A Guide to the C-HPP Workshops in Vancouver
(Web Version, Last Updated Sept 22, 2015)
### Summary of the C-HPP Activities in Vancouver

(Last updated: Sept 22, 2015)

<table>
<thead>
<tr>
<th>SUN, Sept 27</th>
<th>MON, Sept 28</th>
<th>TUES, Sept 29</th>
<th>THURS, Oct 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>HPP General Investigators Meeting</td>
<td>C-HPP (Part 1) Poster Session</td>
<td>C-HPP (Part 3) Principal Investigator Council Meeting</td>
<td>HPP Post-Congress Day</td>
</tr>
<tr>
<td>08:30-15:00 Room 11</td>
<td>7:30 - 09:00 &amp; 16:20-17:30 Exhibit Hall</td>
<td>13:15 - 14:15 Room 12</td>
<td>Venue: SFU Harbour Centre</td>
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<tr>
<td>(Chair: Gil Omenn) 8:30: Gathering/coffee</td>
<td>(Chair: Lydie Lane)</td>
<td>(Chair: Young-Ki Paik)</td>
<td>(Co-Chairs: Gil Omenn, Jennifer van Eyk &amp; Young-Ki Paik)</td>
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<tr>
<td>Progress of HPP</td>
<td>Session 1: 07:30-09:00 (Chr Odd No. 1, 3, 5,...21) Session 2: 16:20-17:30 (Chr Even No. 2, 4, 22, X, Y, Mito.)</td>
<td>Session 1: 08:30 AM, Room 18 C-HPP Deliverables 2016</td>
<td>0830-16:30:</td>
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<tr>
<td>09:00: Overview and Metrics 09:20: C-HPP highlights 09:40: B/D-HPP highlights 10:00: PeptideAtlas/neXtProt 2015 updates 10:20 Human Protein Atlas 2015 10:40 JPR C-HPP 2015 SI Highlights 11:30 Lunch break-out Sessions C-HPP (Rm 18) B/D-HPP (Rm 19) 13:30 Crowd-Sourcing Prot. 14:00 Testis Proteins 15:00: Membrane Proteins 16:00: Reports from Breakout Session 1630: Plan of HPP activities 17:00: Adjourn</td>
<td>Poster Awards (Cash Prize and Award Certificate by HUPO President) will be given to Total 10 Best Outstanding Poster Presenters at the Closing Ceremony.</td>
<td>Lunch will be provided to all PIC members and invited members: C-HPP EC, SSAB, Co-PIs</td>
<td>highlights of Sun-Wed HPP</td>
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<td>(Appendix 2)</td>
<td>(Appendix 4, 5)</td>
<td>(Appendix 6)</td>
<td>(Appendix 7)</td>
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<tr>
<td>C-HPP (Part 2) Bioinformatics Session 13:15 - 14:15 Room: 12</td>
<td>HPP Keynote Session 14:30 - 16:20 Room 11</td>
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<td>(Chair: Eric Deutsch)</td>
<td>(Co-chairs: Gil Omenn and William S. Hancock)</td>
<td>Two keynote talks and multiple invited oral talks will be presented.</td>
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<td>● Topics: “What is sufﬁcient evidence for publishing claims of detection of missing proteins?”</td>
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<td>(Appendix 6)</td>
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<tr>
<td>● Speakers: Eric Deutsch, Reudi Aebersold and more</td>
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<td>(Appendix 3*)</td>
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1. C-HPP EC Meeting: Sunday, 27th Sept, 07:30-08:30 AM Room 19
2. B/D-HPP EC Meeting: Sunday, 27th Sept, 07:30-08:30 AM, Room 18
HUPO Scientific Program at a Glance

Floor Map for C-HPP Workshop Lecture Rooms (11, 12, 18, 19)
Appendix 1

HPP General Investigators’ Meeting in Vancouver
(Last updated 20 September)

Sunday, Sept 27, HPP General Investigators’ Meeting, Room: 11

0830: Gathering/coffee/interactions within groups & SSAB

Progress of the Human Proteome Project
0900   Gil Omenn: Overview and Metrics
0920   Young-Ki Paik:  C-HPP highlights
0940   Jennifer van Eyk: B/D-HPP highlights
1000   Lydie Lane & Eric Deutsch: neXtProt & PeptideAtlas 2015 updates
1020   Mathias Uhlen & Emma Lundberg: Human Protein Atlas 2015

