways in Aortic Aneurysm**

Sarah J. Parker, Cedars Sinai Medical Center, USA

**07:50 HPP03.03: Novel CaMKII Phosphorylation Sites Identified on NaV1.5 by Label-Free Mass Spectrometry**

Anthony W. Herren, University of California, Davis, USA

**08:05 HPP03.04: TMT10-TAILS Analysis of Lymphocytes to Unravel the Role of Proteolysis in B Cell Activation**

Theo Klein, University of British Columbia, Canada

**08:15 HPP03.05: Visualization of Protein Signaling Networks Through Publication Distance**

Maggie Lam, NIH BD2K Center of Excellence at UCLA, USA

**08:25 HPP03.06: The Complexity of Oxidative Modifications**

Mark E. McComb, Boston University School of Medicine, USA

**08:35 HPP03.08: Panel Discussion**



# HPP SESSIONS

MONDAY, SEPTEMBER 28, 2015

07:30 - 09:00 HPP 04: HDPP - Diabetes

CHAIRS: PETER BERGSTEN, SWEDEN & JEAN-CHARLES SANCHEZ, SWITZERLAND  
ROOM 11

The aim of the HUPO Human Diabetes Proteome Project (HDPP) initiative is to enhance the understanding of mechanisms in diabetes development by performing and analyzing large-scale network biology-based experiments.

Diabetes is a disease characterized by inability of normalizing circulating levels of glucose resulting in hyperglycemia. In addition, persons with diabetes often have increased concentrations of fatty acids especially if they are overweight or obese. Therefore, elevated circulating concentrations of glucose and lipid, separated or combined have been implicated in the impaired function observed in different cell types and tissues in individuals with diabetes. Within the HUPO community special expertise is available to generate and analyze complex data sets generated from cells and tissues obtained from healthy and diabetic subjects, animal models of the disease or cell lines.

At previous HDPP workshops, which are held twice a year with one at the HUPO meeting, persons with interest in pursuing diabetes research related to the aim of HDPP have been invited to join the initiative. The resulting group of researchers has worked on different topics. One topic has been to define sets of proteins of interest for understanding diabetes and identify how these sets could be measured and analyzed in an efficient way. Information from these workshops has been disseminated to the general public by the HDPP homepage ([www.hdpp.info](http://www.hdpp.info)).

The 8th HDPP workshop, to be held at the HUPO 2015 meeting in Vancouver, will focus on how sets of proteins of interest discovered by classical omics strategies can be translated in robust assay development to be applied on large cohort of patients. Among the speakers are Dave Goodlett and Ann-Catrin Andersson, who together with the chair and co-chair of the session will address the topic.

**07:30 HPP04.01: Introduction: Progresses since the 13th HUPO meeting in Madrid**

Jean-Charles Sanchez, University of Geneva, Switzerland

**07:45 HPP04.02: Discovery and Validation of Serum Proteome Biomarkers of Type 1 Diabetes Developing Children**

Dave Goodlett, University of Maryland Baltimore, USA

**08:05 HPP04.03: Beta-JUDO: From Pathway Analysis to Target Selection**

Peter Bergsten, Uppsala University, Sweden

**08:25 HPP04.04: Proximity Extension Assays in Diabetes Research**

Ida Grundberg, O-link, Sweden

**08:40 HPP04.05: General Discussion and Proposals**

# HPP SESSIONS

MONDAY, SEPTEMBER 28, 2015

07:30 - 09:00 HPP 05: Human Antibody Initiative

CHAIRS: MATHIAS UHLEN, SWEDEN & TOVE ALM, SWEDEN & EMMA LUNDBERG, SWEDEN  
ROOM 12



BREAKFAST WILL BE PROVIDED DURING THIS SESSION.

The recent discussions within the scientific community and in journals about reproducibility and the quality of antibodies throw light on topics that impact the daily work of most life science researchers. Antibodies and other affinity reagents are commonly used tools across all disciplines of life science, including proteomics, and they are well known to be cross-reactive and have variable success depending on the application. There is a strong need to improve reproducibility in antibody-based proteomic research. Undertaking a number of steps will help reach this goal; first of all affinity reagents must be properly identified and secondly properly validated for the particular application is needed. This session will focus on research programs and initiatives working on identification and quality improvement for affinity reagents, and how we all can contribute to higher quality in proteomic research.

**07:30 HPP05.01: Opening & Welcome**

Emma Lundberg, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

**07:40 HPP05.02: RRIDs The Standard for Research Resource Citation**

Anita Bandrowski, Rancho BioSciences, UCSD, USA

**07:50 HPP05.03: Exploration and Validation of Protein Expression Patterns Using an Integrated Omics Approach**

Cecilia Lindskog, Immunology, Genetics and Pathology, Sweden

**08:00 HPP05.04: Antibody Validation Using siRNA and GFP-Tagged Proteins**

Marie Skogs, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

**08:10 HPP05.05: Affinity Binder Knockdown Initiative**

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

**08:20 HPP05.06: NCI Antibody Characterization Program - An Update Report**

Henry Rodriguez, National Cancer Institute, USA

**08:30 HPP05.07: Alleviating Antibody Anxiety: Generation of Antibodies with Demonstrated Specificity and Reproducibility**

Deepa Shankar, Thermo Fisher Scientific (Life Technologies), USA

**08:40 HPP05.08: Concluding Remarks**

Mathias Uhlen, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

# HPP SESSIONS

MONDAY, SEPTEMBER 28, 2015

07:30 - 09:00 HPP 06: EyeOME - Proteomics: Towards Understanding Biological Pathways in the Eye

CHAIRS: RICHARD SEMBA, USA & MARIUS UEFFING, GERMANY & HYEWON CHUNG, KOREA  
ROOM 19

The EyeOME session has eight speakers who place an emphasis upon biological pathways in the eye that have been revealed through proteomic approaches. The topics include identification of pathways and biomarkers associated with age-related macular degeneration through study of aqueous humor (Hyewon Chung) and tears (Lei Zhou) using SWATH-MS, use of laser capture microdissection and pressure cycle technology to study specific retinal substructures (Sascha Dammeier), and discovery of molecular networks in diabetic retinopathy using a novel transgenic pig model (Stefanie Hauck). New mechanisms of glaucoma have been found through proteomic investigation of the trabecular meshwork (Sanjoy Bhattacharya) and retina (Franz Grus). SWATH-MS has been used to identify dynamic changes in the proteome of human induced pluripotent stem cells in their differentiation to retinal pigment epithelial cells (Richard Semba). A screening approach was used to identify retinal substrates for a disease-associated variant in the protease CAPN5 (Vinit Mahajan).

**07:30 HPP06.01: SWATH-based Comparative Proteomic Analysis of the Aqueous Humor in Patients with Dry Age-related Macular Degeneration**

Hyewon Chung, Konkuk University Medical Center, Korea

**07:40 HPP06.02: Tear Protein Biomarkers for Detection of Age-Related Macular Degeneration**

Lei Zhou, Singapore Eye Research Institute, Singapore

**07:50 HPP06.03: Use of Laser Capture Microdissection with Pressure Cycle Sample Preparation to Analyze the Proteome of Retinal Sub-Structures**

Sascha Dammeier, University of Tuebingen, Germany

**08:00 HPP06.04: Ocular Pathology in the INSC94Y Transgenic Pig, a Novel Model for Diabetic Retinopathy**

Stefanie M. Hauck, Research Unit Protein Science, Helmholtz Center Munich, Germany

**08:10 HPP06.05: Lack of Basement Membrane Protein Degradation in Glaucomatous Trabecular Meshwork**

Sanjoy K. Bhattacharya, University of Miami, USA

**08:20 HPP06.06: Dynamic Changes in the Proteome During the Differentiation of Human Induced Pluripotent Stem Cells into Retinal Pigment Epithelium**

Richard Semba, Johns Hopkins School of Medicine, USA

**08:30 HPP06.07: Glaucoma-Associated Proteomic Changes Provide New Insights in Neurodegenerative Pathways**

Franz Grus, University Medical Center, Johannes Gutenberg-University, Germany

**08:40 HPP06.08: Protease Proteomics: Global Identification of Biological Pathways that Activate Uveitis, Retinal Angiogenesis and Degeneration, and Intraocular Fibrosis**

Vinit B. Mahajan, University of Iowa, USA

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# HPP SESSIONS

MONDAY, SEPTEMBER 28, 2015

13:15 - 14:15 HPP 07: HPP Bioinformatic Session

CHAIRS: ERIC DEUTSCH, USA

ROOM 12

In this workshop, the current and future HPP data guidelines will be discussed. The goal of the workshop is to understand where the existing guidelines have served the HPP well and poorly, and discuss a proposed set of new guidelines, specifically in the context of advancing confident detections of missing proteins. Each subtopic will be introduced separately, followed by discussion by the workshop participants. Full audience participation is encouraged. The major subtopics include: current HPP data guidelines, data deposition in ProteomeXchange, the 1% protein-level FDR requirement, manual inspection of extraordinary claims, consideration of alternate explanations of the data, use of synthetic reference peptides, and the use of SRM to confirm shotgun results.

**13:15 HPP07.01: HPP Bioinformatics Workshop**

Eric Deutsch, Institute for Systems Biology, USA

# HPP SESSIONS

TUESDAY, SEPTEMBER 29, 2015

07:30 - 09:00 HPP 08: CPTAC HPP - CPTAC Data, Tools, and Assays for Cancer Biology

CHAIR: HENRY RODRIGUEZ, USA

ROOM 1

The Clinical Proteomics Tumor Analysis Consortium represents a network of proteomic scientists at multiple locations who coordinate research approaches and data sharing to comprehensively interrogate genomically characterized specimens, initially obtained from The Cancer Genome Atlas collection of highly annotated tumor samples. CPTAC is dedicated to combining state-of-the-art standardized proteomic technologies with genomic analysis and a technological tour de force approach in order to deeply interrogate biospecimen cohorts sized for adequate statistical power. The desired outcome is not only new insights into cancer but also the development of publicly available tools (data, assays, reagents) in proteomics for future studies by the cancer research community. In this workshop CPTAC investigators will describe the tools under development as part of the initial analysis of TCGA tumor specimens, leading to a discussion of the best strategies for moving forward to develop the most informative targeted assays of disease insight.

