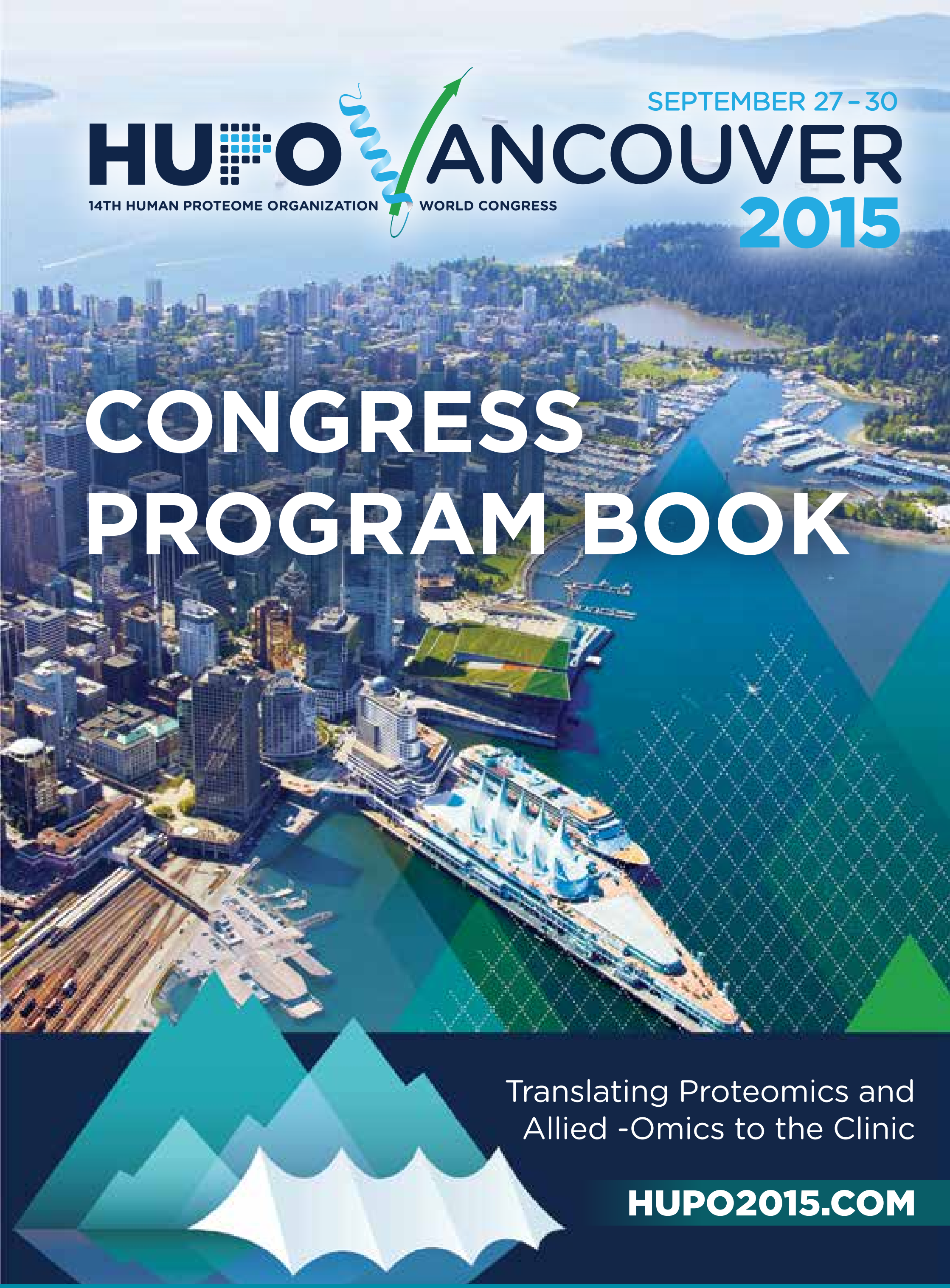
SEPTEMBER 27 – 30

HUPO VANCOUVER 2015

14TH HUMAN PROTEOME ORGANIZATION WORLD CONGRESS



CONGRESS PROGRAM BOOK

Translating Proteomics and
Allied -Omics to the Clinic

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translating the code of life

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- Become part of an international scientific community of over 880 members
- Enjoy a discount on the HUPO Annual World Congress registration fees
- Vote online in the annual election of HUPO Council (Board of Directors) members
- 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

For more information visit **www.hupo.org**

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HUPO and the 14th World Congress would like to sincerely thank the following organizations for supporting the HUPO 2015 Congress:

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HUPO and the 14th World Congress would also like to sincerely thank the following organizations for providing awards:

DISTINGUISHED ACHIEVEMENT AWARD

Journal of
proteome
research

TRANSLATIONAL PROTEOMICS AWARD

TRAVEL AWARDS

BCProteomicsNetwork

CNPN

University
of Victoria

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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!

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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

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SECTION 1

GENERAL CONGRESS INFORMATION

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 **14th 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

