



HUMAN PROTEOME PROJECT

HPP GUIDE TO MADRID AND SEGOVIA

The Human Proteome Project (HPP) has grown to become a strong focus of HUPO activities. Most existing HUPO initiatives have found a focus within the HPP and a wide range of new initiatives and projects have also been started by the HPP. All activities take place in the annual world congress facility, Centro de Convenciones Norte - IFEMA – Feria de Madrid, unless otherwise noted.

Please note that all HPP activities are represented in this guide, but those interested in C-HPP specifics may wish to also the C-HPP Guide which is available at <http://c-hpp.org> (navigate to Documents/Public).

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HPP INVESTIGATORS MEETING • SUNDAY, OCTOBER 5, 10:00 – 17:00

Location: Room D

AGENDA

- 10:00-10:10 **Overview of Progress, Metrics, and Publications from the HPP**
Gil Omenn, *Chair, HPP, Univ. of Michigan, Ann Arbor, MI, US*
- 10:20-10:40 **B/D-HPP Highlights, Priority Protein Lists by Disease, Clinician- Scientist Initiative, Workshops Plan + Discussion**
 - Ruedi Aebersold, *ETH Zurich, Switzerland*
 - Jennifer Van Eyk, *Cedars-Sinai Health System, Los Angeles, CA, US*
- 10:40-11:00 **C-HPP Highlights, Busan and Bangkok Workshops, Congress Workshops + Discussion**
 - Young-Ki Paik, *Chair, C-HPP Initiative, Yonsei Univ., Seoul, Korea*
 - William S. Hancock, *Co-Chair, Northeastern Univ., Boston, MA, US*
- 11:00-11:55 **Update of HPP Metrics: neXtProt (9/14), PeptideAtlas (8/1/14) & GPMdb - Moderator: Gil Omenn**
Bioinformatics Discussions and Standardized Re-Analyses of Major Datasets of Four Major Publications in 2014: Kim et al (Pandey lab, PXD000561); Wilhelm et al (Kuster lab, PXD000865); Guo et al (Mirzaei lab with various proteolytic enzymes); and TCGA datasets
Comments:
 - Amos Bairoch & Lydie Lane, *SIB, Geneva, Switzerland*
 - Eric Deutsch, *Inst. Systems Biology, Seattle, WA, US*
 - Akhilesh Pandey, *Johns Hopkins & Bangalore*; Bernhard Kuster, *TUM, Munich*; Henry Rodriguez, *Bethesda*
- 12:00-12:50 **Discussion over Working Lunch about Inter-Relationships across HPP Components and Bioinformatics Approaches** - Moderator: William S. Hancock (lunch provided by RSVP only)
- 13:00-13:30 **Antibody and MS Resource Pillars**
Cross-Validation with Ab and MS Approaches Including MRM Based Quantitation for HPP
 - Emma Lundberg, *SciLifeLab, Stockholm, Sweden*ProteomeAnalyzer Project
 - Bruno Domon, *Centre Sante' Clinical Proteomics Center, Luxembourg*
- 13:30-14:00 **SSAB Panel, Overview, Strategic Comments from SSAB Members**
Moderator: Mike Snyder, *Stanford Univ., Stanford, CA, US*
 - Cathy Costello, *Boston Univ, Boston, MA, US*; Matthias Mann, *Max Planck, Munich, Germany*; Kate Rosenbloom, *Univ of California Santa Cruz/ENCODE, US*
- 14:00-16:00 **Town Hall Meeting Open Forum – on B/D- and C-HPP Collaboration**
Co-Chairs: Ruedi Aebersold and Young-Ki Paik
Part 1. Integrated Data Management
“Priority Proteins”/“Popular Proteins”, Including PTMs, Splice Isoforms, SNPs/SAAPs, for Specific Diseases; Use of SRM Peptides, Spectral Libraries, and SRMAtlas
 - Jennifer Van Eyk, Ruedi Aebersold, Eric Deutsch and B/D TeamsProteomeExchange Experience: PDX Identifiers and Release of Data on Acceptance, Uploading Large Data Sets
 - Juan Vizcaino, *EBI, Hinxton, UK*Proteogenomics/RNA Seq, Integrated ‘Omics analyses
 - Gyorgy Marko-Varga, Jennifer Harlow, Kate Rosenbloom, Michael Snyder (ENCODE)**Part 2. Biological Impact of Missing Proteins on C-HPP and B/D-HPP Research**
Updates from neXtProt on the missing and orphan proteins
 - Lydie Lane and Amos Bairoch, *SIB, Switzerland*A Strategy for Bioinformaticians to Take a Deep Dive on Chr-Specific Missing Protein Lists (as discussed in Bangkok C-HPP workshop)
 - William S. Hancock and Gyorgy Marko-Varga, *Co-Chairs, C-HPP Consortium*Timing of JPR Special Issue and Standardization of Data Bases for Publication Metrics: What is the Best Theme and Date (middle of 2015) for this Special Issue?
 - Bill Hancock and Young-Ki Paik, *C-HPP Consortium***Part 3. Opportunities to Explore Collaborations Within and Between B/D-HPP and C- HPP**
 - Young-Ki Paik and Ruedi Aebersold, *entire C-HPP & B/D-HPP Groups*
- 16:00-17:00 **Meeting of SSAB with HPP-EC for Feedback:** Mike Snyder and SSAB Group

HPP EARLY MORNING SESSION OVERVIEW

All congress attendees are invited to participate in the early morning HPP sessions. These lively, smaller sessions are an invaluable opportunity to connect with colleagues and contribute to the HPP.

Refer to the following pages for detailed description of the initiative sessions Monday, Tuesday and Wednesday mornings 8:00 - 9:20 am. For details on the Wednesday, October 8 HPP Parallel Session, please refer to the main congress program.

All rooms listed below are in the main congress center.