**07:30 HPP08.01: Overview of CPTAC**

Henry Rodriguez, National Cancer Institute, USA

**07:35 HPP08.02: CPTAC Data Coordinating Center: Data Availability**

Christopher Kinsinger, National Cancer Institute, USA

**07:45 HPP08.03: NetGestalt: CPTAC's portal for Cancer Proteogenomics**

Bing Zhang, Vanderbilt University Medical Center, USA

**08:00 HPP08.04: Targeted Assays for Verification of Biological Insights**

Stefani Thomas, Johns Hopkins University, USA

**08:15 HPP08.05: CPTAC Assay Portal**

Jeff Whiteaker, Fred Hutchinson Cancer Research Center, USA

**08:30 HPP08.06: Moderated Discussion**

# HPP SESSIONS

TUESDAY, SEPTEMBER 29, 2015

07:30 - 09:00 HPP 09: Proteomics Standards Initiative and ProteomeXchange Consortium

CHAIRS: ERIC DEUTSCH, USA & HENNING HERMJAKOB, UK

ROOM 2+3

The HUPO Proteomics Standards Initiative (PSI) defines community standards for data representation in proteomics to facilitate data comparison, exchange and verification. We contribute to data management and integration in all other HUPO initiatives, and have published a modular set of standards for proteomics data representation. For details of the HUPO PSI please see [www.psidev.info](http://www.psidev.info). Based on the HUPO PSI standards, we have developed ProteomeXchange, an international consortium to standardize collection and dissemination of public proteomics data worldwide ([www.proteomexchange.org](http://www.proteomexchange.org)). In this session, we will provide an overview of current PSI activities, with an emphasis on the formats currently in development that need further input from the community. We will also present the current status and future plans for aspects of data deposition in ProteomeXchange. In addition to presentation, there will be time for open discussion and feedback from the community on these activities.

**07:30 HPP09.01: The Proteomics Standards Initiative - Introduction and Status Report**

Eric W. Deutsch, Institute for Systems Biology, USA

**07:45 HPP09.02: Fine-Grained Modelling of Molecular Interactions in PSI MI XML 3.0**

Henning Hermjakob, EMBL-European Bioinformatics Institute, UK

**08:00 HPP09.03: Mass Spectrometry Informatics Formats in Progress**

Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, UK

**08:15 HPP09.04: Open Discussion Focused on Future Projects of the PSI**

**08:30 HPP09.05: ProteomeXchange Consortium - Introduction and Status Report**

Henning Hermjakob, EMBL-European Bioinformatics Institute, UK

**08:45 HPP09.06: Open Discussion Focused on Experiences and Future Projects of ProteomeXchange**

# HPP SESSIONS

TUESDAY, SEPTEMBER 29, 2015

07:30 - 09:00 HPP10: B/D-GPP (Biology/Disease-driven Glycoproteome Project)

CHAIR: HISASHI NARIMATSU, JAPAN

ROOM 8+15

## Session theme

Coordination of proteomics and glycomics for establishment of Glycoproteome Atlas

Most of proteins in the living body are glycosylated and present as glycoproteins. In the previous glycomics initiatives, many technologies were focusing on the analysis of glycans released from glycoproteins. Since two years ago, the Biology/Disease-driven Glycoproteome Project has been aiming at development of new glycoproteomics technologies that are applicable to the biological and medical studies. Glycoproteomics is an Omics-technology for analysis of (1) glycosylation sites, (2) glycan structures, and (3) peptide sequences of intact glycopeptides. This workshop introduces the latest glycoproteomics technologies with six leading researchers who would provide us the recent updates on MS-based glycoproteomics approach, lectin array-based glycan profiling and its application, and perspective on rapidly advancing glycan-related databases. Although there still remain technical difficulties toward the “perfect” glycoproteomics analysis of biological samples such as serum and tissue, we will discuss the possibility of our current technologies for application in the biological and medical areas.

**07:30 HPP10.01: Isomer Specific Glycan and Glycopeptide Sequencing as Tools for Unraveling Disease Glycosylation Signatures**

Daniel Kolarich, Max Planck Institute of Colloids and Interfaces, Germany

**07:45 HPP10.02: Development and Application of a Method to Reveal Large-Scale Glycosylation Site-Specific Glycan Compositions**

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

**08:00 HPP10.03: Alteration in Protein Abundance, Glycoside Occupancy, and Site-Specific Glycosylation Heterogeneity**

Hui Zhang, Johns Hopkins University, USA

**08:15 HPP10.04: Lectin Microarray for Cell Surface Glycosylation Analysis and Biomarker Identification**

Sheng-ce Tao, Shanghai Jiao Tong University, China

**08:30 HPP10.05: Differential Glycome Profiling Analysis of Mouse Tissue Based on Lectin Microarray**

Xia Zou, Shanghai Jiao Tong University, China

**08:40 HPP10.06: From UniProtKB to UniCarbKB and Back Again**

Nicolle H. Packer, Macquarie University, Australia

# HPP SESSIONS

TUESDAY, SEPTEMBER 29, 2015

07:30 - 09:00 HPP 11: Toxicoproteomics

CHAIRS: LEKHA SLENO, CANADA & OLIVER POETZ, GERMANY  
ROOM 11

**07:30 HPP11.01: Welcome**

Lekha Sleno, UQAM, Canada

**Part 1 – Discovery – Chair Lekha Sleno, Canada**

**07:35 HPP11.02: Reactive Drug Metabolites and Covalent Binding**

Lekha Sleno, UQAM, Canada

**07:50 HPP11.03: Virtual-Experimental 2-DE Together with ESI LC-MS/MS as a Toxicoproteomics Platform in Study of Biomarkers**

Stanislav Naryzhny, B.P. Konstantinov Petersburg Nuclear Physics Institute, National Research Center “Kurchatov Institute”, Russian Federation

**Part 2 – Mechanism and Drug-Drug Interaction**

**08:05 HPP11.04: Non-Genotoxic Carcinogens - a Functional Proteomic Study Using High-Content Western-Blotting**

Markus F. Templin, NMI Natural and Medical Sciences Institute at the University of Tuebingen, Germany

**Part 3 – Safety Toxicology**

**08:20 HPP11.05: Proteomic Plasma Profiling Within Human Drug-Induced Liver Injury**

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

**08:35 HPP11.06: Monkey, Dog, Rat and Men - Safety Protein Biomarker Across Species**

Oliver Poetz, NMI Natural and Medical Sciences Institute at the University of Tuebingen, Germany

**08:50 HPP11.07: Closing Remarks**

Oliver Poetz, NMI Natural and Medical Sciences Institute at the University of Tuebingen, Germany



# HPP SESSIONS

TUESDAY, SEPTEMBER 29, 2015

07:30 - 09:00 HPP12: HBPP - Brain

CHAIR: HELMUT E. MEYER, GERMANY

ROOM 12

The HUPO Brain Proteome Project (HBPP) is an international interdisciplinary initiative focusing the investigation of the human brain. The brain is the most complex organ of the human system, which shows various patterns of different tissue layers and cells. In order to investigate the function of the human brain the HBPP members use a broad spectrum of methods combined with a couple of functional analyses such as: mass spectrometry coupled with label free quantification studies, immunohistochemistry, immunological techniques and laser-micro dissection. The strong cooperation between scientist from different fields (affinity proteomics, bioinformatics and biostatistics, proteomics, analytical biotechnology, clinical science, neurobiology, biochemistry, neuroanatomy, neuropathology) is triggered by the aim to understand the biogenesis of neurodegenerative diseases. Special attention is given to the biogenesis of the most common form of dementia, Alzheimer's Disease (AD), Parkinson's Disease (PD), Frontotemporal Dementia (FTD) and other neurodegenerative diseases are topics of the HBPP initiative. The search for biomarkers is also an essential task of the HBPP initiative.

The 24th HUPO Brain Proteome Project (HBPP) workshop will focus on new insights in methods of biomarker research of neurodegenerative diseases. A special tribute will be given to the most important part of the human brain, the hippocampus. But also new hypothesis of the biogenesis of neurodegenerative diseases will be discussed at the 24th HBPP workshop.

The HUPO BPP is an open project – thus, anyone interested in the project shall be welcomed cordially. The latest information will always be publicly available at [www.hbpp.org](http://www.hbpp.org).

