INSIDE

Special Contribution: Gene Editing – a Path Forward for Annotating the uPE1s for the C-HPP

Dr. Ekaterina Poverennaya
Orekhovich Institute of Biomedical Chemistry,
Moscow 119191, Russia

Prof. Andrey Lisitsa,
Orekhovich Institute of Biomedical Chemistry,
Moscow 119191, Russia

The next phase of the C-HPP has pivoted towards the functional analysis of proteins, especially the uPE1 proteins that have absolutely no functional, locational, or structural information, and now resembles the Human Genome 2.0 Program. Among the young scientists, this idea was accepted with enthusiasm and ambition.

What do we have right now, after 6 years of work by the C-HPP? The protocols for the confident identification and quantification of proteins have been delivered. Up to ~87% of the human proteome has been covered [1]. This coverage provides us with an outstanding tool to trace the changes in the molecular landscape in response to disturbances of the genome. We are now in the position to leverage this momentum and take the next steps to implement and expand what has been achieved.

In our view, the logistics of the C-HPP can accept gene editing technology, thus fulfilling the mission in a chromosome-centric way. Here we propose that the chromosome can be unlocked through gene-by-gene editing, followed by measuring the integral response of the whole proteome. The emerging CRISPR/Cas gene editing technology [2] could support the C-HPP with the following the operations on selected genes (Figure 1): (a) knocking off the gene by inserting a stop-codon near the center of the gene to prevent translation; (b) enhancing/depressing gene expression, with subsequent transcriptome-proteome profiling; and (c) tagging the gene and then pulling out the tagged protein for structural-functional analysis (profiling proteoforms [3,4], which can even be resolved in 3D using X-fel). Using a tagged protein is useful for identifying the interacting partners, or deciphering the "hubs" [5]. Tagged proteins allow us to obtain clues about functions that can be followed by sequentially focused functional screens to decipher biological roles and activities.

The more ambitious aspects are to inactivate a chromosome or chromosomes by transferring the XIST gene from the X chromosome. The first steps of this process were published by Jun Jiang et al. [6]; they inactivated the additional chromosome 21 in Down syndrome pluripotent stem cells.

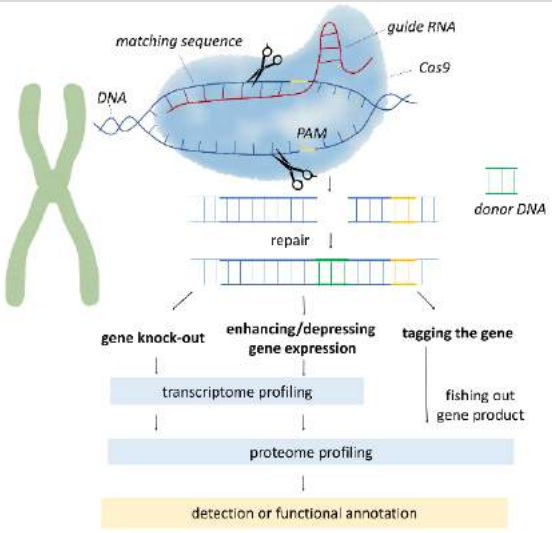

Figure 1. Genome editing using the CRISPR-Cas9 system for C-HPP goals.

In conclusion, a proteome-wide analysis combined with the editing of target genes and/or chromosomes is not only possible but also will probably end up as a springboard into the next phase of the C-HPP.

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The New Release of neXtProt (2018-01-17)

The Swiss Institute of Bioinformatics (SIB) has recently released a new version of neXtProt (2018-01-17; www.nextprot.org) that contains the latest updated human proteome database. In this release, 17,470 validated human proteins (PE1) are included; this number is 393 more than the previous version (2017-1-17). Figure 2 shows how each dataset has been updated and cross-checked to prepare for the new release.

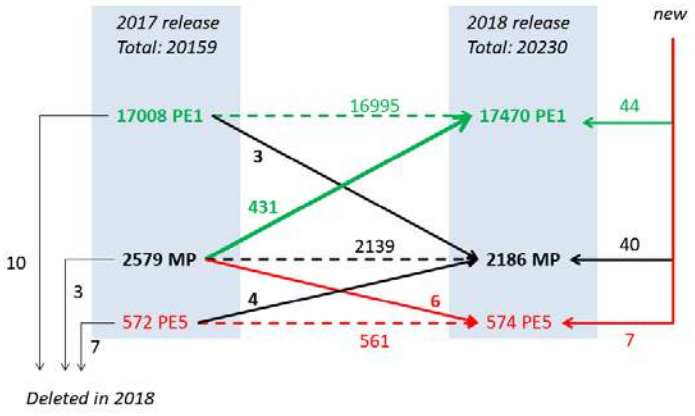
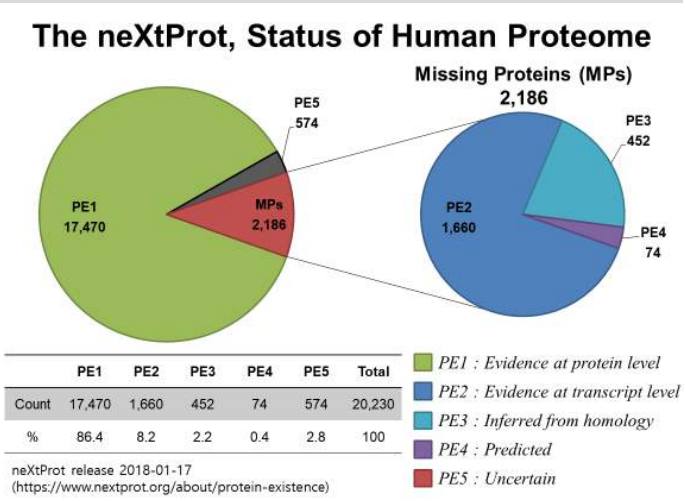


Figure 2. Illustration of changes in the status of annotated proteins between 2017 and 2018 versions (provided by Lydie Lane Team; January, 17, 2018).

Now, there are only 2,186 missing proteins (MPs) with a status of PE2+PE3+PE4 and 574 uncertain proteins (PE5; Figure 3). The recent neXtProt release was generated based on the latest data from the PeptideAtlas (release Human 2018-01), which provides a total of 51 PeptideAtlas datasets obtained from normal tissues, cancer tissues and cell lines, and includes over 1.4 million peptides detected by mass spectrometry (MS). Most importantly, the number of proteins with unknown function is now 2,271, which can be obtained with a SPARQL query of NXQ_00022. Selecting only the validated ones (PE1) from the result list gives a total of 1260 validated proteins with unknown function (uPE1). Data from UniProtKB, Ensembl, IntAct, GOA, and GeneIDs, have also been updated. These data have been complemented with GO molecular function; biological process and cellular component annotations for most of the human protein kinases; and expression information, mutagenesis, and variant phenotype data (Figure 3).

Dr. Lydie Lane
SIB, Switzerland



	PE1	PE2	PE3	PE4	PE5	Total
Count	17,470	1,660	452	74	574	20,230
%	86.4	8.2	2.2	0.4	2.8	100

Figure 3. Distribution and status of human proteins presented in neXtProt (2018-01-17 release)

There are two new rules that reflect the state of PE:

(1) The status of some missing proteins (PE2, PE3, or PE4) has been upgraded to the PE1 level if the entry has GOLD binary interaction data from neXtProt.

(2) Due to the UniProtKB demerging entries encoded by multiple genes, some neXtProt entries now have the same protein sequence and are indistinguishable at the protein level. This list can be retrieved using a SPARQL query of NXQ_00231. The peptides that match such indistinguishable entries are now labeled "pseudo-unique" rather than "found in other entries" and have been used to validate PE if they complied with the HPP guidelines.

The "proteomics" view for entries has been revamped and now loads faster. It is now also possible to search the positional annotations listed in the feature table for a specific category or for text found in the feature description. For instance, searching for selected reaction monitoring (SRM) now returns the number of SRM peptides mapping to the isoform and allows the user to rapidly browse the data for all SRM peptides.

