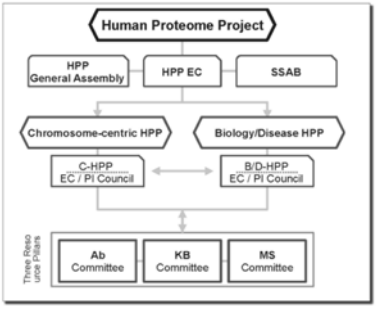
HUMAN PROTEOME PROJECT - INITIATIVE SESSIONS

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

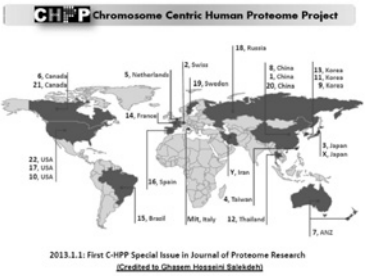
At the conclusion of the congress two HPP-related sessions are scheduled where, in addition to invited speakers, the HPP Executive Committee will report on progress and updates from the Sunday, Monday and Tuesday morning sessions.

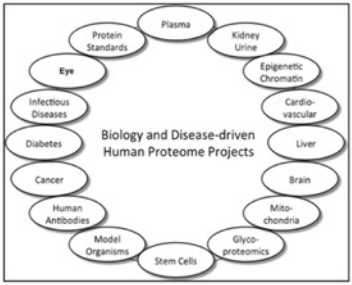
MORE ABOUT THE HPP

An organizational chart for the Human Proteome Project showing the C-HPP, B/D-HPP, resource pillars, the HPP Executive Committee (EC) and HPP Senior Scientific Advisory Board (SSAB). Please also visit www.thehpp.org and www.c-hpp.org for more information.



The teams for the chromosome-centric C-HPP and the biology and disease-driven B/D-HPP are shown here. Details about the members of the teams and the activities of each can be found at www.thehpp.org and www.c-hpp.org.





The Journal of Proteome Research published progress updates from both the C-HPP and B/D HPP leadership in a special January 2013 issue. To-date a total of 48 C-HPP related articles have been published in JPR (January 2013 and June 2013).

- Marko-Varga G, Omenn GS, Paik YK, Hancock WS. **A first step toward completion of a genome-wide characterization of the human proteome.** J Proteome Res. 2013;12:1-5.
- Aebersold R, Bader GD, Edwards AM, van Eyk JE, Kussmann M, Qin J, et al. **The biology/disease-driven human proteome project (B/D-HPP): enabling protein research for the life sciences community.** J Proteome Res. 2013;12:23-7.

HPP Initiative Session 1: PSI/ProteomeXchange/KBpC + C-HPP (Part 1)

Sunday, September 15 8:15 - 9:30 Room 303+304

Organizers:
Eric Deutsch, Henning Hermjakob, Lydie Lane, Bill Hancock

HPP projects are generating massive amounts of proteomics data using a large variety of MS-based techniques. To be exploitable, this data need to be stored and and precisely documented, and made available in a standardized format. To answer these needs, several resources are being developed.

- Eric Deutsch (ISB, USA) will present the PSI efforts to develop standardized data formats and their implementation
- Henning Hermjakob (EBI, UK) will present ProteomeXchange, that simplifies and unifies proteomics data submission to PRIDE and Peptide atlas
- Lydie Lane (SIB, Switzerland) will show how human proteomics data is handled in neXtProt, and how it is integrated with other types of data

Finally, a panel composed of the three speakers and Bill Hancock will host 15 min of Q&A about the optimization of data resources within the HPP.

HPP Initiative Session 2: EyeOME

Sunday, September 15 8:15 - 9:30 Room 301

Organizers:
Richard Semba and Roger Beuerman

In this session, we introduce the Human Eye Proteome Project (HEPP), one of the most recent components of the Biology/Disease-driven Human Proteome Project (B/D-HPP) whose overarching goal is to support the broad application of state-of-the-art measurements of proteins and proteomes by life scientists studying the molecular mechanisms of biological processes and human disease. The goals of the HEPP will be presented (Richard Semba, Baltimore). The session will cover the proteome of human tears and murine retina (Zhou Lei, Roger Beuerman, Singapore), the anterior segment in relation to glaucoma (Deepak Edward, Riyadh, Saudi Arabia), the vitreous proteome in diabetic retinopathy (Edward Feener, Boston), and personalized proteomics for therapy of inflammatory retinal disease (Vinit Mahajan, Iowa City).