Overview of HPP Early Morning Sessions

Open to ALL Congress Attendees

MONDAY, OCTOBER 6 8:00 – 9:20 am	TUESDAY, OCTOBER 7 8:00 – 9:20 am	WEDNESDAY, OCTOBER 8 8:00 – 9:20 am
HPPP (Plasma) <i>Room B</i>	Diabetes <i>Room B</i>	Respiratory Diseases <i>Room B</i>
C-HPP, Part I: New Technology <i>Room C</i>	C-HPP, Part II: Poster Session <i>Inside Poster Hall</i>	C-HPP, Part III: PIC <i>Room C</i>
Cancers I <i>Room D</i>	PSI / ProteomeXchange <i>Room C</i>	Cardiovascular <i>Room D</i>
iMOP <i>Room E</i>	Antibody Proteomics <i>Room D</i>	Computational Mass Spec. <i>Room E</i>
Liver <i>Room F</i>	Cancers II <i>Room E</i>	Mitochondria <i>Room G</i>
Extreme Conditions <i>Room G</i>	Glycoproteomics <i>Room F</i>	Protein Aggregation Diseases <i>Room H</i>
Infectious Diseases <i>Room H</i>	Brain Project <i>Room G</i>	PediOme <i>Room I</i>
EyeOme <i>Room I</i>	Stem Cells <i>Room H</i>	
	Biobanking & Pre-Analytical Sample Assessment <i>Room I</i>	

Please see the following pages for details on each workshop.

HPP EARLY MORNING SESSIONS • MONDAY, OCTOBER 6, 2014, 08:00 – 9:20

**Human Plasma Proteome Project (HPPP)
Plasma Proteomics Underpins a Translational HPP**

Organizers: Mark Baker, Martin Kussman, Eric Deutsch, and Simon Fredericksson
Room B

- 8:00 - 8:12 am Loïc Dayon: A Comprehensive and Scalable Automated Workflow for Human Plasma Proteomics and Its Application to the DiOGenes Clinical Study
- 8:15 - 8:27 am Simon Fredriksson: Multiplexed and Sensitive Immunoassays by the Highly Specific Proximity Extension Assay
- 8:30 - 8:42 am Eric Deutsch: The PeptideAtlas Plasma Proteome Build
- 8:45 - 8:50 am Jochen Schwenk: Affinity Proteomics in Plasma from Cancer Biobanks
- 8:50 - 8:55 am Sadi Mahboob: Targeted Proseek Multiplexed Immunoassays of Candidate Plasma Biomarkers for Dukes' Stage A-D CRC
- 8:55 - 9:00 am Tatjana Sajic: An Inter-Cancer Study of Human Plasma Proteins by glycoSWATH Mass Spectrometry
- 9:00 - 9:20 am Panel: Baker, Aebersold, Omenn, Kussmann, Deutsch, Fredriksson

C-HPP, Part I: New Technology

Organizer: Bill Hancock
Room C

The following topics will be discussed in the New Technology C-HPP session.

- SRM measurement of missing proteins
- RNA analysis, including predicting when transcript forms protein
- Integration of RNA-Seq and proteomics
- Approaches to ASV and SNV characterization such as down top MS, adoption of protein chemistry methods
- Identification of protein families and sharing of specific data across chromosome families

Cancers I

Organizers: Hui Zhang, Christopher Kinsinger and Edouard Nice
Room D

- 8:00 - 8:10 am Hui Zhang: Overview of the Ca-B/D HPP
- 8:10 - 8:25 am Ruedi Aebersold: Quantifying Cancer Related Proteins via Targeting MS Assay
- 8:25 - 8:40 am Christopher Kinsinger: The CPTAC Initiative
- 8:40 - 8:55 am Robert Moritz: MRM
- 8:55 - 9:10 am Edouard Nice: Towards the Human Proteome Analysis of Alternate Clinical Samples
- 9:10 - 9:20 am Open Discussion

iMOP

Organizers: Emøke Bendixen, Sabine Schrimpf
Room E

- 8:00 - 8:05 am Emøke Bendixen: Introduction
- 8:05 - 8:25 am Erik Bongcam-Rudloff: The ALLBIO Project, Beyond Human Centric Bioinformatics Resources
- 8.25 - 8:45 am Fabrize Bertil: Deciphering New Anti-Obesity Mechanisms Using Non-Sequenced Species
- 8.45 - 9:10 am Dorothea Rutishauser: Levels of Chemosensory and Odorant-Binding Proteins from Caterpillar Saliva are Affected by Host Plant and Immune Challenge
- 9.10 - 9:20 am Open discussion

Human Liver B/D Initiative

Organizers: Pumin Zhang and Fernando J. Corrales
Room F

The Human Liver Proteome Project (HLPP) was launched in 2002, aiming to establish a biological atlas of the human liver, uncover the proteomic basis of liver development, physiology and pathology, and develop diagnostics and therapeutics for liver diseases. It is a large-scale international collaborative initiative of the Human Proteome Project (HPP). In the past decade, under the efforts of HLPP international consortium, HUPO has set up standard operating procedures, optimized the strategies for proteomic analysis and investigated the proteomes of liver tissues, healthy and diseased. More specifically, in 2010, Human Liver 1.0 was published, in which 6788 gene products have been identified, whilst in 2013, proteome of liver cellular organelles was profiled and totally 12,168 gene products in human liver were identified. The next goals will be, first, to profile the four major cell types in the liver to produce Liver Proteome 3.0 that will include around 13,000 proteins in total; second, to investigate post-translational modifications of liver proteins, and finally, focusing on the Biology/Disease (B/D)-driven Liver Proteome Project and looking for biomarkers for liver disease.