New advanced search SPARQL queries have been added. These new queries are: (1) identifying proteins with high proline content in the SnorQL interface (NXQ_00225); (2) listing proteins with at least two uniquely mapping peptides larger than 9 or more amino acids (aa) in length found in blood plasma, urine, or cerebrospinal fluid to support markers research (NXQ_00226); and (3) identifying proteins with experimentally determined lengthy alpha-helices (defined as a length longer than 75 or more amino acids), illustrating a query of proteins with a specific secondary structure (NXQ_00230).

The new release of neXtProt is the definitive reference database of the human proteome and is used by the Human Proteome Project (HPP) to assess the progress of completing the map of the human proteome.

Highlights of C-HPP Consortium News

Period of C-HPP Research was Extended: 2012 to 2027 (Decision I)

After discussion at the Co-Chairs (9/16/2017), EC (9/17/2017), and PIC meetings (9/17/2016) in Dublin (Venue: O'Brien Center for Science, University College Dublin), the C-HPP consortium made two important decisions about the working period and the direction of scientific research and as determined by a majority vote (see below).

Decision 1: Extension of C-HPP Period to 2027

Decision 2: The Launch of neXt-CP50 Challenge

Rationale: Considering the current speed of the progress in detection and characterization of MPs (neXt-MP50), it seems unlikely that we will accomplish the goals, which were set early, of completing the annotation of missing proteins, including three post-translational modifications (PTMs) of each of the yet-to-be identified **2,186** MPs within the next 5 years or so. An aspirational goal is to obtain three PTMs critical for the biological function of all proteins, not just the MPs. Thus, it was necessary to extend the proposed 5 years of the current term 2022 to 2027. As Dr. Lee Hood mentioned in the SSAB meeting on Sunday (9/17/2018), it seems a good time for us to think about our project in the past and set out a new direction to accommodate our scientific goals.

C-HPP Principal Investigator Council Meeting in Dublin (O'Brien Center for Science, University College Dublin), Sept 17, 2017

The Launch of the neXt-CP50 Challenge: A Pilot Initiative to Characterize 50 uPE1 Proteins of Unknown Function in 3 years (Decision II)

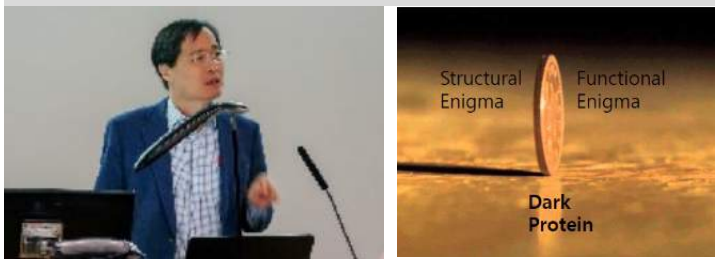
In Dublin, Young-Ki Paik, chair of the C-HPP, presented a pilot project of the functional study of PE1 proteins of unknown function (uPE1), accounting 1260 (neXtProt 2018-01-17 release). The idea behind this proposal came from a long discussion between the C-HPP Co-Chairs. Recently, the C-HPP extended the scope of target proteins from uPE1 to other proteoforms, such as smORFs, lncRNA translation products, missing proteins, and SNP-driven proteins. These proteins are now colloquially called the "**dark proteome**" implying both structural and functional enigmas (see below). On March 1, 2018, the C-HPP announced an official launch of the **neXt-CP50** challenge, a pilot project for the functional study of dark proteins, with a total of 14 teams submitting 50 target proteins for a 3-year project (Table 1).

Table 1 The neXt-CP50 Pilot Project Team (Total 50 uPE1 Proteins; last updated April 18, 2018)

Chr.	PI Name	Total*	1st priority	1st period	2nd priority	2nd period	Comments
2	Lydie Lane	80	5	2018~2019	N/A	N/A	Cross chromosome targets
3	Takeshi Kawamura	56	2	2018~2020	N/A	2021~	
4	Yu-Ju Chen	53	2	2018~2020	8	2021~	
9	Je-Yoel Cho	57	2	2018~2019	8	N/A	
10	Joshua LaBaer	61	2	2018~2020	8	2021~	
11	Jong Shin Yoo	70	2	2018~2020	8	2021~	
13	Young-Ki Paik	26	5	2018~2021			
15	Gilberto Domont	44	2	2018~2020	6	2021~	
16	Fernando Corrales	54	2	2018~2021	4	N/A	
17	Gilbert S Omenn	66	17	2018-2020		-	Development of bioinformatics tool.
18	Alexander Archakov	14	2	2018~2020	14	2021~	
19	Sergio Encarnación-Guevara	68	2	2018~2019	6	2020~	
20	Siqi Lui	35	4	2018~2020	11	2021~	
Y	Ghasem Hosseini Salekdeh	1	1	2018~2020	N/A	N/A	

*website: https://goo.gl/Wf2Qnn, neXtProt release 2018-01-17)

The current members of this pilot project are Chromosome 2, 3, 4, 9, 10, 11, 13, 15, 16, 17, 18, 19, 20, and Y (Table 1). Tentatively, these 14 teams were assigned to the Blue Team of TAMPA (Task force for MP annotation, see C-HPP Newsletter No. 6, 2017) and would replace the previous inactive functional study teams. It is anticipated that new "Blue Team," will carry out functional studies of 'dark proteins' including uPE1 using cell lines, tissues, and model organisms. It is noted that Chr 17 team (PI: Gilbert S. Omenn) committed to development of bioinformatics tool which may allow an *in silico* functional prediction of uPE1. The C-HPP leadership is currently planning key strategies for the next step and will host an open discussion on this project at the upcoming 19th C-HPP workshop in Santiago, Spain (6/16-17) and HUPO Orlando Congress in September (9/30-10/4).



Dr. Young-Ki Paik, Chair of C-HPP Consortium introduced the concept and objectives of neXt-CP50 initiative at the Sunday HPP Investigators meeting on Sept. 17, 2017 (left). This initiative aims to characterize function of dark proteins (right) which may symbolize two sides of the same coin: one side for structural enigma that is being targeted by structural genomics group and the other one for functional enigma that is being targeted by HUPO C-HPP investigators.

HUPO 2017 Award for Discovery in Proteomic Sciences

Prof Chris Overall, Co-Chair of the C-HPP, was awarded the HUPO 2017 Award for Discovery in Proteomic Sciences – sponsored by the Journal of Proteomics-Elsevier BV. The other winner was Prof Ileana Christea, Princeton University. The Award and short presentation were made at the HUPO 2017 congress in Dublin, September 20, 2017.

Dr Overall is best known for two related but distinct scientific achievements. The first is development of new positional proteomic methods for identification of protein N and C termini, e.g., TAILS, PICS, ATOMS, which also allow for identification of protease cleavage sites and substrates in vivo for the first time. Thereby he established the field of degradomics. The second is levering these techniques to reveal new and often unexpected biological roles for proteases in vivo and their aberrations in disease. The significance of his research has been recognized by many previous Awards including: the Tony Pawson Award (2014); and the Proteomass Scientific Society Award (2017). He is an Associate Editor of the Journal of Proteome Research and was elected to the HUPO Executive Council and to Co-Chair the Chromosome-Centric Human Proteome Project.

Highlights from HPP Workshop: September 17 and 21, 2017 in Dublin

University College Dublin

Dr. Gilbert S. Omenn
Chair, HUPO HPP, University of Michigan, MI, USA

About 70 HPP investigators and interested HUPO Congress attendees participated in the post-Congress Workshop at the University College Dublin on September 21, 2017.

