

HUPO 2011
10TH WORLD CONGRESS
4-7 SEPTEMBER 2011

Geneva

HUPO Initiative Programmes



HUP0 Initiative Programmes

SUNDAY 4 SEPTEMBER 2011

09:00-12:00

HPP CONSORTIUM

ROOM L

Organized by Pierre Legrain, Gil Omenn and Young-Ki Paik

Theme Next steps in the development of HPP to become a top scientific initiative.

Goals To establish a formal HPP consortium (Technology, C-HPP and B/D-HPP).

Chair: Gil Omenn/Pierre Legrain

- | | |
|----------------|---|
| 09:00 - 09:10 | Introduction by Gil Omenn |
| 09:10 - 09:25 | Update on the HPP Working Group Activity (2010/2011)
by Pierre Legrain, Manager of HPP WG, CEA, France (PC31) |
| 09:25 - 11:25 | Discussion: "Formation of the HPP Consortium" <ol style="list-style-type: none"> 1. Proposal for the Formation of the Technology Consortium of HPP with IAB inputs: The Three Pillars
Moderator: Bill Hancock, Co-Chair of IAB and of C-HPP Consortium Technology & Bioinformatics Update, Ruedi Aebersold, Mathias Uhlen, Amos Bairoch, Eric Deutsch 2. Update on the Chromosome-Centric HPP (C-HPP) Working Group Activity
by Young-Ki Paik, Chair of C-HPP, YPRC, Korea (PC032/OC074) 3. Presentation of a Proposal for the Formation of Biology/Disease-HPP Consortium
by Gil Omenn & Ruedi Aebersold 4. Leadership: Nomination of Chairs of Technology, B/D-HPP and HPP consortium
Moderator: Pierre Legrain 5. Introduction of Senior Scientific Advisory Board for HPP
Moderator: Young-Ki Paik |
| 11:25 - 11:35: | Conclusions and Action Plans |
| 11:35 - 12:00 | General Discussion |

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MONDAY 5 SEPTEMBER

07:00 – 08:30**HUMAN LIVER PROTEOME****ROOM K**

- 07:00 - 08:30 Chairs: José M. Mato, Laura Beretta & Fuchu He
- 07:00 - 07:15 **OC001**
**SEARCHING FOR NON-INVASIVE BIOMARKERS FOR LIVER INJURY:
EXOSOME AND PEPTIDOME APPROACHES**
Felix Elortza
- 07:15 - 07:30 **OC002**
**PROTEOMIC ANALYSIS OF HEPATOCELLULAR CARCINOMA
IDENTIFICATION OF TARGET PROTEINS AND FUNCTIONAL IMPLICATIONS**
Fernando Corrales
- 07:30 - 07:45 **OC003**
A METHOD FOR PROFILING TRANSCRIPTION FACTORS
Jun Qin
- 07:45 - 08:00 **OC004**
A WORKFLOW FOR IN DEPTH COVERAGE OF THE MOUSE LIVER PROTEOME
Jun Qin
- 08:00 - 08:15 **OC005**
**THE NOVEL ROLE OF AN EXOSOME SECRETION RELATED PROTEIN
IN THE METASTASIS OF HEPATOCELLULAR CARCINOMA**
Ying Jiang
- 08:15 - 08:30 **Concluding remarks**

MONDAY 5 SEPTEMBER 2011

10:30-12:30**HBPP SESSION - HUPO 2011****ROOM K****“Launching Human Brain Proteome Atlas Project”**

- 10:30 - 10:50 **OC021**
Strategies for creating Human Brain Proteome Atlas
Young Mok Park
- 10:50 - 11:10 **OC022**
**Strategies of tissue and cell sampling in early stages of AD in order to
assess and to compensate confounding ante- and post-mortem factors**
Helmut Heinsen
- 11:10 - 11:30 **OC024**
Maldi imaging For neuropathologies investigation.
Michel Salzet (or Isabelle Fournier)

