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PRESIDENT'S NOTE



Dear HUPO Colleagues,

Welcome to Q2 HUPOST 2015. There are many interesting things to report in this newsletter.

Firstly, the HUPO EC has completed its review of society management companies short-listed to replace Scientific Association Management (SAM). We are delighted to announce that the successful tender was awarded to International Conference Services (ICS), Vancouver. We are delighted to have made a smooth transition thanks to Mathias Posch (ICS President), Jenn Abbott (ICS Vice President), Chelsea Prangnell (HUPO Client Manager), and Joanna Baird (HUPO Support Manager). We have already held a number of strategic meetings with ICS, including our recent inaugural EC Strategic Workshop, and will roll out proposed changes in upcoming months - so keep an eye out for these opportunities.

One obvious change you will see is the new format of the HUPOST newsletter. I trust you will enjoy the new format. In addition, the EC felt it was time for one of HUPO's EC to take on responsibility for HUPOST communication. Emma Lundberg has kindly agreed to take on this task and be the inaugural HUPOST Editor. Please send all your ideas to Emma for circulation. She has started with a new template and is looking for regular contributions from all HUPO sectors – young and experienced alike. Emma will address many of the issues updated in previous President's messages – like progress/selection with upcoming Congresses, awards, nominations and elections committee updates – so you won't have to be bored by me as much in the future.

As we look forward to our annual Congress in Vancouver, Canada this year, we first congratulate our colleagues who won HUPO honours selected by the HUPO Awards Committee, chaired by Martin Larsen. One exciting change I have asked Martin and his committee to manage from next year's Congress in Taipei is formal awards for (i) experienced scientists (as we currently have) as well as new awards for; (ii) early career postdoctoral/MD researchers and (iii) PhD students. I would also like to take this opportunity to thank past chair (Catherine Fenselau) and her committee for their many years sterling service.

Vancouver approaches and Christoph Borchers and his ICS PCO team have organised a very special scientific program packed with new ideas and new topics for us to consider and discuss – from what I see, it promises to be another marvelous HUPO World Congress. Please register early and take advantage of discount rates.

Our flagship scientific program, the Human Proteome Project, goes from strength to strength with much interest generated from considerable publication outputs in 2015. As in the past, I have urged us all to "speak the same language" and in this

regard might I let you know that the latest 2015 Human Proteome Project “metrics” manuscript has recently been accepted in JPR. The HUPO EC and HPP EC are now considering endorsing this and distributing a letter indicating so to Editors-in-Chief of major journals. Please consider this important paper, contribute to the debate and pass on comments you have to any HPP or HUPO EC member.

I hope you find the remainder of our refreshed HUPOST interesting and that you continue to make the HUPO family a strong, vibrant scientific and social network.

See you all in Vancouver, BC, Canada!

Mark S. Baker
HUPO President

EDITOR'S NOTE



Dear Colleagues,

I'm pleased to present the first issue of the new HUPOST that I am now editor of. The redesigned newsletter is a part of a long-term strategy to improve the visibility of HUPO. This quarterly newsletter will feature important updates and reports to spread the knowledge of hot topics in proteomics and the HUPO organization and includes the subjects highlighted below.

An important mission for HUPO is to support the Human Proteome Project. In every HUPOST you will now find the **HPP update** where you can read all about the recent advancements and thrilling findings, written by Gil Omenn, chair of HPP. The Q3 issue, scheduled to come out in September, will introduce the **News in Science** update, written by YuJu Chen as chair of the publications committee. To synergize with regional and national proteomics societies, every issue will feature updates from a few national or regional societies as well as a calendar of upcoming events. In this issue we are announcing the prestigious **HUPO award winners**. You can also read about the upcoming HUPO 2015 World Congress including a new mentoring day for young researchers.

In line with the strategy to improve the visibility, HUPO initiated a **tagline competition** in May. We asked members to suggest a memorable and dramatic tagline that reflects HUPO's role in encouraging the advancement of proteomic research through the initiatives of HUPO. Thank you to everyone who submitted such fantastic and creative taglines. The HUPO Executive Committee is reviewing and ranking all options and we will be excited to announce the winner soon!

I urge you to participate in making this newsletter more interesting and engaging by proposing additions or topics by sending an email to office@hupo.org. Between issues you can visit us at our website (www.hupo.org) to read updates and find resources and links to additional information.