Highlights from the Congress and HPP Meetings and Sessions, Sunday, Sept 17, 2017

Mike Snyder, Chair of SSAB, initiated and moderated the discussion at the HPP Investigator meeting. He highlighted the importance of replicable, quantitative analyses throughout biology; the emergence of single-cell analyses with CyTof and MS; contrasts between proteomics and metabolomics in terms of depth of analysis, which are

favorable for proteomics, and the time and cost of analyses; and the growing emphasis on clinical applications and wellness projects. Jenny van Eyk pointed to the dynamics of proteomics studies and new work with cross-linking and protein structures. Eric Deutsch emphasized the statistical validation and localization of proteins with PTMs (mzIdentML now covers PTMs). Nikki Parker mentioned glycoproteins in the secretome.

Drs. Mike Snyder (Chair of SSAB) and Eric Deutsch

Young-Ki Paik introduced a pilot C-HPP initiative, termed neXt-CP50 Challenge that was complementary to the neXt-MP50 Challenge (MP: neXtProt PE2,3,4 predicted proteins): the uPE1 proteins lacking any functional annotation (estimated at 1,232 in the neXtProt version 2017-08-08). He introduced the five new leaders of the C-HPP teams (Chr 3, 6, 19, 21 and X), the schedule of the C-HPP workshops beginning with Santiago, Spain, in June 2018, and referred us to the C-HPP website and wiki. Lydie Lane emphasized the new advanced search tools in neXtProt. There was general discussion about linking the C-HPP and B/D-HPP teams; Jenny van Eyk challenged us to clarify the process for declaring a new project within the HPP, not just in the C-HPP. Likewise, the Early Career Researchers initiative of the B/D-HPP might be better placed under the entire HPP. There are groups in both arms that are pursuing PTMs, splice variants, and functional characterization. Several people called for the HPP to strengthen governance.

Drs. Gilbert S. Omenn, Chair of HUPO HPP (left) and Lydie Lane (right)

Progress on the Missing Proteins neXt-MP50 Challenge

Dr. Christopher Overall presents the update on the neXt-MP50

Chris Overall reported that there were 216 previously PE2,3,4 predicted proteins confidently identified in 2016 by HPP investigators. Comparing neXtProt PE2,3,4 MPs from January 2016 to January 2017, we found the total was reduced from 2,949 to 2,579, a gain of 370, and the total number of PE1 proteins rose from 16,518 to 17,008. Most of these PE1 proteins came from the Swiss-French Chr 2+14 study of sperm and the Chinese consortium study of testis. The assessment of newly identified proteins from the manuscripts submitted to the JPR SI 2017 was still under review, with many candidates, but a relatively modest number fully confirmed. Now that all the manuscripts are published, the best estimate is 73. See the Paik et al. editorial for the December special issue, which provides a good introduction to the multiple strategies for detecting MPs and their yield to date. It is hoped that more C-HPP teams will become active in this neXt-MP50 Challenge. There were many comments.

Progress on the B/D-HPP Popular Proteins Strategy

Dr. Fernando Corrales

The proteomics strategy of building a bridge to organ-focused biomedical researchers with lists of the most studied proteins and suitable SRM assays for quantitative has gained some momentum. Fernando Corrales, from the B/D-Liver Proteome Project and Chr 16, used this approach to focus on the enzymes of one-carbon metabolism pathways in the progression of non-alcoholic fatty liver disease/non-alcoholic steatohepatitis. Jenny van Eyk from the B/D Cardiovascular Proteome team focused on cysteine S-nitrosylation sites involved in some switch functions in the human, mouse, and rat. Their database has 2,955 unique SNO-proteins with 5,826 sites, including myofilaments, myosin H chain, and other proteins of interest. Tadashi Yamamoto described proteomics findings in multiple compartments of the kidney and in urine studies.

Drs. Jenny van Eyk and Tadashi Yamamoto

A major advance is the work of Kun-Hsing Yu, who is now at Harvard Medical School after finishing a post-doc with Mike Snyder at Stanford University. Yu performed a complementary literature search for each of the 22 B/D-HPP groups, including 11 organ systems, using PubMedQuery and PubtatorQuery. Snyder summarized the approach and noted that the work will be prepared for publication in the coming year, hopefully with information about uses by the B/D teams.

Comments from HPP Senior Scientific Advisory Board

In the Sunday HPP investigators meeting on Sunday, the Senior Scientific Advisory Board (SSAB) members Lee Hood, Mathias Uhlen, Cathy Costello, and Mike Snyder provided many useful comments. At the Thursday workshop, Naoyuki Taniguchi and Snyder carried forward these discussions. Taniguchi recommended a roadmap to enhance communication, attention to additional organs like lung, ovary, and prostate; clinical applications; and the renewed glycoproteomics activities. Snyder called the role of the HPP EC critical, supported the focus on PTMs, noted the deliverables from the B/D, acknowledged the interest in lncRNAs and smORFs addressed critically in the annual Metrics paper, and called for more attention to deliverables from each of the B/D and C-HPP teams. Snyder agreed that the ECR initiative should be adopted by the whole of the HUPO, perhaps linked with the Education Committee chaired by Gary Corthals.

Luncheon Meeting with Senior Scientific Advisory Board Members, Sept 17, 2017: Michael Snyder, Cathy Costello, Leroy Hood and Mathias Uhlen


The SSAB Committee Meeting

There was discussion about whether the proposed Pathology Proteomics Initiative should be under the B/D or a new Resource Pillar. Ed Nice, Dan Chan, Mark Baker, and others are actively engaged in the planning, including an upcoming conference in Australia. The tentative advice from the Workshop was to place the Pathology Proteomics Initiative under the B/D and connect it with multiple organ-specific and biofluid teams. We will welcome a well-drafted assessment of alternatives following the Australia conference.


Drs. Gil Omenn and Naoyuki Taniguchi

Relationship with the Journal of Proteome Research

Chris Overall announced that the Editor of the Journal of Proteome Research (JPR), John Yates, and the editorial board had committed to a sixth annual issue on the same schedule because it worked well this year. There was a call for papers in December 2017, using PeptideAtlas 2018-01 and neXtProt 2018-01 as the baselines for analyses and discussion, and the deadline for the submission of manuscripts is May 31, 2018. The review, revision, and re-review process will be completed by September 1, 2018, and the submission of finalized manuscripts for production of the journal will happen by October 1, 2018. The special issue will be published in December 2018. Each accepted manuscript will be published online when accepted.

Mass Spectrometry Resource Pillar Initiative on Post-Translational Modifications



Dr. Sue Weintraub

Sue Weintraub, leader of the rejuvenated MS Resource Pillar, introduced this initiative on Sunday and again at the Post-Congress HPP Workshop on Thursday, Sept 21. She announced the availability of a valuable resource prepared specifically for the HUPO Congress attendees and HPP investigators: a standard sample with 96 phospho-peptides either in solution or in a yeast protein matrix by SynPeptides Ltd. of Shanghai and aliquoted by the Moritz Lab at the Institute for Systems Biology. If you did not sign up at the exhibit hall and did not bring home the vials with these standard samples, you can still obtain them, perform your analyses, and share your results.


Drs. Yingming Zhao, Jystyna Fert-Bober and Hongxiu Yu

Yingming Zhao described extensive work on a family of metabolism-sensitive PTMs: acetyl, propionyl, butyl, crotonyl, hydroxyl-butyryl, malonyl, succinyl...lysyl acylations; histone acylations and HDACs sirtuins, and acyl transferases. He also addressed the different specificities in the different pathways of P300/CBP. Justyna Fert-Bober reported on studies of the citrullination of arginine residues. Removing the positive charges can be impactful and create neoantigens. The increased hydrophobicity increases the retention time. The DIA SWATH workflows have also been developed, and databases in heart and brain have been launched. Hongxiu Yu of Fudan University presented on succinylation, a dynamic PTM important in the HDAC classes of I, II, III, IV, and deacetylase SIRT5. The NADP+ IDH mutations cause excess succinylation, while SIRTS5 de-succinylates and activates PK2. Such changes affect immunoregulation in tumors and tumor cells.