Speakers:

Introduction to the Human Eye Proteome Project

Richard Semba[1], Jan J. Enghild[2], Vidya Venkatraman[3], Thomas F. Dyrlund[2], Jennifer E. Van Eyk[3]
[1]Wilmer Eye Institute, Johns Hopkins University School of Medicine, Baltimore, MD, USA, [2]Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark, [3]Johns Hopkins Bayview Proteomics Center, Johns Hopkins University School of Medicine, Baltimore, MD, USA

Proteome of Human Tears and the Mouse Retina

Zhou Lei[1,2,4], Roger Beuerman[1-4]
[1]Singapore Eye Research Institute, [2]Duke-NUS, SRP Neuroscience and Behavioral Disorders, [3]Ophthalmology, Yong Loo Lin School of Medicine, National University of Singapore, [4]Ophthalmology, University of Tampere Medical Center, Tampere, Finland

The Proteome of the Anterior Segment in Relation to Glaucoma

Deepak Edward[1,2], Rachida Bouhenni[3]
[1]King Khalid Eye Hospital,Riyadh, Kingdom of Saudi Arabia, [2]Wilmer Eye Institute, Johns Hopkins University School of Medicine, Baltimore, MD, USA, [3]Summa Health System, Akron, OH, USA

Vitreous Proteome in Diabetic Retinopathy

Edward P. Feener[1,2], Lloyd P. Aiello[1,3]
[1]Joslin Diabetes Center and Departments of [2]Medicine and [3]Ophthalmology, Harvard Medical School, Boston, MA, USA

Personalized Proteomics for Inflammatory Retinal Disease Therapy

Vinit B. Mahajan[1,2], Jessica M. Skeie[1,2]
[1]Omics Laboratory, [2]Department of Ophthalmology and Visual Sciences, University of Iowa, Iowa City, IA, USA

The Tears as a Source for Proteomic Biomarkers of Human Eye Diseases

Roger Beuerman[1-4], Zhou Lei[1,2,4]
[1]Singapore Eye Research Institute, [2]Duke-NUS, SRP Neuroscience and Behavioral Disorders, [3]Ophthalmology, Yong Loo Lin School of Medicine, National University of Singapore, [4]Ophthalmology, University of Tampere Medical Center, Tampere, Finland

HPP Initiative Session 3: Proteome Biology of Stem Cells

Sunday, September 15 8:15 - 9:30 Room 311+312

Organizers:
Albert Heck and Jeroen Krijgsveld

This session will provide an update of recent efforts gaining insight into various aspects of both embryonic, induced pluripotent and adult stem cell biology using advanced proteomic approaches.

Three talks will be presented followed by discussion.

Speakers:

Deep Subcellular Proteome Profiling of Human Induced Pluripotent Stem Cell by One-Shot Nanolc-MS/MS Analyses with Meter-Scale Monolithic Silica Columns

Mio Iwasaki[1], Masato Nakagawa[1], Yasushi Ishihama[2], Shinya Yamanaka[1,3]
[1]Center for iPS Cell Research and Application, Kyoto University, Japan, [2]Graduate School of Pharmaceutical Sciences, Kyoto University, Japan, [3]Gladstone Institute of Cardiovascular Disease, San Francisco, USA

Proteomic Analysis OF LGR5+ve Intestinal Adult Stem Cells and Their Immediate Undifferentiated Daughters

Javier Muñoz[1,2], Daniel E. Stange[3], Marc van de Wetering[3], Shabaz Mohammed[1,2], Hans Clevers[3], Albert J. R. Heck[1,2]
[1]Biomolecular Mass Spectrometry and Proteomics Group, Utrecht University, The Netherlands, [2]Netherlands Proteomics Center, Utrecht, The Netherlands, [3]Hubrecht Institute, KNAW, Utrecht, The Netherlands

Stem Cells and Neural Development

Akhilesh Pandey
Johns Hopkins University, Baltimore, USA

HPP Initiative Session 4: Human Brain Proteome Project (HBPP)

Sunday, September 15 8:15 - 9:30 Room 313+314

Organizers:
Lea Grinberg, Young-Mok Park, Helmut E. Meyer

The Human Brain Proteome Project is one of the international initiatives of the Human Proteome Organization