Thank you for taking the time to read our newsletter and I look forward to meeting you all in Vancouver.

Emma Lundberg
Editor, HUPOST

COMMITTEE UPDATES

Membership Committee - Emma Lundberg, *Chair*

The membership committee is currently discussing the benefits for HUPO members. If you have any suggestions please send them to office@hupo.org. We continuously seek diversity within HUPO membership. HUPO has created the new Associate Membership level for researchers in national proteomics societies or from related fields of research.

The Human Proteome Project (HPP)

The HUPO Annual world Congress provides an opportunity to convene face-to-face meetings and sessions across the full-range of HPP activities. Prior to the Congress start all registered delegates will have the opportunity to review all aspects of the HPP at the Pre-Congress: HPP General Leadership Meeting. From Monday, September 28 – Wednesday, September 30, a number of HPP activities will be presented in concurrent morning sessions. For more information regarding session organizers and locations, visit the [HUPO 2015 website](#).

Sponsorship Opportunities at HUPO 2015

The 14th HUPO World Congress offers a tremendous opportunity to market to one of the largest international gatherings of researchers, educators, and professionals in the field of human proteomics. For more information on how to increase your visibility and organization's profile by becoming a Sponsor and/or Exhibitor or by holding an Industry Supported Symposium, click here to visit the [Congress website](#).

The 14th Human Proteome Organization World Congress (HUPO 2015) Organizing Committee would like to thank the following companies for their generous support:

Diamond Level



Gold Level



Silver Level



Agilent Technologies

Bronze Level



GenomeCanada

Supporter Level



The HUPO Human Proteome Project: the Human Proteome 2015

at the Milano EXPO C-HPP Workshop and EuPA Annual Meeting, 23-26 June, 2015

Gilbert (Gil) Omenn - Chair, HPP

Remarkable progress continues on the annotation of the proteins identified in the Human Proteome and on finding credible proteomic evidence for the expression of “missing proteins”. Missing proteins are those with no previous protein-level evidence or insufficient evidence to make a confident identification upon reanalysis in PeptideAtlas and curation in neXtProt. Enhanced with several major new datasets made available in 2014, the Human Proteome presented as neXtProt version 2014-09-19 has 16,491 unique confident proteins (PE level 1), up from 13,664 at 2012-12 and 15,646 at 2013-09. That leaves 2948 missing proteins from genes classified having protein existence level PE 2, 3, or 4, as well as 616 uncertain or dubious proteins at PE 5. The 2014-08 PeptideAtlas had 14,928 canonical protein based on mass spectrometry alone, including all the confirmable protein identifications from multiprotease digestion to overcome limitations of trypsin, using HeLa cells (Guo et al); proteomics studies from CPTAC/TCGA/NCI/NIH for colon and breast cancers (<http://cancergenome.nih.gov>); a Human Proteome Map from Kim et al (Pandey lab, PXD000561); and a Draft Human Proteome from Wilhelm et al¹³ (Kuster lab, PXD000865).

As presented in detail by Deutsch et al (JPR C-HPP special issue 2015), these datasets generated large increases in distinct peptides, but much smaller increments in high-confidence canonical protein identification in PeptideAtlas. In PeptideAtlas 2014-08 there are successive increments of 541, 591, 231, and 2 proteins for the CPTAC, Kim, Wilhelm, and Guo datasets, respectively. With the 2015-05 PeptideAtlas revised criteria, these datasets contributed 516, 377, 110, and 4 additional proteins, respectively. Using various proteolytic enzymes (ArgC, AspN, GluC, Lys-C, chymotrypsin, elastase, trypsin) significantly increased protein sequence coverage at 1% protein FDR. However, only very few previously undetected proteins were identified. The colon and breast cancer CPTAC proteomic data gave a substantial increment in protein identifications, while 2015 data for serous ovarian cancers added only a few. Kim et al claimed 17,294 protein matches across 30 normal samples (17 adult and 7 fetal tissues plus 6 hematopoietic cell types), including 2535 of the HPP 3844 then-missing proteins from 2013.

Subsets of these results for Chromosome 22 and Chromosome 12 were published in the C-HPP 2014 JPR special issue. Wilhelm et al¹³ reported evidence for 18,097 of 19,629 SwissProt protein-coding genes (92%). As Matthias Mann noted in his lecture at the HUPO Madrid 2014 Congress, these two datasets lacked protein-level thresholds for false-positives.