Rob Moritz summarized advances in tools and approaches, like inclusion lists, SWATH, and SRM. There are many unidentified peptides; the Trans-Proteomic Pipeline now offers assessment of chimeric spectra. He described evidence of many modified peptides such as D-amino acids, especially Ala and Ser, might be significant in the aging brain and eye. Of course, searching for modified peptides increases the computational burden. Alexey Nesvizhskii and Andy Kong have developed MSFragger. Pengyuan Yang emphasized the expression patterns, splice variants, and PTMs related to the regulation of protein-coding genes, epigenetics, metabolites, and cell biol

Drs. Rob Moritz and Pengyuan Yang

Long non-coding RNAs

Drs. Tong Wang and Gong Zhang

Tong Wang from Guangzhou described the translatome based on full-length RNC-mRNA from initiation fractions on polysomes, as described in 2013. Some 47% of missing proteins have positive evidence in the live translatome. Epigenetic induction may enhance expression. Testis may be a particularly rich organ for study. Based on his presentations at the Tehran Workshop and the Guangzhou Conference this year, we invited Wang to present to the HPP investigators for better recognition of findings to date and critical evaluation of claims of protein translation products.

From studies of nine cell lines, 2,969 lncRNAs were identified. Applying the HPP Guidelines v2.1 of two non-nested proteotypic peptides of at least 9aa in length and a false detection rate (FDR) <1% at the protein level, they identified a substantial number of protein candidates using search engines. They have also performed MRM on many peptides and immunofluorescence on a small subset. The preliminary impression at the Workshop was that a more detailed assessment of the spectra and the

comparisons with spectra of synthetic peptides would be necessary to evaluate these extraordinary claims. Rob Moritz and Eric Deutsch agreed to scrutinize these findings when available.

Gong Zhang described an unpublished de novo sequencing approach, with 13,000 human proteins and 20,000 proteoforms identified in a single experiment on three hepatocellular cancer cell lines. No FDR method or reference database was used. They performed MRM on a Sciex 6500 Q-TRAP instrument and claimed 424 PE2, PE3, or PE4 MPs detected with two peptides of 9 aa. A Chinese biotech offers RNA-Seq translatome analyses at no charge for the C-HPP teams.



HUPO HPP Day Workshop, Dublin 9/21/2017

Bioinformatics Hub and HPP Guidelines for Interpretation of Mass Spec Data v2.1


Dr. Eric Deutsch

Eric Deutsch reported that the Guidelines are being widely used and were kept unchanged for a second year. There are several new developments.

1. A Universal Spectrum Identifier, for claims of findings of missing proteins: PDF screenshots in manuscripts are simply unsatisfactory (e.g., mzspec:PxD002145 //HeLa45_20_160423/scan14321). The identifier will be required for the 2018 JPR C-HPP Special Issue, which will be finalized by April 2018.

2. On the HPP Guidelines Checklist for manuscripts submitted to the JPR, we will now require page numbers and line numbers for each checkmark. Staff will check whether "not applicable" checks are explained; only some authors used that box, Item #10. If spectral quality was not great, the experiment should be repeated, not ignored.

3. We are preparing to clarify the guidelines for DIA-SWATH datasets. If these findings are analyzed like SRM with trace extraction via spectral libraries, SRM guidelines apply, with the display of traces and heavy-labeled reference peptides to demonstrate co-elution and matching of intensity patterns. If these findings are analyzed like shotgun (DIA-Umpire), shotgun guidelines should be applied, spectra displayed, and the spectra of labeled peptides should be shown.

We must talk with companies, as methods of acquisition are quite different.

4. We continue to allow "MP candidate detections" for non-compliant evidence, but it was suggested that they be called "unverified detections."

5. We noticed exceptions to the two non-nested unique 9 aa peptides, as revealed in the 2017 manuscripts. For example, beta-defensin 123 (Q8N688) has only one 9

aa uniquely-mapping tryptic peptide; it was a PE1 protein when the criterion was 7aa. Should we establish an Exceptions Committee? We must work together with neXtProt curators.Should we have guidelines for PTMs and their unmodified peptides? We will work with the MS Resource Pillar team.

In closing, the many attendees expressed enthusiasm for keeping the same format of the pre-Congress (Sunday) HPP Investigators meeting, scientific track, Bioinformatics Hub, and post-Congress HPP Workshop (Thursday). This format capitalizes on the dissemination of information during the Congress and build the aims and deliverables for the future.

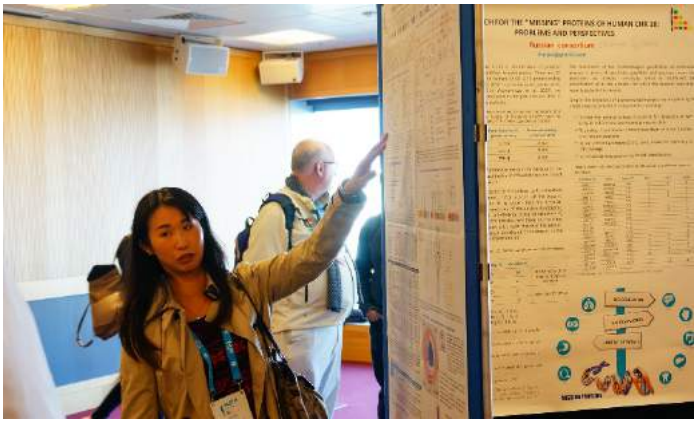
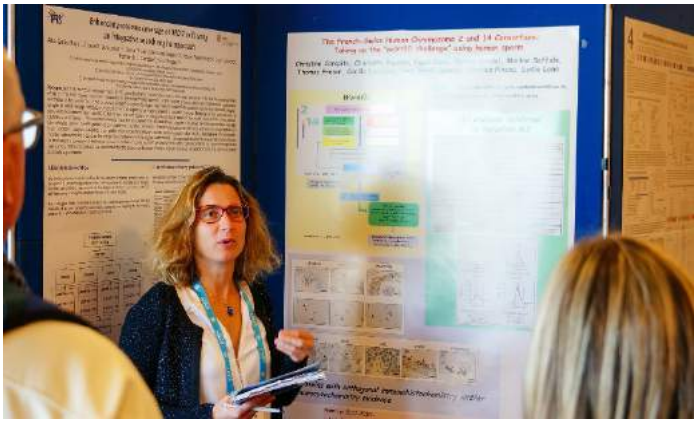
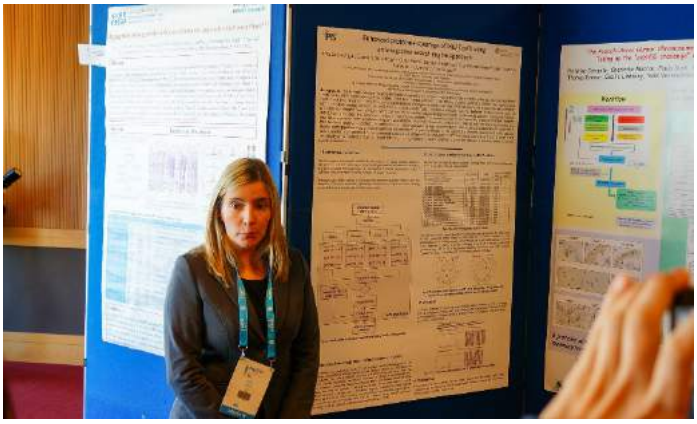
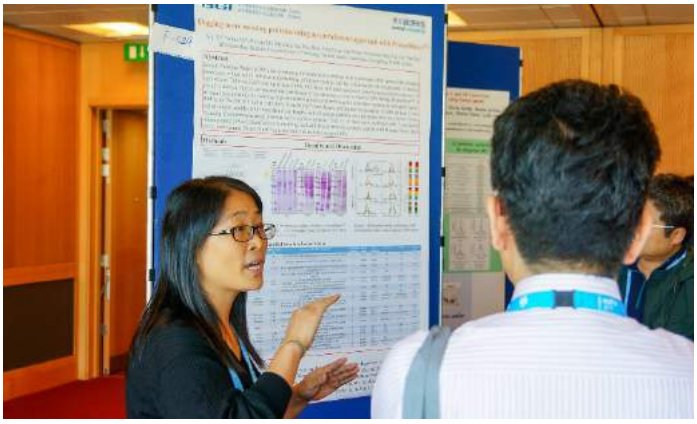
Group Photo taken after Post-Congress HPP Day Workshop in Dublin, Ireland (September 21, 2017).