1040-1130  Highlights of the JPR C- HPP 2015 special issue:
            Bill Hancock, Chris Overall, Deutsch, Paik, Omenn (editors),
Ulrich Eckhard U (Univ. of British Columbia, Vancouver, Canada)
    Recent Progress on TAILS N-terminomics
Pengyuan Yang (Fudan Univ., Shanghai, China)
    Finding missing proteins from epigenetically manipulated human cell lines
Ping Xu (BPRC, Beijing, China)
    Special enrichment strategies for missing proteins
Peter Horvatovich (Univ. of Groningen, Groningen, The Netherlands)
    In vitro transcription/translation system: a versatile tool

1130-1330  Lunch and Breakouts: (Lunch will be served in the foyer.)

1: C-HPP working session with lunch, led by Young-Ki Paik (Rm 18)
   See Appendix 1A
2: B/D-HPP working session with lunch, led by Jennifer van Eyk &
   Fernando Corrales (Rm 19)
3: Members of the resource pillars will go to these breakouts.
Proposed Crowd-Sourcing **Project on Plasma Proteome Variation**, a multiplex SRM/SWATH-MS analysis of priority proteins in HUPO Volunteers (Snyder) Initial comments from **Senior Scientific Advisory Board** (Snyder et al)

1400  
**Panel on the Testis Proteome**: highly enriched for missing proteins  
Charles Pineau (France), Siqi Liu (China), Ghasem Salekdeh (Iran), Cecilia Lindskog (Sweden)

1500  
**Panel on Membrane Proteins**: special challenges  
YuJu Chen (Taiwan), Takeshi Tomonaga (Japan), Akhilesh Pandey (USA), Mathias Uhlen, (Sweden); Lead Discussant: Alexey Nesvizhskii

1600  
**Reports from Breakout Sessions**  
(C-HPP and B/D-HPP leaders)

1630  
**Discussion of Plan of HPP activities for the week**: 20 morning B/D-HPP and C-HPP workshops (M-T-W); Mon lunchtime C-HPP Bioinformatics workshop, Tues Early Career Researchers session, Tues lunchtime C-HPP PI mtg, Tues HPP Congress scientific session, post- Congress HPP Next Steps Thursday Workshop

1700  
Adjourn
Appendix 1A

Agenda for the C-HPP Break-out Session

(Moderated by Young-Ki Paik, Bill Hancock and Lydie Lane)

Part I: Opening Stimulatory Talk: New ideas for missing protein study?

11:30- Use of mouse peptides/tissues for validation of human missing proteins

Christoph H. Borchers, University of Victoria - Genome British Columbia Proteomics Centre

11:45- Q & A

Part II: Update on the C-HPP Restructuring Initiative

11:50- Introduction & Guidance for Group Discussion

<table>
<thead>
<tr>
<th>Group</th>
<th>Chromosome Teams</th>
<th>Remarks</th>
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<tbody>
<tr>
<td>IVTT</td>
<td>5, 10, 15, 16, 19</td>
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<tr>
<td>Cancer</td>
<td>1, 8, 20, 9, 11, 13 (12, 17 can be joined) (Liver, Lung and CRC)</td>
<td>China-Korea Alliance</td>
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<tr>
<td>Reproduction Disease</td>
<td>2, 14, X, Y</td>
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<tr>
<td>Membrane Proteins</td>
<td>4, 7, 18 (more)</td>
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</table>

12:00- Group Discussion with Lunch

Common agenda to be discussed at each group

Examples: (The followings are just minimum number of items to be discussed)

1) Organization, Designate discussion leader (spokesperson) within each group
2) Goal Setting (year 2016; 2017): -Qualitative and quantitative ways
3) Strategy for coordinated research within group
   a. Sharing reagents (clones, ab, assay) and resources (blood, tissues, cell lines)
   b. Cross functional validation of missing proteins using different platforms
   c. Disease target
   d. Missing proteins exchange to help partner
   e. Workshop plans in 2016, DB construction
   f. Working with B/D-HPP group

13:20- Wrap Up (Each leader can prepare the reports in 2 power point slides)
Appendix 2

C-HPP Poster Session (Exhibit Hall)

Monday, Sept 28, Exhibit Hall (07:30-09:00 [Odd No.] and 16:00-17:30 [Even No])

Co-Chairs: Lydie Lane and Peter Horvatovich

Poster sessions are intended to showcase research in a format that is easy to scan and absorb quickly. This session is designed to facilitate more in-depth discussion of the research than is typically possible in a symposium format.