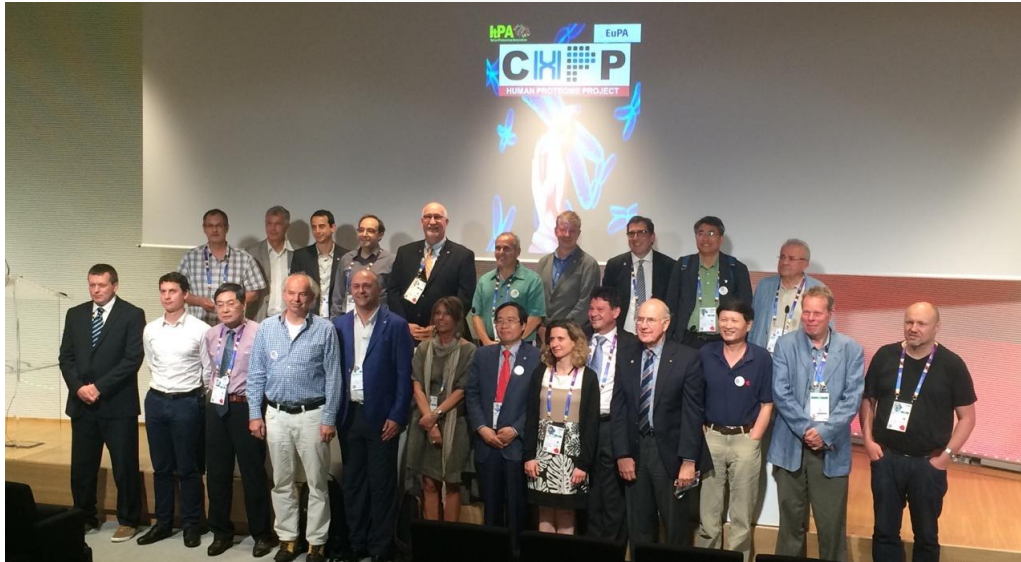
The HPP standard PeptideAtlas and GPMDB reanalyses were unable to confirm at least 4000 claimed protein matches in each of the Kim and Wilhelm datasets. Many investigators have noted unreliable identifications among proteins of interest for their research. For example, Ezkurdia, Tress, and colleagues in Spain were unable to confirm any of the 108 and 200 olfactory receptor (OR) proteins claimed, respectively, in the two datasets. As Juergen Cox presented at the EuPA meeting, his MaxQuant-based method with FDR control of PSMs and protein groups gave <14,000 proteins for the two datasets, similar to PeptideAtlas and GPMDB, with no OR proteins.

Deutsch has concluded that no OR proteins have been credibly identified thus far, including two that were in previous versions of PeptideAtlas. GPMDB contains 425 distinct OR entries; Beavis concluded that only 6 are “green” (good quality) proteins, five based on single small, low complexity peptides that can be assigned to other proteins. The final match is a single peptide from a prostate-specific GPCR. We await analysis of olfactory cortex or olfactory epithelium specimens.

At the EuPA meeting, Cox and Nesvizhskii highlighted the remarkable reanalysis by Savitski, Kuster, et al (MCP May 2015) with a “picked FDR method”, yielding only 14,714 proteins from their own data in ProteomicsDB.

From the point of view of HPP, all investigators are well-advised to process their MS findings through the Trans-Proteomic Pipeline (with Mayu adjustment for large datasets) developed for PeptideAtlas and/or the X!Tandem pipeline developed for GPMDB.

Nesvizhskii discussed the challenge of false positives in proteogenomics studies that seek to identify novel peptides, *i.e.*, peptides not present in the major reference protein sequence databases – RefSeq, UniProt, and Ensembl. He provided guidelines for analyzing the data and reporting the results of proteogenomics studies in the literature. For novel peptides that are highly homologous to peptides in a reference protein sequence dataset, like pseudogenes, false identifications of homologous peptides are underestimated by all decoy database methods. Such peptides must be scrutinized for alternative, more likely explanations (SAAVs or PTMs of abundant proteins).