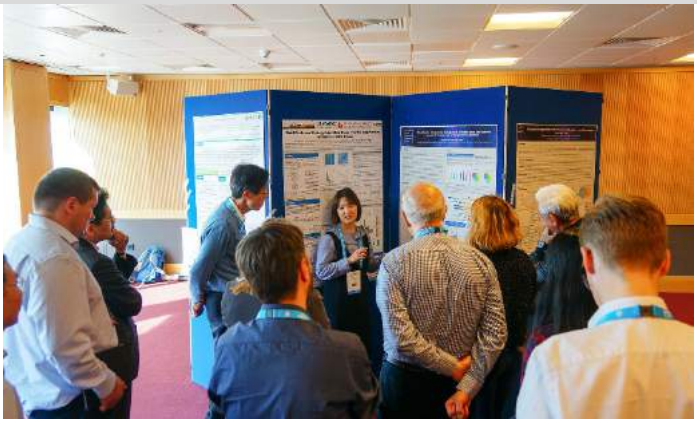
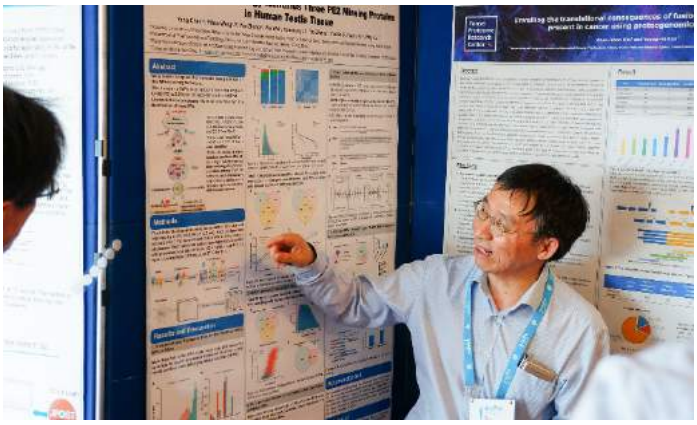
C-HPP Poster Session September 18, 2017 in Dublin

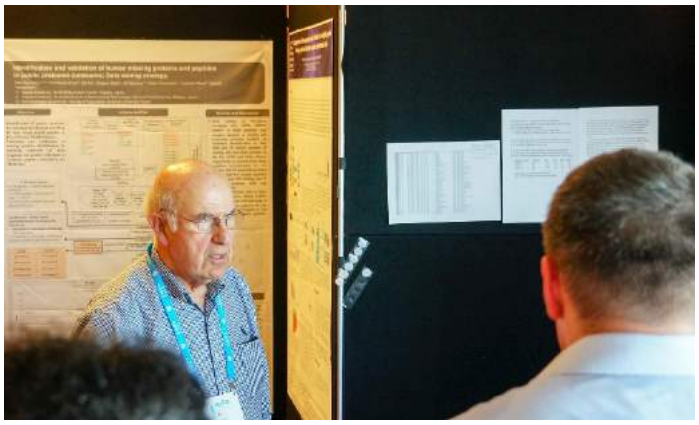
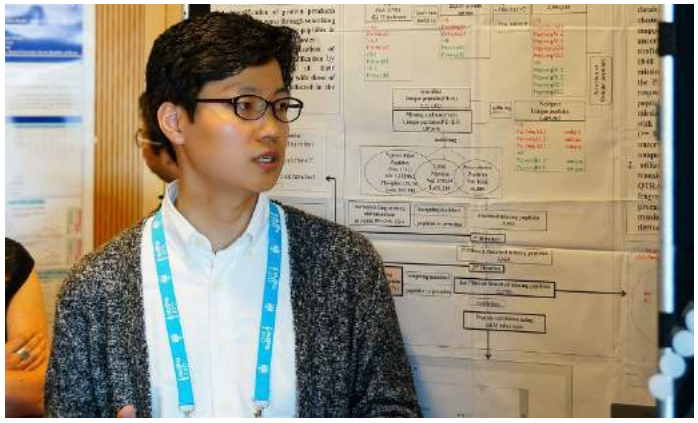
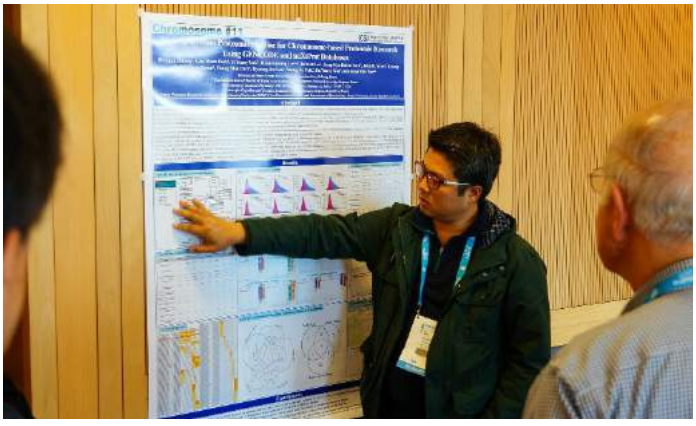
The C-HPP poster session at HUPO 2017 Congress in Dublin was held at the Wicklow Meeting Room 2 of Convention Center Dublin on Monday September 18, 2018 in two parts; the first part in the morning (10:00-11:00) for even number chromosome group and the second part in the afternoon (15:30-16:30) for odd number chromosome group. Many C-HPP chromosome teams participated in the C-HPP poster session which attracted a large and active audiences. The poster presenting authors, mainly PhD students and postdocs, explained their work with

enthusiasm and high scientific details entailing intensive discussion between presenters, audience and the members of Poster Award Committee (Lydie Lane, Peter Horvatovich). The posters covered various subjects that are relevant to the C-HPP such as high-throughput data processing, proteogenomics data integration harboring splicing events, identification of "missing proteins" using various analytical methodologies such as application of multiple proteases and bioinformatics approaches for analyzing rarely accessible samples such as testis. From this poster competition, the following authors received Top 5 best posters awards: Ekaterina Ilgisonis (Chromosome 18), Chia Li Han (Chromosome 4), Alba Garin-Muga (Chromosome 16), Yan Ren (Chromosome 20) and Chae-Yeon Kim (Chromosome 13). We invite all C-HPP groups and HUPO members to submit their work for C-HPP poster award competition in Orlando at HUPO 2018.




C-HPP Poster Session and Poster Awardees (right below).

Publication of Journal of Proteome Research Special Issue (December 1, 2017)

In cooperation with the B/D-HPP investigators, a C-HPP Special Issue was published on December 4, 2017; it is the fifth special issue since the first C-HPP edition in January 2013 (see cover Figure). The editorial members were; Guest Editors: Young-Ki Paik (Yonsei Univ.), Gilbert S. Omenn (Univ. of Michigan), Eric W. Deutsch (Institute of Systems Biol) and Jennifer E. Van Eyk (Cedars-Sinai Medical Centre); Associate Editor: Christopher M. Overall

About Cover: The cover illustration of the JPR SI 2017 issue was from the Ping Xu (Chr1, China) lab and was selected by the guest editors. This figure is a part of his paper entitled "Multi-Protease Strategy Identifies Three PE2 Missing Proteins in Human Testis Tissue" (Yihao Wang, Yang Chen, Yao Zhang, Wei Wei, Yanchang Li, Tao Zhang, Fuchu He, Yue Gao, and Ping Xu; pp 4352–4363 DOI: 10.1021/acs.jproteome.7b00340).