This session will feature talks from the following speakers:

- Opening Remarks: **Pumin Zhang** (Baylor College of Medicine, USA)
- Reference Material-Based Liver Proteome Quantitation: **J Eugene Lee** (Korea Research Institute of Standards and Science, Korea)
- Proteomic Analysis of Human Urine Exosomes and Hepatoblastoma Tissue Samples by Label-Free nLC MS/MS: **Felix Elortza** (CIC bioGUNE)
- Deciphering Essential Genes by Comparative Analysis Transcriptoproteome of Liver Tissue and HepG2 Cell Line: **Andrey Lisitsa** (Institute of Biomedical Chemistry, Russia)
- From Protein Lists to the Pathogenesis of Chronic Liver Disorders. Role of One Carbon Metabolism: **Fernando J Corrales** (CIMA, University of Navarra, Spain)
- Proteomics on Post-Translation Modifications of Proteins: **Ping Xu** (Beijing Proteome Research Center, China)
- **Laura Beretta** (MD Anderson Cancer Center, USA)
- **Tommy Nilsson** (McGill University, Canada)
- **Pengyuan Yang** (Fudan University, China)

Extreme Conditions

Organizer: Evgeny Nikolaev and Irina Larina
Room G

- 8:00 - 8:05 am Evgeny Nikolaev: Introduction
- 8:05 - 8:20 am Irina Larina: Adaptation of Human Organism to Long Space Flight (Institute of Biomedical Problems, Moscow, Russia)
- 8:20 - 8:30 am Saik Olga: System for Automated Literature Mining and Protein Interactome Networks Reconstruction (Institute of Cytology and Genetics, Novosibirsk)
- 8:30 - 8:40 am Igor Popov: Technical Aspects of Proteomic Assays of People Under Extreme Conditions (Talroze Institute for Energy problems of Chemical Physics, Moscow Institute of Physics and Technology, Dolgoprudnyj, Russia)
- 8:40 - 8:50 am Alexey Kononikhin: Proteomics of Exhaled Breath Condensate of People in Extreme Conditions (Talroze Institute for Energy problems of Chemical Physics, Moscow Institute of Physics and Technology, Dolgoprudnyj, Russia)
- 8:50 - 9:00 am Ludmila Pastushkova: Cardiovascular Proteins in the Urine of Healthy Volunteers During the "Dry" Immersion; (Institute of Biomedical Problems, Moscow, Russia)
- 9:00 - 9:10 am Andrew Chambers: Plasma and Urine MRM Assay Development for the Cosmonaut Samples (UVic-Genome BC Proteomics Centre, Victoria, Canada)
- 9:10 - 9:20 am Bruno Domon, Nina Khristenko, Irina Larina, Eugene Nikolaev: Systematic Analysis of Proteins in Urine Samples; Application to the Mars-500 Program; (Luxembourg Clinical Proteomics, (Institute of Biomedical Problems, Moscow, Russia, Institute for Energy problems of Chemical Physics, Moscow, Russia)

Infectious Diseases (HID)

Organizers: Ileana Cristea and Concha Gil

Room H

Infectious diseases are disorders caused by (micro) organisms (viruses, bacteria, fungi and parasites). These have the potential to rapidly become global epidemics and pandemics, and are a leading cause of human disease and death worldwide, 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 and therapeutic agents are required to reduce the mortality of these infectious diseases.

8:00 - 8:05 am HID-HPP Initiative Introduction

8:05 - 8:40 am Round Table Discussion

Panelists: Ileana Cristea, Concha Gil, Manuel Fuentes, Sanjeeva Srivastava, Rafa Cantón, Jesús Fortún, Catherine Costello, Christopher Overall, Frank Schmidt, Joshua LaBaer, Peter Nilsson

Key discussion points:

A. How to organize a community of scientists working in Infectious disease proteomics?

B. Potential scientific goals for this initiative

1. Selection of human proteins related to infectious diseases and immune system response based on published data using literature searches and bioinformatic analysis
2. Definition of human infectious disease-specific protein profiles (viruses, bacteria, fungi and parasites)
3. Selection of microbial proteins useful as diagnostic biomarkers.
4. Development of SRM methods for detection and quantification of human and microbial proteins
5. Generation of PeptideAtlas and SRMAtlas of selected microorganisms
6. Detection and quantification of these proteins by targeted proteomics in clinical samples
7. Detection and quantification of these proteins by affinity or antibodies based technologies
8. Identification of novel host factors for antiviral therapeutic intervention
9. Characterization of host-pathogen protein-protein interactions
10. Building of a web page to freely-access data
11. Collaboration with other HPP Initiatives (e. g. HAI - Antibodies, HPPP – Plasma Proteins, DBI- Disease Biomarkers Initiatives, iMOP- Initiative on Model Organism Proteomes)

C. Contribution to J. Proteomics HUPO 2014 special issue

D. HID-HPP initiative Organization and future actions

8:40 - 8:50 am Discovery and Validation of Biomarkers to Guide Clinical Management of Pneumonia; Climent Casals-Pascual, University of Oxford, UK

8:50 - 9:00 am Label-Free Proteomic Analysis of Environmental Acidification-Influenced Streptococcus Secretome Reveals a Novel Acid-Induced Protein Histidine Triad Protein A (HtpA) Involved in Necrotizing fasciitis Pyogenes; Pao-Chi Liao, National Cheng Kung University, Taiwan

9:00 - 9:10 am Phosphoproteomic Characterization of Influenza A Virus Infected Human Primary Macrophages; Tuula Nyman, Institute of Biotechnology, Finland

9:10 - 9:20 am Open Discussion

EyeOme

The EyeOME: A View on the Proteomics Side of Vision

Organizer: Richard Semba, Marius Ueffing, and Hyewon Chung

Room I

In this session, eight speakers will present the current state-of-the-art of proteomic investigations of the eye. Tear, aqueous, vitreous, and serum sampling offers great potential for identifying biological pathways leading to eye disease. A comprehensive catalogue of eye proteins should provide a solid basis for proteomic studies of the eye. Animal models help increase the understanding of uveitis and diabetic macular edema. Proteomics provides new insight into major causes of blindness and visual disability such as glaucoma, retinal vascular disease, diabetic retinopathy, and age-related macular degeneration.

