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EDITOR'S MESSAGE



Emma K. Lundberg
HUPOST Editor

Dear HUPO friends,

The year of 2016 is coming to an end, and what a year for proteomics! With the multitude of great scientific articles written by HUPO members, many successful conferences and meetings all over the world, computer games and so on, proteomics has clearly transitioned into a key technology across labs and disciplines. No wonder the number

of HUPO members is higher than ever!

In this issue you can read the farewell message from our President Mark Baker. It is a great summary of the priorities made and work performed during his Presidency. Thanks for this time Mark, you have really made a positive impact on HUPO!

I would like to take the opportunity to welcome the next President of HUPO, Mike Snyder, as well as the newly elected council and EC members. Personally, I am looking forward to another two years on the EC and to continue working on making HUPO an even more active, inclusive and vivid society.

This is probably the last time you will read HUPOST in its current format. In 2017 you will hear from us more frequently through our social media channels and the redesigned website. Again I would like to thank all of you that have sent us content for HUPOST – keep it coming! Stories, highlights, news, suggestions and announcements are gladly accepted for inclusion in the HUPOST. To contribute please email the HUPO Office at office@hupo.org. And remember to follow us in social media, you can find us on [Facebook](#), [Twitter](#), and [LinkedIn](#).

Happy holidays and best wishes for the new year!

Emma

PRESIDENT'S FAREWELL



Mark Baker
HUPRO President 2015-2016

Dear Colleagues,

My term as HUPRO President has almost ended and I hope that I have had a positive impact on HUPRO and that we're left it in good shape, well positioned for a bright future. Thank you for the honour and opportunity to lead such an amazing group of people and for your patience with me over the last two years. I anticipated that as incoming

President it would be an *exciting time for proteomics* and I believe that anticipation has been true. After consulting with many of you, our 5 main aims were to; (i) increase HUPRO's financial stability, (ii) refresh HUPRO's democratically-elected committee/initiative structures, (iii) implement strategies to engage all members in HUPRO activities (especially early/mid-career researchers and retiring members), (iv) develop a broad-based communications/marketing/outreach strategy, (v) engage with international bio-banking organisations. I'll let you be the ultimate judge of whether we accomplished lasting change.... but my reflection is that HUPRO appears to have travelled far from where it was a few years back.

As I "pass the buck" to incoming President Mike Snyder, I thought I'd take this opportunity to celebrate what HUPRO has become and hopefully encourage you to continue building a secure, stronger, vibrant and engaged HUPRO in the future.

Firstly, let me especially congratulate our outgoing Executive Committee colleagues – Yu-Ju Chen (Member-at-Large), Bruno Domon (Treasurer), and György

Marko-Varga (Secretary General). In addition, I warmly thank our many outgoing or rotating-off HUPRO Councilors (György Marko-Varga, Aysel Ozpinar, Charles Pineau, George Tsangaris, Yu-Ju Chen, Ghasem Hosseini Salekdeh, Richard Simpson, Tadashi Yamamoto, Catherine Fenselau, Gabriel Padron, Solange Serrano and Richard Smith) for your fantastic collegial support and for so many of you for long service to HUPRO. I also welcome our new HUPRO Councilors and Executive Committee and encourage all members to consider serving our great society next year. We are indeed very fortunate to have such a strong band of motivated contributors at all levels of our society.

I would also like to especially mention the many of you who have re-invigorated HUPRO as an organisation, especially Gil Omenn, Young-Ki Paik, Jennifer Van Eyk, Fernando Corrales and their [Human Proteome Project \(HPP\)](#) teams who have driven the ongoing success of our flagship scientific endeavour. I applaud the HPP leadership for their decisions to (i) drive the capture and re-analysis of proteomics big data through communally-agreed metrics and guidelines, (ii) to revisit long term HPP plans and (ii) to adopt social media and the many other vehicles we now use for HPP knowledge transfer. We need to continue communicating the importance of integrating that HPP knowledge in what it means for humans to "know *thysself*" in strictly molecular terms.