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- 11:30 - 11:50 **OC025**
Biomarker for Neurodegenerative Diseases - Brain Regions of Interest
 Helmut Meyer
- 11:50 - 12:10 **OC023**
The level of DNA hydroxymethylation in Alzheimer's disease (AD) and normally aged brain.
 Harry Steinbusch
- 12:10 - 12:30 **OC026**
Characterization and quantification of α -synuclein – a potential biomarker for Parkinson's disease
 Katrin Marcus

MONDAY 5 SEPTEMBER

EuPA PRESENT AND FUTURE

Chair: Gyorgy Marko-Vargas

13:15 – 15:00

HALL A

OC027

SHAPING THE FUTURE OF THE EUROPEAN PROTEOMICS ASSOCIATION EUPA

Gyorgy Marko-Vargas

MONDAY 5 SEPTEMBER 2011

HUP0 PROTEOMICS STANDARDS INITIATIVE

15:00-17:00

ROOM G

The HUP0 Proteomics Standards Initiative (PSI) defines community standards for data representation in proteomics to facilitate data comparison, exchange and verification. In this session we discuss current status and future plans, and invite feedback from the community and fellow HUP0 Initiatives.

Agenda

- 15:00 – 15:10 **Welcome**
 PSI overview
 Pierre-Alain Binz, SIB.
- 15:10 – 15:25 **Molecular Interactions**
 As a key result of the EU PSIMEx grant, the PSICQUIC common query interface for currently 15 interaction data resources has been published
 Sandra Orchard, EBI

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- 15:25 – 15:40 **Mass Spectrometry**
The Transitions Markup Language (TraML) is a new format being developed for encoding selected reactions monitoring transitions
Eric Deutsch, ISB
- 15:40 – 15:55 **Protein Identifications**
mzIdentML (released) and mzQuantML (under development) provide a full-featured representation for MS-based protein identification and quantification with full evidence track
Martin Eisenacher, MPC Bochum
- 15:55 – 16:05 **MIAPE Quant**
MIAPE guidelines for Mass Spectrometry Quantification are now being defined. These guidelines will help to standardize the reporting for the quantitative data and will allow a better understanding and critical evaluation of these approaches
Salvador Martinez-Bartolomé, ProteoRed
- 16:05 – 16:15 **mzTab**
The mzTab format provides a concise overview of protein identifications and quantitations in a standardized format
Juan Antonio Vizcaino, EBI
- 16:15 – 16:25 **2D case study**
A DIGE study on the effects of salbutamol on the rat muscle proteome - an exemplar of best practice for data sharing in proteomics
Juan Pablo Albar, ProteoRed
- 16:25 – 16:35 **ProteomeXchange**
The ProteomeXchange consortium aims to provide a single point of submission to a network of collaborating proteomics repositories
Henning Hermjakob, EBI
- 16:35 - 17:00 **Open Discussion**

MONDAY 5 SEPTEMBER 2011

HUMAN DISEASE GLYCOMICS / PROTEOME INITIAVE

Chairs: Hisashi Narimatsu, Naoyuki Taniguchi, Anne Dell

17:00-19:00

HALL A

17:00 - 17:20

OC046

FUCOSYLATED ALPHA-FETOPROTEIN(AFP): STRUCTURAL BASIS AND DEVELOPMENT OF ANTIBODY-LECTIN ENZYME IMMUNOASSAY

Naoyuki Taniguchi

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- 17:20 - 17:40 **OC047**
SUGARS IN THE REAL WORLD: ARE CULTURED CELLS A GOOD MODEL
SYSTEM FOR STUDYING PROTEIN GLYCOSYLATION?
Nicki Packer
- 17:40 - 18:00 **OC048**
GLYCOPROTEOMICS APPROACH TOWARD DISCOVERY OF GLYCOBIOMARKERS
Hisashi Narimatsu
- 18:00 - 18:20 **OC049**
ABERRANT O-GLYCOSYLATION OF IGA1 AND PATHOGENESIS
OF IGA NEPHROPATHY
Jan Novak
- 18:20 - 18:40 **OC050**
MASS SPECTROMETRIC STRATEGIES FOR GLYCOMICS AND GLYCOPROTEOMICS
Stuart Michael Haslam
- 18:40 - 19:00 Open Discussion