Christoph Borchers
HUPO 2015
Congress Co-Chair

Pierre Thibault

Pierre Thibault
HUPO 2015
Congress Co-Chair

BRITISH
COLUMBIA

A Message from Premier Christy Clark

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

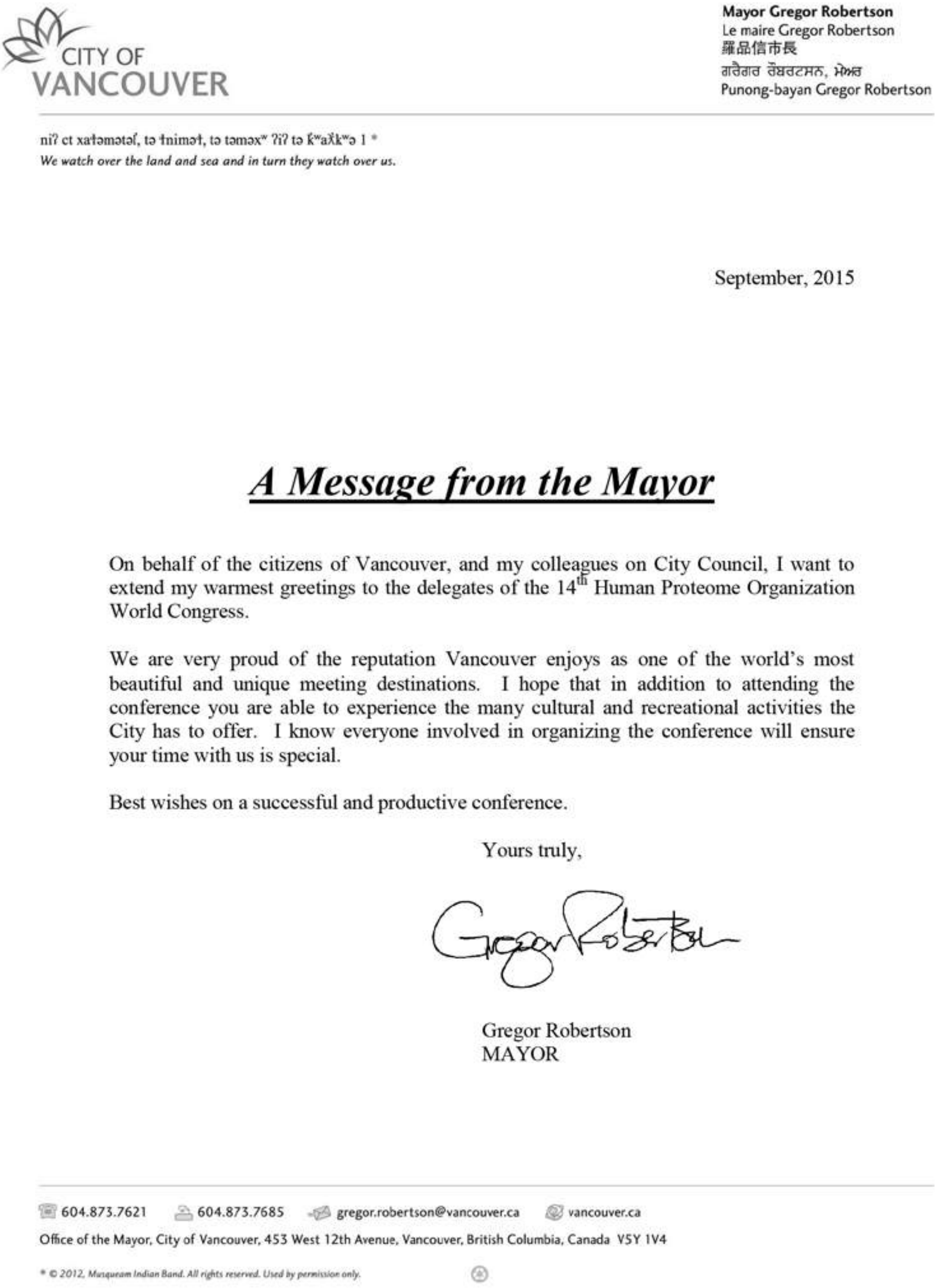
Your meetings will be taking place in our world-class convention facilities, the Vancouver Convention Centre East Building, where experienced staff will help to ensure a successful gathering.

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,

Christy Clark

Christy Clark
Premier



CITY OF
VANCOUVER

Mayor Gregor Robertson
Le maire Gregor Robertson
羅品信市長
ਗਰੈਗਰ ਰੌਬਰਟਸਨ, ਮੇਅਰ
Punong-bayan Gregor Robertson

niʔ ct xaˑɬəmətəl̓, tə ɬnimət, tə təməxʷ ʔiʔ tə k̓ʷaƛ̓kʷə 1 *
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 14th 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.

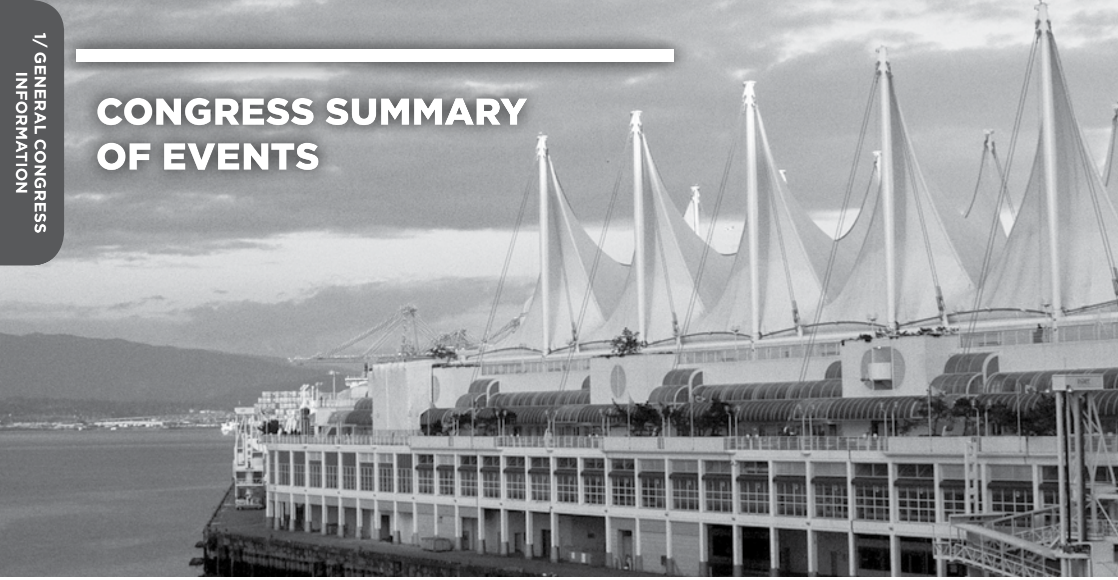
Best wishes on a successful and productive conference.

Yours truly,

Gregor Robertson

Gregor Robertson
MAYOR

☎ 604.873.7621 604.873.7685 gregor.robertson@vancouver.ca vancouver.ca
Office of the Mayor, City of Vancouver, 453 West 12th Avenue, Vancouver, British Columbia, Canada V5Y 1V4



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
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

OFFICIAL NETWORKING EVENTS

Welcome Reception

EXHIBIT HALL (HALL B),
STREET/CONVENTION LEVEL

Sunday, September 27 19:30–21:00

Congress Night ‘Hockey Night in Canada’

EAST BALLROOMS,
STREET/CONVENTION LEVEL

Tuesday, September 29 19:30–22:30

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

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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

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(ex-officio)

PAST PRESIDENT

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(2013-2015)

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Richard D. Smith
Michael Snyder
Pierre Thibault
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 ProteomeXchange 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.

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 Neanthes Arenaceodentata

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 Tinnefeld, 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-Berrocoso, 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 Proteotype

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 Patent-Derived iPSC Using SWATH-MS

HUPO 2015 TRAVEL AWARDS

BCPN Travel Award Winners

BCProteomicsNetwork

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+] 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
HPP03.04 - TMT10-TAILS Analysis of Lymphocytes to Unravel the Role of Proteolysis in B Cell Activation

Nichollas Scott, Canada
P13.01 - Characterization of the Protein Complex Landscape of Murine Tissues

Ameya Ranade, Canada
P02.14 - 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
P04.27 - Immunoaffinity-MS Platform for Antibody Screening and Native Protein Analysis in Biological Fluids

Nikunj Gevariya, Canada
P06.56 - 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
P06.35 - 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

HUPO 2015 COMMITTEES

HUPO 2015
LOCAL ORGANIZING COMMITTEE

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Victoria, Canada

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Monreal, Canada

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Yossef Av-gay
University of
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HUPO 2015 COMMITTEES