Over 2015 and 2016 we held wonderfully successful HUPRO Annual World Congresses in Vancouver and Taipei respectively. and I extend our deepest thanks to Christoph Borchers, Pierre Thibault, Ming-Daw Tsai, Yu-Ju Chen and their teams for the quality of the scientific programs, the smooth overall organization of their meetings, the integration of the HPP into the mainstream program, the development of the "hub" concept and the thoroughly enjoyable, locally-flavoured

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PRESIDENT'S FAREWELL

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social events. I'm positive that Steve Pennington and Andrew Pitt from the British Society of Proteome Research (HUPO2017 in Dublin), David Muddiman from US HUPO (HUPO2018 in Orlando), and Stuart Cordwell from the Australasian Proteomics Society (HUPO 2019 in Adelaide) will continue our traditions of holding fantastic scientific meetings blended with countless fun.

HUPO's financial sustainability was one key priority to address when I took on the job. I am pleased to update you that thanks to Bruno, Rob and the HUPO EC, we have been financially prudent, saving expenditure wherever and whenever possible. Overall, we are in much better financial shape than we were two years ago and I thank you all for your efforts here.

To achieve better long term Congress financial accountability, continuity, knowledge transfer, visibility and engagement of exhibitors/sponsors, Council accepted a recommendation from the taskforce headed up by Secretary-General György Marko-Varga and appointed a CORE-PCO, for a period of 5 years from HUPO2020, with HUPO's current society management company [International Conference Services Ltd \(ICS\)](#) being the successful appointee. You will hear more about this important Council decision as implementation approaches.

The HUPO family is indebted to the outstanding efforts of our many Committees, chaired by highly motivated colleagues as following;(Awards (Martin Larsen), Membership (Emma Lundberg), Marketing (Christoph Borchers), Website (Charles Pineau), Publications (Yu-Ju Chen & Jean-Charles Sanchez) Education & Training (Garry Corthals/David Muddiman), Nominations &

Elections (Henning Hermjakob), Industrial Advisory Board (Aran Paulus, Rob Moritz & Mike Snyder)). You and your respective teams have been unbelievably active as we renewed HUPO, under these various *committees* for management and integrated *initiatives* for our science, coordinated under Gil's remarkable HPP leadership.

I also pass a personal vote of thanks to our wonderful society management team at ICS - especially Chelsea Prangnell, Joanna Rose, Mathias Posch and Aksinia Shier for their insightful inputs, outstanding advice, financial acuity, performance, dedication to HUPO and many efforts above and beyond their duty to help build a HUPO family – you were the best decision we made during my Presidency and it has been a privilege to work with you all.

Finally, I wish you and your families and friends a successful, peaceful and happy holidays and New Year.

I look forward to staying very active in HUPO/HPP progress and to getting together with you to celebrate proteomics next September at HUPO 2017.

Fheiceann tú i Dublin (if not before).

Best always,



Mark Baker
HUPO President

HUPO Congress: September 18-21
HPP workshop day: September 22

Precision Proteomics
for Precision
Biology and Medicine

HUPO 2016 CONGRESS

Dear Participants of HUPO 2016,

On behalf of the Organizing Committee of the 15th Human Proteome Organization World Congress in 2016 (HUPO 2016), we would like to thank you for your enthusiastic participation in the Congress held from September 18th (Sunday) to September 22nd (Thursday), 2016, in Taipei, Taiwan.

We believe that one of the best ways to promote the development of new technologies and their fruitful applications to better understand human disease is to bring together a wide range of diverse expertise for brainstorming on a platform like HUPO Congress. With over 1,100 participants including you, HUPO 2016 is one of the most successful events to have cultivated new initiatives and consensus, focusing on "Precision Proteomics for Precision Biology and Medicine". We hope that this Congress has provided you new perspectives, inspiration and motivation that would allow you to continue making important progress in proteomics.