- 8:00 - 8:10 am Proteomics and Immunoproteomics Biomarker in Glaucoma; Franz Grus, *Experimental Ophthalmology, Department of Ophthalmology, University Medical Center, Mainz, Germany*
- 8:10 - 8:20 am Diagnostic Aspects of Proteomics and Metabolomics in Ophthalmology; Sascha Dammeier¹; Dario Bosch¹; Focke Ziemssen²; Marius Ueffing¹, ¹*Medical Proteome Center, Institute for Ophthalmic Research, Eberhard-Karl-University Tuebingen, Tuebingen, Germany*; ²*Centre for Ophthalmology, University Eye-Hospital, Tuebingen, Germany*
- 8:20 - 8:30 am The Human Eye Proteome Project – Update 2014; Richard D. Semba¹; Pingbo Zhang¹; Randi Turner¹; Sara Ferri¹; Jennifer E. Van Eyk²; Craig Dufresne³, ¹*Wilmer Eye Institute, Johns Hopkins School of Medicine, Baltimore, MD, USA*; ²*Cedars-Sinai Medical Center, Los Angeles, CA, USA*; ³*Thermo Fisher Scientific, West Palm Beach, FL, USA*
- 8:30 - 8:40 am A Peculiar Translational Animal Model for Recurrent Uveitis; Cornelia A Deeg, *Department of Veterinary Sciences, LMU Munich, Munich, Germany*
- 8:40 - 8:50 am The Vitreous is an Accessible Source for Retinal and Choroidal Disease Biomarkers; Vinit B. Mahajan^{1,2}, Stephen H. Tsang³, Jessica M. Skeie^{1,2}, ¹*Omics Laboratory, ²Department of Ophthalmology and Visual Sciences, University of Iowa, Iowa City, IA, USA*; ³*Departments of Ophthalmology, Pathology & Cell Biology, College of Physicians & Surgeons, Columbia University, New York, NY, USA*
- 8:50 - 9:00 am Clinical Vitreous Biopsy Reveals Molecular Signature of the Retina; Jeffrey M. Sundstrom¹, Alexey Nesvizhskii², ¹*Department of Ophthalmology, Penn State Hershey Medical Center, Hershey, PA, USA*; ²*Department of Computational Medicine & Bioinformatics, University of Michigan, Ann Arbor, MI, USA*
- 9:00 - 9:10 am Identification of Protein Biomarkers for Retinal Thickening in Diabetic Macular Edema; Edward P. Feener^{1,3}, Nivetha Murugesan^{1,3}; Allen Clermont^{1,2,3}; Ward Fickweiler¹; Takeshi Kita¹; Lloyd P. Aiello^{1,2,4}, ¹*Joslin Diabetes Center, ²Beetham Eye Institute, Departments of ³Medicine and ⁴Ophthalmology, Harvard Medical School, Boston, MA, USA*
- 9:10 - 9:20 am Exosomal Proteins in the Aqueous Humor as Novel Biomarkers in Patients with Neovascular Age-related Macular Degeneration; Hyewon Chung¹; Ae Jin Choi¹; Jeehyun Yoon¹; Joo Young Bang²; Je-Hyun Baek²; Hyung Soon Park², ¹*Department of Ophthalmology, Konkuk University School of Medicine, Seoul, Republic of Korea*; ²*Diatech Korea Co., Ltd., Seoul, Republic of Korea*

Human Diabetes Proteome Project (HDPP)

Organizer: Martin Kussmann

Room B

Diabetes prevalence has increased dramatically during recent years with rising numbers of both individuals suffering from relative (type 2 diabetes mellitus, T2DM) and absolute (type 1 diabetes mellitus, T1DM) insulin deficiency. To slow down, eventually stop, and ideally prevent this epidemic, deeper knowledge of the pathophysiological mechanisms responsible for impaired function of the multiple organs and cell-types affected is required. We have leveraged a worldwide constellation of expertise into the Human Diabetes Proteome Project (HDPP) initiative to generate systems-level insights into diabetes-associated cellular changes by gathering multivariate data sets over time from specialized cells and organs of healthy and diabetes-affected individuals. The HDPP has begun not only to deliver comprehensive information on disease mechanisms but also to identify proteins and isoforms associated with diabetic pathogenesis and crucial for the development of better diagnostics, therapies and preventions.

- 8:00 - 8:10 am Welcome and Presentation / Introduction of the HDPP Group & Partners;
Martin Kussmann, Chair, Nestle Inst. Health Science (NIHS), Lausanne, Switzerland
- 8:10 - 8:20 am Update on the HDPP Project and HDPP Protein List
Domitille Schvartz and Jean-Charles Sanchez, Univ. Geneva, Switzerland
- 8:20 - 8:35 am HDPP Partner Presentation
Peter Bergsten, Uppsala Univ. Sweden: Beta Cell Function
- 8:35 - 8:50 am HDPP Partner Presentation
Loïc Dayon, NIHS: Mitochondrial Function
- 8:50 - 9:05 am HDPP Partner Presentation
Y.A. Goo Univ. Maryland, USA / Univ. Turku, Finland: The DIPP Study
- 9:05 - 9:20 am Diabetes Protein Panel Project: SRM/MRM Assays (Open Discussion for all presenters and attendees)

C-HPP, Part II: Poster Session

Organizer: Gyorgy Marko-Varga

Inside Poster Hall

Poster Awards (Cash Prize and Award Certificate) will be given to Total 10 Best Outstanding Poster Presenters

Each team needs to load the poster no later than 5 pm, Monday. In addition to the C-HPP, any papers related to common technology or resources can be presented.

Presentation Times: 8:00 - 8:40 am: Group A: Chromosome 1-12 and 8:40 - 9:20 am: Group B: Chr 13-22, X, Y and Related Technologies (bioinformatics, MS, Ab, reagents etc.)

HUPO Proteomics Standards Initiative (PSI) and ProteomeXchange

Organizers: Eric Deutsch and Henning Hermjakob

Room C

The HUPO Proteomics Standards Initiative 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 <http://www.psidev.info>

For a publication list see <http://scholar.google.com/citations?user=oNoChlcAAAAJ>

Based on the HUPO PSI standards, we have developed ProteomeXchange, an international consortium for efficient collection and dissemination of open proteomics data (<http://www.proteomexchange.org>). We will provide an overview of current PSI activities, and discuss practical aspects of data deposition in ProteomeXchange through a short tutorial and Q&A session.