(HUPO). Since its initiation in 2003, the HUPO Brain Proteome Project (HUPO BPP) organizes workshops on a regular basis. The main goal was to intensify collaboration between fundamental research and clinics as well as to discuss recent sub-project results in the field of clinical Neuroproteomics and to establish guidelines and requirements for the future HBPP. At the 16th HUPO BPP workshop which was held in 2011 during the HUPO 10th Annual World Congress in Geneva, Human Brain Proteome Atlas Project (HBPAP) was launched as an international, multidisciplinary initiative by HUPO BPP. The overarching goal of HBPAP is to analyze what are the proteomic compositions of distinctive areas of healthy human brain and how it changes during aging and disease. At HBPAP, several groups will analyze human brain samples using their expertise, and the results will be compared using robust and integrative bioinformatics. This well-orchestrated international collaboration will maximize the project potential and the chances of identifying biomarkers and novel therapeutic targets for Alzheimer's disease.

Speakers:

The Role of Neuroproteomics to Elucidate Neurodegenerative Disease Mechanisms
Lea T. Grinberg
University of Sao Paulo (Brazil) and University of California, San Francisco (USA)

Biomarker Discovery for Alzheimer and Parkinson Disease
Helmut E. Meyer
Medical Proteom-Center, Ruhr-University Bochum, Germany

HPP Initiative Session 5: Liver (HLPP and B/D-HPP-Liver)

Monday, September 16 8:15 - 9:30 Room 303+304

Organizers:
Pumin Zhang, Fernando Corrales

Liver is the central metabolic organ in human body that maintains blood sugar and lipid homeostasis. It also performs many other critical functions essential for survival. Human Liver Proteome Project (HLPP) was launched in 2002 with three objectives: 1) generate an integrative approach leading to a comprehensive protein atlas of the liver, 2) expand the liver proteome to its physiome and pathome to dramatically accelerate the development of diagnostics and therapeutics toward liver diseases, and 3) develop standard operating procedures (SOPs) for other HUPO initiatives. The HLPP Workshop will summarize the progresses made in past few years towards the objectives and discuss plans to move the initiative forward. HLPP participants and everyone else with an interest in liver function are welcome to attend the workshop.

Speakers:

Urine as a Source of Liver Disease Biomarkers and Proteomics Studies with Human Hepatoblastoma Samples
Felix Elortza
CIC bioGUNE, CIBERehd, ProteoRed-ISCIII, Technology Park of Bizkaia, Derio, Spain

Identification of Proteins Driving the Progression of Liver Injury and Potential Biomarkers
Fernando J. Corrales
Division of Hepatology and Gene Therapy, CIMA, University of Navarra, Pamplona, Spain

Towards the System Medicine of Non-Alcoholic Fatty Liver Disease
Tommy Nilsson
The Research Institute of the McGill University Health Centre, the McGill University Health Centre & McGill University, Montreal, Quebec, Canada

HLPP, A Progress Report from Team China
Pumin Zhang
Beijing Proteome Research Center, China and Baylor College of Medicine, Houston, TX, USA

HPP Initiative Session 6: Human Protein Atlas / ABpC

Monday, September 16 8:15 - 9:30 Room 301

Organizers:

Jochen Schwenk, Emma Lundberg, Mathias Uhlen

The Human Antibody Initiative (HAI) aims to promote and facilitate the use of antibodies for proteomics research. In this session we will present recent developments in antibody technologies as well as alternative affinity reagents. In addition to this we will report on the current status of available antibody collections for the human proteome and discuss how to best integrate the antibody-based research with other data in the Human Proteome Project.

Speakers:

Welcome and Introduction

Mathias Uhlén
Science for Life Laboratory, KTH, Sweden and Michael Snyder, Stanford Center for Genomics and Personalized Medicine, USA

Programs for Antibody Generation at NIH and NCI

Salvatore Sechi
NIH, USA

Programs for Antibody and Protein Binder Generation in Europe

Peter Nilsson
KTH-Royal Institute of Technology, Sweden

Programs for Generation of Antibodies in Australia

Ed Nice
Monash University, Australia

Availability of Commercially Antibodies to the Human Proteome

Tove Alm
Antibodypedia, KTH, Sweden

Discussion - the Role of HAI for the HPP

Mathias Uhlén, Michael Snyder
Science for Life Laboratory, KTH, Sweden and Michael Snyder, Stanford Center for Genomics and Personalized Medicine, USA