Session 1: 7:30 - 09:00, Monday, Sept 28
Chromosomes #Odd Numbers (1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21)

Session 2: 16:00 - 17:30, Monday, Sept 28
Chromosomes #Even Numbers (2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, X, Y) and Related Technologies:

- **Evaluation Team for the Best Posters:** Lydie Lane and Peter Horvatovich will organize the evaluation committee for selecting the awardees.

- **Poster Awards** (Cash Prize and Award Certificate Issued by HUPO President) will be given to 10 Best Outstanding Poster Presenters based on the merits of contents, significance of discovery and deliverables.

- In addition to the C-HPP research subjects (e.g., mapping missing proteins, ASV, PTM on each chromosome), any papers related to common technology or resources applicable to C-HPP can also be presented. All eligible presenters (first authors or senior authors) should be one of the C-HPP members (PI, co-PI or participating members).

- All posters need to be loaded on the board between 19:30-21:00 pm, Sunday. At least one author is required to be in attendance at the poster for the entire duration of the designated session to be qualified for Young Investigators’ Award (Session 1: 07:30-09:00, Session 2: 16:00-17:30)
● Posters should be prepared according to the guideline set by HUPO Congress organizer. Poster Presentation Guidelines (see details at http://hupo2015.com/program/information-for-speakers-and-poster-presenters/)

- The maximum poster size is: 4' x 4'. Poster Boards will be Velcro and Push Pin compatible.
- All Posters will be displayed in the Exhibit Hall at the Vancouver Convention Centre, East Building.
- Keep illustrations and text simple, remember that one must be able to read it from a distance.

- **Setup hours:** Sunday, September 27 – 19:30 – 21:00 (during Welcome Reception)
- **Take down hours:** Wednesday, September 30 by 16:30; any posters not removed by 16:30 will be discarded by management.

**Poster Printing Guidelines:** It is important to set up your slide to a size that is proportional to the printed size of the poster. In PowerPoint, go to Page Setup and select Custom. Fill in the proper width and height.

The following printed poster sizes are available:

48 inches (w) x 48 inches (h) – square
48 inches (w) x 24 inches (h) – landscape
24 inches (w) x 24 inches (h) – square

**Maximum poster size:** each poster can be a maximum size of 48 inches wide x 48 inches high.

**Fonts** – Choose two fonts at most, nothing cursive. Stick to sans-serif fonts for legibility: Arial and Helvetica are recommended. If you wish to use a serif font, we recommend Times New Roman (Windows) or Times (Macintosh).

**Excel Charts** – You can paste Excel charts into PowerPoint: from Excel, select your chart and Copy, then in PowerPoint, Paste the chart where you want it to appear. For detailed instructions, please click here.

**Word Text** – insert a text box into your PowerPoint slides, copy the text from your Word document and paste it into the textbox in your slide.

**Image Files** – To add image file, select “Insert”>”Picture”. Images should be good quality and appear clear and sharp on your screen. Since they will be enlarged for printing, we recommend that images are set to a resolution of 300 dpi.

**Backgrounds** – For legibility and viewing ease, we suggest that you keep your backgrounds simple and avoid using dark colors.
In this workshop, the current and future HPP data guidelines will be discussed. The goal of the workshop is to understand where the existing guidelines have served the HPP well and poorly, and discuss a proposed set of new guidelines, specifically in the context of advancing confident detections of missing proteins. Each subtopic will be introduced separately, followed by discussion by the workshop participants. Full audience participation is encouraged. The major subtopics include: current HPP data guidelines, data deposition in ProteomeXchange, the 1% protein-level FDR requirement, manual inspection of extraordinary claims, consideration of alternate explanations of the data, use of synthetic reference peptides, and the use of SRM to confirm shotgun results.
Appendix 4

C-HPP Principal Investigator Council Meeting

Tues, Sept 29, 13:15-14:15, Room 12 (with Lunch)

Chair: Young-Ki Paik  Co-Chairs: Bill Hancock and Lydie Lane

PIC Members Invited to This Meeting (as of August 1, 2015)

<table>
<thead>
<tr>
<th>Chr 1</th>
<th>Chr 2</th>
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<th>Chr 18</th>
<th>Chr 19</th>
<th>Chr 20</th>
<th>Chr 21</th>
<th>Chr 22</th>
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</table>

Additional Invitees:

Co-PIs of each Chromosome team, Members of C-HPP EC & SSAB, Amos Bairoch, Emma Lundberg, Eric Deutsch, Christoph Borchers and *Designated New PI candidates: Peter Horvatovich (for Chr 5), Ed Nice (for Chr 7): We will warmly welcome those additional designated New PI candidates for chromosome teams other than Chr 3, Chr 5 and 7.