Participants at the C-HPP Showcase Workshop at Milano EXPO

Other Highlights from the C-HPP Milano EXPO Workshop, June 23, 2015

Andrea Urbani, Paola Roncada, Young-Ki Paik, *Co-Chairs*

Mathias Uhlen presented the 2015 Human Protein Atlas Tissue Proteome and Tove Alm introduced the HPA-EuPA-HUPO HPP Knockdown Initiative for validating antibody findings. Testis has emerged as the leading example of tissue-specific protein expression, with 999 proteins enriched; despite its great complexity, the corresponding figure for brain is only 330 (so far). In fact, Jong-shi Yoo reported finding only 19 high-confidence missing proteins in human hippocampus, while Charles Pineau et al found 89 missing proteins (plus 5 PE5 candidates) in spermatozoa.

Andrea Urbani (EuPA President) and Mauro Fassano co-chair the HPP Mitochondrial Proteome. Presentations included nuclear and mitochondrial-coded proteins involved in mitophagy in neuro-degenerative disorders (Mauro Fassano,) and findings in liver cancers (Young-Ki Paik). Joshua Labaer (US HUPO President) and Peter Horvatovich (Chr 5) reported use of *in vitro* transcription/translation technology to couple cDNA plasmids and SRM-MS assays for the consortium of Chromosomes 5,10,15,16, and 19. Gyorgy Marko-Varga described the remarkable BioBank of Lund-Malmo's leading hospitals. Gil Omenn reported differential expression of splice variant transcripts and proteins in key breast cancer pathways and pointed to splice isoforms as more specific candidate biomarkers or therapeutic targets. Lennart Martens called the 85% of mass spectra not assigned to peptides "the dark matter of the proteome". Chris Overall has found hundreds of missing proteins by focusing on the normal and neo-N-termini of proteins his TAILS and TopFIND methods in understudied tissues, e.g., 174 missing proteins in dental pulp.

Lydie Lane emphasized that numerous genomic variants have not yet been incorporated into the reference databases, putting us at risk of misidentifying such unrecognized variant proteins and peptides. Complementary to finding missing proteins is recognizing that some proteins cannot be found by current MS methods if no detectable tryptic peptides are produced, the protein is highly hydrophobic, or the protein is subsumed or indistinguishable in sequence from other known proteins. Corrales reported 100 missing proteins among the 837 coded by Chr 16, with an estimate of 30% for those not detectable. They are applying SRM to the confirmation of missing proteins, as has Chromosome 18 (Alex Archakov) and Chromosomes 2 and 14 (Pineau and Lane). Some proteins may require induction, for example, by infection or inflammation for beta-defensins, with DEFB1 and DEFB29 most commonly detected, probably in stomach or urine (Pengyuan Yang).

In closing, the HPP investigators have committed to more stringent guidelines for identification of previously-missing proteins and especially novel proteins. PeptideAtlas has raised its threshold to two peptides of 9 or more amino acids, and neXtProt to two peptides of 7 aa or one of 9aa, as well as searching for missing peaks in the spectra and finding SAAV or PTM peptides that better explain the spectra. Allowance is made for proteins with only one uniquely-mapping or proteotypic peptide. We also recommend use of synthetic peptides, SRM assays, or SWATH-MS to enhance the confidence in the peptide identifications.

HUPO AWARD WINNERS 2015

The Human Proteome Organization presents a number of distinguished awards annually at the World Congress. HUPO gratefully acknowledges the support of the Industrial Advisory Board, Journal of Proteome Research (ACS Publications), and Elsevier as sponsors of three of the annual awards. The HUPO Executive Committee and the Awards Committee would like to sincerely thank all those who submitted nominations for the 2015 Award Winners.

It is with great enthusiasm that we present the 2015 HUPO Award Winners! Please visit the [HUPO Awards Page](#) for more information on the accomplishments of these outstanding scientists.

Distinguished Achievement in Proteomic Sciences *Sponsored by the Journal of Proteome Research*

Amanda Paulovich, *Fred Hutchinson Cancer Research Center, Seattle, Washington*

Discovery in Proteomic Sciences *(Shared by two recipients)*

Bernhard Kuster, *Technische Universitat Munchen, Germany*

Akhilesh Pandey, *Institute of Genetic Medicine and Department of Biological Chemistry, Oncology and Pathology*

John Hopkins University School of Medicine, Baltimore, USA

Science and Technology Award *Sponsored by the Industrial Advisory Board*

(Norman) Leigh Anderson, Morteza Razavi, Selena S. Larkin, *SISCAPA Assay Technologies, Inc., Washington, DC*

Translational Proteomics Award *Sponsored by Elsevier*

Jennifer Van Eyk, *Cedars Sinai Medical Center, Los Angeles, CA*

Distinguished Service Award

Catherine Costello, *Center for Biomedical Mass Spectrometry, Boston University School of Medicine*

INDUSTRIAL ADVISORY BOARD (IAB)

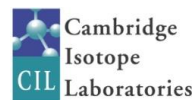
The HUPO Industrial Advisory Board (IAB) is comprised of industry partners engaged in the field of proteomics. IAB member companies meet regularly to provide valuable input on technology and product innovations to the HUPO Council and its Executive Committee for the benefit of members and to identify industry trends that will position HUPO to meet the future challenges of its partners and organization.