HPP Initiative Session 7: Cancer

Monday, September 16 8:15 - 9:30 Room 302

Organizers:

Hui Zhang Center for Biomarker Discovery and Translation, Department of Pathology, Johns Hopkins University, USA

Juan Pablo Albar CEI-UAM+CSIC Proteomics Platform, Spain

The Cancer-HPP attempts to generate and disseminate the assays and resources to support the analysis of biological networks underlying biological processes and cancer. The use of emerging mass spectrometry (MS)-based platforms such as selected reaction monitoring (SRM) or targeted data extraction for candidate proteins from SWATH MS data has become an increasingly popular method for quantitative analysis of target proteins. It has been shown that the use of synthetic peptide standards and isotope dilution makes identification and accurate quantitation of proteins in a multiple laboratories possible. Therefore, the assays, once developed, can be easily transferred and used in other laboratories. Acceptance of high throughput MS assays for proteins or protein modifications has been limited due to the difficulty in establishing assays and the availability of the

assays comparing to using traditional antibody based assays, here we propose an international effort to target cancer proteins in each cancer type. By working together, we can create a synergistic effort to work with a list of cancer protein targets, develop assays, and make assays available. We further discuss the procedure to accrue a list of target proteins from each cancer type, the strategy for assay development, quality control, and procedure and materials needed for transferring the established assays to a new laboratory.

Speakers:

CPTAC - a Proteogenomics Network for Cancer

Christopher Kinsinger

Clinical Proteomic Tumor Analysis Consortium (CPTAC), National Cancer Institute, USA

Analysis of Tissue Biopsies by PCT-SWATH

Guo Tiannan

ETH Zurich, Institute of Molecular Systems Biology, Switzerland

Proteomics-Based Studies on Colorectal Cancer

Edouard Nice

Clinical Biomarker Discovery and Validation, Monash Antibody Technologies Facility, Monash University, Australia

Integrative Analysis - Bridging the Gaps in Genetic Information Flow between Genomic and Proteomic Data

Zhen Zhang

Biomarker Discovery and Translation, Johns Hopkins University, USA

Breast Cell Index and Atlas Projects

Peter James

Department of Immunotechnology, Lund University, Sweden

Human Proteome Knowledge Discovery Gateway: Progress and Perspective

Dong Li, Fuchu He

State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, National Center for Protein Sciences, National Engineering Research Center for Protein Drugs, China

Panel Discussion including:

Hisashi Narimatsu

Research Center for Medical Glycoscience (RCMG), National Institute of Advanced Industrial Science and Technology (AIST)

Tadashi Kondo

Division of Pharmacoproteomics, National Cancer Center Research Institute, Japan

Sam Hanash

Clinical Cancer Prevention-Research, Red & Charline McCombs Institute for the Early Detection and Treatment of Cancer, The University of Texas MD Anderson Cancer Center, USA

Leigh Anderson

SISCAPA Assay Technologies, Inc, USA

Ignacio Casal

ProteoRed-ISCIII, CIB-CSIC, Spain

HPP Initiative Session 8: HKUPP + HPP

Monday, September 16 8:15 - 9:30 Room 311+312

Organizers:
Mark Baker and Tadashi Yamamoto

The following topics will be discussed: (1) comparative analyses across plasma and other biofluid and organ proteomes, like the plasma/urine/kidney study pending; (2) joint workshops, like Plasma & CVD in Sydney and Plasma and HKUPP in Boston and Yokohama; (3) the move from shotgun to targeted proteomics in biomarker discovery especially to overcome the domineering effect of highly abundant proteins and their peptides in plasma; (4) the strategy of identifying biomarker candidates in diseased tissues and then following the proteins into the periphery for convenient analysis; and (5) emphasis on protein variants from alternative splicing, PTMs, and mutations.