**07:30 HPP12.01: Welcome Address**

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

**07:35 HPP12.02: What Are the Triggers of Alzheimer's Disease?**

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

**07:47 HPP12.03: Platelet Extracellular Vesicles (PL-EVs) Are Carriers of Proteins Involved in Vascular- and Neurodegenerative Diseases**

Gerd Schmitz, Institute for Clinical Chemistry and Laboratory Medicine, Germany

**07:59 HPP12.04: Proteome-wide Characterization of Signalling Interactions in the Hippocampal Ca4/dg Subfield of Patients with Alzheimer's Disease**

Young Mok Park, Institute for Basic Science (IBS), Korea

**08:11 HPP12.05: Human Protein Atlas Enabled Neuroproteomic Profiling of Body Fluids**

Anna Häggmark, SciLifeLab, KTH - Royal Institute of Technology, Sweden

**08:23 HPP12.06: H2S Role in Amyotrophic Lateral Sclerosis: Unravelling New Cellular and Molecular Mechanisms**

Andrea Urbani, Santa Lucia Foundation, Italy

**08:35 HPP12.07: Chitinase 3-Like Proteins as Candidate Cerebrospinal Fluid Biomarkers for Multiple Sclerosis**

Philippe Marin, Institut de Génomique Fonctionnelle, France

**08:47 HPP12.08: The Past, the Present and the Future of HBPP**

Katrin Marcus, KTH - Royal Institute of Technology, Sweden  
Peter Nilsson, KTH - Royal Institute of Technology, Sweden  
Daniel Martins-De-Souza, University Campinas, Brazil

# HPP SESSIONS

TUESDAY, SEPTEMBER 29, 2015

07:30 - 09:00 HPP13: PediOme - Paediatrics and Proteomics: Back to the Beginning

CHAIRS: ALLEN EVERETT, USA & HANNO STEEN, USA

ROOM 19

In this session recent advances in pediatric proteomics will be presented and discussed. The presentations will highlight the use of a wide range of proteomics technologies in different clinically relevant settings pertaining to pediatric patient population. Examples will include the application of a wide range of technologies including iTRAQ, SILAC, label free quantification, data independent acquisition methods, SomaScan and ELISA to identify and verify biomarkers for a wide range of pediatric diseases: i) diagnostic urinary biomarkers for different causes of abdominal pain, ii) prognostic serum biomarkers to prognosticate onset and/or activity of Type 1 Diabetes (T1D) before the appearance of T1D associated autoantibodies, and iii) predictive serum biomarkers to predict disease progression and response to therapies Duchene muscular dystrophy patients. A part of the session will be devoted to a discussion led by the session chairs about the progress of the PediOme to date, as well as the specific plan for future progress of this important initiative.

**07:30 HPP13.01: Introduction to the PediOme**

Allen Everett, Johns Hopkins, USA

**07:40 HPP13.02: Proteomics Starts with a Pee - Urine Proteomics for the Discovery of Biomarkers for Pediatric Diseases**

Hanno Steen, Boston Children's Hospital, USA

**08:00 HPP13.03: Serum Proteomes Distinguish Children Developing Type-1 Diabetes**

Dave Goodlett, University of Maryland Baltimore, USA

**08:20 HPP13.04: Development and Implementation of Biomarkers in Duchenne Muscular Dystrophy**

Yatrib Hathout, Children's National Medical Center, USA

**08:40 HPP13.05: Discussion**

13:15 - 14:15 HPP14: C-HPP PIC Meeting

CHAIR: YOUNG-KI PAIK, KOREA

ROOM 12

**13:15 HPP14.01: C-HPP PIC Meeting**

Young-Ki Paik, Yonsei University, Korea, Republic of

# HPP SESSIONS

WEDNESDAY, SEPTEMBER 30, 2015

07:30 - 09:00 HPP15: mtHPP (mitochondria)

CHAIR: MAURO FASANO, ITALY

ROOM 1

In this session the speakers will focus on the update of the mitochondrial HPP project, an initiative started as an activity of the Italian Proteome Association and subsequently extended to involve collaborators from other countries. After a broad summary of previous activities, four talks will span from interactomics to metabolism, from methodology to spatial proteomics. Sufficient time is allotted for general discussion at the end of the session.

**07:30 HPP15.01: Introduction and Resume**

**07:40 HPP15.02: Mitochondrial Networks and Their Association with Neurodegenerative Disorders**

Mohan Babu, University of Regina, Canada

**07:53 HPP15.03: The Mitochondrial Proteome as Observed in the Human Protein Atlas**

Emma Lundberg, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

**08:06 HPP15.04: Mitochondrial Proteomic Analysis of Triple-Negative Breast Cancer Cells**

Italia Bongarzone, Fondazione IRCCS Istituto Nazionale Tumori, Italy

**08:19 HPP15.05: High Density Coverage of Mitochondrial Proteome: A Progress Update**

Maurizio Ronci, University of Chieti-Pescara, Italy

**08:28 HPP15.06: The Multi-Mode Acquisition Analysis of Mitochondrial Proteins.**

Hans Vissers, Waters Corporation, UK

**08:36 HPP15.07: Discussion and Perspectives**

# HPP SESSIONS

WEDNESDAY, SEPTEMBER 30, 2015

07:30 - 09:00 HPP16: Human Liver Proteome Initiative

CHAIRS: FERNANDO CORRALES, SPAIN & PUMIN ZHANG, USA  
ROOM 2+3

## Topics for discussion:

- Configuration of protein priority lists in regard of liver physiology and disease (NAFLD, liver fibrosis, HCC).
- Proteogenomics in the liver (interactions with TCGA and CPTAC).
- Meetings

The liver is a central organ in human body that controls metabolic homeostasis, provide essential substances to the organism and allow detoxification of xenobiotics. In addition to its biological function, liver physiology is peculiar in different aspects, including its regeneration capacity. Despite the intense research performed during the last couple of decades, there are still many open questions in regard of the molecular mechanisms underlying liver function and, most importantly, liver disease. This constraint largely restricts the development of more efficient diagnostic and therapeutic strategies for the better management of the patients. In the postgenomic era, the Human Liver Initiative started in 2002 aiming to define a comprehensive and dynamic map of the human liver proteome. During this session latest results about key issues in liver biology will be presented and discussed, including methods to define cell specific proteome profiles within the liver, definition of factors responsible for maintaining the differentiated phenotype of hepatocytes and mechanisms by which regulation of the protein methylation pattern might contribute to liver injury.

### 07:30 HPP16.01: Liver Proteome with A Cellular Resolution

Chen Ding, Beijing Proteome Research Center, China

### 07:45 HPP16.02: Maintenance of Hepatocyte Identity

Pumin Zhang, Baylor College of Medicine, USA

### 08:00 HPP16.03: Methylthioadenosine Phosphorylase as Regulator of the Methylproteome in Liver Cells

Fernando Corrales, Cancer Research Center, Spain

### 08:15 HPP16.04: Presentation - Title TBC

Pengyuan Yang, Fudan University, China

### 08:30 HPP16.05: General Discussion

# HPP SESSIONS

WEDNESDAY, SEPTEMBER 30, 2015

07:30 - 09:00 HPP17: iMOP  
(Multi Organism Proteomes)

CHAIR: EMOKE BENDIXEN, DENMARK  
ROOM 8+15

iMOP, the initiative on multi organism proteomes, aims to present proteome research from non-human species. iMOP members are working with classical animal models to study human diseases but also focus on a wide range of species which greatly affect human health, including farm animals and crop species, pathogens, as well as the microbiome of humans and farm animals. This year's workshop will include presentations on animal models for studying inflammatory bowel disease (Allan Stensballe) and proteogenomic approaches to improving the health state of honeybees (Leonard Foster), HipA-mediated mechanisms in E.coli (Maja Semanjski), and studies of mucosal microbiota from rat colon, (Nico Jehmlich). As always, we will include a plenum discussion on how the iMOP community can improve proteome research in non-human species.

**07:30 HPP17.01: Animal Models for Inflammatory Bowel Diseases**

Allan Stensballe, Aalborg University, Denmark

**07:50 HPP17.02: Protegenomics and Selection of Health Traits in Honeybees**

Leonard J. Foster, University of British Columbia, Canada

**08:10 HPP17.03: Proteomic Characterization of HipA-Mediated Mechanisms of Bacterial Persistence in E.coli**

Maja Semanjski, University of Tuebingen, Germany

**08:25 HPP17.04: Revealing the Response of the Active Mucosal Microbiota from the Rat Colon to a Change in Diet**

Nico Jehmlich, Helmholtz-Centre for Environmental Research, Germany

**08:40 HPP17.05: Plenum Discussion of iMOP Work and Progress**

# HPP SESSIONS

WEDNESDAY, SEPTEMBER 30, 2015

07:30 - 08:15 HPP 18a: Human Proteomics at Extreme Conditions

CHAIRS: EVGENY NIKOLAEV, RUSSIAN FEDERATION & IRINA LARINA, RUSSIAN FEDERATION ROOM 11

This will be the second session of the Extreme Conditions initiative. This year discussion of research in molecular bases of physiology of sport of high achievements will be included into the program.