Up to date, 164 C-HPP-related papers have now been published. In this special issue, 27 papers addressed the HPP goals of progressively completing the human protein parts list and advancing the usefulness of proteomics for the broader community (Paik et al., 2017, JPR Editorial). Those 27 manuscripts were categorized into four subjects: (i) Metrics of Progress and Resources, (ii) Missing Protein Detection and Validation, (iii) Analytical Methods and Quality Assessment, and (iv) Protein Functions and Disease. Notably, authors reported 73 missing protein detections that met the HPP guidelines using several novel approaches.

As we have done in past years, the C-HPP headquarter office freely distributed one copy of the printed version of the JPR SI 2017 to all the C-HPP PIs and HPP leaders by regular mail. This issue was printed only once for the C-HPP group, and there are a limited number of copies.

17th C-HPP Workshops/Symposium in Tehran, Iran (April 27-28, 2017)

17th C-HPP Symposium/Workshop in Tehran, Iran (April 27-28, 2017).

Opening Remarks by Dr. Ghasem Hosseini Salakdeh (upper) and welcome remarks by Dr. Gourabi, Head of the Royan Institute (down).

The 17th C-HPP symposium/workshop was held in Tehran, Iran, during April 27-28, 2017, and included contributions from the leadership and well-known scientists from around the globe. The participants shared their latest findings on the progress of the C-HPP concerning each individual chromosome and very recent approaches to overcome the challenges facing the discovery of missing proteins. More than 300 Iranian scientists, researchers, and students attended this symposium.

In this meeting, in addition to ongoing efforts, the prospective programs to maintain collaboration, resource and information sharing, and the formation of a newly organized working group termed TAMPA were discussed. Following the welcome words of Dr. Gourabi, Head of the Royan Institute, and Dr. Hosseini Salekdeh, Symposium Chairman, this meeting held several scientific sessions and an open discussion.

The sessions were: Introduction and Overview, Uncovering Missing Proteins, Functional Study of Missing Proteins with Disease Implication, Invited Special Lectures, Young Investigator Invitation Session, General Discussion on All Pending Issues, and Working Group Formation: Networking and Interaction through the C-HPP Clusters. Dr. Gil Omenn joined this session using Skype from his home (at the early time of 2-3 a.m. in Michigan, USA) and gave us many constructive suggestions and stimulating comments on the issues.

Plenary lecture by Dr. Young-Ki Paik (upper) and special comments given by Dr. Gil Omenn through the Skype Teleconference (down).

All the participants thanked him for his dedication to this productive discussion session, which was one of the most vibrant forums using tele-video mediation. All the participants were invited to attend a local tour of the Royan Institute where the research on the stem cell proteomics and reproduction biology is actively carried out.

From upper: Drs. Christopher M. Overall, Fernando J. Corrales, Charles Pineau and Je Yoel Cho at the 17th C-HPP Symposium in Teheran.

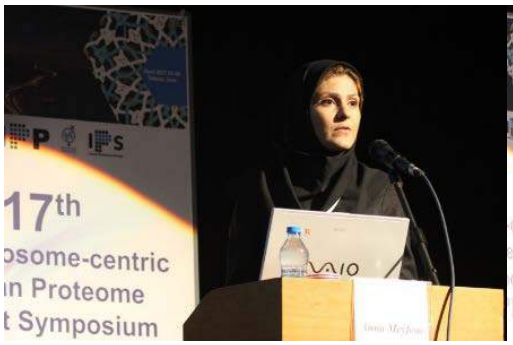
Having the C-HPP symposium in Iran provided an opportunity to understand the enthusiasm and contribution of Iranians to the proteomics research in Chromosome-based missing protein study, human reproduction, and stem cell biology happening at the global level. Despite limited resources and instrumentation such as mass spectrometry facilities, Iranian scientists are working hard on proteomics through collaborations with various groups across the world.

(For details, see Meyfour A et al., Proteomics, 2018, https://onlinelibrary.wiley.com/doi/abs/10.1002/pmic.201800012)

▲Dr. Paola Roncada

▲Dr. Gong Zhang

▲Mr. Dehua Li



▲Dr. Anna Meyfour

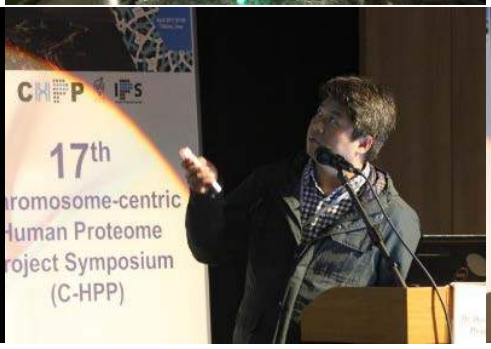

▲Dr. Fan Zhang

▲Dr. Mehdi Alikhani

▲Dr. Seul-Ki Jeong

▲Dr. Tadashi Yamamoto

▲Dr. Anarea Urbani



▲Dr. Heeyoun Hwang


▲Dr. Alexander Archakov

Summary of Discussion on the C-HPP Progress

In Dublin, there were several oral presentations by new PIs of C-HPP consortium as well as group discussions on various topics in Sunday (9/17) or Thursday (9/21). The following summary was prepared by HQ office for the record of meeting.

Speakers	Key Points
Chr. 3  **Dr. Takeshi Kawamura** (Tokyo Univ., Japan)	**On-going original efforts** - Peptides derived from multiply modified histones tend to co-elute on HPLC and give complex chimera MS/MS spectra. - Currently developing an analysis pipeline with sophisticated algorithm to resolve the chimera spectra. - Data-independent acquisition causes the similar issue, trying to overcome it. - Limited amounts of separated chromosomes require greatly enhanced detection sensitivity.
Chr. 6  **Dr. Yassene Mohammed** (Univ. of Victoria, Canada)	**Guiding targeted proteomics to detect human MPs by dissecting mouse proteins** - Using mouse tissue, they attempted to determine which issue has a homolog of human MPs. - 195 mouse proteins were detected in various tissues that correspond to human MPs. - Among 29 proteins, the salivary glands had the highest no of homologs of human MPs - Validation of this finding is now underway.  **PI: Dr. Christoph Borchers**
Chr. 19  **Dr. Sergio Encarnación-Guevara** (Encarnacion-Guevara, UNAM, Mexico)	**To identify more missing proteins through high coverage proteomics technology.** - Purification of proteins containing zinc finger domains using immobilized metal ion affinity chromatography - Proteomics of umbilical cord. Endothelial cells (human umbilical vein, endothelial cells) - Brian proteomics, mainly in cancer research. - Secretome in cervical cancer cell lines - Membranome in breast cancer cell lines with specific treatments for protein solubilization and fractionation.
Chr. 21  **Dr. Albert Sickmann** (Leibniz-Institut für Analytische Wissenschaften Dortmund, Germany)	**Strategy – Sample material acquisition** - Access to - specimen from Down Syndrome patients; skin biopsy material; Mouse - Homology search for proteins from chr. 10, 16 and 17. - Comparison with a dataset of about 12000 proteins from 42 tissues. - Probing for missing proteins with SIL based - MRM / PRM assays were done for Amniotic fluid cells with diagnosed free 21 trisomy karyotype. We aim to include chorionic villus samples into our further investigations
Chr. X  **Dr. Yasushi Ishihama** (Kyoto Univ., Japan)	**Introduction of jPOST Repository** - To facilitate the sharing and reuse of promising datasets, jPOSTrepo was constructed and operated (https://repository.jpostdb.org/). - It has unique features, including high-speed file uploading, flexible file management and easy-to-use interfaces. - This repository has been launched as a public repository containing various proteomic datasets and is available for researchers worldwide. - With linked to ProteomeXchange, end users share and store all datasets.