The detailed Congress data and photos are available on the HUPO 2016 Website. Please do not forget to visit www.hupo2016.org for snapshots of these memorable moments you shared with us.

Finally, we would like to express our sincere appreciation to all of you again! We also hope that you all have enjoyed your stay in Taipei!

Yours Sincerely,



Dr. Ming-Daw Tsai
Congress Chair, HUPO 2016



Dr. Yu-Ju Chen
Congress Co-Chair, HUPO 2016



HUPO Congress: September 18-21
HPP workshop day: September 22



*Precision Proteomics
for Precision
Biology and Medicine*



Human Proteome Project

Update on the Human Proteome Project (HPP)

Gil Omenn, HPP Chair

At the 15th annual HUPO Congress in Taiwan 18-22 September 2016, the Human Proteome Project presented 12 scientific sessions from B/D-HPP groups as part of Track 1 of the three-day Congress program, held an all-day HPP Investigators meeting, hosted a Bioinformatics Hub throughout the Congress for discussion of special topics and drop-in consultations, had a C-HPP poster competition, and presented a Mentoring Day for Early Career Researchers. The following day we had a productive HPP strategy workshop at beautiful Sun Moon Lake in the Central Highlands.

The Biology and Disease-driven component of the HPP, led by Jennifer van Eyk and Fernando Corrales, has delivered three important initiatives: Kusebauch et al published a comprehensive SRM Atlas in the 28 July issue of *Cell* covering >99% of the predicted human proteins with 166K proteotypic peptides, spectral libraries, expected transitions, and access to labeled synthetic peptides; the passionate engagement of Early Career Researchers (ECR) includes a Mentoring Day, a manuscript competition, a travel awards program, and a seat on the B/D-HPP Executive Committee; and production of useful lists of “popular proteins” with the 50 proteins most published by subject-matter researchers on heart, cerebrum, intestine, liver, lung, and kidney, by Lam et al in the 4th annual JPR special issue. We strongly recommend that the 22 Biology and Disease HPP teams and 25 chromosome and mitochondria teams of the C-HPP apply this approach.

The Chromosome-centric C-HPP, led by Young-Ki Paik, Lydie Lane, and Chris Overall, has teams around the

world tackling the 24 individual chromosomes plus mitochondria to identify and characterize proteins whose coding genes are on the respective chromosome. There has been substantial progress on building the protein parts list from all sources. There are 19,467 protein-coding genes according to neXtProt (excluding 588 dubious/uncertain genes, labeled PE5). During the past four years of the HPP, the annual Human Proteome metric of PE1 proteins with highly confident protein-level evidence has progressed from 13,664 in 2013 to 15,646 in 2014, 16,491 in 2015, and 16,518 in the 2016-02 version of neXtProt. The latest increment was reduced due to the implementation of more stringent Mass Spectrometry Data Interpretation Guidelines v2; of 485 proteins that would have been PE1 under the earlier v1 Guidelines, 432 were reclassified as PE2, 3, or 4. See the Metrics and Guidelines papers in the 4th JPR special issue released on 4 November 2016 <http://pubs.acs.org/toc/jprobs/current>.

The 2290 PE2 predicted proteins have tissue-based transcript expression data that guide us where to search for evidence of protein expression. This strategy was implemented admirably this year by the C-HPP Chromosome 2/Chromosome 14 consortium focusing on the large number of genes (879) with testis-specific or testis-enriched expression, as shown by the Human Protein Atlas. From studies of testis and sperm, 253 previously missing proteins were reported as compliant with the HPP Guidelines v2. Once these (and other) findings have been subjected to reanalysis by PeptideAtlas and incorporated into the 2017-02 version of neXtProt, we project that the number of PE1 proteins will rise to at least 16,873 (87% of the 19,467

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H Human Proteome Project

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predicted proteins) and the number of missing proteins (still PE2,3,4) will decrease at least from 2949 to 2696.