**07:30 HPP18a.01: The New Approaches to the Quantitative Analysis of a Long Flight Influence on the Blood Proteome**

Eugene N. Nikolaev, The Institute of Energy Problems of Chemical Physics RAS, Russian Federation

**07:35 HPP18a.02: Mass-Spectrometry Based Blood Serum Peptidome Analysis of Athletes under Physical Overstrain**

Georgij Arapidi, Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry, RAS, Russian Federation

**07:40 HPP18a.03: Analysis of Protein and Biological Processes Dynamics Based on Urine of Healthy Volunteers Exposed 105-day Isolation**

Irina Larina, IMBP RAS, Russian Federation

**07:45 HPP18a.04: Permanent Proteins in the Urine of Healthy Humans During the Mars-500 Experiment**

Liudmila Pastushkova, IMBP RAS, Russian Federation

**07:50 HPP18a.05: Proteome and Metabolome Analysis of Exhaled Breath Condensate Before and After Space Flight, Proteomics Study of Human Body Adaptation During the Space-flight: Correlation Between Blood, Urine and Exhaled Breath Condensate Assays**

Igor Popov, Emanuel Institute of Biochemical Physics RAS, Moscow Institute of Physics and Technology, Russian Federation

**07:55 HPP18a.06: Sportomics: Building a New Concept in Metabolic Studies and Exercise Science**

L. C. Cameron, Adriana Bassini, Laboratory of Protein Biochemistry - Center of Innovation in Mass Spectrometry - Federal University of State of Rio de Janeiro, Department of Biochemistry and Sportomics - Olympic Laboratory, Olympic Committee - Brazil

**08:00 HPP18a.07: Monitoring of Physiological Changes Occurring as a Result of Impact of Erythropoietin**

Marina G. Rodchenkova, Emanuel Institute for Biochemical Physics, Russian Academy of Sciences, Moscow, Russia, Russian Federation

**08:05 HPP18a.08: Development of The New Approaches To Proteome Analyses of Physiologically Diluted Urine, HYPERLINK**

Andrew Percy, University of Victoria Genome British Columbia Proteomics Centre, Canada

**08:10 HPP18a.09: Variation of Urine Proteome During MARS 500 Program**

Bruno Domon, Luxembourg Clinical Proteomics Center, Luxembourg

# HPP SESSIONS

WEDNESDAY, SEPTEMBER 30, 2015

08:15 - 09:00 HPP18b: Skeletal Muscle Proteome

CHAIRS: LUIGI FERRUCCI, USA & KURT HOJLUND, DENMARK  
ROOM 11

Maintenance of the contractile function and energy metabolism of skeletal muscle is essential for autonomy and quality of life in humans. Though, the health and function of muscle is threatened in many situations. Muscle dystrophy in its many forms is the main genetic diseases affecting children and young adults. A progressive decline in muscle mass and strength as well as changes in energy metabolism and mitochondria in muscle are a hallmarks of aging that may cause physical disability. A rapid decline in muscle mass, often referred as cachexia, accompanies debilitating diseases, such as chronic infections, cancer, kidney failure and heart failure. Common chronic diseases, such as diabetes, autoimmune diseases and osteoarthritis often accelerate the age-associated decline in muscle mass and contribute to disability. The specific mechanisms that lead to impaired muscle function in these conditions have been poorly characterized but probably include functional anomalies in energetic metabolism. Etiological diagnoses are based on medical history and physical examination complemented by genetic studies and histological examination of biopsies, which are laborious and have limited sensitivity and specificity. A comprehensive proteomic analysis of skeletal muscle biopsies may increase our understanding of the mechanisms leading to different clinical forms of muscle pathology and also improve diagnosis. Likely specific skeletal muscle proteins undergo specific changes in abundance and/or post translational modifications (PTMs) such as e.g. phosphorylation and acetylation in aging, type 2 diabetes and different other pathologies and the stoichiometric relationships between different proteins and their PTMs change as well. A number of studies have reported maps of skeletal muscle proteins humans, using a number of different discovery-mode and targeted proteomic technologies, usually in small sample on unselected individuals or patients with selected diseases. An assemblage of the data from these studies suggests that as many as 7000 proteins can be detected in muscle tissues. However, an analysis of changes in muscle proteins with aging in individuals free of major diseases and drug treatments is currently not available. These data could serve as a critical reference to dissect changes in proteins that occur with disease as opposed to "normal" aging, therefore increasing their contribution in our understanding of musculoskeletal diseases and expanding their diagnostic value.

In this session, we will provide both an introductory overview of the potential values and uses of skeletal muscle proteomics in aging, type 2 diabetes and other diseases. We present the design and preliminary data from the Genetic and Epigenetic Signatures of Translational Aging Laboratory Testing (GESTALT) a study performed by the Intramural Program of the National Institute on Aging in Baltimore whose aims include the characterization of muscle proteins with aging in a group of very healthy men and women dispersed over a wide age range (20-100 years). Finally, we present studies of the proteomes and phosphoproteomes of human skeletal muscle and isolated muscle mitochondria, as well as quantitative studies of changes in the muscle proteome associated with obesity and type 2 diabetes.

Both the introductory remarks and the examples reported should stimulate a wider interest in proteomic characterization of muscle in humans and, hopefully, will encourage more collaborative research between international groups of this important research topic.

## 08:15 HPP18b.01: Mapping the Skeletal Muscle Proteome: A Functional Approach

Kurt Hojlund, University of Southern Denmark, Denmark

Luigi Ferrucci, National Institute on Aging (NIA), USA

# HPP SESSIONS

WEDNESDAY, SEPTEMBER 30, 2015

07:30 - 09:00 HPP19: Infectious Diseases (HID)-BD-HPP

CHAIRS: CONCHA GIL, SPAIN & ILEANA M. CRISTEA, USA  
ROOM 12

The HID-BD-HPP initiative was established last year at the HUPO-2014 in Madrid. The main goal of this initiative is to organize a community of scientists working in Infectious disease proteomics. Infectious diseases are caused by pathogenic microorganisms, such as bacteria, viruses, parasites or fungi. These infectious are a leading cause of illness and death throughout the world, in particular in low income countries. Lower respiratory infections, HIV/AIDS and diarrheal diseases are ranked in the top ten causes of death globally, whereas malaria and tuberculosis are two of the major ten causes of death in low income countries. In developed countries infectious diseases are also important in immunosuppressed patients and transplant recipients. New diagnostic tests, therapeutic agents and vaccines are required to control these infectious diseases. International collaboration of scientists working in Infectious diseases and proteomics is essential to promote these researches.

## 07:30 HPP19.01: Introduction

Ileana Cristea, Princeton University, USA

## 07:40 HPP19.02: The Current State Of-Art of Proteomics Investigations on Infectious Diseases (Viruses, Bacteria, Fungi and Parasites)

Sanjeeva Srivastava, IIT Bombay, India

Joshua LaBaer, The Biodesign Institute at Arizona State University, USA

Frank Schmidt, University Medicine Greifswald, Germany

Concha Gil, Universidad Complutense de Madrid, Spain

## 08:30 HPP19.03: Round Table

Manuel Fuentes, Cancer Research Center, Spain

Catherine Costello, Boston University School of Medicine, USA

### Topics for discussion:

- How can the scientists working in Infectious disease proteomics collaborate?
- Development of SRM methods for detection and quantification of human and microbial proteins
- Detection and quantification of these proteins by affinity or antibodies based technologies
- Building of a web page to freely-access data
- Diffusion of HID-HPP activities (reports, special issues,..)
- Organization and future actions.



# HPP SESSIONS

WEDNESDAY, SEPTEMBER 30, 2015

07:30 - 09:00 HPP 20: Proteomics of Protein Misfolding and Aggregation Diseases

CHAIRS: MELINDA REZELI, SWEDEN & PAOLA PICOTTI, SWITZERLAND  
ROOM 19

Protein misfolding and aggregation diseases (PMAD), exemplified by Parkinson's or Alzheimer's disease and systemic amyloidoses, are characterized by an abnormal deposition of protein aggregates of regular three-dimensional structure (amyloid). The B/D PMAD working group aims at developing proteomics assays for proteins that are relevant to the study, diagnosis and therapy of protein aggregation diseases. These assays are tested and refined on a set of relevant patient samples (for clinical applications) and on samples from model organisms and cell culture (for basic research). Besides developing assays for measuring protein abundances, a peculiarity of our initiative is that it will attempt also the development of proteomics assays for "aberrant protein conformations", those typically generated in PMADs. In this workshop of the PMAD working group we will present the current status of the project, summarize the assays for PMAD targets developed and validated so far and discuss future directions.

**07:30 HPP20.01: Introduction**

**07:40 HPP20.02: Alpha-Synuclein Proteoforms in Parkinson's Disease**

Melinda Rezeli, Lund University, Sweden

**07:50 HPP20.03: : Probing the Mechanism of Aggresome Formation in Parkinson Disease**

Catherine E. Costello, Boston University School of Medicine, USA

**08:00 HPP20.04: Probing the Conformational Changes of Amyloidogenic Proteins in Biological Samples**

Yuehan Feng, ETH Zurich, Switzerland

**08:20 HPP20.05: Targeted Proteomics to Study Neuronal Physiology**

Hanno Langen, F. Hoffmann-La Roche Ltd, Switzerland

**08:30 HPP20.06: Narrow Range pI Plasma Protein Abundances as Alzheimer Disease Biomarker**

Mohammad Pirmoradian, Karolinska Institute, Sweden

**08:40 Wrap Up**

# HPP SESSIONS

THURSDAY, OCTOBER 1, 2015

08:30 - 17:45 Post-Congress HPP Workshop Day

CHAIR: GIL OMENN, USA

SFU HARBOUR CENTRE, JOSEPH AND ROSALIE SEAGAL CENTRE, 515 WEST HASTINGS ST.

REGISTRATION FEE: 50 CAD



LIGHT REFRESHMENTS AND LUNCH WILL BE INCLUDED

**08:30 Highlights from Sunday-Wed from HPP  
(Selected Workshop Presentations from C-HPP and B/D-HPP, 4min each)**

**09:30 Strategies for Identifying the neXtProt and HPP “Missing Proteins”**

- Lessons from Multiple HPP Groups and JPR Manuscripts and Monday Bioinformatics Workshop

Eric Deutsch, Institute for Systems Biology, USA

- Validation of Claims of Detecting Missing & Novel Proteins and Isoforms

Alexey Nesvizhskii, University of Michigan-Ann Arbor, USA

- Searching for and Credibly Identifying or Proteins

Eric Deutsch, Institute for Systems Biology, USA

Bonghee Lee, Gachon University, Korea

Michael L. Tress, Spanish National Cancer Research Centre (CNIO), Spain

- More Stringent Guidelines Established by Peptide Atlas & neXtProt

Lydie Lane, Swiss Institute of Bioinformatics, Switzerland

- Realizing That Some Predicted Proteins Will Not Be Detectable by Mass Spectrometry, Should We Adjust the Denominator?