- | | |
|----------------|---|
| 8:00 - 8:15 am | The Proteomics Standards Initiative – Introduction and Status Report
Eric Deutsch, ISB Seattle |
| 8:15 - 25 am | Fine-grained modelling of molecular interactions in PSI MI XML 3.0
Henning Hermjakob, European Bioinformatics Institute, Cambridge, UK |
| 8:25 - 8:35 am | Mass Spectrometry Informatics
Gerhard Mayer, MPC, Bochum, Germany |
| 8:35 - 8:55 am | Submitting Your Data to ProteomeXchange – A Mini-Tutorial
Juan Antonio Vizcaino, European Bioinformatics Institute, Cambridge, UK |
| 8:55 - 9:05 am | Representing Imaging MS Data
Juan Antonio Vizcaino, European Bioinformatics Institute, Cambridge, UK |
| 9:05 - 9:20 am | Open Q&A session |

Antibody Proteomics

Organizers: Tadashi Yamamoto and Mathias Uhlen

Room D

- Antibody Atlas; Fredrik Ponten or Emma Lundberg
- Antibodypedia; Tove Alm
- Antibodyregistry.org and the Resource Identification Initiative: Identifying Research Resources in Biomedical Literature, One Antibody at a Time; Tadashi Yamamoto
- AntibodyRegistry; Anita Bandrowski
- Monoclonal Antibody-Based Strategies for Missing proteins; Ed Nice
- Development and Validation of a High Specificity, High Affinity Antibodies; Simon Brasch (Abcam)

Cancers II

Roundtable Discussion Chaired by Joseph Kagan

Organizers: Hui Zhang, Christopher Kinsinger and Edouard Nice
Room E

Chair/Moderator: Jacob Kagan

Discussion Panel: Bill Hancock, Bryan Krastins, Christopher Kinsinger, Connie Jimenez, Daniel Chan, Edouard Nice, Henry Rodriguez, Hui Zhang, Jacob Kagan, Joshua LaBaer, Josip Blender, Mark Baker, Peter James, Robert Moritz, Ruedi Aebersold, Shoba Ranganathan, Sam Hanash, Zhen Zhang

Key Discussion Points

- Mining the existing datasets and databases
- Dissemination of data and resources: generation and/or linking of appropriate websites
- Generation of a directory of key players, skills, cancer targets, and available assays
- Key persons to take responsibilities
- Prioritization of targets in the top 5 cancers
- Use of animal models
- Understand the normal/personalized medicine

Glycoproteomics / HGPI

Organizer: Hisashi Narimatsu
Room F

Through the past three pilot studies, the Human Disease Glycomics/Proteome Initiative (HGPI) had tried an evaluation and standardization of glycomic technologies for discovery and application of disease-related glycome. To establish the glycomic technologies, there are many technical problems even now. However, disease/biology-driven glycomic studies should make solid progress into the analyses of glyco-conjugates such as glycoproteins or glycopeptides rather than released glycans. This research direction was proposed and agreed by many committee members at the last two HGPI sessions in the HUPO annual meetings at Boston and Yokohama.

In this session, we would like to discuss on the researches generating the large-scale knowledge on glycomes, glycosylation site maps, and recent hot technologies on site-specific glycomics, as well as the construction of database for the resultant huge resources.

Tentative Speakers:

- Novel Protocol for Preparation and nLC-MS/MS Characterization of Proteoglycan Linkage Region Glycopeptides of Human Plasma, Urine and Cerebrospinal Fluid Samples; **Goran Larson**; *Institute of Biomedicine, University of Gothenburg*;
- Mass Spectrometry-Based Novel Techniques and Methods for N-Glycomics; **Haojie Lu**, *Ying Zhang*, *Yan Cai*, *Jing Jiao* and *Pengyuan Yang*; *Dept of Chemistry, Institutes of Biomedical Sciences, Fudan University*
- Construction of the Standard Method for Mouse Tissue Glycome Mapping in HUPO BD-GPP Initiative; **Atsushi Kuno**¹, *Jun Iwaki*¹, *Maki Yoshida*¹, *Atsushi Matsuda*¹, *Takashi Sato*¹; *Yoko Itakura*², *Masashi Toyoda*², *Binbin Tan*³, *Sheng-Ce Tao*³, *Yan Zhang*³, *Hiroyuki Kaji*¹, *Hisashi Narimatsu*¹; ¹*Glycomedicine Technology Research Center, National Institute of Advanced Industrial Science and Technology*; ²*Department of Vascular Medicine, Tokyo Metropolitan Institute of Gerontology*; ³*Ministry of Education, Key Laboratory of Systems Biomedicine, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University*
- Development and Application of a Method for the Glycopeptide-Based Site-Specific Glycomic Analysis; **Hiroyuki Kaji**, *Azusa Tomioka*, *Erika Noro*, *Maki Sogabe*, *Takashi Sato*, *Toshihide Shikanai*, *Hisashi Narimatsu*; *Glycomedicine Technology Research Center, National Institute of Advanced Industrial Science and Technology*

HPP EARLY MORNING SESSIONS • TUESDAY, OCTOBER 7, 2014, 08:00 – 9:20, continued

Human Brain Project

Organizers: Lea T. Grinberg, Young-Mok Park, Fouzi El Magraoui, Helmut E. Meyer
Room G

- 8:00 - 8:02 am Welcome Address; Helmut E. Meyer
- 8:02 - 8:14 am Bridging Old and New Anatomic-Proteomic Characterization of Human Brain Subcortical Nuclei; Enrique Santamaría Martínez
- 8:14 - 8:26 am Proteomic Characterization of Neuromelanin Granules; Katrin Marcus
- 8:26 - 8:38 am Autoantibodies as Disease Markers in ALS and Other Neurodegenerative Diseases; Caroline May
- 8:38 - 8:50 am Molecular Predictive Diagnosis of Preclinical Alzheimer's Disease: On the Way Towards the Development of Future Preventive Treatment Options; Jens Wiltfang
- 8:50 - 9:02 am Discovery of Regulated Brain Proteins in Mouse Multiple Sclerosis Models and the Presence of Their Homologues in Human CSF; Frode Berven
- 9:02 - 9:20 am Open Discussion

