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## President's Message



geographic region.

I congratulate Fernando Corrales, Juan Calvete, and Concha Gil for organizing an outstanding and diverse program for the Congress in Madrid. We also had the opportunity to recognize the leadership of our friend Juan Pablo Albar who contributed so much to the proteomics community. The 2014 HUPO congress was a great success scientifically and in attendance.

The annual congress is the time for renewal of HUPO governance. The 2015 Executive Committee will be under the leadership of Mark Baker, President. It also welcomes new members, Gyorgy Marko-Varga as Secretary General and Emma Lundberg and Yu-Ju Chen elected as Members-at-Large. A new HUPO Council was elected from a strong slate of candidates, demonstrating interest for HUPO governance. This election resulted in a new Council of diverse age, gender, and

During the HUPO congress, we had very fruitful discussions with representatives of national proteomics societies. HUPO now offers free associate member status to their members. This initiative provides a number of advantages, including receiving HUPO newsletters and information about workshops and training courses, ensuring all information of interest is disseminated throughout the global HUPO community. The major benefit for full members of HUPO remains a discounted Congress registration fees and discounts for subscriptions to several journals. I also had the opportunity in Madrid to sign with Stephen Pennington and Andrew Pitt from the British Proteomics Society (BPS) the MOU for their successful bid to host the HUPO2017 Congress in Dublin.

The year 2014 has been a very productive, and I would like to emphasize a few key points.

1. B/D HPP and C-HPP were reinforced as two arms of the same HPP program, thanks to their respective leaderships. Many scientists are now engaged in both arms of our strategic HPP adventure.
2. The status of "missing proteins" is now clarified; they totaled 3,844 in 2013 and only 2,948 in 2014. We are on track to make solid progress in the hunt.
3. The Human Protein Atlas v13 was released on 6-7 November 2014 – have a look at the new data and informational content it covers - it's great!
4. The Proteome Analyzer project is aimed at the development and commercialization of robust, moderate cost, high-throughput mass spectrometers suitable for clinical laboratories and epidemiological studies. They have made significant progress, including discussions with manufacturers.
5. The Nature publication of a pair of papers claiming 17,294 and 18,097 protein identifications raised many questions with some focused on the appropriateness of FDR filters at the protein level... Both publishing teams were present in Madrid and robust positive discussion covered how to deal with false positive and negative results. It was decided that a group of leading bioinformaticians will examine the methods to reduce false-positives while not losing too many true-positives.
6. The openness of the proteomics community to other large scale studies was also illustrated by the presentation of genomic, transcriptomic, and epigenomic studies of common cancers coupled with proteomic analyses. It was further recommended that working on "popular proteins" in disease-specific research will make proteomics an essential toolbox component of future biomedical studies.
7. Finally, the Segovia post-Congress HPP Workshop was again a lively and interesting day of presentations and discussions.



*Continued on page 2*

## HUPO Awards Presented at Congress



**Professor Pier Giorgio Righetti** receives the Award for Distinguished Achievement in Proteomic Sciences sponsored by ACS *Journal of Proteome Research*.



**Professor Neil L. Kelleher** receives the Award for Discovery in Proteomics Sciences.



**Professor Daniel W. Chan** receives the inaugural award for Translation Proteomics presented by Jean-Charles Sanchez, Editor-in-Chief of *Translational Proteomics*.



The Award for Science and Technology was presented jointly to **Subhasish "Babu" Purkayastha** (AB SCIEX), **Rosa Viner** (Thermo Fisher Scientific), **Andrew Thompson** (Proteome Sciences plc), and **John Rogers** (Thermo Fisher Scientific).

## President's Message, continued

As you all know, HUPO has benefited for the past three years from the very professional support from Scientific Association Management (thanks again to Judith Sjoberg and Jennifer Watson). We are presently looking for alternative administrative support of HUPO that may offer the possibility to contribute to the present development and future growth of activities related to our flagship Human Proteome Project. The HUPO Council also decided to consider options around a model involving a preferred/core Congress PCO for the running of future annual Congresses, with the scientific program remaining under the responsibility of the local organizers supported by their national proteomics society.