Fernando Corrales, Cancer Research Center, Spain, Ulrike Kusebauch, Institute for Systems Biology, USA

**11:15 SRM/SWATH-MS: How to Assist HPP Investigators and the Broad Community to Utilize These Advances from the B/D-HPP? How to Improve the Workflows, Especially for Low-Abundance Proteins and Complex Tissues?**

Robert L. Moritz, Institute for Systems Biology, USA, Jennifer van Eyk, Cedars Sinai Medical Center, USA, Christoph Borchers, University of Victoria, Canada

12:00 Lunch

13:00 HPP Deliverables for 2016: C-HPP

14:00 HPP Deliverables for 2016: B/D-HPP

15:00 HPP Deliverables for 2016: Antibody Pillar

15:20 HPP Deliverables for 2016: MS Pillar

15:40 Summary and Discussion of Goals and Deliverables for 2016-2017

16:30 Reception

17:45 Adjourn

SECTION 8  
**INDUSTRY  
SESSIONS**

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# INDUSTRY SESSIONS

## AT A GLANCE

MONDAY, SEPTEMBER 28  
13:15-14:15

TUESDAY, SEPTEMBER 29  
13:15-14:15

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**Room 1****Thermo Scientific**

From Markers to Assays:  
Accelerating Translational  
Proteomics

**Thermo Scientific**

Pushing the Boundaries  
of Comprehensive  
Proteome Profiling

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**Room 2+3****Bruker Daltonics**

New Solutions in LC/MS  
Based Proteomics

**Wako Laboratory  
Chemicals**

A Versatile Protein Tagging  
System for Recombinant  
Protein Production,  
Isolation, and Detection  
in Mammalian Cells

---

**Room 8+15****Waters Corporation**

Improving Multi-omic  
Workflows for the  
Discovery and  
Development of  
Novel Biomarkers

**SCIEX**

Testimonials in  
OneOmics™: Next  
Generation Proteomics  
at Work

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**Room 11****Agilent Technologies**

Multi-omic Analysis for  
Integrated Biology

# INDUSTRY SESSIONS

MONDAY, SEPTEMBER 28

Monday, September 28 | 13:15-14:15

LUNCH WILL BE PROVIDED FOR ALL SESSIONS

Space is limited for Industry Sessions.

To register and for further information please visit: [hupo2015.com/program/industry-seminars/](http://hupo2015.com/program/industry-seminars/)

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## Room 1

### Thermo Scientific

#### From Markers to Assays: Accelerating Translational Proteomics

- An Integrated Molecular View of Triple Negative Breast Cancer  
SPEAKER: JUDIT VILLEN, PH.D., UNIVERSITY OF WASHINGTON GENOME SCIENCES
- Advances in Parallel Reaction Monitoring: Quantifying Protein Pathways  
SPEAKER: BRUNO DOMON, PH.D., LUXEMBOURG CLINICAL PROTEOMICS CENTER

---

## Room 2+3

### Bruker Daltonics

#### New solutions in LC/MS based proteomics

- Novel and Robust nanoLC/UHR Q-TOF MS Workflow Solution for Deep Proteome Characterization  
SPEAKER: DR. OLE VORM, BRUKER DALTONICS, ODENSE
- Where Genomics Can't Go: Practical Applications of Proteomics in Agriculture and Medicine  
SPEAKER: DR. LEONARD FOSTER, DIRECTOR, CENTRE FOR HIGH THROUGHPUT BIOLOGY, UBC
- Quantitative Protein Degradomics: TAILS Strategies to Identify Missing Proteins  
SPEAKER: DR. CHRIS OVERALL, CENTRE FOR BLOOD RESEARCH, UBC

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# INDUSTRY SESSIONS

MONDAY, SEPTEMBER 28

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**Room 8+15 Waters Corporation**  
**Improving Multi-omic Workflows for the Discovery and Development of Novel Biomarkers**

- Quantitative Multi-Omic Solutions for Translational Research  
SPEAKER: DAVID HEYWOOD, SENIOR MANAGER, OMICS BUSINESS DEVELOPMENT, WATERS CORPORATION
- Pushing the Limits for Targeted Mass Spectrometry  
SPEAKER: PROFESSOR HASMIK KESHISHIAN, BROAD INSTITUTE OF MIT AND HARVARD

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**Room 11 Agilent Technologies**  
**Multi-omic analysis for Integrated Biology**

- Mass Spectrometry Based Metabolomics – the Nuts and Bolts  
SPEAKER: UTE ROESSNER, PH.D. – METABOLOMICS AUSTRALIA, SCHOOL OF BIOSCIENCES, THE UNIVERSITY OF MELBOURNE
- Enhancing Statistical and Pathway Analysis of Protein Discovery Results with Peptide-level Information  
SPEAKER: CHRISTINE MILLER, AGILENT TECHNOLOGIES

# INDUSTRY SESSIONS

TUESDAY, SEPTEMBER 29

**Tuesday, September 29 | 13:15-14:15**

LUNCH WILL BE PROVIDED FOR ALL SESSIONS

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**Room 1      Thermo Scientific**  
**Pushing the Boundaries of Comprehensive Proteome Profiling**

- How to Boost your nanoLC-MS Performance and Throughput in Proteomics  
SPEAKER: PAUL TAYLOR, THE HOSPITAL FOR SICK CHILDREN
- Pushing the Boundaries of Proteomics through Accurate Multiplexed Quantification  
SPEAKER: WILHELM HAAS, PH.D., MASSACHUSETTS GENERAL HOSPITAL CANCER CENTER AND HARVARD MEDICAL SCHOOL

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**Room 2+3      Wako Laboratory Chemicals**  
**A Versatile Protein Tagging System for Recombinant Protein Production, Isolation, and Detection in Mammalian Cells**

SPEAKERS:

DR. JUNICHI TAKAGI,  
PROFESSOR, LABORATORY OF PROTEIN SYNTHESIS AND EXPRESSION,  
INSTITUTE FOR PROTEIN RESEARCH, OSAKA UNIVERSITY

MR. TAKU FUNAKOSHI,  
GENE TECHNOLOGY UNIT LEADER, NEW PRODUCTS DEVELOPMENT  
DEPARTMENT, WAKO PURE CHEMICAL INDUSTRIES

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# INDUSTRY SESSIONS

TUESDAY, SEPTEMBER 29

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**Room 8+15** **SCIEX**

**Testimonials in OneOmics™: Next-Generation Proteomics at Work**

- Prostate Cancer Companion Biomarker Discovery Using SWATH® Acquisition 2.0 and OneOmics™  
SPEAKER: HUGO GAGNON, PH.D., CHIEF OPERATING OFFICER,  
PHENOSWITCH BIOSCIENCE
- Combining Next Generation Proteomics and NGS through OneOmics™ to Gain New Insights Into Human Spermatogenesis  
SPEAKER: CHARLES PINEAU, PH.D., DIRECTOR OF THE PROTEOMICS CORE  
FACILITY BIOGENOUEST





NEW SPECIAL ISSUE

# The Chromosome-Centric Human Proteome Project

**GUEST EDITORS**

Young-Ki Paik  
*Yonsei University*

Gilbert S. Omenn  
*University of Michigan*

**CO-EDITORS**

Chris Overall  
*University of British Columbia*

William S. Hancock  
*Northeastern University*

[tinyurl.com/JPRChromosomelssue](http://tinyurl.com/JPRChromosomelssue)

Journal of  
**proteome**  
research

SECTION 9  
**POSTERS**

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# POSTERS

POSTERS WILL BE DISPLAYED FOR THE ENTIRE DURATION OF THE CONGRESS

## Poster Setup Time:

Sunday, September 27 19:30 – 21:00  
during Welcome Reception

Monday, September 28 07:30 – 10:00

## Poster Take Down:

Wednesday, September 30 By 16:30

POSTERS NOT TAKEN DOWN BY 17:00 ON WEDNESDAY WILL BE DISCARDED BY MANAGEMENT

## Presenting Author Stand By Time

Time in which Poster Presenters remains at his/her poster board and is available to discuss their research personally with interested delegates.

### ENDING ON ODD POSTER NUMBER

Monday, September 28 10:00–11:10  
and 16:20–17:30  
(Networking Breaks)

### ENDING ON EVEN POSTER NUMBERS

Tuesday, September 29 10:00–11:10  
and 16:20–17:30  
(Networking Breaks)

**All Oral and Mini Oral Abstract Presenters have been invited to prepare a Poster in addition to their Oral/Mini Oral Presentations. Poster presentations for Oral and Mini Oral Presenters will be labeled with their Oral/Mini Oral Presentation number (eg CS01.01)**

- P01 Human Proteome Project
- P02 Sample Preparation for Proteomics
- P03 Regenerative Medicine and Stem Cells
- P04 New Technological Advances in Proteomics
- P05 Top Down Proteomics and Macromolecular Complexes
- P06 Cancer Proteomics
- P07 New Advances in Biomarker Discovery
- P08 Proteomics at Pharma
- P09 Proteomics of Microbes and Infectious Diseases
- P10 Structural Proteomics
- P11 Other
- P12 Epigenetics and Histone Landscape
- P13 Protein Networks and Computational Biology
- P14 Membrane Proteomics
- P15 Phosphoproteomics and Cell Signaling
- P16 Neurological Disorders
- P17 Translational Proteomics
- P18 Cardiovascular and Haematological Proteomics
- P19 Protein Modifications (Other than Phosphoproteins)
- P20 Imaging Mass Spectrometry
- P21 Glycomics in Biology and Diseases
- P22 Subcellular Proteomics
- P23 Personalized Medicine
- P24 Proteogenomics
- P25 Metabolomics and Metabolic Diseases
- P26 Chemical Proteomics and Drug Discovery
- P27 Proteomics and Cell Immunity
- P28 Integrated OMICS
- P29 Standardization in Proteomics