HUPO 2015
SCIENTIFIC ORGANIZING COMMITTEE

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Sydney, Australia

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Victoria, Canada

Maxey C.M. Chung
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of Singapore
Singapore, Singapore

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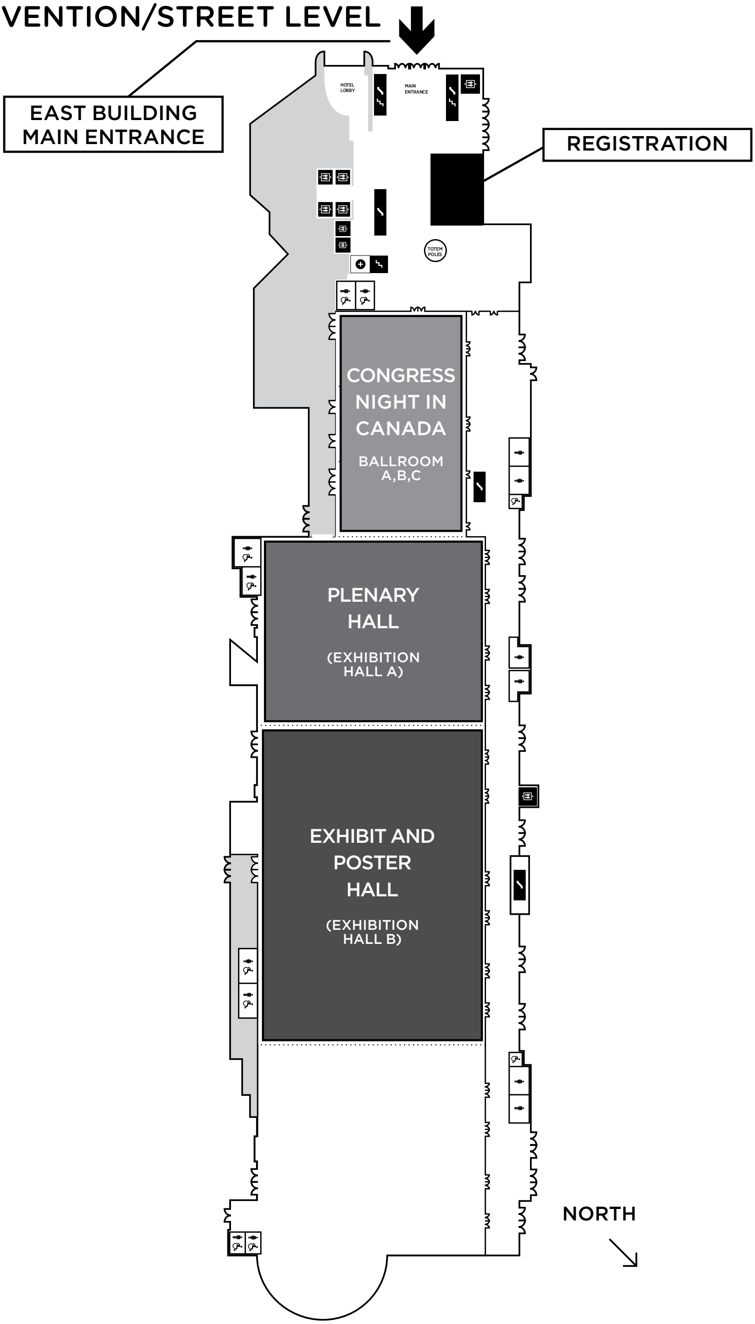
John Yates
The Scripps
Research Institute
LaJolla, USA

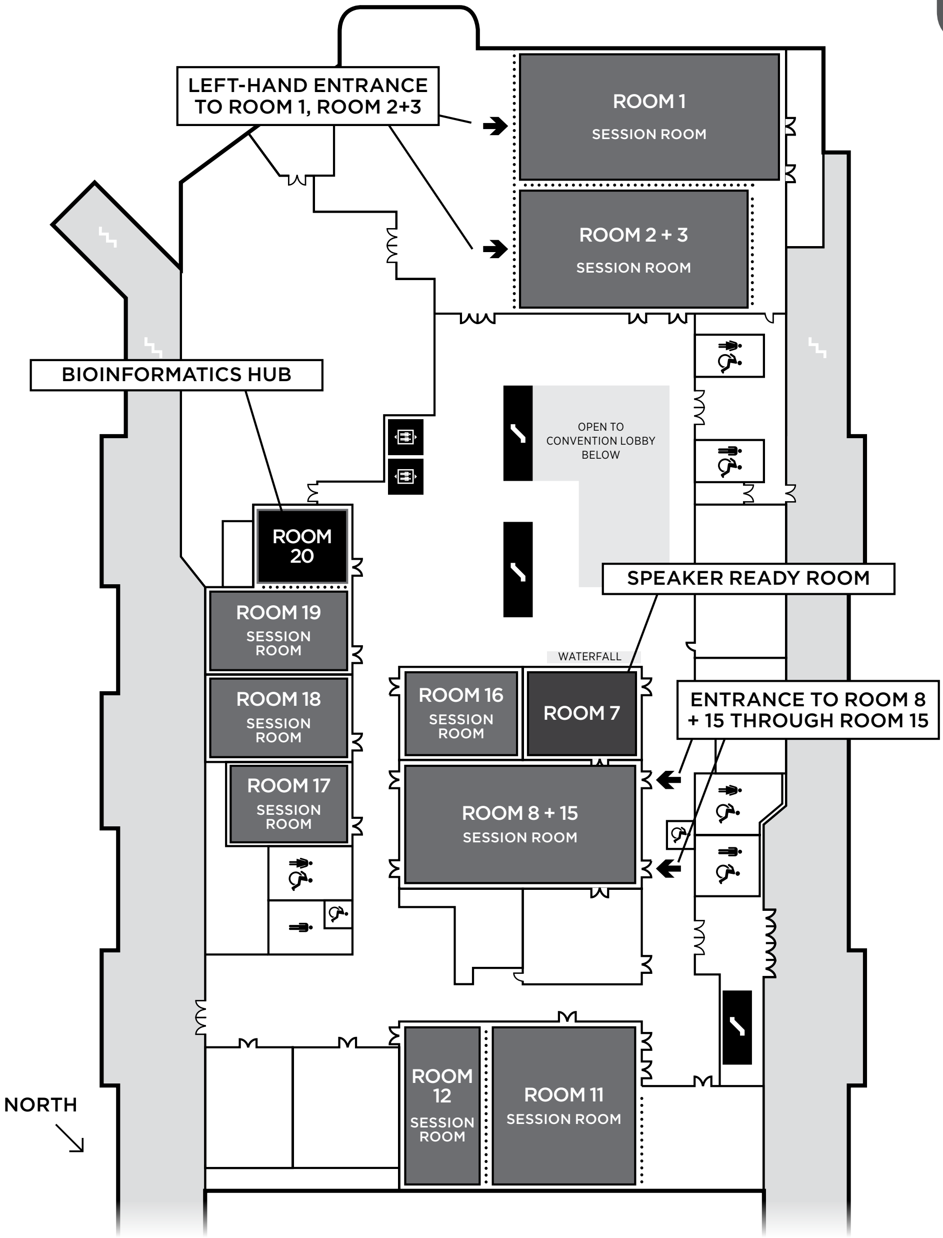
CONVENTION CENTRE, EAST BUILDING

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

LinkedIn **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.