Agenda (tentative)

1. Welcome Remarks

2. Discussion and Approval of the New PI candidates who will replace the current PIs (Chr 3, Chr 5, Chr 7, possibly more from Sunday 27th Break-out session) who will start their terms from January 1, 2016.

3. Discussion and Approval of C-HPP Restructuring Plans (see attached Appendix 6)

4. Discussion and Approval of Nomination and Election of the C-HPP Co-Chair Who Represents ‘America’ (North and South)

5. 2016 Plans:
   ●14th C-HPP Workshop in Shanghai, China in 2016
Vote on - “Option 1: May 20-21\textsuperscript{st}” or “Option 2: May 27-28\textsuperscript{th}”

(Consider “ASMS meeting in 2016”: 6/5-9, San Antonio, TX)

● JPR SI publication plans (Bill Hancock)

● Cross-Chromosome Workshops and more.

6. Open discussion on how to further stimulate C-HPP Activities; Separate HPP Mtg etc.
Proposal for Restructuring C-HPP Teams

(Draft ver. 2.0)

1. Aims

● To stimulate activity of each team and work performance of chromosome-based proteomics research in a cooperative manner, resulting in more credible and reproducible results.

● To improve efficiency and make a closer working relationship between chromosome teams and their resource pillar towards completion of the scientific goals.

● To make a strong research focus of chromosome teams using the advanced proteomics platform technologies and resources, enabling secure research funding.

2. Why we need restructuring?

● As the technology in proteomics research and large scale competitive publications came out recently, it was necessary for us to closely re-examine the direction of ongoing projects and C-HPP teams’ operation to ensure we continually are at upfront in the studies of Chromosome-based proteomics.

● At the juncture of a half past in Phase I (2012.9-2018.9), the C-HPP leadership felt that some changes in our working structure and consortium operation are necessary as the strong demands on better corporation between teams are emerging, making necessary to develop a team approach to achieve our scientific goals.

● It is also noticed that at present there exist some differences among the consortium teams with respect to research productivity (e.g., publications to JPR special issues, 2013-2015), efficiency of collaborations, level of secured funding and team management. Thus, to improve the current situation, leadership of C-HPP and HPP had an informal meeting in Milano, Italy (June 25, 2015) and they came up with an idea on restructuring the current C-HPP teams.
C-HPP leadership felt that the structural changes need to be done stepwise without disturbing overall organization. This new move will give us a golden opportunity to reshape the leadership (PI) of our individual chromosome teams, if necessary, and build new team networks to achieve our scientific goals.

3. Expected Outcomes

- Restructuring our C-HPP associated teams with a strong focus on the project will bring streamline in the leadership of each team and logistical strategy on completing the project. It will also be a good chance in getting more efficient research works for clustered teams.

- This new move will not only stimulate less active teams by giving them an opportunity to identify a new PI as well as additional working members but also make synergistic outputs by working together with other teams across chromosomes under the specific goals (e.g., missing protein validation, data integration, disease mechanism, biological studies using the same resources and technology platform).

- Regarding more efficient collaboration within HPP group, since C-HPP has a strong technological aspect to improve detection of proteoforms (including missing proteins), we can enhance our collaboration with B/D-HPP teams. For instance, if we identify a missing protein or a proteoforms, we can provide the analytical method to study their functionalities. This should define the collaboration with B/D-HPP teams with addition that they can be a source of precious sample collection for the studies of biological/pathological implications of missing proteins, important for both teams.

- With restructured team, more efforts will be put on metrics to unequivocally define those newly detected protein/proteoforms. Further to this, we can build a consensus on identification of cell types, tissues or biological conditions providing the highest probability of detecting a given protein/proteoform. This also brings improved methods and workflows allowing detection and quantification of missing proteins/proteoforms.

Proposed Action Items by Each Team

We want to suggest that each PI may use the following steps to implement successful changes to each team’s chromosome-based research: of course, they can have modified steps of the suggested one. The discussion topics also include PI change, recruitment of new members, identification of collaborative teams and sharing funds in addition to the given topics, ‘team clustering’ or ‘cross chromosome study group formation’.