## P01 – HUMAN PROTEOME PROJECT

### **P01.01: Virtual-Experimental 2-DE in Combination with ES LC-MS Gives a Clearer View of Proteomes**

Stanislav Naryzhny, Institute of Biomedical Chemistry, Russian Federation

### **P01.02: New Insights into the Evolutionary Characteristics of Missing-Protein-Encoding Genes**

Dong Yang, Beijing Proteome Research Center, China

### **P01.03: Antibodypedia - The Wiki of Antibodies**

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

### **P01.04: Most Genes Have a Single Highly Expressed Dominant Splice Isoform**

Michael L. Tress, Spanish National Cancer Research Centre (CNIO), Spain

### **P01.05: Automated Quantitative Method for Biomarker Assessment of Salivary Proteins**

Andrew J. Percy, University of Victoria, Canada

### **P01.06: Gene-centric Knowledgebase as a Tool for Estimating Protein Species Number**

Elena A. Ponomarenko, Institute of Biomedical Chemistry, Russian Federation

### **P01.07: Platelet-Derived Extracellular Vesicles - A Key to Understand Alzheimer's Disease**

Fouzi El Magraoui, Leibniz Institute for Analytical Sciences (ISAS), Germany

### **P01.08: Proteomics Analysis of Human Ureter for Urine Biomarker Discovery**

Yoshitoshi Hirao, COI-s Biofluid Biomarker Center, Institute for Research Collaboration and Promotion, Japan

### **P01.09: Proteogenomics Analysis of Novel Transcripts and Isoforms Using the Human MiTranscriptome Assembly**

Fernando J. Corrales, Center for Applied Medical Research, Spain

### **P01.10: Changes on the Methyl Proteome Triggered by a Deficiency on MTAP in Liver Cells**

Fernando J. Corrales, Center for Applied Medical Research, Spain

### **P01.11: New features of GenomewidePDB v 2.0**

Seul-Ki Jeong, Yonsei Proteome Research Center, Korea

### **P01.12: SRM-Assay Database for Reproducible Protein Quantification in Different Types of Biomaterial**

Ekaterina V. Ilgisonis, IBMC, Russian Federation

### **P01.13: The First Master Proteome of Single Chromosome: Example of Human Chromosome 18**

Alexander I. Archakov, Institute of Biomedical Chemistry, Russian Federation

### **P01.14: The Combo-Spec Search Method Improves the Current Search Methods Used to Identify Missing Proteins**

Jin-Young Cho, Yonsei Proteome Research Center, Korea

### **P01.15: What Can Housekeeping Gene/Protein Studies Tell Us?**

Bingyun Sun, Simon Fraser University, Canada

### **P01.16: Chromosome-Centric Approach to Unraveling the Human Interactome**

Ekaterina V. Poverennaya, Institute of Biomedical Chemistry, Russian Federation

### **P01.17: Reference Molecular Map of Individual Monocyte Lineages of the Spanish Healthy Population**

Fernando Corrales, ProteoRed-ISCI, Center for Applied Medical Research (CIMA), Spain

### **P01.18: Comprehensive Proteome Analysis of OCT Embedded Frozen Human Renal Cortex by LC-MS/MS**

Bo Xu, Niigata University, Japan

### **P01.19: Human Proteome Project in Cancer**

Hui Zhang, Johns Hopkins University, USA

### **P01.20: Quantitative Nuclear Proteomics of Schizophrenia**

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

### **P01.21: Integration of -Omics Datasets for Comprehensive Protein Expression Profiling for the C-HPP**

Manuel Fuentes, Cancer Research Center, Spain

### **P01.22: Chromosome-Based Proteomic Study for Identifying Novel Protein Variants from Human Hippocampus**

Heeyoun Hwang, Korea Basic Science Institute, Korea

**P01.23: Mass-Spectrometry Based Blood Serum Peptidome Analysis of Athletes under Physical Overstrain**

Georgij Arapidi, Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry, RAS, Russian Federation

**P01.24: Proteomics of Ocular Diseases**

Jeya Maheshwari Jayapal, Aravind Medical Research Foundation, India

**P01.25: Alternatively Spliced Homologous Exons Are Highly Enriched at the Protein Level**

Michael L. Tress, Spanish National Cancer Research Centre (CNIO), Spain

**P01.26: Bioinformatic Approach for Analyzing Missing Proteins in neXtprot Database**

Amr Elguoshy, Niigata University, Japan

**P01.27: MI-PVT: Michigan Proteome Visualization Tool**

Bharat Panwar, University of Michigan, USA

**P02 - SAMPLE PREPARATION FOR PROTEOMICS**

**P02.01: Evaluation of a 96-well Immunodepletion Platform for Multiplex MRM Assay of Proteins in Human Plasma**

Gordon Nicol, Sigma Aldrich, USA

**P02.02: Sample Preparation for Low Amount Cumulus Samples**

Claudia Fortes, Functional Genomics Center Zurich, Switzerland

**P02.03: Phosphopeptide Enrichment Strategies for Mass Spectrometry Analysis**

Jae Choi, Thermo Fisher Scientific, USA

**P02.04: STAGE-Digging: A Novel In-Gel Digestion Processing for Proteomic Samples**

Paolo Soffientini, IFOM, the FIRC Institute of Molecular Oncology, Italy

**P02.05: The SingleShot Workflow: Parallel Analysis of Changes in Gene and Protein Expression**

Anton Posch, Bio-Rad Laboratories, Germany

**P02.06: An Efficient Platform for Basic Reversed-Phase Off-Line Fractionation Enables Deep Proteome Coverage**

Dorte B. Bekker-Jensen, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Denmark

**P02.07: A High-Performance, Scalable and Universal Phosphoproteomics Platform**

Sean J. Humphrey, Max Planck Institute for Biochemistry, Germany

**P02.08: A Novel Approach for Fabricating Functionalized Plate for Sample Enrichment and MS Analysis**

Chao-Jung Chen, China Medical University, Taiwan

**P02.09: Comparison of Protein Extraction Efficiencies of Dried Blood Spots and Dried Plasma Spots**

Dieter Stoll, University of Applied Sciences Albstadt-Sigmaringen, Germany

**P02.10: Strong Cation Exchange Separation of Peptides Using a Spin Column Format (ProTrap XG)**

Kirsten M. Jones, Dalhousie University, Canada

**P02.11: Quantitative Peptide Assay for Optimized and Reproducible Sample Preparations**

Paul Fayad, Thermo Fisher Scientific, Canada

**P02.12: A Systematic Investigation Reveals an Unexpected Side Modification Caused by Lysine Guanidination**

Xumin Zhang, Fudan University, China

**P02.13: High pH Reversed-Phase Peptide Fractionation in a Convenient Spin-Column Format**

Sergei Snovida, Thermo Fisher Scientific, USA

**P02.14: Methodology Development for Quantification of Tightly Adsorbed Proteins**

Ameya V. Ranade, Simon Fraser university, Canada

**P02.15: Automated Protein Digestion to Reduce the Sample Preparation Bottleneck**

Christie Hunter, SCIEX, USA

**P02.16: Protein Fractionation Using a Dissolvable Acrylamide Gel and Its Application to Top-Down Proteomics**

Nobuaki Takemori, Ehime University, Japan

**P02.17: Low Cost Semi-Automated In-Gel Tryptic Digest for High-Throughput Proteomics**

Michelle M. Hill, The University of Queensland, Australia

**P02.18: Trypsin Coated Polymer Nanofibers and Its Application to Protein Digestion under the Pressure Cycle**

Han Sol Kim, Korea University, Korea

**P02.19: Improved Speed & Reproducibility of Protein Digestion Using Novel Sample Preparation Technology**

Kevin Doolan, Thermo Fisher Scientific, UK

**P03 – REGENERATIVE MEDICINE AND STEM CELLS**

**P03.01: Proteomic Analysis of Infantile Haemangioma**

Jonathan Dunne, Gillies McIndoe Research Institute, New Zealand

**P03.02: Candidate Surface Biomarkers of Transformed Mesenchymal Stem Cells by Quantitative (Glyco)Proteomics**

Julian Saba, Thermo Fisher Scientific, USA

**P04 – NEW TECHNOLOGICAL ADVANCES IN PROTEOMICS**

**P04.01: HiRIEF LC/MRM-MS: Toward Increased Coverage of the Human Plasma Proteome**

Vincent R. Richard, McGill University, Canada

**P04.02: Accuracy and Sensitivity of Proteome Quantitation Using TMT - An Evaluation of Recent Developments**

Anna Chen, Mission San Jose High School, USA

**P04.03: TMT 10-Plex Quantitation by Travelling Wave IMS-QToF Mass Spectrometry**

Roy Martin, Waters Corp, UK

**P04.04: ELISA-PLA: A Sensitive and Specific Protein Post Translational Modification Detection Method**

Qing He Tong, Fudan University, China

**P04.05: Extending the Quantitative Information of the Glioblastoma Proteome Using SuperQuant**

Frank Kjeldsen, University of Southern Denmark, Denmark

**P04.06: Improved Peptide Identification Using Variable Window SWATH Acquisition, UPLC and DIA-Umpire**

Brett Larsen, Mount Sinai Hospital, Canada

**P04.07: Behavioral and Proteomic Analysis of Stress Response in Zebrafish(Danio rerio)**

Sameh Magdeldin, Niigata University, Japan

**P04.08: Protein Post-Translational Modifications of Mouse Kidney Using OFFGEL Prefractionation**

Sameh Magdeldin, Niigata University, Japan

**P04.09: Development of LC-Electrochemistry-MS for Disulfide Mapping: Application to Notch3 Protein Fragments**

Linda Switzar, Leiden University Medical Center, Netherlands

**P04.10: Targeted Tissue-Enriched Proteomics in Kidney Tissue**

Masato Habuka, Institute of Nephrology, Medical and Dental School, Niigata University, Japan