Proteome Biology of Stem Cells

Organizers: Javier Muñoz, Jeroen Krijgsveld, Albert Heck
Room H

- 8:00 - 8:20 am Reprogramming *in vivo* Produces Teratomas and iPS Cells with Totipotency Features; Maria Abad (CNIO, Madrid, Spain)
- 8:20 - 8:40 am Proteome profiling of human healthy and tumor colon organoids; [Alba Cristoba](#), Marc van de Wetering, Henk van den Toorn, Hans Clevers, Albert Heck, Shabaz Mohammed (Biomolecular Mass Spectrometry and Proteomics Group, Utrecht, The Netherlands)
- 8:40 - 9:00 am Characterisation of a novel spontaneous model of epithelial to mesenchymal transition using a primary prostate cancer cell line using quantitative label-free proteomics (SWATH™); [David Boocock](#), Clare Coveney, Naomi Dunning-Foreman, Jayakumar Vadakekolathu, Matthew Nicklin, Graham Hickman, Graham Pockley, Sibylle Heidelberger, Thomas Knapman, Robert Rees (John van Geest Cancer Research Centre, Nottingham, UK)
- 9:00 - 9:20 am Dynamics of locus-specific chromatin composition in stem cells; Mahmoud-Reza Rafiee and [Jeroen Krijgsveld](#) (European Molecular Biology Laboratory, Heidelberg, Germany)

Biobanking and Pre-Analytical Sample Assessment

Organizer: Andrea Urbani
Room I

- 8:00 - 8:15 am Opening and General Concepts; Andrea Urbani
- 8:15 - 8:35 am Biobanking Workflow for Proteomics Investigation; Gyorgy Marko Varga
- 8:35 - 8:55 am Integrating and Developing Quality Controls in System Biology; Garry Corthals
- 8:55 - 9:00 am Direct Analytical Sample Quality Assessment (DASQ) for Biomarker Investigation: Qualifying CSF Samples; Viviana Greco
- 9:00 - 9:15 am Round Table Discussion for the Preparation of Seeding Initiative on Standardization and Biobanking
- 9:15 - 9:20 am Closing; Andrea Urbani

HPP EARLY MORNING SESSIONS • WEDNESDAY, OCTOBER 8, 2014, 08:00 – 9:20

Respiratory Diseases

Organizer: Rainier Bischoff

Room B

This workshop has the goal to establish Respiratory Disease as a new area in the B/D-HPP program of HUPO.

- 8:00 - 8:10 am The Need to Establish a Respiratory Disease Area as Part of the B/D-HPP Program (Rainer Bischoff, University of Groningen, Netherlands)
- 8:10 - 8:20 am What We Can Learn from Proteogenomics Approaches (Peter Horvatovich, University of Groningen, Netherlands)
- 8:20 - 8:30 am Biobanking (Gyorgy Marko-Varga, Tom Fehniger, Lund University, Sweden)
- 8:30 - 8:40 am The Role of Glycans in COPD (Naoyuki Taniguchi, RIKEN and RIKEN-Max Planck Joint Research Center, Japan)
- 8:40 - 8:50 am The Clinical Need for Proteomics Research in Respiratory Disease (Xiangdong Wang, Fudan University, Shanghai, China)
- 8:50 - 9:20 am Panel Discussion: Consortium Building, Sub-Topics (e.g. asthma, COPD), Funding Opportunities / Strategies

C-HPP, Part III: Principal Investigators Council

Organizer: Young-Ki Paik

Room C

This meeting is intended for Principal Investigator Council members and guests (by invitation).

1. Approval of new Chr 16 PI
2. A New Strategy for Stimulating C-HPP Activities.
3. Election of the C-HPP EC member-at-large
4. 2015 C-HPP workshop plans
5. 2015 JPR Special Issue on thematic topics with publication timing may possibly be explored.
6. Organization Matters

Looking to the Future: The Cardiovascular Initiative

Organizers: Jennifer Van Eyk, Catherine Costello, Peipei Ping, Vidya Venkatraman, Maggie Lam

Room D

Session Chair: Peipei Ping, PhD

Popular Proteins in the Heart

8:00 - 8:10 am Jennifer Van Eyk, PhD; Peipei Ping, PhD; Vidya Venkatraman, PhD; Maggie Lam, PhD Cedars-Sinai Medical Center; University of California Los Angeles

Perspectives and Updates on Proteomics in Cardiovascular Sciences

- 8:10 – 8:20 am Moving to Populations in Biomarkers; Manuel Mayr, MD, PhD, King's College, London
- 8:20 – 8:30 am Dynamic Regulations of the Cardiac Proteome; Maggie Lam, PhD, University of California, Los Angeles
- 8:30 – 8:40 am PTM in Heart Disease - Which Are Your Favorite?; Melanie White, PhD, The University of Sydney, Australia
- 8:40 – 8:50 am Large-Scale Pre-Clinical/Clinical Profiling; Jun Qu, PhD, University at Buffalo
- 8:50 – 9:00 am The Complexity of Oxidative Modifications; Catherine Costello, PhD, Boston University School of Medicine
- 9:00 – 9:20 am Panel Discussion

CompMS - HUPO Computational Mass Spectrometry Initiative

Organizers: Henning Hermjakob
Room E

CompMS is a new, joint initiative of HUPO and the International Society for Computational Biology (ISCB). It promotes the efficient, high quality analysis of mass spectrometry data through dissemination and training in existing approaches and coordination of new, innovative approaches. The CompMS initiative aims to exploit synergies between different application domains, in particular proteomics and metabolomics. We aim to

- build a community of scientists working in computational mass spectrometry
- integrate experimental and theoretical research
- bridge the gaps between proteomics, metabolomics, and other MS-driven fields

For more information on CompMS please see <http://compMS.org>.

This will be the constitutive meeting of CompMS as a HUPO initiative, and will provide an opportunity for all attendees to engage with the initiative and its future activities.