In conclusion, this is my last contribution to HUPOST as the HUPO president. I would like to take the opportunity to thank all of you, especially the members of the HUPO EC and HUPO Council who worked with me to secure our organization and reinforce its scientific activities. It was an honor to serve HUPO at different levels of the organization for many years. Whilst it's time for me to leave the stage, please be assured that I'll continue to be part of our community and to enjoy with all of you the many scientific achievements to come.

Pierre Legrain  
HUPO President



Above Pierre Legrain applauds recipients of the Student Poster Awards. Below **Fiorella Solari** receives the Young Investigator Award from Pierre Legrain.



## HUPO Executive Committee 2014

Pierre Legrain, President (France)  
 Mark Baker, President-Elect (Australia)  
 Catherine Costello, Past President (U.S.A.)  
 Maxey C.M. Chung, Secretary General (Singapore)  
 Bruno Domon, Treasurer (Luxembourg)  
 William Hancock, Vice President, (U.S.A.)  
 Gilbert S. Omenn, Member at Large (U.S.A.)  
 Michael Snyder, Member at Large (U.S.A.)

## HUPO Executive Committee 2015

Marl Baker, President (Australia)  
 Pierre Legrain, Past President (France)  
 Michael Snyder, Vice President, (U.S.A.)  
 Gyorgy Marko-Varga, Secretary General (Sweden)  
 Bruno Domon, Treasurer (Luxembourg)  
 Yu-Ju Chen, Member at Large (Taiwan)  
 Emma Lundberg, Member at Large (Sweden)

## HUPO Council Election Results

HUPO Council consists of an equal number of representatives from each world region: Eastern (Asia/Oceania), Central (Europe/Africa), and Western (the Americas). These scientists were elected for terms that will begin January, 2015

### Eastern

- Peter Hoffmann, University of Adelaide (Australia)
- Bonghee Lee, Gachon University (Korea)
- Hisashi Narimatsu, Natl Institute of Advanced Industrial Science & Technology (Japan)
- Marc Wilkins, Macquarie University (Australia)
- Ho-Jeong Kwon (Korea)
- Jun Qin (China)

### Central

- Bruno Domon, CRP-Santé (Luxembourg)
- Albert Heck, Utrecht University (Netherlands)
- Matthias Mann, Max Planck Institute of Biochemistry (Germany)
- Charles Pineau, Biogenouest Proteomics Core Facility (France)
- Jonathan Blackburn (South Africa)
- Paola Roncada (Italy)

### Western

- Chris Overall, University of British Columbia (Canada)
- Mike Snyder, Stanford University (USA)
- Pierre Thibault, University of Montreal (Canada)
- Ana Paulina Barba (mexico)
- Daniel Martins de Souza (Brazil)

## HUPO Council Meets in Madrid



The HUPO Council met on Sunday, 5 October in Madrid. After reports by HUPO Officers (Secretary General and Treasurer), new members of the Executive Committee were elected. Council diversity appointments from the three regions (West, Middle and East) were also ratified. See *election results*.

The Committee reports, Initiative reports and Congress reports were presented by the respective chairs or representatives. The membership report generated discussion on the issue of a nominal subscription fee charged to national societies to enable their members to become associate members of HUPO. It was decided that no fees will be charged, but National societies must provide their member lists to HUPO in order to enroll their members as Associate members of HUPO. This revised plan was presented to the Presidents of the Regional and National Societies at their meeting on 6 October.

The selection of a new management company for HUPO administrative office and a preferred PCO for the Congress were discussed. The Congress management has become urgent with the Yokohama Congress yielding only a minimal surplus to HUPO. Requests for proposals have been developed for HUPO management and the preferred PCO to be distributed after the Congress.

On 6 October the General Assembly of Members (GAM) was held in the late afternoon. Officers presented the HUPO financial statements, election results, and announcement of the venue for HUPO 2017. The organizers of the Madrid Congress were thanked.

Maxey Chung  
 Secretary General



## Key Scientists Retire from HUPO Council

These colleagues are retiring from HUPO Council after many years of service. Although they will remain active participants in HUPO, we want to acknowledge and thank them deeply for their leadership on the Council and the Executive Committee.



HPP and C-HPP.