MONDAY 5 SEPTEMBER 2011
HUP0 CARDIOVASCULAR INITIATIVE
Chair: Peipei Ping

17:00-19:00
HALL B

- 17:00 -17:30 Proteome Biology of Cardiovascular Medicine: On the Boat of
Translational Research
Peipei Ping
- 17:30 -18:00 Reorganization of cyclic nucleotide signaling pathways in dilated
cardiomyopathic hearts
Arjen Scholten
- 18:00 -18:30 Human Protein Knowledgebase for the Heart and Soul
Henning Hermjakob
- 18:30 - 19:00 Open Discussion

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MONDAY 5 SEPTEMBER 2011

17:00-19:00

PROTEOME BIOLOGY OF STEM CELLS INITIATIVE

HALL C

Chairs: J. Krijgsveld , A. Heck

- | | |
|---------------|--|
| 17:00 - 17:20 | <p>OC051
 USING MASS SPECTROMETRY BASED PROTEOMICS TO UNRAVEL KEY MOLECULAR COMPONENTS IN STEM CELL BIOLOGY
 A. Heck</p> |
| 17:20 - 17:40 | <p>OC052
 PROTEOME ANALYSIS OF HAEMATOPOIETIC STEM CELLS AND MULTIPOTENT PROGENITOR CELLS
 D. Klimmeck</p> |
| 17:40 - 18:00 | <p>OC061
 QUANTITATIVE PROTEOMICS TO UNRAVEL NEURAL PROGENITOR/STEM CELLS (NPCS) INTERCELLULAR COMMUNICATION
 A. Bachi</p> |
| 18:00 - 18:20 | <p>OP086
 GLYCOBIOLOGY AND GLYCOMICS OF EMBRYONIC STEM CELLS
 S. Dalton</p> |
| 18:20 - 18:40 | <p>OC053
 IN DEPTH QUANTITATIVE PROTEOMICS ON HUMAN EMBRYONIC STEM CELL DIFFERENTIATION
 B. Blagoev</p> |
| 18:40 - 19:00 | <p>Open Discussion</p> |

MONDAY 5 SEPTEMBER 2011

17:00-19:00

PROTEOMICS MASTER CLASSES

ROOM G

Chair: Thierry Rabilloud

DETERMINATION AND STUDY OF PHOSPHOSITES IN PROTEINS

Speakers : Martin Larsen, Garry Corthals, Tine Thingholm

The HUP0 master classes aim at giving an advanced knowledge on hot topics to researchers who are not beginners in proteomics but are not necessarily experts in these precise topics. To this purpose, experts in the field will be present for the duration of the workshop to answer the practical and fundamental questions of the audience in a workshop/round table style.”

HUP0 Initiative Programmes

MONDAY 5 SEPTEMBER 2011

17:00-19:00

MANUAL INTERPRETATION OF ELECTRON TRANSFER
DISSOCIATION (ETD) MASS SPECTRA OF PEPTIDES

ROOM L

Speaker: Donald F. Hunt,

Electron transfer dissociation mass spectrometry is a break-through technology for sequencing post-translationally modified peptides. In this technique, radical anions of polyaromatic hydrocarbons (fluoranthene and azulene) are employed to transfer electrons to the carbonyl group in the polyamide backbone of multiply charged peptides generated by electrospray ionization. Capture of an electron into the peptide backbone reduces the positive charge on the ion by one, and forms a carbonyl radical anion that then abstracts a proton from a nearby protonated amino group. The resulting carbonyl radical triggers cleavage of the adjacent nitrogen-carbon bond to produce fragments of type c' and z•.