8:00 – 8:10 am	Introduction to the Computational Mass Spectrometry Initiative, Oliver Kohlbacher (U Tuebingen)
8:10 – 8:30 am	Computational Challenges in Spatial Mass Spectrometry, Laurent Gatto (U Cambridge)
8:30 – 8:50 am	Spatial Metabolomics Using Imaging Mass Spectrometry, Theodore Alexandrov (U Bremen / EMBL Heidelberg)
8:50 – 9:20 am	Open Business Meeting of the HUPO Initiative for Computational Mass Spectrometry

Mitochondria

Organizers: Andrea Urbani
Room G

8:00 – 8:05 am	Opening, Andrea Urbani
8:05 – 8:17 am	Characterization, Design, and Function of the Mitochondrial Proteome: From Organs to Organisms, Peipei Ping
8:17 – 8:29 am	Decoding the Mitochondrial Interaction Landscape in Neurodegenerative Diseases, Mohan Babu
8:29 – 8:41 am	The Mitochondrial Proteome from the Human Protein Atlas Perspective, Emma Lundberg
8:41 – 8:53 am	Mitochondrial Proteomics of Cellular Models of Parkinson's Disease Pathogenesis, Mauro Fasano
8:53 – 9:05 am	Bacterial Resistance and Host Mitochondria Rearrangements, Alessio Soggiu
9:05 – 9:17 am	Investigating Mitochondria Proteome in Fatigue Syndrome, Federica Ciregia
9:17 – 9:20 am	Wrap up

Protein Aggregation Diseases B/D HPP Working Group

Organizers: Paola Picotti
Room H

8:00 - 8:10 am	Introduction
8:10 - 8:20 am	Amyloidoses: fatal diseases caused by Misfolded Proteins; Bouke Hazenberg (University of Groningen, Netherlands)
8:20 - 8:30 am	Targeted MS Assays for the Clinical Diagnosis and Subtyping of Systemic Amyloidoses in Subcutaneous Fat Aspirates; Paul Boersema (ETH Zurich, Switzerland)
8:30 - 8:40 am	Proteomics in the Understanding and Management of Systemic Amyloidoses: The Pavia Experience; Giampaolo Merlini (University of Pavia, Italy)
8:40 - 8:50 am	Disease developments in Parkinson and Malignant Melanoma; Melinda Rezeli (Lund University)
8:50 - 9:00 am	Towards MS-Based Conformational (Bio)Markers?; Paola Picotti (ETH Zurich, Switzerland)
9:00 - 9:20 am	Wrap-up

PediOme

Pediatric Proteomics Initiative (PediOme): Exploring Child Health with Proteomics

Organizers: Allen Everett and Vera Ignjatovic

Room 1

Overview of the project will be followed by these talks:

- Differences in Platelet Proteome and Secretome between Children and Adults: The Role in Protection from Thrombosis and Cardiovascular Disease. - Vera Ignjatovic
- The Regenerative Abilities of Resident Cardiac Stem Cell Depends on Secreted Paracrine Factors - Sunjay Kushal
- Monitoring the Status of Infants Being on Nursing in Incubators by Urine Proteome Analysis. - Alexey Kononikhin
- Urine Proteomics for the Discovery of Non-Invasive Diagnostic Biomarkers for Pediatric Diseases. - Hanno Steen
- Omics in Nutrition and Its Perspectives for Pediatrics Research and Healthcare - Martin Kussmann

Human Proteome Project

15:00 – 16:50, Room A

Chair: Gil Omenn

- 15:00 – 15:25 **Comparative proteomics and the role of Multi-Organism Proteomes in the HPP**; Emøke Bendixen; *Aarhus University, Aarhus, Denmark*
- 15:25 – 15:50 **Multilayered Genetic and Omics Dissection of Mitochondrial Activity**; Johan Auwerx; *Laboratory for Integrative and Systems Physiology, Ecole Polytechnique Fédérale de Lausanne, Lausanne, Switzerland*
- 15:50 – 16:05 **Overview of Progress, Strategies, and Metrics of the Human Proteome Project**; Gilbert S. Omenn; *University of Michigan, Ann Arbor, MI, USA*
- 16:05 – 16:20 **Acceleration of Work Plan for C-HPP**; Young-Ki Paik; *Yonsei Proteome Research Center, Yonsei University, Seoul, Korea*
- 16:20 – 16:50 **Panel and General Audience Discussion**; Confirmed Panelists: Ruedi Aebersold, Catherine Costello, Bill Hancock, Pierre Legrain, Michael Snyder, Mathias Uhlen, Jennifer Van Eyk

Post Congress Workshop in Segovia, Spain

Interested participants are invited to [register here](#) (required). Segovia is located approximately one-hour from Madrid (by train or bus). Transportation TO Segovia on Wednesday evening (October 8) will be provided for all registered participants (by bus). Participants are responsible for their own hotel room Wednesday (Oct 8) and/or Thursday (Oct 9).

- [Hotel options in Segovia](#) (participants must book their own hotel)
- [Venue Map for Segovia](#) (location of Oct 9 meeting)
- [Return transportation options](#) (Segovia to Madrid)
- For additional logistics information, please contact Lola Segura mdsegura@proteored.org



Efforts to Accelerate the HUPO Human Proteome Project Preliminary Program

(Draft Ver 4.3, 9/11/2014)

To the memory of Juan Pablo Albar

Bus departing Madrid for Segovia will be provided for all participants who register in advance. For details, go to <http://www.hupo2014.com/newtrends.html>

08:45-09:10 Coffee and Welcome

Fernando Corrales, Concha Gil

Young-Ki Paik, Bill Hancock, Jennifer Van Eyk, Tadashi Yamamoto, Pierre Legrain, Gil Omenn

09:10-10:00 Common Reagents and Resources for HPP Networks

09:10-09:35 A Tissue-Based Map of the Human Proteome: Cross-validation of HPA antibody data with MS, RNA-seq and other publicly available data; **Ulrika Qundos**, SciLife Lab, Stockholm, Sweden

09:35-09:45 Develop Effective Antibody Capture Reagents for the Missing or Orphan Proteins and for Characterization of Proteoforms of Well-Known Proteins; Collaboration between ProteinAtlas and Monash Monoclonal Ab facility; **Ed Nice**, Monash University, Australia

09:45-10:00 Develop and Facilitate Utilization of Common Bio-Banking Samples; **Gyorgy Marko-Varga**, Lund Univ., Sweden and **Henry Rodriguez**, NCI, USA

10:00-11:45 Defining Highly Informative Sets of Proteins for Studies of Specific Diseases: Moving from HPP Focus on the Missing Proteins to the 80% Known Proteins