**Maxey Chung** joined the Executive Committee only in 2013 as Secretary General, but has been a Councilor since 2006. He has taken on many assignments to foster global communication and cooperation among the regional and national HUPO organizations. Maxey has served on many committees and initiatives over the years, chaired the Awards Committee (2009-2012) and now is active with

**Cathy Costello** has served on many HUPO committees and on the Executive Committee as President and Past President. Her leadership moved HUPO into more advanced and cost effective management systems, including new online transaction methods and new web site.



**Bill Hancock** has driven the Industrial Advisory Board and the alliances between HUPO and several journals, including the ACS sponsorship of the Distinguished Achievement in Proteomic Sciences Award. Bill retires after 14 years on HUPO Council and a number of years on the Executive Committee. As Chair of the Nominations and Elections Committee and active participant in the HPP, Bill leaves a lasting, positive influence on HUPO.



**Gil Omenn** has been a Councilor since 2005 and has been one of the most productive members of the Executive Committee. He spearheaded the development of a number of initiative projects, most importantly the Human Proteome Project (HPP), which in only three years has enlisted broad global participation and support. Gil also served as co-organizer of the 2012 World Congress in Boston.



On behalf of the HUPO EC and the HUPO council, and on a personal note, I would like to emphasize how great, pleasant and inspiring it has been working with these colleagues: sharing views on many subjects, solving issues when necessary, always having in mind the best for our organization and our community. Thanks, my friends!

Pierre Legrain

## HPP: Madrid Reported by Gil Omenn

**HPP Investigators and Teams played large roles in the HUPO Annual Congress in Madrid.** There were 3 Workshops by C-HPP and 21 Workshops by B/D-HPP and related teams: plasma, cancers I, cancers II, iMOP, liver, \*extreme conditions, \*infectious diseases, EyeOme, diabetes, PSI/PX, antibody proteomics, glycoproteomics, brain, stem cells, \*respiratory diseases, cardiovascular, \*mitochondria, \*protein aggregation diseases, \*PediOme, \*biobanking & pre-analytical sample assessment, and \*computational mass spectrometry (\* = first time workshop). Appended is the Activity Document our staff prepared for Madrid plus Segovia. We hope to have summaries from the rapporteurs and chairs of these sessions, though only a few have been collected so far. There is no doubt that the HPP generated a lot of the discussion and excitement in Madrid.

### Segovia Post-Congress HPP Workshop

The main observations or conclusions from our lively and interesting day of presentations and discussions in Segovia were these:

- We should promote wide usage of neXtProt, PeptideAtlas, GPMdb, SRM, SWATH, HPA, and Antibodypedia across the life sciences community, with a focus on annotation for pathways, networks, and protein interactions.
- All HPP teams should reach out to colleagues on other C- and B/D-HPP teams to characterize proteins and protein isoforms of known proteins.
- We all should focus on **Missing Protein** lists and identify proteins that are not findable due to no or few tryptic cleavage sites, too hydrophobic, too basic, only expressed under unusual stress conditions or in very unusual cell types or at extremely low concentrations.
- We should all use the October 2014 updated **neXtProt tables**; we were invited to volunteer to participate in the beta-testing of the neXtProt SPARQL query scheme.
- We should further scrutinize the Kim et al and Wilhelm et al datasets and papers to see which proteins survived in PeptideAtlas and/or GPMdb and neXtProt, and which not. Groups should examine those proteins and protein families they know best.
- We should commission a group of leading bioinformaticians to examine the methods to reduce false-positives while not losing too many true-positives as we saturate the protein parts list.
- We should find ways to participate in B/D initiative to name priority proteins (Aebersold) or "popular proteins" (van Eyk) for specific disease categories. We should submit comments and protein nominees, critique those released, and promote their use in the integration of proteomics with other omics.

## Future Congresses

[Vancouver, September 27 – 30, 2015](#)

