

Fostering international proteomic initiatives to better understand human disease

LAUNCH OF C-HPP

Now, the Wheels Are Ready to Roll Over the Next 10 Years

In Boston, you are invited to witness a historic moment when the HUPO's C-HPP consortium of 24 national and international teams (Figure 1) officially embark on a 10-year global collaboration to produce a reference map of the entire human proteome according to 20,300 protein coding gene numbers. Overcoming earlier skepticism, this chromosome-centric human proteome project, a part of HUPO HPP has now built the necessary infrastructure for the big task. The objective of the C-HPP is to map and annotate all proteins, the body's building blocks, encoded by the genes on each human chromosome and to use this knowledge in Biology, Health and Disease studies (1). Using the three technological pillars (MS, Ab and bioinformatics knowledge base, KB) (2) and integrated omics techniques based on the backbone of cellular and molecular biology, the C-HPP consortium of 24 national/international teams will systematically define the entire set of human proteins in terms of their protein evidence matched with gene and cellular location with characterization of major post-translational modifications.

The immediate task of the C-HPP will find the major protein form for each of the 20,300 protein coding genes and define the missing proteins as lacking evidence in NextProt or containing no mass spectral evidence in the public databases (1, 3). During the past years, throughout the several standards initiatives, proteomics has been proven as the reproducible technique and with the new generation of mass spectrometers the field is now ready for this large task.

We expect that the C-HPP initiative will provide an efficient model of managing resources building on the genome initiatives and initially funded with a mixture of chromosome and individual project funding.



HPP Plenary Session, Geneva Congress
Sept 7, 2011

From left: Gil Omenn, Michael Snyder, Bill Hancock, Cathy Costello, Ruedi Aebersold, Mathias Uhlen, Denis Hochstrasser, Young-Ki Paik

The initiatives will also draw governmental grants and industry-support to further study the C-HPP list of novel and 'missing' proteins as disease biomarker candidates or drug targets. The concept of the C-HPP was first introduced with chromosome 13 as an initial target by Young-Ki Paik in Amsterdam, August 16, 2008 and was based on HUPO's gene centric proposal initiated by John Bergeron in late 2007 (4).

Since then C-HPP has been established as part of HPP through several joint workshops in Toronto (2009), Sydney (2010), Busan (2011), Geneva (2011) and Beijing (2012). As laid out in Figure 2, our strategy is to 1) organize and perform chromosome-centric protein identification and characterization using carefully-selected human samples, 2) construct a web of bioinformatics for the C-HPP (including existing platforms such as PRIDE, GPMDB, PeptideAtlas, UniProt and ProteinAtlas) and emerging initiatives (such as NextProt, ProteomeXchange, Tranche, and HUPO PSI strategy), and 3) integrate

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PRESIDENT'S MESSAGE



Catherine E. Costello
HUPO President

Dear Colleagues and Friends of HUPO,

I am pleased and honored to be serving as HUPO President. I am especially thrilled that I will have the opportunity to welcome you to Boston, my hometown, for the 11th World Congress, September 9 - 13, 2012. Be sure to check the Congress web site (www.hupo2012.com) to review the creative and outstanding program. And, of course, *don't forget to register*.

Much has happened since January. Most significantly, HUPO has been filing documents to complete the transition from HUPO's existing Canadian corporation and to our new non-profit corporation in the U.S. HUPO has taken this route with the advice of the *ad-hoc* committee appointed by the EC in 2009 and with the approval of the EC and the Council. The main reason for a change was to make the administrative management of HUPO more efficient, cost effective and flexible; we have accomplished this by contracting with Scientific Association Management, a U.S. company with extensive experience and success in the management of scientific associations and conferences.

This move ultimately provides to HUPO a high level of managerial expertise and a depth of staffing that will assure that our future operations run smoothly. This change will not affect in any way your HUPO membership. All of HUPO structure remains unchanged - just a new

mailing address and telephone.

You received in August two important notices.