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

Genome
BritishColumbia
Leading > Investing > Connecting

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

HUPO HUMAN PROTEOME ORGANIZATION 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 restaurants 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.

SUPPORTED BY

BRUKER

WIRELESS INTERNET

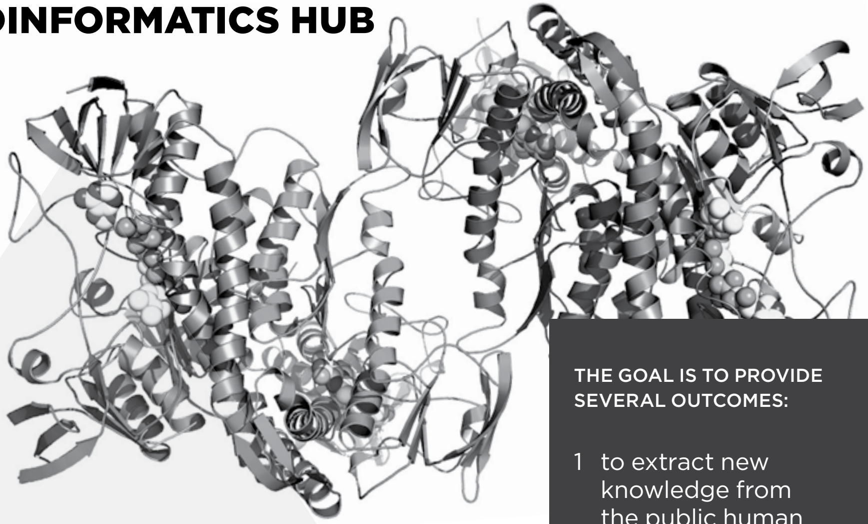
HUPO is providing free Wi-Fi throughout the Vancouver Convention Centre. To ensure a positive Wi-Fi experience for all users please do not use your own wireless Hotspot device. These additional Wi-Fi devices create significant RF interference which can interfere with all Wi-Fi networks. Please turn these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

DISCLAIMER

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.

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THE BIOINFORMATICS HUB AT HUPO 2015 IS SPONSORED BY

NIH Big Data to Knowledge (BD2K)

UVic Genome BC
PROTEOMICS CENTRE

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.

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

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

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

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

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

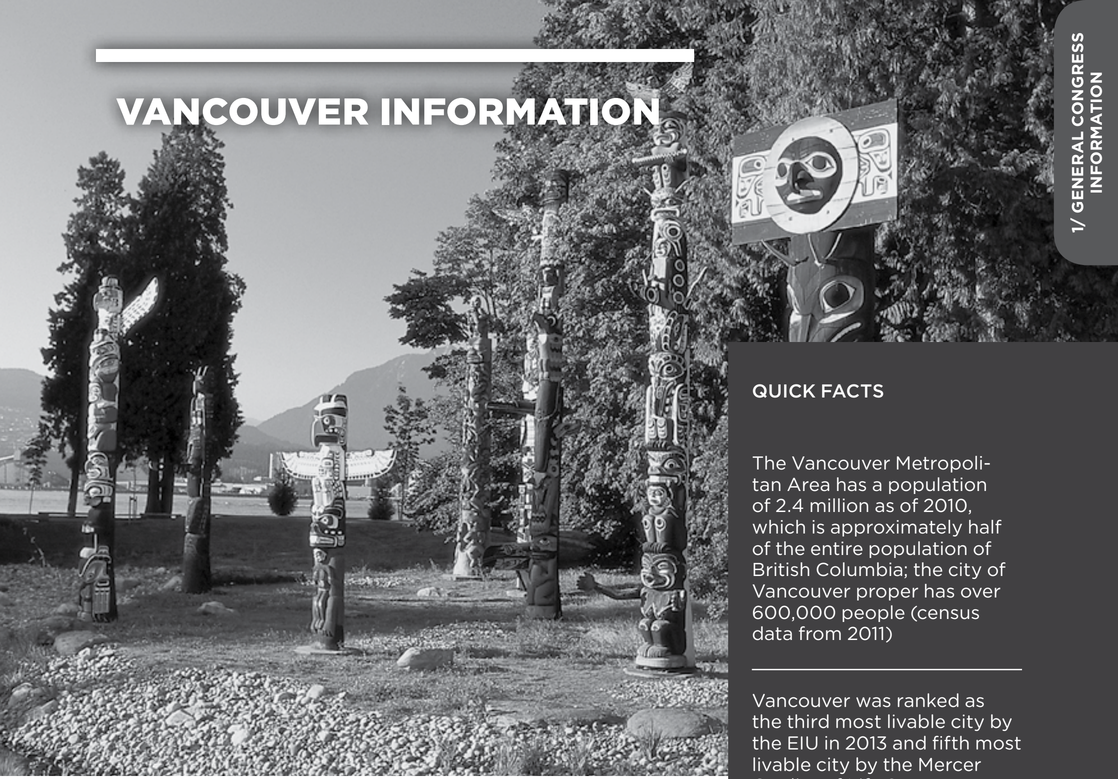
Whistler and Shannon Falls

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

VANCOUVER INFORMATION



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!

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 multicultural 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

Join the conversation!