Membership in the IAB facilitates communication and input between industry partners to support the proteomics community and to recognize these partners as HUPO affiliates. HUPO supports industry allies active in the development of innovative technologies and appropriate standards that are responsive to the constant changes in the scientific proteomics environment. For more information on the IAB please visit the [HUPO website](#). If your company is interested in joining the IAB please download the [IAB Brochure and Sign-up Form](#).

Thank you to our [2015 IAB Members!](#)



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MENTORING DAY AT HUPO 2015

The HUPO 2015 Organizing Committee is excited to invite you to our first ever organized Mentoring Day! During this one-day session, young scientists will have the opportunity to hear from world-renowned scientists from a wide variety of science, technology and business fields. They will give presentations and reflect on their education, careers, field, choices, work history, and what an early career scientists need to know today for a rewarding future career in science and technology. The keynote(s) will share their personal stories and their creative ways of using science, technology, and the choices they made in their careers and everyday lives.

The day will be an excellent networking opportunity! Throughout the day, the participants will have an opportunity to interact, brain storm and chat with our speakers. The participants will learn about activities you might participate in order to enhance your experience, and gather resources that will help your future career. Join us and have fun while getting inspiration for a successful scientific career! We have some of the best speakers in the world and a tremendous opportunity to get involved in a wonderful networking atmosphere with your peers.

Date: Sunday, September 27, 2015
Time: 9:00 - 15:30
Location: Vancouver Convention Centre
 East Building, Meeting Room 8+15
 HUPO Members - 80 CAD
 Non HUPO Members - 130 CAD

Speakers:

- Ruedi Aebersold
- Beth Anderson
- Leigh Anderson
- Mark Baker
- Jeff Chapman
- Catherine Costello
- Donna Edmonds
- Luigi Ferrucci
- Christie Hunter
- Hanno Langen
- Emma Lundberg
- Gilbert Omenn
- Fred Regnier
- Henry Rodriguez
- Jochen Schwenk
- Salvatore Sechi
- Mike Snyder
- Pothur Srinivas
- Jennifer Van Eyk
- John R. Yates III

The scientific committee has put together an outstanding scientific program. To register for any additional sessions and to see more information, visit the [HUPO2015 Scientific Program page](#).

SAVE THE DATE! SEPTEMBER 27-30, 2015



HUPOST VANCOUVER 2015
 14TH HUMAN PROTEOME ORGANIZATION WORLD CONGRESS
 SEPTEMBER 27-30

PROGRAM HIGHLIGHTS

Plenary Sessions with world renowned Speakers:

- Ruedi Aebersold
- Emma Lundberg
- Ute Roessner
- Steven Carr
- John Yates,
- Fuchu He,
- Aled Edwards

Pre-Congress Workshops

30 Keynote sessions with more than:

- 60 Keynote Presentations
- More than 200 oral abstract presentations

More than 30 interest groups and workshop sessions

Translating Proteomics and Allied -Omics to the Clinic

HUPO2015.COM

NATIONAL & REGIONAL SOCIETY UPDATES

The Human Proteome Organization encourages the formation of national and regional human proteome-related societies. For a comprehensive list of proteomics societies, please visit <https://www.hupo.org/national-and-regional-societies/>.

This issue of HUPOST introduces the regular featuring of these societies. If you wish for your society to be featured in a particular quarterly issue of the HUPOST, please email office@hupo.org.



British Society for Proteome Research (BSPR)

BSPR is a registered incorporated charity (Registered Company No. 6319769, UK Charity No. 1121692).

It represents both the Human Proteome Organization (HUPO) and the European Proteomics Association (EuPA) in the UK and Ireland and is affiliated to the Society of Biology.