1. An electronic ballot for the election of new Council members. (Please vote online by Sept. 10!)
2. A notice of the vote that will occur at the General Assembly of members in Boston to dissolve the Canadian corporation.

I want to thank and commend our former Montreal staff, Wehbeh Barghachie and Sylvie Ouellette. They have both moved on to new opportunities and we wish them all the best.

This has been an exciting year for HUPO worldwide, with many very well attended national and regional proteomics meetings, workshops, courses and active committees. I have had the pleasure of joining meetings in Lorne, Australia (Australasian), Beijing (Asia Oceania), Niigata, Japan and US-HUPO. All featured excellent speakers, both current leaders and impressive emerging leaders, many interesting posters and workshops and engaging social events. The HPP had

intensive sessions in Beijing that laid much of the groundwork for presentations that will be made at the Boston meeting and in upcoming focused issues of proteomics journals. Several other Initiatives also sponsored sessions. The Liver Proteome Project presented the book that has been assembled to summarize their results.

I congratulate the **winners of the 2012 HUPO Awards:**

Michel Desjardins, *Discovery Award in Proteomics Sciences*

Carol V. Robinson, *Distinguished Achievement in Proteomic Sciences*

Mark S. Baker, *Distinguished Service Award*

David Creasy and John Cottrell, *Science and Technology Award*

Each recipient has made outstanding contributions to our science and we are proud to honour them this year.

I look forward to seeing many of you in Boston and to visiting with you during meetings of your national and regional societies.

Cathy Costello, HUPO President

HUPO Staff, Scientific Association Management



From left: Brent Watson, Marin Walker, Lori Stevens, Miquela Sena, Jennifer Watson, Cindi Lilly, Judith Sjoberg

HUPO

Boston 2012

11th Annual World Congress
September 9 – 13, 2012

Hynes Convention Center
Boston, Massachusetts

DON'T MISS THE PRE-CONGRESS PROGRAM

SUNDAY, SEPTEMBER 9, 2012

Clinical Day

New Technologies and Standardization of Proteomics Symposium

Short Courses

- Advanced Protein Identification Informatics
- Quantitative Bottom-Up Proteomics: Discovery and Targeted Analyses
- Systematic PTM Analysis

Register for the Congress and Pre-Congress Programs online today at www.hupo2012.com.

ORGANIZERS

Michael Snyder, *Chair*
Stanford University

Catherine C. Fenselau
University of Maryland

William Hancock
Northeastern University

Gilbert S. Omenn
University of Michigan



KEYNOTE SPEAKERS

Neil L. Kelleher
Northwestern University



Susan Lindquist
Whitehead Institute for Biomedical Research
Massachusetts Institute of Technology



Stuart L. Schreiber
Broad Institute of Harvard and MIT
Harvard University

PLENARY SPEAKERS

Natalie Ahn, *University of Colorado at Boulder*

Wolfgang Baumeister, *Max Planck Institute for Biochemistry*

Anne-Claude Gingras, *Samuel Lunenfeld Research Institute*

Samir Hanash, *Fred Hutchinson Cancer Research Center*

Hanno Langen, *Roche Molecular Laboratories*

Ulf Landegren, *Uppsala University*

Jeremy Nicholson, *Imperial College London*

Jun Wang, *Beijing Genomics Institute*

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**REGISTER
ONLINE**

PRE-CONGRESS PROGRAMS, SUNDAY, SEPTEMBER 9, 2012

Five full-day programs includes four fee-based programs (three short courses and one symposium) and one free program.