At the post-Congress HPP Workshop, there was extensive strategic discussion about accelerating progress on identifying and validating the remaining missing proteins, enhanced by HPP Scientific Advisory Board members Cathy Costello, John Yates, and Naoyuki Taniguchi and by comments from a HUPO-wide survey that had stimulated 162 responses. The C-HPP announced a Top-50 Challenge for a coordinated effort across every chromosome to identify the most tractable 50 predicted proteins for detection, combined with use of SRM or other methods for confirmation. A new web resource (missingproteins.org) with structured information from the literature was released at this Congress by the Australian team led by Mark Baker. The strategic discussion recognized the many reasons why proteins may be undetectable by mass spectrometry. Of the 16,518 PE1 proteins as of neXtProt v2016-02, 14,629 were based on PeptideAtlas for mass spectrometry, while 1860 were based on a variety of non-MS methods. Present MS methods will not detect proteins of very low abundance (which include those with inaccessible chromatin or very low transcript expression), proteins lacking lysine and arginine residues such that tryptic digestion cannot yield peptides of 9 to 50 aa in length, proteins in highly homologous protein families such that the detected peptides cannot be distinguished, or proteins not solubilized from membranes. Such proteins may justify an adjustment in the denominator of potentially detectable proteins.

There was strong sentiment for accelerating the long-planned work, now incorporated into the neXtProt, PeptideAtlas, and GPMdb databases, on splice variants, PTMs, N-termini, and sequence variants and their functional and pathological features. This strategy reinforces the decisions to link the B/D-HPP teams with the C-HPP and its informal clusters focused on cancers, neurodegenerative disorders, reproductive biology, membrane proteins, and the in vitro transcription/translation platform.

It was agreed that there will be a 5th annual HPP Special Issue of the Journal of Proteome Research in 2017; the Call for Papers was announced by JPR on 4 November 2016, with a deadline of 31 May 2017. The JPR confirmed that the HPP Guidelines v2.1 and Checklist will apply. We hope that investigators throughout the world will find these guidelines helpful for routine mass spectrometry reporting, especially respecting the protein-level FDR <1%, and for “extraordinary claims” of detection of previously undetected proteins and/or translation products from lncRNAs or pseudogenes or small ORFs; (hupo.org/guidelines). The latter include careful scrutiny of the spectra, use of thresholds of 9 aa in length and 2 uniquely-mapping proteins for peptide-to-protein matches, and careful consideration of alternative protein matches, especially to sequence variants or isobaric PTMs of abundant proteins. These more probable matches have been shown to explain many claims of previously unreported proteins. Independent researchers from around the world are warmly welcomed to submit their papers that match the broad thematic priorities specified.

BIOINFORMATICS HUB AT THE HUPO 2016 WORLD CONGRESS

-Written by Eric Deutsch, Yves Vandenbrouck and Lennart Martens

The Bioinformatics Hub is a place where bioinformaticians gather together with three aims: (i) to provide their advice, knowledge, and support to anyone with a relevant question; (ii) to discuss current issues and challenges in proteomics informatics with the entire community; and (iii) to work on interesting, synergistic projects and to freely exchange tools, algorithms and know-how with each other, across all labs, seniorities and levels of experience.

The Bioinformatics Hub at the HUPO 2016 World Congress in Taipei was highly successful in bringing together many researchers interested in computational proteomics and bioinformatics to discuss topics important in the field. The hub was open daily from 8:30 – 5:30 during the congress,

and the on-line program dynamically updated hourly with ongoing activities. Some of the more prominent topics addressed included discussions over the HPP Data Interpretation Guidelines v2.1, The HPP 50 Missing Protein Challenge, the proposed JPR Bioinformatics/Computational Resources Special Issue, use of preprint servers for computational proteomics manuscripts, Missing-ProteinPedia, privacy implications of proteomics data, OmicsDI, glycoproteomics informatics, quality control formats, and proteogenomics data file formats. Work on these topics will proceed based on these discussions, and we look forward to another exciting Bioinformatics Hub at next year's HUPO World Congress. See the Bioinformatics Hub web site for more information: <https://github.com/CompMS/Overview/wiki/HUPO-2016>