Speakers:

Proteomic Analysis of Nephron Segments of Formalin-Fixed Paraffin-Embedded Human Kidney Tissues
Tadashi Yamamoto, Keiko Yamamoto, Yutaka Yoshida, Bo Xu, Ying Zhang, Sameh Magdeldin
HKUPP

A Collective Analysis of Three Human Subproteomes Using PeptideAtlas
Eric Deutsch, Terry Farrah, Tadashi Yamamoto, Julian Watts, Micheleen Harris, Zhi Sun, Gil Omenn
HPPP

Different Levels of Variability in the Human Plasma Proteome
Yansheng Liu, Ben Collins, Ludovic CJ Gillet, Alfonso Buil, Emmanouil T. Dermitzakis, Lin-Yang Cheng, Olga Vitek, Ruedi Aebersold
Institute of Molecular Systems Biology, ETH Zurich

Quantification of Peptides in Clinical Samples Based on High-Resolution Mass Measurements
Bruno Domon
Luxembourg Clinical Proteomics Center, Luxembourg

HPP Initiative Session 9: Human Diabetes Proteome Project (HDPP)

Monday, September 16 8:15 - 9:30 Room 313+314

Organizers:
Jean-Charles Sanchez, Peter Bergsten, Martin Kussmann

Diabetes mellitus is a complex multifactorial disease characterized by hyperglycemia and deranged lipids, which have been linked to diabetes-related complications. The Human Diabetes Proteome Project (HDPP) consortium was created at HUPO 2012 to unravel molecular mechanisms leading to diabetes and to understand the dysfunctions induced by glucose and free fatty acids. During the first year, the partners of HDPP identified the short-to-mid term objectives of the project. Various omics datasets will be collected, mainly by analyzing insulin producing cell lines, islets, and human blood from different conditions. Data integration as well as network biology approaches will be applied to enhance our knowledge of pathways centrally involved and deregulated in diabetes. Existing projects from the partners are already delivering omics data on human islets, rodent beta-cells, mitochondria, glycation in human blood as well as key results on modifications associated to beta-cell dysfunction. Based on the three pillars of the B/D-HPP projects, HDPP has already made publicly available (www.hdpp.info) three key protein resources [1]: (1) the 1'000 diabetes-associated protein (the 1000-HDPP) database with links to their neXtProt, Peptide Atlas and Human Protein Atlas references; (2) a list of 5'300 human islet

proteins; and (3) a list of 2'500 rodent beta-cell proteins. All results obtained so far through the HDPP initiative will be presented in the HDPP workshop held at the 12th HUPO world congress.

[1] Topf F., Schvartz D. *et al*. The Human Diabetes Proteome Project (HDPP): From Network Biology to Targets for Therapies and Prevention. *Translational Proteomics* 2013, in press.

Speakers:

The Human Diabetes Proteome Project (HDPP): 2013 Update
Jean-Charles Sanchez
Geneva University, Switzerland

A Systems Omics Perspective of Diabetes
Michael Snyder
Stanford University, USA

Beta-cells and Mitochondrial Function
Martin Kussmann
NIHS, Switzerland

The Study of Glucotoxicity on Rat INS-1E Pancreatic Beta-Cells
Domitille Schvartz
Geneva University, Switzerland

Genome Wide Methods and Proteomics in Biomarker Discovery for Type 1 Diabetes
Dave Goodlett
University of Maryland, USA

NIDDK Funding Opportunities
Salvatore Sechi
NIH, USA

HPP Initiative Session 10: C-HPP (Part 2) - Poster Session

Tuesday, September 16 8:15 - 9:30 Exhibition Hall

Organizers:
Young-Ki Paik, Bill Hancock, Gyorgy Marko-Vargas

There is a special section within the Exhibition Hall dedicated to HPP-related posters. For C-HPP there will be a number of posters representing each chromosome. Chromosome/C-HPP-related posters will be attended during this special early morning poster session.

Posters relating to both the B/D-HPP and C-HPP are welcome in this special section of the exhibition hall. Posters may be displayed throughout the congress week to maximize viewing opportunities.

HPP Initiative Session 11: C-HPP (Part 3) - Bioinformatics

Tuesday, September 17 8:15 - 9:30 Room 303-304

Organizers:
Young-Ki Paik, Bill Hancock, Gyorgy Marko-Vargas

In this session, chaired by Bill Hancock, the C-HPP consortium members from 25 countries will discuss general matters related to protein database, updated status on the missing proteins, integration of both ENCODE and Metabolomics data into the C-HPP scaffold.