MPP

Dr. Mark Baker
(Co-Chair of HPP EC, Macquarie Univ. Sydney, Australia)

MissingProteinPedia Case study

- Mark Baker highlighted recent update of MPP Quinquennial PE2-4 Data
- He demonstrates usefulness of MPP for HPP study.
- Comments on the olfactory receptors, PRAME family proteins and taste receptors.

SRM Cluster

Dr. Alex Archakov
(Institute of Biomedical Chemistry, Moscow, Russia)

Aims of SRM Cluster

Final goal is full coverage of human exome by SRM-Proteome.
Intermediate steps:

- Creation of SRM proteome of single human chromosome
- SRM confirmation of doubtful proteins detected by other technologies.
- Searching of MPs not detected by other technologies
- SRM identification and quantification of proteins expressed by different chromosomes into the blood of healthy and diseased people for medical purpose.

Co-Chair

Dr. Christopher M. Overall
(UBC, Vancouver, Canada)

Cross-Chromosome Strategy

- Rare Tissues and Cell Lines Cluster: He discussed on the way to access to those rare tissues through a close collaboration with clinical teams for identifying MPS.
- Coordinate with B/D-HPP for access to disease tissues and fluids for MP discovery.
- List tissues on Wiki that each team is accessing so other teams can look for collaborations
- Stem cell sources?
- Human fetal tissue sources?
- Ab reagent etc. available for the community

HPP-Day Post-Congress

Group Discussion by **Dr. Eric Deutsch**
(ISB, Seattle, WA, USA)

Some suggestions from the floor (Thursday, Sept 21, 2017)

- Universal spectrum identifier must cite for MPs with spectrum position, numbers
- Referring proper page numbers for each check list item not just “V”. 1
- Need clarification/guidelines for DIA, SWATH datasets.
- Need guidelines for validating Ab. based and targeted MS based.
- Expansion of MP identification requirements from “need two non-nested, unique (peptide uniqueness checker), high quality, more than 9 aa long” rule to “if there are only weak spectrum matched, use them and show that they are the best match and no other/better choices”.

▲HUPO2017 Registration

▲HUPO2017 Gala Evening in Guiness House

▲UCD, a Place for 18th C-HPP Workshop

▲C-HPP PIC Meeting (9/17)

▲A Deep Dive on PTMs on C-HPP Workshop

▲The Convention Centre Dublin, a Place for 2017 HUPO Congress

2018 JPR Special Issue

Call for Papers

Submission Deadline: 31th May 2018

CHPP HUPO translating the code of life

The *Journal of Proteome Research* will publish its sixth annual Special Issue dedicated to highlight progress on the HUPO Human Proteome Project (HPP) in the broader sense. The Special Issue considers papers encompassing both the Chromosome-Centric Human Proteome Project (C-HPP) and the Biology and Disease Human Proteome Project (B/D-HPP). In addition, we will now consider short definitive reports, submitted in the *Letters* format, on the discovery of a Missing Protein(s). To be considered, the missing protein(s) must meet the Guidelines v 2.1 and are put in the context of both the HPP and biological setting in which they were discovered. We anticipate this format will encourage many teams, particularly of the B/D-HPP, to highlight such protein discoveries in a disease and biological context.

Guest Editors

Young-Ki Paik, *Yonsei University*
Eric Deutsch, *Institute for Systems Biology*
Fernando Corrales, *Centro Nacional de Biotecnología (CSIC)*
Gilbert S. Omenn, *University of Michigan*

Associate Editor

Christopher M. Overall, *The University of British Columbia*

Thematic Priorities:

- Completing the high resolution draft of the human proteome with new strategies and results leading to confident identifications of neXtProt missing proteins (PE2-4) according to the C-HPP Guidelines v 2.1 or recent updates
- Reports on the protein list of individual chromosomes and groups of chromosomes, annotating known proteins and their isoforms/proteoforms and/or credibly identifying missing proteins (PE2-4)
- Creation of protein lists for the B/D-HPP groups systems for deposition into ProteomeXchange
- Produce and utilize "popular proteins" lists in B/D-HPP and contribute to the identification of "missing proteins"
- Generation of post translational modifications (PTM) libraries for chromosome-based protein sets
- Proteomic studies of proteoforms produced by proteolytic processing, PTMs, alternative splicing (ASV), coding non-synonymous single nucleotide polymorphisms (cSNPs), chromosome abnormalities
- Biological mechanistic analyses inspired from proteomics data in diseases or biological processes
- Use of targeted proteomics, especially SRM and MS-SWATH, to extend chromosome-based protein findings
- Disease studies utilizing chromosome information, characterizing amplicons, *cis*-regulated pathways or networks
- Integration of genomic, transcriptomic, epigenomic, or metabolomic data with proteomics, using bioinformatics
- Combined analyses with MS, RNASeq and antibodies for targeted studies of tissue samples
- Biomarker discoveries based on the identification of novel ASVs, PTMs or cSNPs in proteomic studies.

Submission Procedure

Manuscripts must be submitted by 31th May, 2018 to be considered for this Special Issue. Manuscripts must be submitted electronically through the ACS Paragon Plus Environment online submission system. Specify in the authors' cover letter that the manuscript is intended for the HPP Special Issue.

Review and Publication Process

Initial editorial review will determine whether manuscripts are appropriate for the HPP Special Issue. Papers must fulfill the HPP checklist (http://www.thehpp.org/guidelines/HPPDataGuidelines_2.1.0.pdf) to be considered for publication. The completed checklist *must* be included with the cover letter. The full MS data submission to ProteomeXchange *must* also be completed prior to initial submission and the PXD number provided in the abstract. Nonconforming papers will be returned unreviewed. All relevant papers will go through full peer review. As papers are accepted they will go online and be available in time for HUPO-2018 in Orlando. Due to the publication schedule, only papers that are accepted by September 1, 2018 will be published in the December 2018 HPP Special Issue. Those papers requiring more time for revision or falling outside of the scope of the Special Issue will be considered for later regular issues of the journal.

HPP Data Guidelines

Papers must conform to both the *Journal of Proteome Research* mass spectrometry guidelines and the HPP guidelines v 2.1 (see Deutsch et al. http://pubs.acs.org/doi/abs/10.1021/acs.jproteome.6b00392) in order to be sent to review and for acceptance. Please check for any changes to the HPP guidelines available online at http://www.thehpp.org/guidelines/ before submission. All papers must analyze their data using the Human PeptideAtlas release 2018-01 and neXtProt release 2018-02. Papers not doing so will be returned without review.

Special Message on the JPR Special Issue Submission

Dear HPP members,

I have been informed by the Editor that the Journal of Proteome Research Staff are having problems processing all submissions so far for the HPP JPR Special Issue. Processing is at a crawl as as NONE so far have come with the HPP checklist.

This is slowing down the handling as papers are not further considered or reviewers assigned until a completed checklist is received.

From last year, N/A is not a proper option on the checklist if the item checked actually needs to be done. All N/As are carefully reviewed and papers will be returned for completion.

In particular the PXD number must be provided in the abstract and main text.

Thanks so much and we look forward to your papers!

Christopher Overall
Associate Editor
Journal of Proteome Research

Journal of proteome research ACS Publications Most Trusted. Most Cited. Most Read.

Human Proteome Project CHPP

Introduction of Short Form Paper for 2018 JPR Special Issue

Christopher M. Overall, Co-Chair of C-HPP and Associate Editor of JPR and and 2018 JPR SI has recently announced that JPR SI 2018 introduces the letters format for identifying missing proteins and other discoveries relevant to HPP project. According to his statement, discovery of a missing protein or proteins can now be as a short definitive report, submitted in the Letters format. To be considered for publication as a Letter, the missing protein(s) must meet the Guidelines v 2.1 and be cast in the context of both the HPP and biological setting in which they were discovered. We anticipate this format will encourage many teams, particularly of the B/D-HPP, to highlight such protein discoveries when found in disease and biological sample analyses as a side finding that otherwise may be lost or further detailed as it were an incidental finding in a more biological focused analysis. Letters have a maximum length of four journal pages and should contain sufficient experiment detail for the research to be reproduced. There should be no more than 3 figures, 2 tables and 20 references. A separate Table of Contents Graphic is required, but does not count toward the 4-page or Figure limit.