HUPO

16TH HUMAN PROTEOME ORGANISATION WORLD CONGRESS
THE CONVENTION CENTRE DUBLIN, IRELAND 17 - 21 SEPTEMBER 2017

Visit our website www.hupo2017.ie



11th January 2017
Opening of Registration



11th January 2017
Call for Abstracts



5th April 2017
Close of Abstracts



31st May 2017
Notifications of Acceptance



14th June 2017
End of Early Registration



16th August 2017
End of Regular Registration

About HUPO2017

The HUPO2017 Congress is focussed on the theme of "Integrated Proteomics for Healthcare Systems". Our vision is to create a vibrant scientific meeting that will bring together the existing world leaders in the field of proteomics with those in allied disciplines to foster and support the development of a new generation of multi-disciplinary forward looking scientists. Together we have the opportunity to carry forward new capabilities for advancing our knowledge of the Human Proteome to significantly enhance our understanding of health, disease and ageing to create unprecedented impact.

The Congress will celebrate past achievements, present new disruptive advances in proteomics and showcase opportunities in multi-disciplinary research. This will be achieved by a balanced scientific programme that encompasses previous milestone developments in proteomics, the current state of the art and newly emerging advances.

The programme will include sessions covering each of the twelve current HUPO Initiatives and the Biology/Disease driven Human Proteome Proteome Project (HPP). In recognition of the increasing role of proteomics and complementary 'omics technologies in personalised medicine there will be a special focus on the application of proteomics to disease diagnosis, therapeutic protein production (and characterisation) and drug development as well as the analysis and integration of proteomic data. The presence of world-leading major international pharmaceutical biopharmaceutical and information technology companies in Ireland provides a wonderful opportunity for cross discipline information exchange and personal networking.

Some of the key objectives of HUPO2017 Dublin are to:

- Provide a great forum for the presentation of key achievements in proteomics to date
- Embrace a forward looking perspective to deliver an inflection point – a milestone event – in the evolution of proteomics
- Engage new constituencies with the field of proteomics to support new scientific and business opportunities
- Elicit a change in global engagement of the field with the other stakeholders including the public

Programme

We are currently undertaking detailed planning of the Scientific Programme and welcome your input - ideas for sessions and specific speakers - please send them to the organising committee before the end of 2016. To stay informed of programme developments visit the website regularly and sign up to announcements.

The programme will include sessions covering each of the twelve current HUPO Initiatives and the Biology/Disease driven Human Proteome Proteome Project (HPP).

We are delighted to announce that **Professor Leroy Hood** will give an Opening Plenary lecture on Sunday 17th September. For those who don't know: Prof Hood was involved in the development of instruments critical for contemporary biology – including automated DNA sequencers, DNA synthesizers, protein sequencers, peptide synthesizers, and an ink jet printer for constructing DNA arrays. Together these instruments opened the door to high-throughput biological data and the era of big data in biology and medicine. Given the aims of the HUPO2017 Dublin Congress it is fitting that Prof Hood has graciously agreed to open the event.

Other invited and confirmed speakers include:

Ruedi Aebersold; Jonathan Bones; Christoph Borchers; Ben Cravatt; William Gallagher; Albert Heck; Thomas Joos; Joshua Labaer; Matthias Mann; Lennart Martens; Rob Moritz; Andrew Percy; Pauline Rudd; Mike Snyder; Matthias Uhlen and Alain van Gool.