Speakers:
- Siqi Liu (BGI, China) will present the survey results of RNA-Seq service through the C-HPP consortium and give some update on the RNA-Seq database which can be useful for the consortium members.
- Peter Horvatovich (University of Groningen, Netherlands) will present recent progress in WiKi on the C-HPP
- Reports from the web browsers (Rob Goode, Ping Xu, Siqi Liu, Andrey Lisita, and Seul-ki Jeong)
- Updates from Protein atlas and Monash antibody initiative (Emma Lundberg and Ed Nice)
- Encode update (Kate Rosenbloom and Mike Snyder)

HPP Initiative Session 12: HGPI Glycoproteomics

Tuesday, September 17 8:15 - 9:30 Room 301

Organizer:

Hisashi Narimatsu Research Center for Medical Glycoscience (RCMG), National Institute of Advanced Industrial Science and Technology (AIST)

The aim of Human Disease Glycomics / Proteome Initiative (HGPI) is to identify disease-related glycosylation changes in blood and other body fluids for developing glycobiomarkers of cancer, inflammation, auto-immune disease, other chronic fibrotic disease and so forth. To discover such glycan alterations, development of reliable technologies to reveal glycan structures was necessary. Thus, the pilot studies for standardization of glycan structural analyses were carried out as international collaboration with participation of worldwide laboratories with various distinctive technologies. Thus far, two pilot studies were completed successfully on the analyses of common purified glycoproteins for each of N- and O-glycans. The results and assessment of the used methodologies were published[1,2]. Presently, the third pilot study on glycan structural analyses of complex mixtures (soluble and insoluble fractions of two kinds of cell lysates) is progressing; now the analyses of the data contributed by 10 participants have been ongoing. The overview will be reported in the initiative session in Yokohama.

Recently, as described by P. Lagrain et al.[3], HUPO launched a global Human Proteome Project (HPP), which was designed to map the entire protein set in humans. HPP consists of two major branches: C-HPP (Chromosome-Centric HPP) and B/D HPP (Biology and Disease-driven HPP). Through this organizational reformation, all pre-existing initiatives will be incorporated into one of the B/D-HPP. Then, taking upon this opportunity, a new international collaboration project was proposed by the current chair of HGPI, Narimatsu, in 11th Annual World Congress held in Boston, 2012. The new project is designed to expand disease glycomics to glycoproteomics and named tentatively as the B/D-driven Glycoproteome Project (B/D-GPP). In this initiative session in Yokohama, the proposal to the project and latest technologies on N- and O-glycoproteomics will be introduced.

1, Wada Y, et al. (2007) Glycobiol.
2, Wada Y, et al. (2010) MCP
3, Legrain P, et al. (2011) MCP

Speakers:

Summary of the First to Third Pilot Studies of Human Disease Glycomics/Proteome Initiative (HGPI)

Hiromi Ito
Department of Biochemistry, Fukushima Medical University

Proposal of a New International Collaboration Under the HPP: Biology/Disease-driven Glycoproteome Project (B/D-GPP) and Current Resources

Hisashi Narimatsu
Research Center for Medical Glycoscience (RCMG), National Institute of Advanced Industrial Science and Technology (AIST)

Dissection of the Human GalNAc O-glycoproteome? Mapping Specific Functions of Individual Polypeptide GalNAc-transferase Isoforms by Zinc-finger Gene Engineering of Human Cells

Katrine ter-Borch Gram Schjoldager
Department of Cellular and Molecular Medicine, University of Copenhagen

HPP Initiative Session 13: iMOP - Initiative on Model Organism Proteomes

Tuesday, September 17 8:15 - 9:30 Room 302

Organizers:
Michael Hengartner, Sabine Schrimpf

Fundamental pathways and biological processes are conserved across species, and studies of model organisms play an important role for understanding human biology and health. The continuous improvement and use of mass spectrometry have led to a dramatic increase in proteome coverage, and to the inclusion of an increasingly broad range of model organisms over the recent years. However, new model organism species are typically supported by only small communities. To form a broader model organism proteomics community, the initiative on model organism proteomes (iMOP; www.imop.uzh.ch) was integrated into HUPO. The research interest of the iMOP community is already quite diverse; however, we still encourage more research groups to join iMOP. Current iMOP members either focus on the interaction between humans and other organisms at the proteome level or and they are interested in the relevance of model organism proteomes to the human proteome. They run inter- and intra-species proteome and transcriptome comparisons to address evolutionary aspects and pathway development. iMOP members also focus on species that are important for food production and on host-pathogen-interactions. The iMOP initiative distributes proteomics knowledge to a wide range of model organism communities that are otherwise not closely linked. iMOP will contribute to the human proteome project (HPP) by providing comparative studies across species.