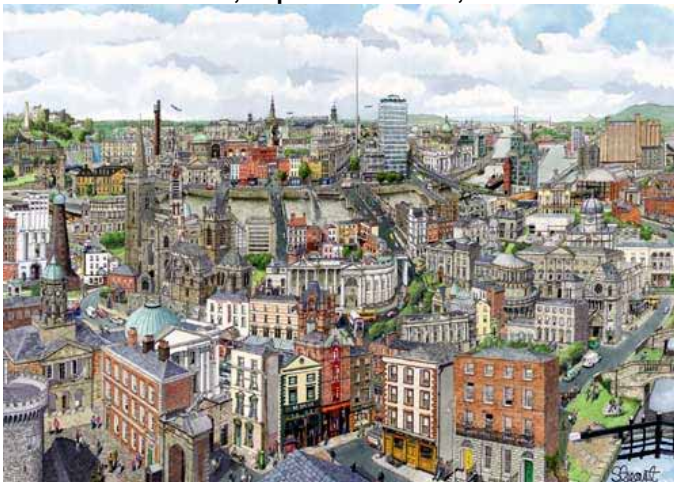
Registration opens January 27, 2015



Taipei, September 18 – 22, 2016



Dublin, September 17 – 20, 2017

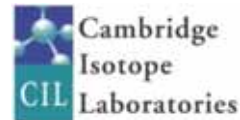


## Industrial Advisory Board

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. 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. Please contact [office@hupo.org](mailto:office@hupo.org) for details on IAB membership.



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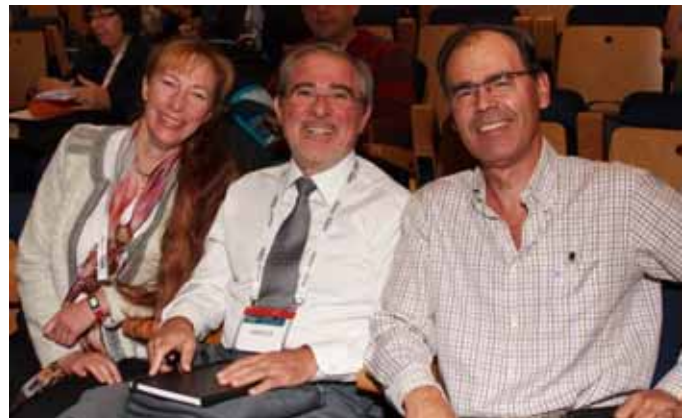


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## HPP – The Year in Review

The year 2014 has been a busy and productive time for the HUPO Human Proteome Project (HPP) and its component parts.