The objectives of the BSPR are to advance the science of proteomics and to promote the study and research in this and related areas for the benefit of all. It enables scientists working in the field of proteomics to keep up-to-date with current developments both nationally and internationally and to meet and exchange ideas with other workers. Unlike many learned societies we have members from a wide range of organisations including

industry and the health service, as well as research and academic institutions.

The BSPR hold high-quality annual meetings with trade exhibition, poster sessions, speaker/poster prizes and student travel bursaries. For [this year's meeting](#) at the University of Reading (July 20-22) we have an impressive line-up of keynote and plenary international speakers. In 2014 we appointed our first BSPR Lecturer (Juri Rappsilber), whose remit is to present both basic principles in proteomics and cutting-edge research at invited lectures across the country.

The Society also underwrites regional proteomics workshops and in 2017 will host the HUPO World Congress in Dublin. Our regularly updated website keeps members and other interested parties informed of recent developments in proteomics and forthcoming UK and overseas meetings on related topics.



Canadian National Proteomics Network (CNPN)

CNPN is a not-for-profit, federally incorporated organization created to provide a co-operative mechanism for building the proteomics research

infrastructure in Canada and to further a better understanding of proteomics in the Canadian life-sciences community. CNPN sponsors scientific conferences, seminars and forums to create a national

focus for scientific collaboration and education. An annual CNPN symposium is held alternatively in major Canadian cities.

CNPN is governed by a Board of Directors that serve 4-year terms. Every two years approximately half of the board member terms expire at the annual conference. An on-line vote ensures that members express their votes in favor of the incoming Board members. Officers are selected by the current Board of Directors.

HUPO COUNCIL ELECTION 2015

The Human Proteome Organization is pleased to announce the official list of candidates for the HUPO Board of Directors (HUPO Council) direct election. HUPO expresses thanks to these candidates who are willing to stand for election for council terms beginning in 2016.

The election period for HUPO Council is September 4 to September 28, 2015. Again this year, the vote is conducted online. All active HUPO members will receive an email containing a secure election ID code. Simply click on the link provided and cast your anonymous vote.

Election 2015 Calendar

Election Website Opens	September 4, 2015
Election Closes	September 28, 2015
Results Announced	September 29, 2015 (During the General Assembly at HUPO 2015 in Vancouver)

Candidates - Central Region



Emøke Bendixen
Department of Molecular Biology and Genetics
Aarhus University, Denmark



Lennart Martins
VIB Medical Biotechnology Center
Ghent University, Belgium



Fernando J. Corrales
Center for Applied Medical Research (CIMA)
University of Navarra, Spain



Evgeny Nikolaevich Nikolaev
The Institute of Biochemical Physics
Russian Academy of Sciences, Russia



Henning Hermjakob
European Bioinformatics Institute, UK



Jean-Charles Sanchez
School of Medicine
University of Geneva, Switzerland



Jeroen Krijgsveld
European Molecular Biology Laboratory (EMBL),
Germany



Jochen M. Schwenk
Royal Institute of Technology, Sweden

HUPO COUNCIL ELECTION 2015 - Candidates - Western Region



Natalie G. Ahn
BioFrontiers Institute
University of Colorado at Boulder, USA



Ulrike Kusebauch
Institute for Systems Biology, USA



Christoph H. Borchers
UVic Genome BC Proteomics Centre
University of Victoria, Canada



Robert Moritz
Institute for Systems Biology, USA



Gilberto B. Domont
Proteomics Unit, Institute of Chemistry
Universidade Federal do Rio de Janeiro,
Brazil



David C. Muddiman
W. M. Keck FTMS Laboratory
North Carolina State University, USA



Sergio Encarnación-Guevara
Center for Genomic Sciences
University of México, Mexico



Sophie Paczesny
Herman B. Wells Center for Pediatric Research
Indiana University, USA



Ying Ge
University of Wisconsin-Madison, USA



Sheng Pan
Department of Medicine
University of Washington, USA



Yetrib Hathout
Proteomics Core Facility
Children's Research Institute, USA



Victoria Pando-Robles
Instituto Nacional de Salud Pública
Mexico



Donald F. Hunt
University of Virginia, USA



Akhilesh Pandey
McKusick-Nathans Institute of Genetic Medicine
Johns Hopkins University, USA



Alexander R. Ivanov
The Barnett Institute of Chemical and
Biological Analysis
Northeastern University, USA