@hupo_org

/humanproteomeorg

#HUPO2015

SEPTEMBER 27 – 30

HUPO VANCOUVER

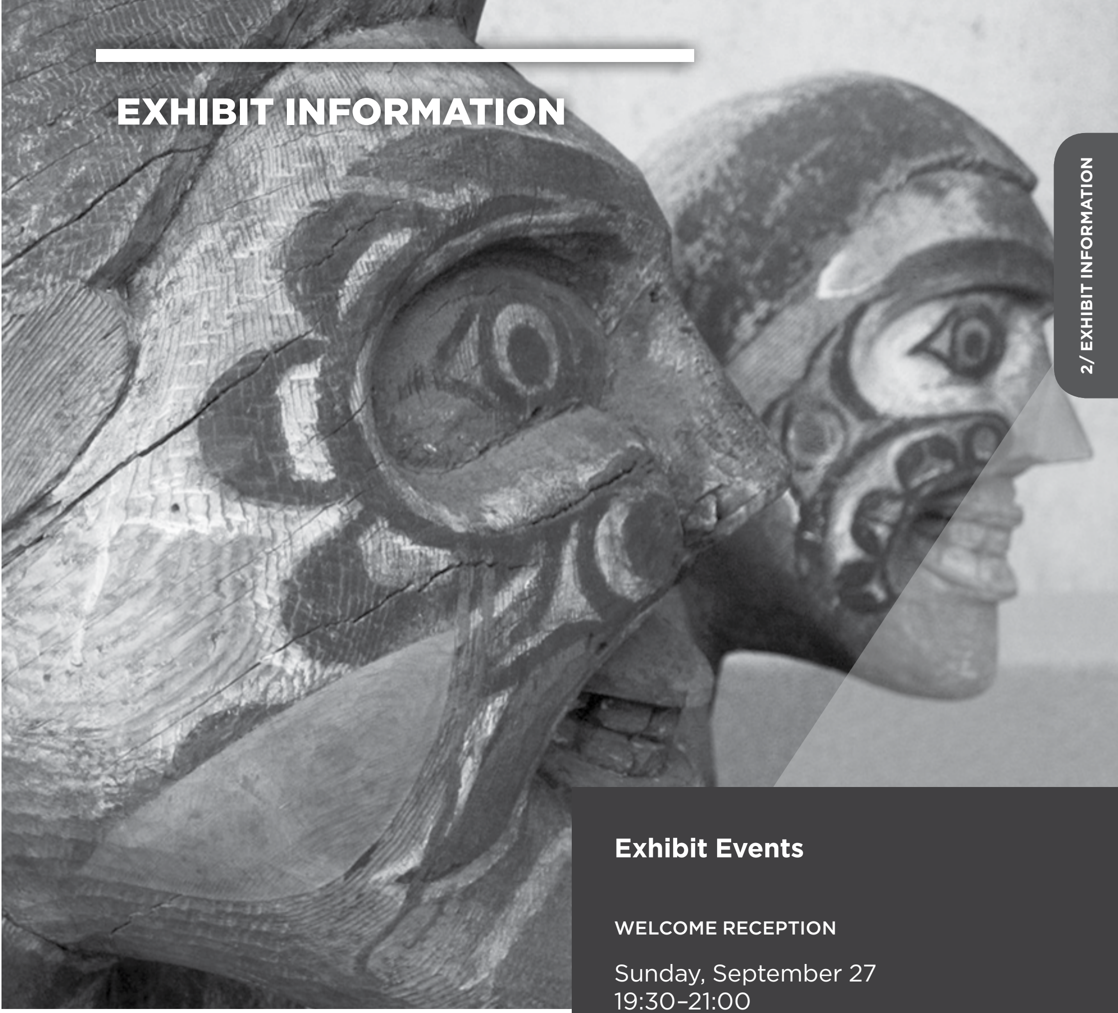
14TH HUMAN PROTEOME ORGANIZATION WORLD CONGRESS

2015

SECTION 2

EXHIBIT INFORMATION

EXHIBIT INFORMATION



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

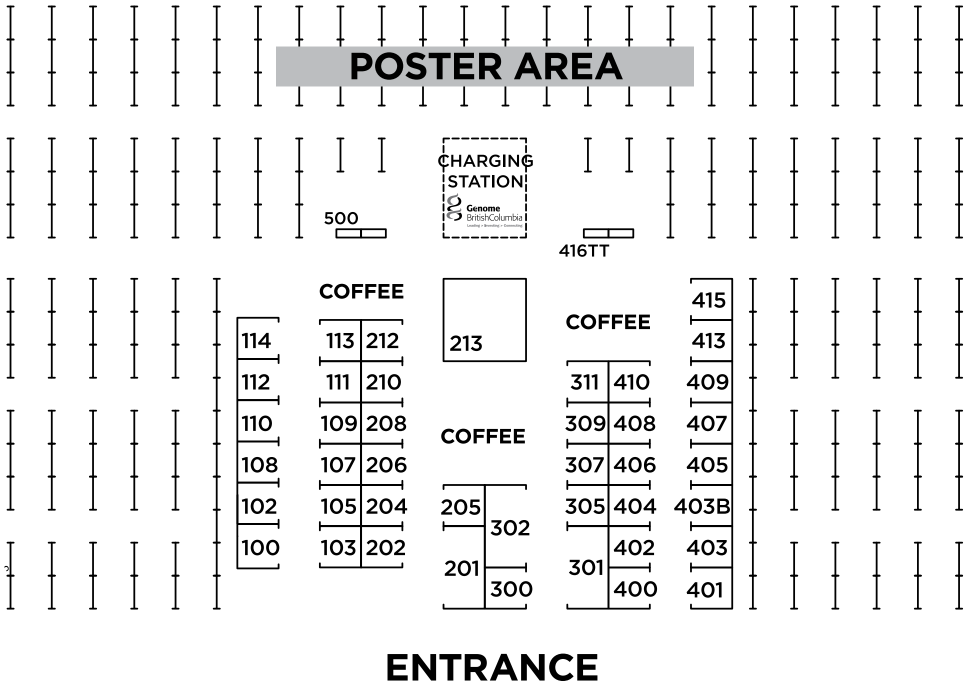


EXHIBIT INFORMATION

EXHIBITOR LISTING

ALPHABETICAL BY EXHIBITOR

COMPANY	BOOTH #
Abcam	112
Agilent Technologies	302
Atlas Antibodies	204
BC Proteomics Network	102
BIOCRATES Life Sciences AG	407
Biotech Support Group LLC	107
Bruker Daltonics	213
Cambridge Isotope Laboratories, Inc.	212
Canadian National Proteomics Network	102
Cell Signaling Technology	202
Denator	208
Elsevier	408
EMD Millipore Corporation	100
Fluidigm Corporation	406
GE Healthcare	113
Genome BC	210
Genome Canada	210
HUPO 2016, Taipei	403
HUPO 2017, Dublin	403B
HUPO, Human Proteome Organization	401
IMSC 2016	402
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Pressure BioSciences, Inc.	311
PROOF Centre of Excellence	416TT
Protein Metrics Inc.	404
ProteinSimple	415
Proteintech Group, Inc.	111
Proteome Software	305
Rapid Novor Inc	108
SCIEX	300
SENGENICS	110
Sigma-Aldrich Life Sciences	205
Silantes GmbH	409
The Metabolomics Innovation Centre	405
Thermo Scientific	301
UVic Genome BC Proteomics Centre	309
Veritomyx	410
VICI Valco Instruments	109
Wako Laboratory Chemicals	114
Waters Corporation	201

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
205	Sigma-Aldrich Life Sciences
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

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

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 multipeptide Mass Spectrometry standards for absolute quantification, called QPrEST.

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 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 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.

Cambridge Isotope Laboratories, Inc. (CIL) is the world leader in the manufacture of stable isotope-labeled (13C, D, 15N, 17O, 18O) compounds used for quantitative MS-based applications. CIL has many products to meet the needs of the proteomic community: MRM Proteomics kits, MouseExpress® 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

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

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.

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.

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.

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.