- **Advanced Protein Identification Informatics**

A master short course organized by Natban Edwards

Level: Advanced (intended for practicing proteomics informaticians)

- **Clinical Day**

Presentations from leading experts and young investigators and small group discussions. Organized by Daniel W. Chan and Mark M. Baker

- **New Technologies and Standardization of Proteomics - Free to all congress attendees, no registration required**

Organized by Christoph Borchers and Bruno Domon

- **Quantitative Bottom-Up Proteomics: Discovery and Targeted Analyses**

A short course organized by Sanford Markey

Level: Intermediate (for those doing or planning quantitative proteomics; familiarity with mass spectrometry assumed)

- **Systematic PTM Analysis**

A short course organized by Yingming Zhao

Level: Intermediate (for those with some background on mass spectrometry or PTMs who want more knowledge and skills)

DON'T MISS CONGRESS CLOSING EVENT



Top of the Hub
RESTAURANT & LOUNGE

6:00 - 8:00 PM

Wednesday, September 12

Skywalk Observatory

Prudential Center



A leisurely walk from the Congress location to

elevators that soar to the 52nd floor

- Breath taking views
- Food
- Music

Purchase tickets at the Congress: \$30



REGISTRATION FORM

First Name _____ Last Name _____ Email (important, receipt will be sent by email) _____ Telephone _____

Company or Institution (will be printed on name badge) _____

Address _____

City _____ State/Region _____ Zip/Postal Code _____ Country _____

Become a member of HUPO (or renew your membership for 2012) and save on Congress registration:

- HUPO 2012 Membership, \$100
 HUPO 2012 Student or Post-Doc Membership, \$60
 For Students or Post-docs: Full-time Student Post-doc Yr1 Post-doc Yr2
 Post-doc Yr3 Post-doc Yr4 Post-doc Yr5
- Enter membership amount \$ _____

CONGRESS REGISTRATION, September 9 - 13, 2012. Check one below.

- | | | |
|--|--|--|
| Early-Bird Registration Fees Received before May 4 | Regular Registration Fees Received May 5 – June 30 | Late-Onsite Registration Fees After June 30 |
| <input type="checkbox"/> **Member, \$400 <input type="checkbox"/> Non-member, \$500 | <input type="checkbox"/> **Member, \$450 <input type="checkbox"/> Non-member, \$550 | <input type="checkbox"/> **Member, \$500 <input type="checkbox"/> Non-member, \$600 |
| **To register as a member, 2012 member dues must be paid. | | Enter registration amount \$ _____ |

Students and Post-Docs - To qualify for these special rates must be a full-time student or post-doc at the time of the Congress. Once registered online, please fax or email a copy of your valid student ID or letter from your advisor as proof of your student or post-doc status.

- | | | |
|--|---|---|
| Early-Bird Registration Fees Received before May 4 | Regular Registration Fees Received May 5 – June 30 | Late-Onsite Registration Fees After June 30 |
| <input type="checkbox"/> **Stud. or Post-Doc Member, \$200 <input type="checkbox"/> *Stud. or Post-Doc Non-Member, \$260 | <input type="checkbox"/> **Student or Post-Doc Member, \$225 <input type="checkbox"/> *Stud. or Post-Doc Non-Member, \$285 | <input type="checkbox"/> **Stud. or Post-Doc Member, \$275 <input type="checkbox"/> *Stud. or Post-Doc Non-Member, \$335 |
| **To register as a student or post-doc member, 2012 member dues must be paid. *All students or post-docs must submit proof of status via email or fax to the Congress office. | | Enter registration amount \$ _____ |

Guest Registration, for accompanying persons, includes opening reception, coffee on Monday morning, and tour of Boston on Monday afternoon. Does not include exhibit halls or scientific sessions.

\$100 x _____ number of guests

Enter guest registration amount \$ _____

Congress Social Event, Wednesday, September 12, 2012, Congress Social Event is **not** included in Congress Registration Fee.

\$30 x _____ number of Congress Event Tickets

Enter the Congress Social Event amount \$ _____

PRE-CONGRESS REGISTRATION. Pre-Congress programs are open to everyone. It is not necessary to register for the Congress to participate in the Pre-Congress activities. Select Pre-Congress option below.