Karen Wang
Novartis Institutes for BioMedical Research
USA



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

HUPO COUNCIL ELECTION 2015 - Candidates - Eastern Region



Stuart Cordwell
Core Facility in Mass Spectrometry
The University of Sydney, Australia



Tony Purcell
Department of Biochemistry
Monash University, Australia



Fuchu He
Beijing Proteome Research Center
National Core Facility for Protein Sciences
China



Shoba Ranganathan
Macquarie University, Australia



Michelle Hill
University of Queensland Diamantina Institute
Australia



Sanjeeva Srivastava
Department of Biosciences and Bioengineering
Indian Institute of Technology, India



Vera Ignjatovic
Murdoch Children's Research Institute
The University of Melbourne, Australia



Tesshi Yamada
Division of Chemotherapy and Clinical Research
National Cancer Research Institute, Japan



Edouard Nice
Monash University, Australia



Jong Shin Yoo
Korea Basic Science Institute
Republic of Korea

HPP Clinical Scientist Travel Grant | Call for Applications

The Human Proteome Project (HPP) was established by the Human Proteome Organization (HUPO) to explore the human proteome and to enable the routine, reliable and broad application of state-of-the-art measurements of proteins and proteomes by life scientists studying the molecular mechanisms of biological processes and human disease¹. This will be accomplished through the generation of laboratory and informational resources that support both research and routine measurement of the process- or disease relevant proteins².

To accomplish these goals, the HPP is reaching out to clinical scientists or clinicians who are using or consider using proteomics for their research projects. HPP is supporting six clinical scientists with a travel grant to attend the 2015 HUPO World Congress in Vancouver, Canada that will take place from September 27 – October 1. Travel grant recipients will receive up to USD \$1,000 to offset travel and hotel costs in addition to complimentary congress registration. The recipients are expected to actively participate in the HUPO congress, particularly in the activities and discussions related to the HPP. Further information on HPP activities in Vancouver can be found here: <http://hupo2015.com/program/hpp-sessions/>.

Applications are due by August 6, 2015. For more information and instructions visit the [Awards Page](#) on the HUPO website.

Reference:

¹ Aebersold R, Bader GD, Edwards AM, van Eyk JE, Kussmann M, Qin J, Omenn GS. (2013) The Biology/Disease-driven Human Proteome Project (B/D-HPP): Enabling Protein Research for the Life Sciences Community. *J Proteome Res.* 2013 Jan 4;12(1):23-7. doi: 10.1021/pr301151m.

² Lane, L.; Bairoch, A.; Beavis, R. C.; Deutsch, E. W.; Gaudet, P.; Lundberg, E.; Omenn, G. S., Metrics for the Human Proteome Project 2013-2014 and strategies for finding missing proteins. *J Proteome Res* 2014, 13, 15-20.

EVENTS IN PROTEOMICS

If you would like to include your meetings in the HUPOST or on the [HUPO website](http://hupo.org), please email the details to office@hupo.org.

Future HUPO Annual World Congresses

- [HUPO 2015 Vancouver](#)
September 27-30, 2015



- [HUPO 2016 Taipei](#)
September 18-22, 2016



- [HUPO 2017 Dublin](#)
September 17-20, 2017



Regional & National Proteomics Society Events

- [British Society for Proteome Research 2015 Meeting](#)
July 20-22, 2015
University of Reading, United Kingdom
<http://www.bspr.org/event/bspr-meeting-2015>
- [5th Nordic Proteomics Symposium](#)
August 23-25, 2015
Malmö, Sweden
<https://www.malmokongressbyra.se/>
- [Mountain Village Science Series](#)
August 26-28, 2015
Karlova Studanka, Czech Republic
<http://www.moviss.org/>
- [UCIBIO training course "Biomarker Discovery using Proteomics Techniques"](#)
August 31-September 4, 2015
Caparica, Portugal
<http://www.requimte.pt/ucibio/ucibio-training-course-proteomics>
- [5th International Conference on Proteomics & Bioinformatics](#)
September 1-3, 2015
Valencia, Spain
<http://proteomicsconference.com/>
- [5th Symposium on Structural Proteomics](#)
November 19-20, 2015
Halle, Germany
<http://www.structuralproteomics.net/>
- [Joint EMBL-EBI/Wellcome Trust Course: Proteomics Bioinformatics](#)
November 11-15, 2015
Cambridge, United Kingdom
<http://www.ebi.ac.uk/>