Of course - the scientific programme will be complemented by an interesting and 'only in Ireland' offering of social events and opportunities that will include - the Opening Reception in the buzzing Sponsor and Partner Exhibition space in the Convention Centre, a fun packed Congress Gala Evening at the iconic Guinness Storehouse, a range of tour opportunities from boat trips around Dublin bay to pub tours around Dublin streets and for the more 'active' we'll be offering early morning cycling, opportunities to rock climb with a two-time Everest summiter and, for the more mindful, yoga and meditation. All this during the Congress and a range of post-Congress tours of Ireland afterwards.

Please visit the Congress website for regular updates and interesting facts - for example: did you know that the Rotunda Hospital in Dublin - only a short walk from the Convention Centre - is the world's first and oldest maternity hospital? It was funded in part by concert fundraisers (an early example of crowd-funding) and the hospital's former operating theatre is now the Gate Theatre.



Contact



hupo2017@conferencepartners.com



www.hupo2017.ie

HUPO INDUSTRIAL ADVISORY BOARD

Created in 2006, the HUPO Industrial Advisory Board (IAB) facilitates communication and input from 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.

The IAB Mission

To provide HUPO leadership (the Executive Committee) valuable input on technology and product innovation for the benefit of members and to identify industry trends that will position HUPO to meet the future challenges of its partners and organization.

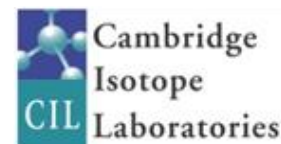
Interested in joining HUPO as an IAB member?

Contact the HUPO Office office@hupo.org

Benefits of an IAB Membership

- Two complimentary individual HUPO memberships available for company employees (value \$200).
- Involvement in Human Proteome Project (HPP) with regular updates from project leadership.
- Direct connection with HUPO Executive Committee and Congress Organizers via monthly IAB calls.
- IAB sponsored Science and Technology Award, established in 2011, awarded to an industrial scientist. IAB representatives solicit and vet nominees. Award recipient presents a talk at the annual HUPO Congress.
- Selection of abstracts for the New Technological Advances in Proteomics presentations at the annual HUPO Congress.

The Human Proteome Organization wishes to thank the following IAB members for their participation in 2016!



Genentech



EVENTS IN PROTEOMICS

HUPO is pleased to post meeting announcements for HUPO-related national and regional societies and for proteomics workshops and symposia. If you have an announcement please email office@hupo.org.

HUPO WORLD CONGRESSES

HUPO 2017 Dublin

September 17-21, 2017

www.hupo2017.ie



HUPO 2018 Orlando

September 30 - October 3, 2018



HUPO 2019 Adelaide

More details coming soon



HPP WORKSHOPS

16th C-HPP Workshop - Including Collaborations with B/D-HPP

December 10-14, 2016

<http://www.brprot.org/16chppworkshop/>

The mitochondrial Human Proteome Project (mt-HPP) Workshop

February 16-17, 2017

<https://hupo.org/event-2362215>

27th HUPO Brain Proteome Project Workshop

May 9-10, 2017

<https://hupo.org/event-2362215>

REGIONAL & NATIONAL EVENTS

II-Caparica Christmas Conference on Sample Treatment

December 5-7, 2016

<http://www.sampletreatment2016.com>

6th BrMASS & 1st IbMS

December 10-14, 2016

<http://ibero2016.brmass.com.br>

PSI & AOPO 2016

December 14-17, 2016

www.psiaoapo2016.org

HUPO 2018 IN ORLANDO, FLORIDA



US HUPO President David Muddiman signed the MOU (memorandum of understanding) to finalize the hosting of HUPO 2018 in Orlando, Florida, USA. This marks the third annual world congress to be held in the United States (2006 Long Beach, 2012 Boston).

Joshua LaBaer (Biodesign Institute, Arizona State University), Ileana Cristea (Princeton University), Robert Moritz (Institute for Systems Biology), and John R. Yates III (The Scripps Research Institute) have been selected as the congress program organizers.