Sunday, September 9:

- Quantitative Bottom-up Proteomics (Short Course) Systematic PTM Analyses (Short Course)
 Adv. Bioinformatics Symposium Clinical Day

- | | | |
|---|--|--|
| Early-Bird Registration Fees Received before May 4 | Regular Registration Fees Received May 5 – June 30 | Late-Onsite Registration Fees After June 30 |
| <input type="checkbox"/> Regular, \$150 <input type="checkbox"/> *Stud. or Post-Doc, \$75 | <input type="checkbox"/> Regular, \$160 <input type="checkbox"/> *Stud. or Post-Doc, \$75 | <input type="checkbox"/> Regular, \$180 <input type="checkbox"/> *Stud. or Post-Doc, \$80 |
| *All students or post-docs must submit proof of status via email or fax to the Congress office. | | Enter the total amount for the Pre-Congress option(s) \$ _____ |

Enter **TOTAL** amount \$ _____

Check is enclosed for total amount in U.S. dollars, payable through U.S. bank. Make check payable to **USHUPO-Long Beach**

Charge total amount to my AmEx, VISA or MasterCard. Sorry, no other cards are accepted.

Credit Card Number (AmEx, VISA, or MasterCard) _____ Exp date _____

Card holder's name _____ Card holder's signature _____

Mail or Fax to:

HUPO Congress Office, 2019 Galisteo Street, Building I-1, Santa Fe, NM 87505 (USA)
 Fax: (505) 989-1073 (Faxed registrations must include credit card information.)

Cancellations: All cancellations must be in writing and must be received by August 15, 2012. No refunds will be made for cancellations received after August 15, 2012. All refunds are subject to an administration fee of \$50 US.

C-HPP Continued from page 1

information derived from the C-HPP initiative with results from the study of cellular and biochemical processes in coordination with the B/D-HPP program (deliverables) (3).

The starting point for the project is the current list of proteins in the UniProt, while the end point will be reached when the comprehensive C-HPP database is 100%-matched with 20,300 protein coding genes, including at least one representative alternative splice variant and amino acid polymorphism resulting from a nsSNP, tissue localization and 3 classes of PTMs in whole-chromosome sets (22 autosomal, X, Y). This ambitious plan will be carried out in two phases composed of profiling stage (6 years) and validation stage (4 years) (1, 3). Throughout this 10-year project, C-HPP will generate information useful for the search for new biomarkers and drug targets and also study disease gene families clustered in each chromosome (e.g., cytokine gene family in Chromosome 17). C-HPP outputs will be integrated with results of disease studies from the parallel B/D-HPP project.

To overcome data variations from different laboratories due to the diversity of instrument and bioinformatics platforms and quality criteria, C-HPP will work closely with proteomics journals, and utilize existing data (GPMDB, PeptideAtlas, PRIDE), literature curation (Uniprot, neXtProt), and standardization programs (PSI, CPTAC, Unimod, ABRF, ASMS) to ensure that the data collection is efficient, with consistent QA/QC.

The C-HPP has already encouraged formation of chromosome-formatted databases (www.nextprot.org/, www.gpm.org/) in which new data sets are integrated with existing datasets. We expect that it will be necessary to update the guidelines over time in order to incorporate changes in areas such as new gene annotation, transcriptome variations, evolution in proteomic technologies and bioinformatics (3).



(Chr 3) Yu Ju Chen (Chr 4), Rainer Bischoff (Chr 5), Paul Keown (Chr 6), Mark Baker (Chr 7), Pengyuan Yang (Chr 8), Joshua Labaer (Chr 9 or 10), Jong Shin Yoo (Chr 11), Visith Thongboonkerd (Chr 12), Young-K Paik (Chr 13), Jérôme Garin (Chr 14), Gilberto B. Domont (Chr 15), Juan Pablo Albar (Chr 16), William S. Hancock (Chr 17), Alexander Archakov (Chr 18), György Marko-Varga (Chr 19), Siqui Liu (Chr 20), John Bergeron (Chr 21), Charles Lee (Chr 22), Tadashi Yamamoto (Chr X), Ghasem Hosseini Salekdeh (Chr Y) Recently, two working groups, Chromosome informatics group (led by Bill Hancock) under KB pillar and Resources and Reagent Group (led by Gyorgy Marko-Varga) under AB pillar were established to deal with data management and web operation and various resources including Recombinant DNA stocks, MRM Peptide banks, stem cells, cultured mammalian cells, antibodies (mAb, pAb etc, adaptor) and protein standards, respectively.