JPT Peptide Technologies, GmbH

JPT is an ISO certified provider of innovative peptide products and services focused on proteomics, developing immune therapeutics & diagnostics and enyzme profiling. JPT has a large portfolio of proprietary products such as SpikeMixTM Peptide Pools & SpikeTidesTM 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

MCP MOLECULAR & CELLULAR PROTEOMICS

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.

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optys
Our Passion Translating into Your Success

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.

BSi
Bioinformatics Solutions Inc.

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.

PBI Pressure BioSciences Inc.

Pressure BioSciences, Inc.

Pressure BioSciences, Inc. ("PBI") (OTCQB: PBIO) 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 | Centre d'
EXCELLENCE
Biomarker solutions for health care.
Biomarqueurs – Solutions en soins de santé.

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

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

EXHIBIT INFORMATION

COMPANY PROFILES

SENGENICS

Sengenics core technology is the patented Immunome™ autoantibody 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.

EXHIBIT INFORMATION

COMPANY PROFILES

UVic Genome BC Proteomics Centre

The Proteomics Centre (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.


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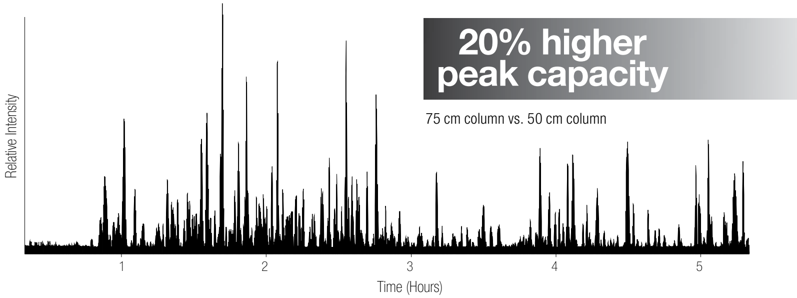
20% higher
peak capacity
75 cm column vs. 50 cm column
Relative Intensity
1
2
3
4
5
Time (Hours)

SECTION 3

PROGRAM
SUNDAY, SEPTEMBER 27

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

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, SCIEX, 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:

Genome BritishColumbia
Leading > Investing > Connecting

GenomeCanada

SPEAKER SPONSOR:

UVic Genome BC
PROTEOMICS CENTRE

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 Ledeboer, 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 **Charcterization 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

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

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

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

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

BREAKFAST WILL BE PROVIDED DURING THIS SESSION.

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

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 Cenralized 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 Steinfelder, 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, Insitute 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 & 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 Guldbrandsen, 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-Acetylglucosaminyltransfease 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 Llombart, 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, Genenetech, 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

ℹ 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 Srvastava, 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

CIL Cambridge Isotope Laboratories, Inc.
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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-Berrocoso, 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 Cerciello, 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 Immunopeptidome 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, Universite 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 Immunopeptidomes**

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, Novarts 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 Pennsylmania 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 β-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

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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 Patent-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, Saudia 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**

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 Stagljar, 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

12:15 **CS14.04: A β-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: TGFβ1 Induces Membrane Proteomce Changes in Colorectal Cancer Cells**

Harish R. Cheruku, Macquarie University, Australia

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

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

ℹ 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

ℹ 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

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

13:15 – 14:15 **SCIEX: Testimonials in OneOmics^{TM}: Next Generation Proteomics at Work**

Room 8+15

ℹ 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**

Maxey 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 NESVIZHSKII, 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: THIBAULT 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

HUPO VANCOUVER

14TH HUMAN PROTEOME ORGANIZATION WORLD CONGRESS

SEPTEMBER 27 – 30

2015

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

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 Cytokinesis**

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 Tinnefeld, 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 THIBAULT, CANADA & JUERGEN KAST, CANADA

ROOM 2+3

SESSION GENEROUSLY SUPPORTED BY

CNPN

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 µL 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 α-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

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

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 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, Universite de Montreal, 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 EDRN, 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). 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).

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 proper 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

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 Univeristy, 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. 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). 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 HPP 10: 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 HPP 12: 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.

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 HPP 13: 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**
Yetrib Hathout, Children’s National Medical Center, USA

08:40 **HPP13.05: Discussion**

13:15 - 14:15 HPP 14: 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 HPP 15: 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 HPP 16: 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 HPP 17: 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 protegenomic approaches to improving the health state of honeybees (Leonard Foster), HipA-mediated mechanisms in E.coli (Maja Semanjscki), 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 HPP 18b: 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 stochiometric 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 HPP 19: 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: Anitobody 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

INDUSTRY SESSIONS

AT A GLANCE

	MONDAY, SEPTEMBER 28 13:15–14:15	TUESDAY, SEPTEMBER 29 13:15–14:15
Room 1	**Thermo Scientific** From Markers to Assays: Accelerating Translational Proteomics	**Thermo Scientific** Pushing the Boundaries of Comprehensive Proteome Profiling
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^{TM}: Next Generation Proteomics at Work
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/

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

INDUSTRY SESSIONS

MONDAY, SEPTEMBER 28

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

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

Space is limited for Industry Sessions.
To register and for further information please visit: hupo2015.com/program/industry-seminars/

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

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

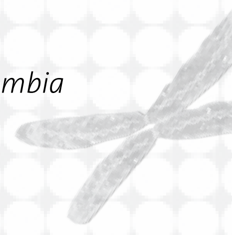
INDUSTRY SESSIONS

TUESDAY, SEPTEMBER 29

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



SECTION 9

POSTERS

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
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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-ISCIII, 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 Univeristy, 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

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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-Diging: 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

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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 µQLISA 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
Annika 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,CBLS, 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 Aquisition 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 Ahrné, 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

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Jingxi Pan, University of Victoria, Canada

P05.02: Metaproteomic Analysis, next Generation Environmental Assessment
Susana Cristobal, Linköping 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

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David Cantor, Macquarie University, Australia

P06.02: Quantitative Mass Spectrometry Reveals Markers for Colorectal Tumors
Anuli C. Uzozie, University of Zurich, Switzerland

P06.03: Multiplexed Immunoassays for Cytokine Profiling in 3D-In Vitro Tumor-Stroma Cell Culture Models
Dieter Stoll, University of Applied Sciences Albstadt-Sigmaringen, Germany

P06.04: Data Independent Quantitation of the Rab GTPase Family
Franziska C. Hundt, Ruhr-University Bochum, Germany

P06.05: Proteomic Analysis of Circulating Extracellular Vesicle for Diagnostic Biomarker of Breast Cancer
Pyong-Gon Moon, Kyungpook National University, Korea

P06.06: Development of a Risk Stratification Test to Discern Aggressive and Non-Aggressive Prostate Cancer
Sandra Goetze, Swiss Federal Institute of Technology Zurich (ETH), Switzerland

P06.07: Large-Scale Analysis of Melanoma Tissue Samples
Maria E. Yakovleva, Lund University, Sweden