The purpose of the workshop is to provide instruction on how to manually interpret peptide ETD mass spectra. Following a lengthy tutorial about ion structures, fragmentation pathways, predictable changes in fragment ion isotope patterns, etc., we will outline a general approach for the manual interpretation of peptide ETD spectra, solve the sequence of several post-translationally modified peptides, assign homework spectra, and reconvene on the second day of the workshop to go over the homework problems and to explore additional applications of this powerful technology. A packet of lecture notes and handouts will be provided. Attendees should bring an inexpensive calculator, pad of paper, and a small ruler.

TUESDAY 6 SEPTEMBER 2011

07:00-08:30

HKUPP INITIATIVE (KIDNEY AND URINE INITIATIVE)

ROOM K

Chairs: Tadashi Yamamoto, Harold Mischak, Roby Langham

07:00 - 07:15

[OC054](#)

PARTICIPATION OF HUMAN KIDNEY AND URINE PROTEOME PROJECT (HKUPP)
INITIATIVE IN CROSSINITIATIVE ANALYSIS AND HUMAN PROTEOME PROJECT

T. Yamamoto

07:15 - 07:30

[OP055](#)

COMPARISON OF ON-SITE PROTEOMICS STUDY ON LASER MICRODISSECTED FFPE
AND FROZEN HUMAN GLOMERULUS TISSUES

B. Xu

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- 07:30 - 07:45 **OP056**
L-FABP AND H-FABP AS MARKERS FOR ACUTE RENAL INJURY:
A CLINICAL PROTEOMICS STUDY
H. Dihazi
- 07:45 - 08:00 **OP057**
Mass spectrometric characterization of human urine proteome changes induced by
space flight
Kononokhin A.S
- 08:00 - 08:15 **OP058**
Extensive profiling of human urine proteome: construction of SRM transitions for
quantification of urinary biomarkers for acute and chronic kidney diseases.
Y. Yoshida
- 08:15 - 08:30 **Open Discussion**

TUESDAY 6 SEPTEMBER 2011

HAI SESSION (HUMAN ANTIBODY INITIATIVE)

Chairs: Michael Snyder and Mathias Uhlen

10:30-12:30

ROOM K

- 10:30 – 10:40 **Welcome and short background to HAI**
Michael Snyder and Mathias Uhlen
- 10:40 – 10:55 **NIH Protein capture reagents**
Salvatore Sechi
- 10:55 – 11:20 **Recombinant antibodies with phage ESCape**
Michael Snyder
- 11:20 – 11:45 **The Human Protein Atlas**
Mathias Uhlen
- 11:45 – 12:10 **Antibodypedia - a portal for validated antibodies**
Kalle Jonasson
- 12:10 – 12:30 **HAI contribution to the HPP - discussion**
Michael Snyder and Mathias Uhlen

HUP0 Initiative Programmes

TUESDAY 6 SEPTEMBER 2011

12:45-15:00

C-HPP CONSORTIUM

ROOM E

Organized by Young-Ki Paik, Bill Hancock and György Marko-Varga

Theme Setting up short-term and long-term plans coupled to the C-HPP Guidelines
Goals To execute C-HPP guidelines and organization of the C-HPP sub-committees
Co-Chairs Young-Ki Paik, Bill Hancock and György Marko-Varga

12:45 - 12:55 **Introduction-Key Issues for the Execution of C-HPP Guidelines**
 by Young-Ki Paik, Chair of C-HPP Consortium

12:55 - 13:20 **Major Technological Issues for the C-HPP: Web portal, data submission, samples, data integration, etc.**
 by Bill Hancock, co-chair of C-HPP consortium

C-HPP Web Portal by Amos Bairoch

Data Submission & Integration by Henning Hermjakob (EBI) & Eric Deutsch (ISB)

Geomics / Transcriptomics by Michael Snyder

Samples and Affinity Reagents by Mathias Uhlen

13:20 - 14:10 **Introduction of New C-HPP Teams Since Sydney Congress**
 Chair: György Marko-Varga
 5 minutes for each presentation