The C-HPP consortium has built the web site (www.c-hpp.org) where the key element of each chromosome team's vision is described in the form of project summary. To continue to make our momentum alive, the consortium is now preparing a special issue targeting January 1, 2013 where the members can contribute to their manuscripts focusing on one of four different categories of subjects: the parts list of individual chromosomes, database and biology/disease studies, and tools and resources. In 2013, we are also looking forward to have 7th workshop in Berlin, Free Univ., Germany which will be held in conjunction with Proteomic Forum 2013. This will further extend our network to reach out more EU member countries.

In conclusion, many thanks should go to Dr. John Bergeron who is pioneer to drive the concept of HPP, Dr. Gil Omenn and Dr. Pierre Legrain for their outstanding leadership on the HUPO HPP consortium and all participants of the C-HPP consortium for their enthusiastic support and passion on this new brand type of integrated omics research. We believe the input arising from early skepticism and helpful criticism on this project has made our consortium stronger and more sustainable.

Thank you!

See you all in Boston!

Young-Ki Paik (chair), Bill Hancock (co-chair) and Gyorgy Marko-Varga (co-chair)

References

- 1: Paik YK et al. and Hancock, WS; The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. *Nat Biotechnol.* 2012, 30:221-3.
- 2: Legrain P et al., Omenn, GS The human proteome project: current state and future direction. *Mol Cell Proteomics.* 2011 Jul;10(7):M111.009993.
- 3: Paik YK et al. and Hancock, WS, Standard guidelines for the chromosome-centric human proteome project. *J Proteome Res.* 2012 Apr 6;11(4):2005-13.
- 4: A gene-centric human proteome project: HUPO--the Human Proteome organization. *Mol Cell Proteomics.* 2010 Feb;9(2):427-9.

The leadership of the C-HPP has been well established as 6 membered EC: Young-Ki Paik (Chair), Bill Hancock (Co-Chair), György Marko-Varga (Co-Chair), Fuchu He, Charles Lee, Carol Nilsson. Senior Scientific Advisory Board (chaired by Mike Snyder) will oversee this committee which will be supported by the principal investigator council. The current membership of the consortium is: Fuchu He (Chr 1), Pierre-Alain Binz (Chr 2), Toshihide Nishimura

ANNOUNCEMENTS

COUNCIL ELECTIONS

The election period for the HUPO Board of Directors (HUPO Council) is August 17 to September 10. Again this year, the vote is conducted online.

The email that members receive contains a secure election ID code. Click on the link and cast your anonymous vote.

| | |
|------------------------------|--|
| Election Website Opens | August 17, 2012 |
| Election Closes | September 10, 2012 5:00 PM EST |
| Results are announced | September 11, 2012 during the General Assembly |

NEW HPP WEB PORTAL

www.thehpp.org

HUPO INDUSTRIAL ADVISORY BOARD



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NOTICE

Meeting of the General Assembly All members are urged to attend

2012 General Assembly/Meeting of the Members
5:45 PM

September 11, 2012

Ballroom B, 3rd level, Hynes Convention Center

900 Boylston Street, Boston, MA

in conjunction with HUPO World Congress

www.hupo2012.com

- Financial report
- Election results
- Member vote to dissolve the Canadian charter of HUPO in favor of the new HUPO non profit corporation in the U.S.
- The U.S. non-profit corporation will assume all responsibilities, liabilities, and commitments associated with the Canadian corporation. The conversion will be transparent to members whose membership in HUPO will remain unchanged.

To be environmentally friendly, all the necessary documents are posted in PDF format to www.hupo.org.



Human Proteome Organization

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