P06.08: Quantitation and Evaluation of Candidate Biomarkers of Pancreatic Cancer in Plasma Using MRM Method
Weimin Zheng, Department of Chemistry, Fudan University, China

P06.09: Functional Characterization of a Novel NF1-Related Protein TCTP by the Interactome Analysis
Daiki Kobayashi, Kumamoto University, Japan

P06.10: Hypoxia-Induced Alternative Splicing Proteomics in Cancer Cell Lines
Pang-Hung Hsu, National Taiwan Ocean University, Taiwan

P06.11: Discovery of Pulmonary Disorder Biomarkers by In-Depth Proteomic Analysis of Pleural Effusions
Pei-Jun Liu, Chang Gung University, Taiwan

P06.12: A Proteomic Investigation for Detection of Early Stage CRC Biosignatures
Mark S. Baker, Macquarie University, Australia

P06.13: Cell Phase Specific Proteomic Profiling of Newly Synthesized Proteins Using SILAC-TMT Quantification
Eva Papachristou, Cancer Reasearch UK Cambridge Institute,University of Cambridge, UK

P06.14: Immuno-MALDI for Quantifying Akt1 and Akt2 Phosphorylation in Colorectal Cancer
Robert Popp, University of Victoria, Canada

P06.15: SWATH-MS Profiling of NSCLC Cell Lines: Defining Mechanisms of Erlotinib Resistance
Sarah A. Hayes, Bill Walsh Translational Cancer Research Laboratory, Australia

P06.16: Optimizing MS Based Methods to Characterize MHC-I Peptidome in Response to Cellular Stimulation
Qui Phung, Genentech, Inc., USA

P06.17: Discovery of Biomarkers for Oral Cancer by Proteomic Profiling of Tumor Interstitial Fluids
Chia-Wei Hsu, Chang Gung University, Taiwan

P06.18: Molecular Consequences of PC1/3 Inhibition in Macrophages and Application in Immunotherapy
Marie Duhamel, Laboratoire PRISM, Inserm U-1192, France

P06.19: Acidosis-Induced Proteome Pattern of AT-1 Prostate Carcinoma Cells
Christian Ihling, Martin Luther University Halle-Wittenberg, Germany

P06.20: Proteomic Analysis of Tumor-Associated Macrophages in an In Vivo Tumor Microenvironment
Evelyne Maes, University of Antwerp, Belgium

P06.21: Identication of Tyrosine-Phosphorylated Proteins Upregulated during EMT Induced with TGF-B
Akiko Okayama, Yokohama City University, Japan

P06.22: Comprehensive Transcriptomic and Proteomic Analysis of Retinoblastoma
Ravikanth Danda, Sankara Nethralaya, India

P06.23: Proteomic Analysis of the Resection Margin at Different Distances of a Gastric Cancer
Gilberto B. Domont, Federal University of Rio de Janeiro, Brazil

P06.24: Tracing Growth Factor Driven Resistance to EGFR Inhibition by Chemical- and Phosphoproteomics
Heiner Koch, Technische Universitaet Muenchen, Germany

P06.25: Proteomic Analysis of the Transcriptional Program Induced by TWIST in Human Fibroblasts
Ignacio Casal, Centro de Investigaciones Biológicas, Spain

P06.26: SWATH Quantitation Using Ion Libraries from Multiple Cancer Cell-Types Identifies Drug Resistance
Christoph Krisp, Australian Proteome Analysis Facility, Australia

P06.27: Verification of Serological Biomarkers for Lung Adenocarcinoma by Targeted Mass Spectrometry
Pao-Chi Liao, National Cheng Kung University College of Medicine, Taiwan

P06.28: YBX1 Induces Oncogenicity via Release of Angiogenic Factors into the Tumour Microenvironment
David W. Greening, La Trobe Institute for Molecular Science, Australia

P06.29: Detection of Aggressive Prostate Cancer Subforms by LC-MS and MALDI Imaging
Corinna Henkel, Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany

P06.30: In-Depth Proteome Characterization of Intraductal Papillary Mucinous Neoplasm Pancreatic Cysts
Misol Do, Seoul National University College of Medicine, Korea

P06.31: Epithelial to Mesenchymal Transition Induced by SNAI1 Operates throughout Epigenetic Mechanisms
Camila Palma, Ribeirao Preto Medical School - University of Sao Paulo, Brazil

P06.32: Large Scale Systematic Proteomic Quantification from Non-Metastasis to Metastasis Colorectal Cancer
Hong Jin, Fudan University, China

P06.33: HSP60-Silencing Disrupts Mitochondrial Proteostasis and Promotes Tumor Progression
Haiping Tang, Tsinghua University, China

P06.34: Protein-Chain Quantitation by Targeted MS for Exploration of the Cancer-Thrombosis Connection
Yassene Mohammed, University of Victoria, Canada

P06.35: Characterization of the Interactome of RSK Isoforms to Decipher Their Roles in Cancer Cells
Antoine Méant, Institute for Research in Immunology and Cancer (IRIC), University of Montreal, Canada

P06.36: Verification of Biomarkers in Uterine Aspirates by LC-PRM to Improve Diagnosis in Endometrial Cancer
Elena Martínez, Vall D'Hebrón Research Institute, Spain

P06.37: TP53-Mediated Regulation of Exosome Proteins and microRNA
Xiaohang Zhao, Cancer Institute & Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, China

P06.38: Quantification of Mutant SPOP Proteins in Prostate Cancer Using SRM-MS
David Camp, Pacific Northwest National Laboratory, USA

P06.39: SRM Verification of Circulating Ovarian Cancer Biomarkers at Early Detection Research Network (EDRN)
Karin Rodland, Pacific Northwest National Laboratory, USA

P06.40: Elucidating Metastatic Changes during Ovarian Cancer Progression by LCM Proteomics
Fabian Coscia, Max Planck Institute of Biochemistry, Germany

P06.41: Exosome Omics Study for Molecular Backgrounds of Drug Response towards Personalized Medicine
Kosuke Hirota, National Cancer Center Research Institute, Japan

P06.42: Drug-Centric Proteomics for Molecular Backgrounds of Drug Response towards Personalized Medicine
Zhiwei Qiao, National Cancer Center Research Institute, Japan

P06.43: Discover the Interactome of the Potent Oral Cancer Oncoproteins by Quantitative Proteomics Analysis
Lang-Ming Chi, Chang Gung Medical Foundation, Taiwan

P06.44: A Multiplexed Cytokeratin MRM Panel for the Classification of Lung Cancer Patient Pleural Effusions
Anna Perzanowska, Institute of Biophysics and Biochemistry PAS, Poland

P06.45: Quantitative Analysis of AKT/mTOR Pathway Using Immunoprecipitation and Targeted Mass Spectrometry
Bhavin Patel, Thermo Fisher Scientific, USA

P06.46: Single-Shot Proteomics Profiling and Quantification of Human Prostate Cancer Cells
Wei Yang, Cedars-Sinai Medical Center, USA