Chromosome 1	(China) by Fuchu He
Chromosome 2	(Switzerland) by Pierre-Alain Binz (OC077)
Chromosome 3	(Japan) by Toshihide N.Shimura
Chromosome 6	(Canada) by Paul Keown
Chromosome 7	(Australia) by Mark Baker
Chromosome 11	(Korea) by Jong Shin Yoo
Chromosome 14	(France) by Jerome Garin & Charles Pineau

14:10 - 14:35 **Update on the ongoing C-HPP**
 Chair: William Hancock

Chromosome 18 (Russia) by Alex Archakov
 (OP081/OP077) & A.V Lisirsa (OP078 / OP080)

Chromosome 19 (Sweden / others) by Juan Pablo Albar & György Marko-Varga (OP076)

Others (Until time is permitted)

14:30 - 15:00 **Setting Up the Action Plans, Guidelines, and Governance: General discussion**
 Chair: Young-ki Paik

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TUESDAY 6 SEPTEMBER 2011

EUPA COMPANY AFTERNOON

15:00-17:00

ROOM E

TUESDAY 6 SEPTEMBER 2011

INITIATIVE ON MODEL ORGANISM PROTEOMES (iMOP) (OC098)

Chairs: S. Schrimpf, M. Hengartner

15:00-17:00

ROOM F

15.00 – 15.10	Introduction Michael Hengartner
15.10 – 15.35	PaxDB Christian von Mering
15.35 – 16.00	Farm animal proteomics (OC099) Emøke Bendixen
16.00 – 16.25	Plant proteomics (OC100) Joshua Heazlewood
16.25 – 16.50	Host-pathogen interaction Dirk Bumann
16.50 – 17.00	General discussion about iMOP

TUESDAY 6 SEPTEMBER

PROTEOMICS MASTER CLASSES

Chair: Thierry Babilloud

17:00 – 18:30

ROOM E

HOW TO BUILD EFFICIENT SRM ASSAYS

Speakers: Ruedi Aebersold, Steve Carr, Susan Abbatiello

The HUP0 master classes aim at giving an advanced knowledge on hot topics to researchers who are not beginners in proteomics but are not necessarily experts in these precise topics. To this purpose, experts in the field will be present for the duration of the workshop to answer the practical and fundamental questions of the audience in a workshop/round table style.”

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TUESDAY 6 SEPTEMBER 2011

17:00-18:30

PROTEOMICS REPOSITORIES AND JOURNALS – A PARTNERSHIP MADE IN H...?

ROOM F

Chairs: Henning Hermjakob and Juan Pablo Albar

Proteomics repositories and journals are the two disseminators of proteomics data and results, so clearly this is a partnership made in heaven, or is it?

In the standard reference example of genomics, the world used to be easy: You generate a sequence, you submit it to a repository, and you publish on it. In proteomics, the situation slowly developed in this direction, but this development is far from complete, and even the “standard” genomics model is starting to creak under the pressure of high throughput sequencing.

In this workshop we will discuss past, present, and future of the interplay between journals and repositories, how well the current situation is serving the community, and which directions future developments should/could take.

Agenda:

- | | |
|---------------|--|
| 17:00 – 17:10 | Welcome and ProteomeXchange concept
Chair: Henning Hermjakob, European Bioinformatics Institute |
| 17:10 – 17:40 | A journal, or a database?
Scott Edmunds, BGI Shenzhen; Editor in chief, GigaScience journal |
| 17:40 – 18:00 | Raising the standards
Robert Chalkley, UCSF; Editor, Molecular and Cellular Proteomics journal &
Henning Hermjakob, European Bioinformatics Institute |
| 18:00 – 18:30 | Podium discussion
Chair: Juan Pablo Albar,
Participants: Scott Edmunds, Robert Chalkley, Eric Deutsch
Christopher Kinsinger, Juan J. Calvete |

This workshop is sponsored by the EU ProteomeXchange grant.