10:00-10:40 Priority Protein Lists with Ready-to-Use SRM Peptides and Spectral Libraries; **Peter Bergsten**, Uppsala University, Sweden (for Diabetes-HPP)

The Proteome-wide SRM Resources: Peptides, Spectral Libraries, PASSEL Database; **Robert Moritz and Eric Deutsch**, ISB, USA

Report on HPP Inter-Laboratory Performance with SRM/MRM Assays; **Christoph Borchers**, University of Victoria, Canada

Extended SWATH Library that makes >10,000 Human Proteins Precisely Measurable; **George Rosenberger**, ETH Zurich, Switzerland

Efforts to Accelerate the HUPO HPP, *continued*

10:40-11:30 Popular Proteins, Quantitative Assays, Functional Networks and Pathways

Peipei Ping, CV-HPP, heart and vascular diseases

Fuchu He and **Pengyuan Yang**, CN-HLPP: liver diseases

Hui Zhang and **Ruth Huttenhain** + others in Cancer-HPP: cancers

Tadashi Yamamoto, HKUPP: Kidney diseases

New Experimental Tools: organ-on-a-chip, non-natural amino acid-based assays

11:30-11:45 Bridging from the Proteomics Research Community to the Clinic

The ProteomeAnalyzer Project of the B/D-HPP: robust, moderate cost, high throughput; **Bruno Doman**, Luxembourg

11:45-13:00 Combined C-HPP + B/D-HPP Studies of Proteome Biology and Disease

11:45-12:05 Demonstration of Joint Efforts on MS-based Automated PTM Analysis and Biological Characterization of Brain Proteins and Glioblastoma; **Jong Shin Yoo**, KBSI, Ochang Korea and **Young-Mok Park**, Korea (HBPP)

12:05-12:20 Demonstration of Utilizing Combined Resources and Technologies from B/D-HPP and C-HPP to Search for Cancer Biomarkers; **Gyorgy Marko-Varga**, Lund University (Chr 19), **Hui Zhang**, Johns Hopkins, Chair, Cancer-HPP

12:20-12:40 Management of RNA Seq Data for Mapping Isoforms (C-HPP) and Characterizing Biological Functions (with B/D-HPP); **Ravi Sirdeshmukh**, Bangalore, India

12:40-13:00 Combined Tools for Characterizing Membrane-Embedded Missing Proteins with Disease Implications (AO-HUPO Membrane Proteome Initiative); **Takeshi Tomonaga**, National Institute of Biomedical Innovation, Ibaraki, Osaka, Japan and **Yu-ju Chen**, Taipei, Taiwan (Chr 4)

13:00-14:00 Lunch

14:00-15:30 Data Resources, Data Standards, and Common Informatics Tools

14:00-15:00 Update on HPP Metrics for High-Confidence Protein Identifications and Missing Proteins combining PeptideAtlas, GPMdb, neXtProt, Human Protein Atlas and including major 2014 datasets

- Reinforcement of Policies on Dataset Deposition with ProteomeXchange, Stringent Protein FDR thresholds, and Reanalysis with Standardized PeptideAtlas and GPMdb Pipelines
- Creation of the Integrated HUPO Human Proteome Browser (Caper, TPB, Genome-wide PDB): Ed Nice, Fuchu He, Ping Xu, Ian Smith, Mark Baker, Anthony Beitz, Dong Li, Young-Ki Paik (Working Group for IHPB)
- Recognition of Reasons Proteins can be Hard to Detect: restricted tissue expression, low abundance, high hydrophobicity or basicity, embedded in membranes, low MW, members of highly homologous protein families

Lydie Lane & Amos Bairoch, neXtProt, SIB, Geneva, Switzerland

Eric Deutsch, PeptideAtlas, ISB, Seattle, USA

Ulrika Qundos, Human Protein Atlas, SciLife Lab, Stockholm, Sweden

Alberto Pascual-Montano and **Fernando Corrales**, Spain

15:00-15:30 Focus on PTMs, ASVs, Protein Interactions, protein and glycan chemistry

Bill Hancock, Northeastern University, Boston, USA

Naoyuki Taniguchi, RIKEN Advanced Science Institute, Japan

Cathy Costello, Boston University, USA

Gil Omenn, Univ. of Michigan, Ann Arbor, MI, USA

15:30-17:00 Town Hall Meeting on Future Directions of the HPP

Everyone in the proteomics community is warmly invited to actively participate. We welcome a broad discussion about the development, integration, and wide application of C-HPP, B/D-HPP and Technology Pillars.

- How to make proteomics an essential component of “functional genomics” and integrated ‘omics research?
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- How to connect with investigators not part of HPP, including clinical investigators, pathologists, geneticists, biologists?
- How to emphasize characterizing the biology of the many proteoforms of known proteins, while sustaining the effort to complete the parts list?
- How to assist and mobilize less active teams in both B/D-HPP and C-HPP consortium?
- How to accelerate HPP development through coordination between B/D-HPP, C-HPP, and Resource Pillars?
- What should be the focus of the next J Proteome Research C-HPP/HPP Special Issue for mid-2015?

Efforts to Accelerate the HUPO HPP, *continued*

Conclusions and Perspectives

Cathy Costello, Pierre Legrain, Mark Baker, HUPO Presidents
Gil Omenn, Chair, HPP Consortium

17:30-19:30 Segovia City Tour

20:30-23:00 Dinner

Organizers (2014 Post-Congress Workshop in Segovia)

Organizations: PROTEORED and HUPO HPP Consortium
Fernando Corrales, Pamplona, Spain
Concha Gil, Madrid, Spain
Gil Omenn, Chair, HUPO HPP Consortium
Tadashi Yamamoto, Chair, HUPO Initiative Committee
Young-Ki Paik and Bill Hancock, Chair and co-Chair, C-HPP Consortium
Ruedi Aebersold and Jennifer van Eyk, Co-Chairs, B/D-HPP Consortium

For more information, please contact Lola Segura mdsegura@proteored.org

Go to <http://www.hupo2014.com/newtrends.html> for information on the following:

- Registration
- Hotels in Segovia (You are responsible for booking your own hotel.)
- Return transportation to Madrid