We will take the opportunity to discuss the future aims and focus of iMOP during the session. The following speakers will give 15-min talks followed by five minute discussion. The session will conclude with general discussion.

Speakers:

The Methylproteome Network of *Saccharomyces cerevisiae*

Marc R. Wilkins
University of New South Wales, Australia

Secretome Protein Profiling of Growth Interaction between *Listeria monocytogenes* and *Lactobacillus lactis* subsp. *lactis*

Paola Roncada
Lazzaro Spallanzani, Italian Experimental Institute, Milan, Italy

Acetyl-phosphate Links Metabolism to Global Acetylation Dynamics in *E. coli*

Brian Tate Weinert
University of Copenhagen, Denmark

HPP Initiative Session 14: Proteome Analyzer: A New High Throughput Platform

Tuesday, September 17 8:15 - 9:30 Room 311+312

Organizer:
Bruno Domon, representing the Mass Spec HPP Pillar

The proteomics community consistently seeks simple, cost-effective tools to analyze full proteomes

(or part thereof) that are routinely applicable in research laboratories. Consequently, there is thus an immediate need for instruments and solutions that enable a rapid, simultaneous, and systematic analysis of very large sets of proteins. Over the past decades, *RNA-sequencing* has shown a successful path forward in the genomics arena, which could provide guidance as a model for proteomics community.

This session aims to be a forum to discuss and to delineate the characteristics of an ideal analytical platform allowing routine proteomic experiments, where end-users (biologists, clinicians), manufacturers, and analytical biochemists share their experience and needs. This should guide the design of a "generic proteome analyzer" and to formulate engineering requirements. The discussion will cover all aspects of a proteomic experiment, including the sample preparation, the separation of the peptides, the mass spectrometric analyses, and the analysis of the data, thus providing an integrated solution.

Two working groups will be formed with the objectives of discussing issues, and needs for different types of applications, and to outline engineering requirements of a *Proteome Analyzer*.

Two "variants" of a *Proteome Analyzer* will be considered during this session, which fulfill distinct purposes and needs, and thus may (or may not) have different requirements:

- "*High-throughput western blot like Proteome Analyzer*" to help biologists to identify and detect proteins in samples in a targeted way, and
- The proteomic analog of a "*RNA-Seq*" *Analyzer*": that could perform routine and systematical characterization of the proteome components.

This session will meet for a brief introduction and then break into two working groups for guided discussion. At the end of the session, both working groups will come back together for a brief summary.

- Working Group I: Proteome Analyzer I: Large-scale Western Blot Surrogate. Chairs Ruedi Aebersold and Mark Cafazzo (representative of IAB)
- Working Group II: Proteome Analyzer II: RNA-Seq Proteome Analog. Chairs Mike Snyder and Andreas Huhmer (representative of IAB)

HPP Initiative Session 15: Cardiovascular

Tuesday, September 17 8:15 - 9:30 Room 313+314

Organizers:

Jenny Van Eyk, Cathy Costello, Peipei Ping

Worldwide, cardiovascular disease is the number one cause of mortality. Understanding the physiological and pathological proteomes of the many cell types and organs that comprise the heart and vascular system is required for improved diagnosis and therapies. The aim of this initiative is to i) bring together a diverse group of investigators in the area of heart and vascular diseases, ii) to support scientists in basic, clinical and translation research with respect to training and the application of proteomics and iii) to assist in the translation of proteomics into clinical medicine.

Session will include:

The Initiative for Cardiovascular Translation (What are the Big Clinical Questions?)
Peipei Ping and Young Clinical Investigator Awardee

Challenges in CVD Tissue Analysis (Proteomic Analysis of Left Ventricular Tissues in Dilated Cardiomyopathy Mouse Models)
Mitsuhiro Nishigori

How to Handle the Really Difficult and Challenging Cardiovascular Proteomes (Systematic Characterization of Human Platelets in Arterial Vascular Disorders by Quantitative Proteomics)
Albert Sickman

Global thoughts Across Species and Cardiovascular Proteomes (A Plasma Membrane Proteomic Analysis of Mouse and Human Cardiovascular Proteins)
Antony Gramolini

Thoughts on Proteome Analysis of Disease Stage Classification (Aortic Aneurysm Stage Classification Utilizing Protein Profiles)
Hiroaki Yaji

Summary and Next Steps
Cathy Costello and Jenny Van Eyk