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WEDNESDAY 7 SEPTEMBER 2011

07:00-08:30

IAB WORKSHOP AND AWARD

ROOM E

Chairs: A. Paulus, Bill Hanckok

- | | |
|---------------|---|
| 07:00 – 07:25 | The Orbitrap story: from dream to mainstream
Alexander Makarov - Thermo Fisher Scientific, Bremen, Germany
Winner - HUP0 Science and Technology Award |
| 07:25 – 07:35 | Advanced mass spectrometry for speed independent proteomics
Jim Landridge, Director, Proteomics - Waters |
| 07:35 – 07:45 | New approaches for improving assay reproducibility for quantitation of peptides and new approaches for improving protein identification
Keith Waddell, LC/MS Application Solutions Manager - Agilent |
| 07:45 – 07:55 | Integrated Mass Spectrometry-based Solutions: Around the Proteome in 10 Minutes
Andreas Hühmer, Director of Proteomics Marketing - Thermo Fisher |
| 07:55 – 08:05 | PTMScan Technology: Innovative Tools for Pathway Profiling, Biomarker Discovery and Target Identification
John-David Herlihy, Pharma Service and Technical Application Specialist - Cell Signaling Technology |
| 08:05 – 08:15 | Extending the reach of proteomics - tools and trends
Ron Bonner, Principal Scientist - ABSciex |
| 08:15 – 08:25 | Advancements in low abundant proteins detection and consistency of proteome analysis
Roumen Bogoev, Senior Product Manager - BioRad |

WEDNESDAY 7 SEPTEMBER 2011

10:30-12:30

HUMAN PLASMA PROTEOME INITIATIVE

ROOM K

Chairs: Gil Omenn, Ruedi Aebersold, Mark Baker

- | | |
|---------------|--|
| 10:30 – 11:00 | OC117
THE HUP0 HUMAN PLASMA PROTEOME PROJECT: 2011 UPDATE
Gil Omenn |
| 11:00 – 11:30 | OC118
ENABLING COMPREHENSIVE PROTEOMICS MEASUREMENTS WITH THE DEVELOPMENT OF THE COMPLETE HUMAN PEPTIDE- AND SRM-ATLAS
Robert Moritz |

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- 11:30-12:00 **OC119**
CEDAR: A MULTI-TIERED PROTEIN IDENTIFICATION SCHEME FOR SHOTGUN PROTEOMICS, APPLIED TO THE HUMAN PLASMA PEPTIDEATLAS
 Eric Deutsch
- 12:00-12:30 **PC033**
THE HUMAN PLASMA PROTEOME IN PEPTIDEATLAS
 Eric Deutsch

WEDNESDAY 7 SEPTEMBER 2011

13:15-15:00

HPP PLENARY SESSION

Organized by Gil Omenn, Pierre Legrain and Young-Ki Paik

- Theme** Future Direction of HPP
Goals To establish the global commitment and engagement for the HPP
Moderator Young-Ki Paik,

Topic - I : Technology and Biology/Disease-Driven Human Proteome Project (B/D-HPP)

- 13:15 - 13:30 **Network-Centric Human Proteome Project**
 Ruedi Aebersold

- 13:30 - 13:45 **Human Antibody Resources for HPP**
 Mathias Uhlen

Topic-II: Chromosome-Centric Human Proteome Project (C-HPP)

- 13:45 - 14:00 **Encode the Human Parts List**
 Michael Snyder

- 14:00 - 14:15 **Studies on Chromosome Biology and Cancer Proteomics within C-HPP (OC075)**
 Bill Hancock

Topic-III: Clinical Implications of HPP and Concluding Remarks

- 14:15 - 14:30 **Clinical proteomics: are we missing opportunities?"**
 Denis Hochstrasser

- 14:30 - 14:45 **HPP Goals and Vision**
 Cathy Costello

- 14:45 - 15:00 **General Discussion**