**P04.11: Molecular Dissection of a Proteome**

Rebecca A.T. Pattison, Centre for Proteome Research, Institute of Integrative Biology, UK

**P04.12: The Thermal Stability of the Human Proteome**

Bernhard Kuster, Technische Universität München, Germany

**P04.13: Zeptomole Detection of Serum Biomarkers Using Surface Plasmon Resonance Imaging (SPRI)**

Marinella G. Sandros, University of North Carolina at Greensboro, USA

**P04.14: High-Density Protein Microarrays for Antibody Validation and Autoimmunity Profiling**

Ronald Sjöberg, KTH - Royal Institute of Technology, Sweden

**P04.15: Electrochemical Detection of Ovarian Cancer Biomarker HE4 Based on  $\mu$ QLISA Principle**

Zuzana Bilkova, University of Pardubice, Czech Republic

**P04.16: Systematic Exploration of Subcellular Redox Status by Methionine-Containing Peptide Enrichment**

Ya-Ju Hsieh, Chang Gung University, Taiwan

**P04.17: Sensitive Approach to Identify HLA-DR Peptides Facilitating Individual Patient Characterization**

Tina Heyder, Karolinska Institutet/University Hospital, Sweden

**P04.18: Click-MS: Tagless Protein Enrichment Using Bioorthogonal Chemistry for Quantitative Proteomics**

Annik Borrmann, Radboud University, Netherlands

**P04.19: Why to Use Ultra-High Resolution Quadrupole Time of Flight Instruments for Proteomics Applications?**

Stephanie Kaspar, Bruker Daltonik GmbH, Germany

**P04.20: Towards a “Load and Play” Solution for Parallel Reaction Monitoring Assays**

Bruno Domon, L.I.H., Luxembourg

**P04.21: Human Proteome Array Revealed That hnRNP K Binds and Affects the Accumulation of Mature miR-122**

Chien-Sheng Chen, National Central University, Taiwan

**P04.22: A New Approach for Better Identification of Cellular Peptide Using Tandem Mass Spectrometry**

Yet-Ran Chen, Academia Sinica, Taiwan

**P04.23: mzDB: A File Format Optimized for the Efficient Analysis of Large LC-MS/MS and SWATH-MS Datasets**

David Bouyssié, CNRS; IPBS (Institut de Pharmacologie et de Biologie Structurale), France

**P04.24: A Comprehensive Database and Search Method for Large-Scale Metaproteomics**

Sandip Chatterjee, The Scripps Research Institute, USA

**P04.25: SWATH-ID: An Instrument Method Which Combines Identification and Quantification in a Single Analysis**

Stephen A. Tate, Sciex, Canada

**P04.26: An Alternative Mass Spectrometry View of the Proteome**

LeRoy B. Martin, Waters Corporation, USA

**P04.27: Immunoaffinity-MS Platform for Antibody Screening and Native Protein Analysis in Biological Fluids**

Dimitrios Korbakis, University of Toronto, Canada

**P04.28: Increased MS Protein Identification Rates Using 75 cm Long Nano LC C18 Separation Columns**

Stephan Meding, Thermo Fisher Scientific, Germany

**P04.29: A Novel MS1-Based Strategy for Accurate Proteomic Quantitation with Extremely Low Missing Value**

Jun Qu, University at Buffalo, CBL, USA

**P04.30: Deep, Single Shot Human Cell Line Protein Profiling Using DIA and Spectronaut on a Q Exactive HF**

Oliver Rinner, Biognosys AG, Switzerland

**P04.31: A Robust SRM Assay for UMOD and Albumin in Urine**

Qin Fu, Cedar Sinai Medical Center, USA

**P04.32: Data Acquisition and Processing to Apply Inter-Peak Isotope Spacing for Turnover Analysis**

John C. Price, Brigham Young University, USA

**P04.33: Ultrafast, High Sensitive microLC/MS/MS for Peptide Quantitation in Highly Targeted Assays**

Remco Van Soest, SCIEX, USA

**P04.34: Compression and Rapid Visualisation of Quantitative LC-MS Data Based on Raw Signal Decomposition**

Andrew W. Dowsey, University of Liverpool, UK

**P04.35: A High-Efficient Yeast BiFC Approach for Genome-Wide Interactome Mapping**

Jian Wang, Beijing Institute of Radiation Medicine, China

**P04.36: A Comparison of Three-Dimensional Strategies in Mining the Human Plasma Proteome**

Yan Zhao, State Key Laboratory of Proteomics, China

**P04.37: Functionalized Polymer Material for Enrichment and In-Situ Digestion of Membrane Proteins**

Mingxia Gao, Fudan University, China

**P04.38: High Retention Time Precision and Mass Accuracy LCMS Platform for Deep Label-Free Proteome Profiling**

Alexander Boychenko, Thermo Fisher Scientific, Germany

**P04.39: A QPrEST Derived Peptide Resource for Targeted Proteomics**

Fredrik Edfors, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

**P04.40: Ultrasensitive Proteome Analysis by On-Line Cell Digestion and Nano-LC-MS Identification**

xiangmin Zhang, Fudan University, China

**P04.41: A New Method to Control Ratio Distortion in Isobaric Labeling Experiments**

Erik Ahn , Biozentrum, University of Basel, Switzerland

**P04.42: Probing Plasma of Patients with Cardiovascular Disease Using a 120-plex Immuno-MRM Assay**

Eric W. Kuhn, Broad Institute, USA

**P04.43: Development of a Reference Peptide Library for Targeted Serum Proteomics Using a Cell-Free System**

Nobuaki Takemori, Ehime University, Japan

**P04.44: A Cross-Platform Comparison of Data Independent Acquisition Methods for Proteomic Analysis**

Xin Ku, Shanghai Jiaotong University, China

**P04.45: Quantitative Profiling of Cyp P450s Using DIA and Processed Using Cloud Computing**

Sibylle Heidelberger, Sciex, UK

**P04.46: Low Attomole Limit of Quantification on the Orbitrap Fusion Lumos Tribrid Mass Spectrometer**

Romain Huguet, Thermo Fisher Scientific, USA

**P04.47: DOSCAT: Double Standards in Proteomics for Mass Spectrometry and Quantitative Western Blotting**

Richard J. W. Bennett, Centre for Proteome Research, University of Liverpool, UK

**P04.48: Identification of Peptide Fragments of Gut Microbiota Proteins in Human Blood Serum**

Georgij Arapidi, Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry, RAS, Russian Federation

**P04.49: Retention Time Independent SWATH Acquisition Scoring**

Stephen A. Tate, SCIEX, USA

**P05 – TOP DOWN PROTEOMICS AND MACROMOLECULAR COMPLEXES**

**P05.01: Middle-Down HDX-MS for Structural Characterization of Antibodies at Single Residue Resolution**

Jingxi Pan, University of Victoria, Canada

**P05.02: Metaproteomic Analysis, next Generation Environmental Assessment**

Susana Cristobal, Link ping University, Sweden

**P05.03: Interactome Analysis of Key Protein Complexes Responsive to DNA Damage and Replication Stress**

Barbora Salovska, Faculty of Military Health Sciences in Hradec Kralove, Czech Republic

**P05.04: Cold Vaporization of Tissue with a Picosecond Infrared Laser for Top down Proteomics**

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

**P05.05: Optimizing Top down Analysis of Proteins on an Orbitrap Fusion Lumos Tribrid Mass Spectrometer**

Romain Huguet, Thermo Fisher Scientific, USA

**P06 – CANCER PROTEOMICS**

**P06.01: av 6, Plasminogen and Latent TGF-  Drive Colorectal Cancer Aggression**

David Cantor, Macquarie University, Australia

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Anuli C. Uzozie, University of Zurich, Switzerland

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Marcelo V. De Sousa, University of Brasilia, Brazil

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Tae-Sung Yoon, UST/KRIBB campus, Korea

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Ashraf Elamin, Philip Morris International, Switzerland

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Benjamin A. Garcia, University of Pennsylvania School of Medicine, USA

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Nicholas E. Scott, University of British Columbia, Canada

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Aleksandra Nita-Lazar, National Institute of Allergy and Infectious Diseases, USA

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Hyobin Jeong, Institute for Basic Science, Korea

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Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, UK

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Andrew Collins, University of Liverpool, UK

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Mathieu Lavallée-Adam, The Scripps Research Institute, USA

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Noemi Del Toro, EMBL-European Bioinformatics Institute, UK

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Mauro Fasano, University of Insubria, Italy

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Joerg Gsponer, University of British Columbia, Canada

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Susana S. Novoa-Herran, Universidad Nacional de Colombia, Colombia

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Shin Kawano, Research Organization of Information and Systems, Japan

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Simon Perkins, University of Liverpool, UK

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Anne-Claude Gingras, Lunenfeld-Tanenbaum Research Institute, Canada

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Shamim Mushtaq, Ziauddin University, Pakistan

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Geert Baggerman, VITO/University of Antwerp, Belgium

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Haruhiko Kamada, National Institute of Biomedical Innovation and Nutrition, Japan

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Benjamin Ruprecht, Technical University of Munich, Germany

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Yih-Cherng Liou, National University of Singapore, Singapore

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Anna-Kathrine Pedersen, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Denmark

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Hongbo Guo, University of Toronto, Canada

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Asfa Alli Shaik, Institute of Molecular and Cell Biology, Singapore

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Tanveer S. Batth, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Denmark

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Michael Blank, Thermo Fisher Scientific, USA

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Moreno Papetti, NNF Center for Protein Research University of Copenhagen, Denmark