A promotional banner for the HUPO 2018 congress. The top left features the HUPO logo and the text "2018 ORLANDO, FLORIDA, USA" and "Human Proteome Organization". The center text reads "September 30 – October 3, 2018" and "Loews Pacific Hotel". The bottom left says "17th Annual World Congress". The bottom right features the "US HUPO from genes to function" logo. A large, stylized "SAVE THE DATE!" stamp is overlaid on the right side. The background is a blue sky with palm trees and the Universal Orlando logo.

COMING SOON - HUPO AWARDS NOMINATIONS OPEN FEB 1 2017!

The Human Proteome Organization presents a number of distinguished awards annually at the World Congress. These awards recognize the outstanding efforts and achievements of individuals (or groups) advancing the field of proteomics. HUPO gratefully acknowledges the support of the Journal of Proteome Research (ACS Publications), the Journal of Proteomics (Elsevier BV), Clinical Proteomics (BioMed Central), and the HUPO Industrial Advisory Board, for their generous support in sponsoring the awards.

The following awards will be presented at the 2017 HUPO World Congress, which will be held in Dublin from September 17-21, 2017. All award recipients will present a talk during the award session at the Congress Closing Ceremony. [Nominations open February 1, 2017.](#)

IMPORTANT DATES AND DEADLINES:

[February 1, 2017](#) - Nominations open

[April 17, 2017](#) - Nominations close

[May 31, 2017](#) - Award winners notified

First week of June, 2017 - Award winners announced

Distinguished Achievement in Proteomic Sciences

\$3,000, Sponsored by the Journal of Proteome Research (Published by ACS Publications)

Recognizes a scientist for distinguished scientific achievements in the field of proteomic science.

Discovery in Proteomic Sciences Award

\$3,000, Sponsored by the Journal of Proteomics (Published by Elsevier BV)

Recognizes a scientist for a single discovery in the field of proteomics.

Clinical and Translational Proteomics Award

\$3,000, Sponsored by Clinical Proteomics (Published by BioMed Central)

This award recognizes a scientist in the field of clinical and translational proteomics.

Science and Technology Award

\$3,000, Sponsored by the HUPO Industrial Advisory Board (IAB)

Recognizes an individual or team in private industry who played a key role in the commercialization of a proteomics technology, product, or procedure. The emphasis of the award is on making the technology, product, or procedure widely available, which is different from the basic scientific invention.

Distinguished Service Award

\$3,000, sponsored by HUPO

The Distinguished Service Award recognizes an exemplary member of the proteomic research community whose dedicated service has made indispensable contributions to the organization and mission of HUPO. The Service Award is presented every other year and will next be awarded in 2017.

CALL FOR PAPERS | JPR HPP SPECIAL ISSUE

Journal of Proteome Research will publish its fifth annual Special Issue dedicated to the HUPO Human Proteome Project (HPP). The scope of the 2017 Special Issue has expanded to highlight progress on the HPP in the broader sense. Thus, starting in 2017, the annual Special Issue will now consider papers encompassing both the Chromosome-Centric Human Proteome Project (C-HPP) and, for the first time, the Biology and Disease Human Proteome Project (B/D-HPP).

We warmly invite independent laboratories to submit articles addressing the thematic priorities.

To read more and to submit your research [click here](#).

INTERNATIONAL WORKING GROUP FOR ANTIBODY VALIDATION

An *ad hoc* International Working Group for Antibody Validation, including participants from the HUPO Antibody Initiative, was formed to formulate appropriate approaches for validating antibodies used in common research applications, and to provide guidelines to ensure antibody reproducibility. The working group recommend five conceptual ‘pillars’ for antibody validation to be used in an application-specific manner, as outlined in the figure below.

The recommendations are summarized in the figure below and in the publication “A proposal for antibody validation”, Uhlén et al. *Nature Methods*. 2016 Sept.

<http://www.nature.com/nmeth/journal/vaop/ncurrent/full/nmeth.3995.html>