Step 1: Each PI of chromosome team may consult his/her team members first and discuss what type of changes would enhance their current operation as well as collaboration to achieve their goals. If this step goes well, then they proceed to step 2.

Step 2: Each team will identify potential new members (e.g., PI, co-PIs, supportive groups,
associate members etc.) and partner(s) and start contacting them by email or phone calls before the Vancouver Sunday (Sept 27) workshop. If necessary, they can seek some advice from the C-HPP co-chairs.

**Step 3:** C-HPP will hold a Break-out session from 11:30 to 13:30 at Room 18, Sunday, Sept 27, in Vancouver Convention Center. In this meeting, they can freely exchange their view on this proposal for their own team development and the potential benefits from this restructuring effort, and each PI reports the outcomes from this discussion to whole group at the meeting. More specifically, **13:30 “Interaction with SSAB and Reports from Breakout Sessions** (led by Mike Snyder). We also would like to encourage all teams to establish team’s long-term plans (2015.9-2018.9, Phase I and 2018.9-2022.9, Phase II) including the research funding.

**Step 4:** All decisions made at this meeting will be reported to C-HPP EC and also be ratified by PIC members at PIC meeting on Tuesday, 13:15-14:15, at Room 12. Although this will conclude the debate on the restructuring plan, we will continue to put our all efforts to improve our organizational operation to accomplish our scientific goals throughout the project period (till Sept 10, 2022).
Appendix 6 HPP Keynote Session:

“The Progress and Challenges of the HUPO Human Proteome Project”

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>09:29-10:15</td>
<td>Appendix 6 HPP Keynote Session</td>
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<tr>
<td>09:30</td>
<td>CS 19: Human Proteome Project</td>
</tr>
<tr>
<td>Date:</td>
<td>09-29-2015</td>
</tr>
<tr>
<td>Time:</td>
<td>14:30 - 16:20</td>
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<tr>
<td>Location:</td>
<td>Room 11</td>
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<tr>
<td>Chairs:</td>
<td>Gilbert S. Omenn, USA &amp; William Hancock, USA</td>
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<tr>
<td>14:30</td>
<td>CS19.01: The Progress and Challenges of the HUPO Human Proteome Project</td>
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<td>Gilbert Omenn, University of Michigan, USA</td>
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<td>14:35</td>
<td>CS19.02: Strategic Points for Dealing with Missing Protein Mapping in the C-HPP</td>
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<td>Young-Ki Paik, Yonsei University, South Korea</td>
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<td>15:00</td>
<td>CS19.03: Controlling False Discovery Rates (FDRs) in Genome-Wide Proteomics Datasets</td>
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<td>Juergen Cox, Max Planck Institute for Biochemistry, Germany</td>
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<td>15:30</td>
<td>CS19.04: How Does an Extra Chromosome 21 Modulate the Quantitative Human Proteome?</td>
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<td>Yansheng Liu, ETH Zurich, Switzerland</td>
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<td>15:50</td>
<td>CS19.05: Mining Missing Proteins Based on the Transcriptomics and Proteomics to the Individual Tissue Tissues</td>
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<td>Qidan Li, Beijing Institute of Genomics, Chinese Academy of Sciences, China</td>
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<td>16:00</td>
<td>CS19.06: Call for a Testis-Epididymis Proteome Project</td>
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<td>Charles Pineau, Inserm U1085 - Inserm, France</td>
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<td>16:00</td>
<td>CS19.07: Refining the Human Proteome: Analyzing Human Tissues by RNA-Seq, Proteomics and Antibodies</td>
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<td>Hannes Hahne, Technische Universität München, Germany</td>
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<td>16:05</td>
<td>CS19.08: Urinary Proteins Originating Uniquely from Each Nephron Segment</td>
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<td>Tadashi Yamamoto, Niigata University, Japan</td>
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<td>16:10</td>
<td>CS19.09: Detection of Chromosome 16 Missing Proteins - Spanish HPP</td>
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<td>Concha Gil, Universidad Complutense de Madrid, Spain</td>
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<td>16:15</td>
<td>Q&amp;A</td>
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Post-Congress HPP Next Steps Workshop
(Last updated 20 September)

Oct 1, Thursday: Post-Congress HPP Workshop Day (Ticketed session)

Location: SFU Harbour Centre, Joseph and Rosalie Seagal Centre, 515 West Hastings Street; Registration fee: 50 CAD/Light refreshments and lunch included.