1. The 2<sup>nd</sup> C-HPP special issue of J Proteome Research appeared on schedule in January 2014 with 32 articles from and related to the HPP. An additional 6 articles appeared during April-June for a total of 38 (on top of 48 in the 2013 special issue). C-HPP continued its practice of having 2 or 3 major workshops each year, including at the annual HUPO Congress. Many of the chromosome-centric teams reported substantial research and/or bioinformatics analyses. Larger cross-team collaborations are still to be developed. Young-Ki Paik, Bill Hancock, and Gyorgy Marko-Varga continue to provide strong leadership to the C-HPP. Young-Ki Paik announced in Madrid that progress of each C-HPP team would be assessed in 2015.
2. An updated set of Metrics for the HPP had nearly 2000 additional highly confident protein identifications, compared with the 2012-2013 metrics. The neXtProt PE1 numbers were 13664 in 2012, 15646 in 2013, and now 16491 in 2014. Removal of 638 PE level 5 genes from the denominator of protein-coding genes left 3844 PE2+PE3+PE4 proteins to be identified in 2013, which was reduced to 2948 “missing proteins” in 2014. It was recommended before the August Bangkok C-HPP Workshop that each team could scrutinize its chromosome-specific list from neXtProt of genes with missing proteins and annotate the predicted features of that protein, the tissue expression of any transcript evidence, and the strategy to find it. Chr 17 provided an example of a list with columns for listings in GPMdb and in Human Protein Atlas. At the end of the Bangkok Workshop many teams expressed interest in proceeding with such analyses.
3. The B/D-HPP made progress on disease-related priority protein lists accompanied by full SRM resources for targeted quantitative analysis. A summary of all of the 2013 Yokohama B/D workshops was published in Proteomics in April 2014. There were several new B/D teams created in 2014: extreme conditions, protein aggregation diseases, and computational mass spectrometry (formed from MS pillar + B/D). Jennifer van Eyk succeeded Ruedi Aebersold as Chair of the B/D-HPP, effective Oct 2014.
4. Planning for the Proteome Analyzer project of the B/D-HPP progressed, with completion of a survey in time for the Madrid Congress. The goal is to engage multiple major manufacturers in the development and commercialization of robust, moderate cost, high-throughput mass spectrometers suitable for clinical laboratories and epidemiological studies. Bruno Domon leads this project.
5. The community was surprised by the publication by Nature of a pair of papers by Kim et al (Pandey lab) and Wilhelm et al (Kuster lab) claiming 17294 and 18097 protein identifications, but using no FDR filter at the protein level. Although they both generously cited the publications from the HPP, they did not follow the guidance about quality thresholds for protein matches. They did study many tissue and cell types, they used high-end instruments, and they registered their raw data sets with ProteomeXchange and made the data fully available for scrutiny. Both PeptideAtlas and GPMdb subjected those datasets to the standard re-analysis pipelines using X!Tandem and TransProteomicPipeline, respectively, finding about 13,000 high-quality protein matches. Each added about 500 proteins to the cumulative number of proteins identified in PeptideAtlas. Claimed protein products from pseudogenes and from such gene families as olfactory receptors were not confirmed in these reanalyses. Moreover, an independent analysis of the 108 olfactory receptor proteins reported by Kim et al and the 200 reported by Wilhelm et al was published in JPR July 2014 by Ezkuria et al of Spain; they were unable to justify any of those matches from the spectra provided. Beavis tested another kind of probe, checking for claims of detection of Y-chromosome-specific gene products in females; many were reported in these datasets, including in ovarian specimens.  
 The HPP leadership decided to avoid a confrontation about these papers. Pandey was already a prominent member of C-HPP (Chr 22 leader), and Kuster participated in the Yokohama Congress. They were given prominent places on the Madrid Congress program and triggered a lot of discussion about how to avoid excessive inclusion of false-positive identifications, without losing true positives as one approaches saturation of the proteome. This topic warrants a serious organized effort from our KnowledgeBase resource pillar/C-HPP Bioinformatics group. They did not address the specific reports on olfactory receptor proteins and Y-specific proteins.  
 In his plenary lecture in Madrid, Matthias Mann noted that “the field of Proteomics over a long time had established high standards for protein expression evidence, with stringent FDR thresholds, but now faces the circumstances of recent papers that took a different approach.
6. The long-running TCGA genomic, transcriptomic, and epigenomic studies of common cancers now are being coupled with proteomic analyses from the NCI CPTAC. CPTAC leaders and investigators are closely associated with the B/D-Cancer-HPP, which held two workshops in Madrid. These datasets will be highly valuable for others in the HPP.
7. The Human Protein Atlas released on 6-7 November 2014 its v13 with four subatlases presenting tissue expression, intracellular localization, cancer biology, and cell line findings. Science magazine of 7 November included a hard copy poster, which can be found also at [www.proteinatlas.org](http://www.proteinatlas.org). Teams annotating missing proteins can search HPA for immunohistochemical evidence (and transcript evidence) to guide further studies. HPA tightened its criteria for “supportive evidence”, a contrast with the approach of Kim et al and Wilhelm et al on the mass spec side. PrEST antigens have been utilized in mass spectrometry; further collaborations across antibody profiling and mass spectrometry would enhance the confidence of findings from both approaches.
8. The Human Protein Atlas released on 6-7 November 2014 its v13 with four subatlases presenting tissue expression, intracellular localization, cancer biology, and cell line findings. Science magazine of 7 November included a hard copy poster, which can be found also at [www.proteinatlas.org](http://www.proteinatlas.org). Teams annotating missing proteins can search HPA for immunohistochemical evidence (and transcript evidence) to guide further studies. HPA tightened its criteria for “supportive evidence”, a contrast with the approach of Kim et al and Wilhelm et al on the mass spec side. PrEST antigens have been utilized in mass spectrometry; further collaborations across antibody profiling and mass spectrometry would enhance the confidence of findings from both approaches.