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Garry L. Corthals, University of Amsterdam, Netherlands

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Zuzana Bilkova, University of Pardubice, Czech Republic

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Steven Pelech, Kinexus Bioinformatics Corporation, Canada

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Steven Pelech, Kinexus Bioinformatics Corporation, Canada

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Rui Zhai, Beijing Proteome Research Center, China

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Mats Borén, Denator, Sweden

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Steven Pelech, Kinexus Bioinformatics Corporation, Canada

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Naoyuki Sugiyama, Kyoto University, Japan

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Concha Gil, Universidad Complutense de Madrid, Spain

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Pia Jensen, University of Southern Denmark, Denmark

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Rolf Nölker, University of Greifswald, Germany

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Emmanuelle Lezan, Biozentrum, University of Basel, Switzerland

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Sylvie Bourassa, CHU de Québec/Laval University, Canada

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Katrin Marcus, Ruhr-University Bochum, Germany

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Shilian Liu, Department of Biochemistry and Molecular Biology, China

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Jason Rogalski, University of British Columbia, Canada

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Philippe Marin, Institut de Génomique Fonctionnelle, CNRS UMR5203, INSERM U1191, Université de Montpellier, France

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Ute Distler, University Medical Center of the Johannes-Gutenberg University Mainz, Germany

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Candelaria Merino-Jiménez, Cinvestav, Mexico

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Jessica Holmén Larsson, University of Gothenburg, Sweden

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Andreas Schroetter, Leibniz-Institut fuer Analytische Wissenschaften - ISAS - e.V., Germany

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Peter Nilsson, SciLifeLab, KTH - Royal Institute of Technology, Sweden

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Anna Häggmark, SciLifeLab, KTH - Royal Institute of Technology, Sweden

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Luis Cubano, Universidad Central del Caribe, Puerto Rico

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Hwan-Ching Tai, National Taiwan University, Taiwan

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Jia Mi, Uppsala University, Sweden

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SATYA Saxena, Johnson and Johnson, USA

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Pernille Lassen, University of Southern Denmark, Denmark

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Laxmikanth Kollipara, Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany

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Andrea Urbani, Santa Lucia Foundation, Italy

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Marina G. Rodchenkova, Emanuel Institute for Biochemical Physics, Russian Academy of Sciences, Moscow, Russia, Russian Federation

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Nikhat Ahmed Siddiqui, Ziauddin University, Pakistan

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Ilijana Begcevic, University of Toronto, Canada

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Mari DeMarco, University of British Columbia & St Paul's Hospital/Providence Health Care, Canada

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Kirti Sharma, Max Planck Institute for Biochemistry, Germany

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Garry Wong, University of Macau, Macau

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Pan Fang, Institute of Biomedical Science, Fudan University, China

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Young Mok Park, Institute for Basic Science (IBS), Korea

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Juliana Almada Colucci, Universidade Federal de São Paulo, Brazil

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Peter D.E.M. Verhaert, Lund University, Sweden

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Julie A. D. Van, University of Toronto, Canada

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Timothy K. Chataway, Flinders University, Australia

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Toshiyuki Mikami, Sumitomo Dainippon Pharma, Japan

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Frøde S. Berven, University of Bergen, Norway

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James Langridge, Waters Corp, UK

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Sun Tae Kim, Pusan National University, Korea

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Sun Tae Kim, Pusan National University, Korea

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Ana Konvalinka, Toronto General Hospital, University of Toronto, Canada

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Jean Charles Sanchez, Centre Medical Universitaire, Switzerland

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CHRISTINA Schiza, University of Toronto, Canada

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Felix Leung, Mount Sinai Hospital, Canada

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M Marta Guarna, University of British Columbia, Canada

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Theano D. Karakosta, Mount Sinai Hospital, Canada

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Nawal Boukli, Universidad Central del Caribe, Puerto Rico

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Thomas Frohlich, Ludwig-Maximilians-Universitaet Muenchen, Germany

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Georg J. Arnold, Ludwig-Maximilians-Universitaet Muenchen, Germany

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Claudia Fredolini, KTH - Royal Institute of Technology, Sweden

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daniel Lopez-Ferrer, Thermo Fisher Scientific, USA

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Michael Merchant, University of Louisville, USA

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Lucilene D. Santos, Botucatu Medicine School (FMB-UNESP)/Center for the Study of Venoms and Venomous Animals (CEVAP), Brazil

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Leticia G. Pontes, Botucatu Medicine School (FMB-UNESP)/Center for the Study of Venoms and Venomous Animals (CEVAP), Brazil

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Johannes P.C. Vissers, Waters Corp, UK

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Jake Cosme, University of Toronto, Canada

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Christopher M. Tracy, University of Utah, USA

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Manuel Fuentes, Cancer Research Center, Spain

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Melinda Rezeli, Lund University, Sweden

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Mark E. McComb, Boston University School of Medicine, USA

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Joel A. Kooren, Cedars Sinai Medical Center, USA

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John E. Wiktorowicz, University of Texas Medical Branch, USA

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Albert Sickmann, Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany

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Daniel Soetkamp, Cedars-Sinai Medical Center, USA

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Ashraf Elamin, Philip Morris International, Switzerland

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Maggie PY. Lam, UCLA, USA

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A Chakraborti, Post Graduate Institute of Medical Education and Research, India

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Sanjay S. Bhandari, University of Leicester, UK

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Nikolaus Fortelny, University of British Columbia, Canada

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Jenny Albanese, Sciex, USA

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Guy G. Poirier, Centre de recherche du CHU de Quebec, Canada

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Honggang Huang, University of Southern Denmark, Denmark

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Gene O. Hart-Smith, UNSW, Australia

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Dong Li, The Academy Of Military Medicine Science, China

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Weixuan Chen, Georgia Institute of Technology, USA

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Rebecca Pferdehirt, Genentech, Inc., USA

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Rosa Viner, Thermo Fisher Scientific, USA

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Min Jueng Kang, Seoul National University, Korea

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Thibault Mayor, The University of British Columbia, Canada

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George Rosenberger, ETH Zurich, Switzerland

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Philipp F. Lange, University of British Columbia, Canada

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Eric Wolf, University of Toronto, Canada

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Selene Swanson, Stowers Institute for Medical Research, USA

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Justyna Fert-Bober, Cedars-Sinai Medical Center, USA

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Jeroen AA. Demmers, Erasmus MC, Netherlands

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Don-Ha Park, Yonsei Proteome Research Center, Yonsei University, Korea

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Maria Ibáñez-Vea, University of Southern Denmark, Denmark

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Yi-Ju Chen, Academia Sinica, Taiwan

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Navratan Bagwan, Centro Nacional de Investigaciones Cardiovasculares, Spain

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Jenny Albanese, SCIEX, USA

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Chien-Yun Lee, National Chung Hsing University-Academia Sinica, Taiwan

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Takayoshi Suzuki, National Institute of Health Sciences, Japan

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Lekha Sleno, UQAM, Canada

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Yi-Yun Chen, Academia Sinica, Taiwan

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Ping Xu, Beijing Proteome Research Center, China



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Xiaodong Wang, University of Victoria, Canada

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David Heywood, Waters, UK

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Justin Chang, Waters, UK

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Michael Becker, Bremen Daltonik GmbH, Germany

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Ping Cao, Amgen, USA

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Jean-Charles Sanchez, University of Geneva, Switzerland

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Tara Schroeder, Thermo Fisher Scientific, USA

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Jiangming Huang, Fudan University, China

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Michael Caragata, The University of Queensland, Australia

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Yoshimi Haga, The University of Tokyo, Japan

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Andras Guttman, University of Debrecen, Hungary

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Stephanie Kaspar, Bruker Daltonik GmbH, Germany

### **P21.08: In-Depth Analysis of Site-Specific N-Glycosylation in Vitronectin from Human Plasma**

Heeyoun Hwang, Korea Basic Science Institute, Korea

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Atsushi Kuno, National Institute of Advanced Industrial Science and Technology (AIST), Japan

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Samir Karaca, Max Planck Institute for Biophysical Chemistry, Germany

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Malene M. Joergensen, Aalborg University Hospital, Denmark

### **P22.03: Reinforcement-Polarity Dependently Regulated Synaptic Proteins in a Learning Paradigm in Mice**

Thilo Kähne, University Magdeburg, Germany

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Matthew Jessulat, University of Regina, Canada

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Rikke Baek, Aalborg University Hospital, Denmark

### **P22.06: Multiplexed Quantitative Profiling of Mitochondria from the USP30 Knockout Mouse**

Lilian Phu, Genentech, USA

**P22.07: Subcellular Proteomic Study of Skeletal Muscle by Evaluated Fatty Acid Level**

Sai Ming Ngai, The Chinese University of Hong Kong, Hong Kong

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Kimberly A. Lee, Cell Signaling Technology, USA

**P23.02: Development of Companion Diagnostics for RCC (Renal Cell Carcinoma) Treatment with mTOR Inhibitor**

Ryosuke Watanabe, National Institute of Biomedical Innovation, Japan

**P23.03: Discovery of Biomarker Candidates for NSCLC Treatment Using CTOS (Cancer Tissue-Originated Spheroid)**

Ryosuke Watanabe, National Institute of Biomedical Innovation, Japan

**P23.04: Array-Based Signaling Pathway Profiling for Cancer Therapy Personalization**

Tesshi Yamada, National Cancer Center Research Institute, Japan

**P23.05: Targeting Modified Single Amino Acid Variants in Cancer Cell Lines by Parallel Reaction Monitoring**

Christoph Taumer, University of Tuebingen, Germany

**P23.06: Molecular You Corporation (MYCO): Comprehensive Omic Analysis for Personalized Preventive Medicine**

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