Co-Chairs: Gil Omenn, Jennifer van Eyk & Young-Ki Paik

0830 Highlights from Sunday-Wed from HPP---selected workshop presentations from C-HPP and B/D-HPP (lightning style, 4 min + question) (chairs van Eyk & Paik)

Invited Speakers (in part)

Heeyoun Hwang (KBSI, Korea): Chromosome-based proteomic study for identifying novel protein variants from human hippocampal tissue using customized neXtProt and GENCODE databases

Katerina Poverennaya (Institute of Biomedical Chemistry, Russia): Master proteome of Chr18. Update 2015

Yi-Ju Chen (Institute of Chemistry, Academia Sinica, Taiwan): In-depth Membrane Proteome Profiling of Lung Cancer Tissues and Cells for Mining Missing Proteins

Elena Ponomarenko (Institute of Biomedical Chemistry, Russia): Gene-centric Knowledgebase as a Tool for Estimating Protein Species Number

And more (TBA)

0930 Strategies for identifying the neXtProt and HPP “missing proteins” (protein existence levels PE 2,3,4) and novel proteins (attributed to pseudogenes, IncRNAs, PE5 protein entries)

0930 Lessons from multiple HPP groups and JPR manuscripts and Monday Bioinformatics
Workshop (Deutsch)
0950 Validation of claims of detecting missing & novel proteins and isoforms (Nesvizhskii, Cox, Yoo)
1010 Searching for and credibly identifying OR proteins (Tress, Deutsch E. Bonghee Lee)
1030 More stringent guidelines established by PeptideAtlas & neXtProt (Lane)
1050 Realizing that some predicted proteins will not be detectable by mass spectrometry, should we adjust the denominator? (Corrales, Ulrike Kusebauch)

1115 SRM/SWATH-MS: (van Eyk, Borchers, Moritz) How to assist HPP investigators and the broad community to utilize these advances from the B/D-HPP? How to improve the workflows, especially for low-abundance proteins and complex tissues?

1200 Lunch with informal discussions

1300 HPP Deliverables for 2016: multiple presenters and active discussion

1300 C-HPP (Paik, Hancock, Lane, He, Archakov, Chen, Yamamoto, LaBaer, Salekdeh):
Emphasis on cross-chromosome collaborations (based on the proposed ‘Clustering Plans’ discussed in Sunday Lunch Breakout)

13:05-13:15: IVTT group
Josh LaBaer (Chr 10) and Gyorgy Marko-Varga (Chr 19)
“In Vitro Transcription/Translation (IVTT)” platform involving Chr 5, 10, 15, 16, 19

13:15-13:30: Cancer group
Fuchu He (Liver Cancer), Je-Yoel Cho (Lung Cancer) and Bill Hancock (CRC/Breast)
China-Korea alliance (Chr 1, 8, 20; 9, 11, 13) and Chr 12 and 17 (To be confirmed later)

13:30-13:40: Reproduction group
Lydie Lane (Chr 2) and Ghasem Hosseini Salekdeh (Chr Y)
Chr2 (Swiss), 14 (France), Y (Iran), X (Japan)

13:40-13:50: Membrane proteins group
Yu-Ju Chen (Chr 4) and Alex Archakov (Chr 18)
Chr 4 (Taiwan), 7 (Australia/NZ) and 18 (Russia)

13:50-14:00 Q & A

1400 B/D-HPP (van Eyk, Corrales, EC, and B/D team leaders):
Popular proteins/ priority proteins (Borchers)
Cancer B/D (Zheng)
New technologies: oxidation in vivo, unnatural amino acids, iPSCs/organs on a chip, biobanking
Early Career Researchers: Mentoring Day and manuscript competition
Physician-scientists initiative
1500 **Antibody Pillar** (Lundberg, Uhlen): tissue proteome; Knock-down Validation Initiative; collaborations with mass spectrometry

1520 **MS pillar** (Domon, Moritz, Rappsilber): Computational MS (conference in Germany end of August); Cross-linking and MS (new initiative)

1540 **Summary and Discussion of Goals and Deliverables for 2016-2017** (All, including SSAB members)

1630 **Adjourn** (Fletcher Room must be vacated)

1630-1745 **Reception** in nearby room