## HPP – The Future

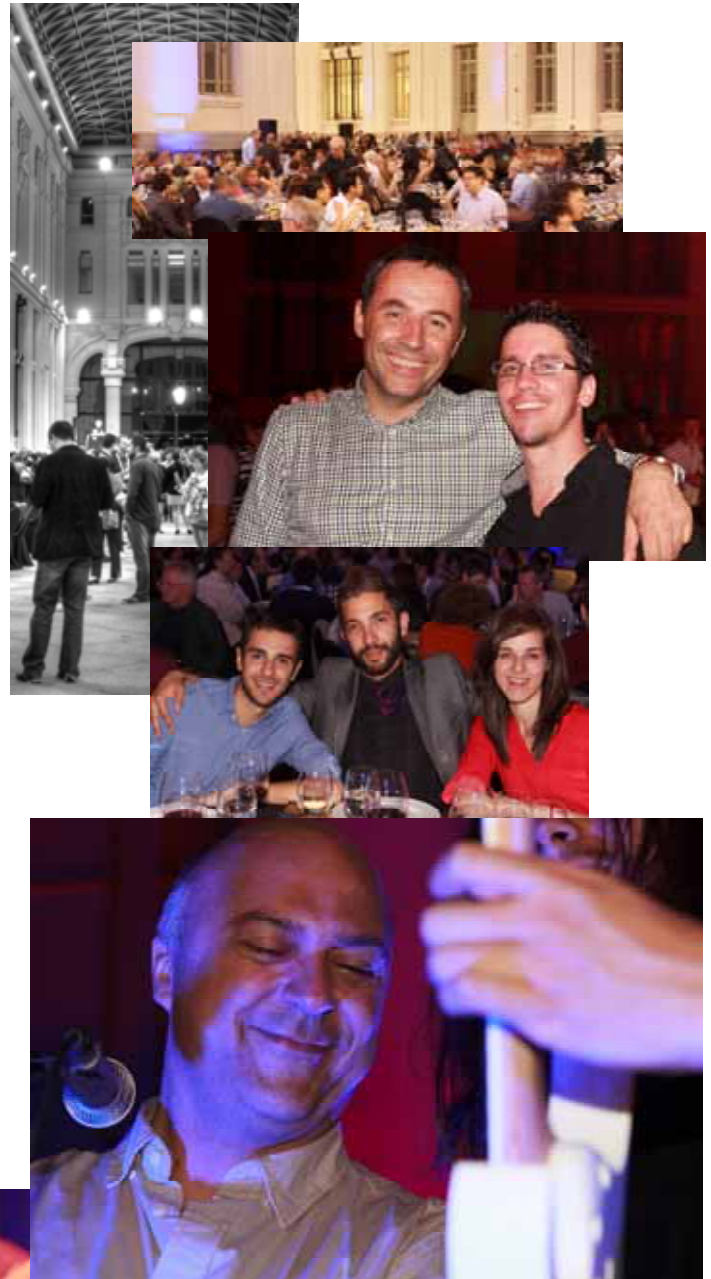
We expect to have continued HPP progress over the coming year with highlights at periodic workshops and the Vancouver Congress in September.

- a) We need to accelerate our analyses of the “missing proteins” for which direct protein evidence is lacking or insufficient; these correspond to the PE2 + PE3 + PE4 genes. We should scrutinize the quality of evidence and potential ambiguous matches for proteins proposed as PE5 gene products.; those passing such assessment should added via PeptideAtlas and neXtProt to our known list (PE1, if evidence is sufficient). A cross-C-HPP effort that utilizes all available data could start from the chromosome-specific lists from neXtProt, PeptideAtlas, and GPMdb to annotate the missing proteins in detail, informed especially by the Human Protein Atlas and transcript expression across tissues.
- b) There are special targeted analyses recommended by protein families, by amplicons, and for probing the quality of evidence for claims of matches to pseudogenes and other PE5 genes.
- c) There should be more effort to confirm known protein identifications and characterize protein concentrations and modifications from mutations, PTMs, and splice variants, using SRM/MRM and using antibodies from HPA and other sources.
- d) More linked analyses by mass spec and antibody profiling on the same specimens would build confidence about the evidence from both strategies.
- e) Priority proteins recommended by the B/D-HPP or “popular proteins” from disease-specific research, as championed by Jennifer van Eyk, should be promoted for use throughout the biomedical research community. This effort would address our broadest goal: to make proteomics an essential component of all studies linking genotypes and phenotypes.
- f) New mass spectrometers from our Proteome Analyzer project should begin to populate clinical and epidemiological laboratories.
- g) We should have a lively program of activities at the 2015 HUPO Congress in Vancouver 27-30 September 2015.



HPP reports by Gil Omenn

## Memorable Madrid . . .



There are many Congress photos posted online:  
[www.hupo.org](http://www.hupo.org)