P06.47: Proteomic Profile of EGF-Stimulated Ovarian Cancer Cells during Epithelial to Mesenchymal Transition
Mariana L. Grassi, Ribeirao Preto Medical School - University of Sao Paulo, Brazil

P06.48: Proteomic Identification of Malignant Pleural Mesothelioma-Related Molecules
Kiyoshi Yanagisawa, Nagoya University Graduate School of Medicine, Japan

P06.49: Interactome-Wide Analysis Reveals the Actin-Regulating Function of TNFAIP2 in NPC Cells
Hao-Ping Liu, National Chung Hsing University, Taiwan

P06.50: Profiling of Autoantibodies for the Stratification of Prostate Cancer
Elisa Pin, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

P06.51: Secretome of Naïve Senescent Mesenchymal Stromal Cell Promotes Senescence in ARH-77 Myeloma Cells
Servet Ozcan, Erciyes University, Turkey

P06.52: New Workflows Combine Albumin Depletion and On-Bead Digestion, for Quantitative Serum Proteomics
Matthew Kuruc, Biotech Support Group LLC, USA

P06.53: Statistical and Pathway Analysis of Protein Data
Christine Miller, Agilent Technologies, USA

P06.54: Ubiquitination Profiling Identifies Sensitivity Factors for IAP Antagonist Treatment
Anita Izrael-Tomasevic, Genentech, Inc., USA

P06.55: A Novel DIA Workflow for More Sensitive and Accurate SILAC Quantitation for Protein Kinome
Scott Peterman, Thermo Scientific, USA

P06.56: Omega-3 Fatty Acid-Enriched Diet Favors a Reduction of Murine TRAMP-C2 Prostate Tumor Growth Compared to Omega-6 Fatty Acid-Enriched Diet
Nikunj R. Gevariya, Cancer Research Center, Laval University, Canada

P06.57: Proteomics Analysis of Cisplatin Resistance in Ovarian Cancer Cells
Yuling Chen, Tsinghua University, China

P06.58: SWATH-MS and Proseek® Oncology Proteomic Biosignatures of Dukes' Staged Colorectal Cancer
Mark S. Baker, Macquarie University, Australia

P06.59: Verification of Biological Insights Gained from Global Proteomic Analysis Using SWATH and SRM
Stefani Thomas, Johns Hopkins University, USA

P06.60: Discovery of Metastasis-Related Biomarkers in Lung Cancer by Quantitative Tissue Proteomics
Chia-Jung Yu, Chang Gung University, Taiwan

P06.61: NetGestalt CPTAC Portal: Empowering Biologists with Cancer Proteogenomic Data
Bing Zhang, Vanderbilt University Medical Center, USA

P06.62: Quantitative Proteomics of Isogenic BAP1-Deficient Cells Lines for Targeted Therapy Discovery
Jenna Kenyani, Institute of Translational Medicine, UK

P06.63: Studying of Malignant Ascites as a Unique Tumor Microenvironment
Victoria Shender, Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry, RAS, Russian Federation

P06.64: Insight on Colorectal Carcinoma Infiltration by Studying Perilesional Extracellular Matrix
Cinzia Magagnotti, Ospedale San Raffaele, Italy

P06.65: Quambalarine B Induces Metabolic and Proteomic Rearrangement in Leukemia Cells
Petr Novak, Charles University, Czech Republic

P06.66: Proteomic/Transcriptomic Characterisation of a Prostate Cancer Cell Line Model of Spontaneous EMT
David J. Boocock, Nottingham Trent University, UK

P06.67: Proteomic Analysis of Serum Biomarkers for Gastric Cancer
Lylia Drici, University of Southern Denmark, Denmark

P06.68: Development of Assays for Measuring CUZD1, a Pancreas-Specific Protein, in Biological Fluids
Sofia Farkona, University of Toronto, Canada

P06.69: Stroma COL6A3 Is a Prognosis Marker of Colorectal Carcinoma Revealed by Quantitative Proteomics
Feng Liu, Institutes of Biomedical Sciences, Fudan University, China

P06.70: Development of a Global Phosphotyrosine Proteomic Method for Analysis of Cancer Cell Lines
Yuichi Abe, National Institute of Biomedical Innovation, Health and Nutrition, Japan

P06.71: Proteomic Study Revealing Roles of MET and Caveolins in Exosome-Induced Hepatoma Motility
Terence C. W. Poon, University of Macau, Macau

P06.72: Novel Protein Biomarkers for Subtype Stratification and Immunotherapy in Pancreatic Cancer
Laura Kuhlmann, DKFZ, Germany

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Mohammad Pirmoradian, Karolinska Institutet, Sweden

P07.02: Overcoming the Challenges in Data Independent Acquisition (DIA) via Orbitrap Technology
Yue Xuan, Thermo Fisher Scientfic, Germany

P07.03: Quantitative Analysis of the Soluble Proteome of Airway Epithelial Cells in COPD
Tina Heyder, Karolinska Institutet/University Hospital, Sweden

P07.04: MRM-Based Proteins Diagnostic of Chronic Obstructive Pulmonary Disease Exacerbations
Zsuzsanna Hollander, PROOF Centre of Excellence, Canada

P07.05: Evaluation of New Biomarkers of Resistance to Trastuzumab in the Treatment of HER2+ Breast Cancer
Barbara Cardinali, IRCCS AOU San Martino - IST National Institute for Cancer Research, Italy

P07.06: Intelligent Workflows for Proteomics Data Analysis
Arzu Tugce Guler, Leiden University Medical Center, Netherlands

P07.07: Respiratory Disease Confirmation via Proteome Analysis of Exhaled Breath Condensate
Eugene N. Nikolaev, Energy Problems Of Chemical Physics Russian Acad. Sc., Russian Federation

P07.08: Discovery of Autoantibody Biomarkers for Oral Cancer Detection Using Protein-Array Analyses
Ya Ting Chang, Molecular Medicine Research Center, Taiwan

P07.09: Tear Proteins of Dry Eye Patients Respond to Environmental Stress
Roger Beuerman, Singapore Eye Research Institute, Singapore

P07.10: Systems-Wide Proteome Analysis of Hepatocellular Carcinoma Tissues by Targeted Proteomic Platform
Dohyun Han, Seoul National University Hospital, Korea

P07.11: Development of Meta-Markers for Recurrence Lung Cancer Using Multiple Reaction Monitoring
Yong-In Kim, BK21 Plus and Research Institute for Veterinary Science, College of Veterinary Medicine, Seoul National University, Korea

P07.12: Affinity Proteomics for the Identification of Biomarkers of Drug-Induced Liver Injury in Humans
Maria Mikus, KTH - Royal Institute of Technology, Sweden

P07.13: A Biomarker Panel to Rule-Out CT-Scan Lesions in Mild Traumatic Brain Injury
Linnea Lagerstedt, University of Geneva, Switzerland

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Zuzana Bilkova, University of Pardubice, Czech Republic

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