MPs must meet both the JPR technical and the HPP MP Guidelines including figure(s) of the annotated spectra and the data uploaded to ProteomeXchange with a PXD number included in the abstract. To be reviewed the HPP Checklist items must be fulfilled and the checklist submitted.
(see Deutsch et al. http://pubs.acs.org/doi/abs/10.1021/acs.jproteome.6b00392)

For the HPP Checklist please see this: checklist (http://www.thehpp.org/guidelines/HPPDataGuidelines_2.1.0.pdf and the MP HPP Guidelines, please see this: http://www.thehpp.org/guidelines/

Finally, in the cover letter please clearly state and, in the header, that the paper is for the 2018 HPP Special Issue, Associate Editor Christopher Overall.

Deadline for submission is May 31

I would appreciate any updates on anticipated papers with titles by March 31 to aid in preselection of reviewers so as to facilitate processing and Editorial Consideration on submission. Please consider that we receive many papers simultaneously submitted at the deadline. If you prefer faster processing please try and beat the deadline as much as possible.

19th C-HPP Workshop in Santiago, Spain, 2018

Highlights of the 19th Chromosome Centric Human Proteome Project Workshop

The 19th Chromosome Centric Human Proteome Project Workshop will be held in Santiago de Compostela, Spain, over the weekend of June 16-17, 2018, as a companion event to the XII EuPA Congress 2018. We cordially invite all scientists and parties interested in discussing the status and future directions of the Chromosome Centric Human Proteome Project. The workshop will cover the most pertinent questions of the project, which include the following topics:

- Completeness of the human proteome and new developments to identify missing proteins, and highlights of the next 50 missing proteins (MP50) program
- Start of the uPE1 project, which aims to identify the unknown function(s) of human proteins identified with high confidence (PE1 category in neXtProt)
- Discussion of the future directions of the Human Proteome Project, focusing on the bright proteome (known, HPP PE1 proteins) and dark proteome (unknown, missing proteins, uPE1 proteins, and dark structural proteins)
- Inclusion of translated small open reading frames (smORFs) and long non-coding RNAs; sequence variants; splice isoforms; and proteins and peptides with post-translation modifications
- Bioinformatic infrastructure of the (C-)HPP project
- Recent results and future directions of the B/D-HPP and joint actions with the C-HPP teams

The status and future endeavors of the C-HPP are addressed in a recent review by the members of the C-HPP Executive Committee (EC) in Expert Review of Proteomics entitled "Advances in the Chromosome-Centric Human Proteome Project: looking to the future." Questions about and suggestions for the workshop can be addressed to the organizer, Fernando Corrales (corrales@cnb.csic.es, Spanish National Centre for Biotechnology, Madrid, Spain). The continuously updated workshop program is available at C-HPP Wiki. We are looking forward to meeting all interested persons at this event

19th C-HPP Symposium/Workshop

June 16-17 2018

Santiago de Compostela, Spain

Venue: Faculty of Medicine, University of Santiago de Compostela

(In the heart of the old city, close to Hotel Monumento San Francisco (EuPA meeting venue); last updated: 4-21-2018).

Saturday, June 16th	
8:00-8:20	Registration
8:20-8:30	Welcome Message. Fernando J. Corrales.
8:30-9:00	The Human Proteome Project. Gil Omenn.
9:00-9:20	C-HPP: Progress Update and Future Direction: Young-Ki Paik (C-HPP Chair).
9:20-11:00	neXt-MP50 Challenge: Update. Chris Overall. • Keynote presentation 1 (20 min). Charles Pineau. • MP success and new strategies. - The proteome of human cerebrospinal fluid and the identification of missing proteins (10 min). Charlotte Macron (Chr 2). - Short oral C-HPP group 2 (10 min). Christoph Borchers (Chr 6). - Missing protein detection in human embryonic tissues using a proteogenomics approach (10 min). Fernando J. Corrales (Chr16). - Short oral C-HPP group 4 (10 min). Miguel Marcilla (Chr 16). • Discussion (40 min).
11:00-11:30	Coffee break.
11:30-13:30	Bioinformatics, Green team (Lydie Lane, Co-Chair Eric Deutsch). Update on the Status of Target Proteins --MPs, uPE1, smORFs, lncRNAs and others. • Introduction (10 min; Lydie Lane). • Re-using and integrating public proteomics data to improve our knowledge of the human proteome (20 min; Juan A. Vizcaino (ProteomeXchange)). • Keynote presentation 2 (20 min; Jong Shin Yoo (Chr 11)). • Action plan to decipher functions of Chr18 encoded proteins in the frame of neXt-CP50 Challenge (15 min; Elena Ponomarenko (head bioinformatics Chr 18)). • Short oral C-HPP group 3 (Chr. 5) (15 min; Peter Horvatovich (Chr 5)). • Discussion (40 min).
13:30-15:00	Lunch break.
15:00-17:00	neXt-CP50 Challenge: functional annotation, Blue team. Young-Ki Paik. • Keynote presentation 1 (20 min; Gilberto Domon (Chr 15)). • Keynote presentation 2 (20 min; Lydie Lane).

	• Sensitivity and specificity of mass-spectrometric proteomic technologies as factors determining the prospects for the CHPP project (10 min; Alexander Archakov (Russian Team Chr 18)). • Short oral C-HPP group 2 (10 min; Fernando J. Corrales (Chr 16)). • Short oral C-HPP group 3 (10 min; Andrea Urbani (Mt)). • Deciphering Functional roles of missing proteins by Comprehensive integration of affinity proteomics, MS/MS & RNA-sequencing datasets in Chronic Lymphocytic Leukemia tumor B cells and healthy B cell subpopulations in the context of the Chromosome-Centric Human Proteome Project (10 min; Manuel Fuentes (Chr 16)). • Discussion (40 min)
17:00-19:00	C-HPP EC and HPP Leaders meeting.
EuPA and C-HPP dinner.	

Sunday, June 17th	
9:00-11:00	Young Investigators session. • Proteogenomics: Combining Next Generation Sequencing and Mass Spectrometry in Candida albicans (12+3 Q&A min; Mónica Franch). • Speaker 2 (12+3 Q&A min; Seul-Ki Jeong, YPRC). • Differential Immune Recognition of the Candida albicans yeast and Hyphal cell surface Proteomes in invasive Candidiasis (12+3 Q&A min; Aida Pitarch (UCM)). • Speaker 3 (12+3 Q&A min; Yong-In Kim (Korea Research Institute of Standards and Science). • Speaker 4 (12+3 Q&A min; Catarina Oliveira (UCM)). • Speaker 6 (12+3 Q&A min; Heeyoun Hwang, KBSI) • Speaker 7 (12+3 Q&A min).
11:00-11:30	Coffee break
11:30-13:30	Long-term plans and directions for C-HPP (Young-Ki Paik, Christoph M. Overall) • Re-structuring C-HPP Teams for Phase II (2019-) • Strategies for the identification of MPs (Using info available on public proteome databases, proteogenomics, proteoforms, small ORFs, etc.). • Strategies for the functional annotation of Dark Proteome (MPs, uPE1, smORFs and lncRNA proteins) (Russian team proposal, and others). • Synergies and interactions across C-HPP and B/D-HPP groups (samples, data sharing…). • Other issues
13:30-14:00	Next C-HPP meetings and other business. • 2018 JPR SI Update Christoph M. Overall • 2018 HUPO Congress Workshop Plans Young-Ki Paik • 2019 C-HPP Workshop Plans in St. Malo (Charles Pineau)

Future C-HPP Scientific Workshops (2018-2020)

Meeting Title	When/Where	Local Host
19th C-HPP Workshop http://www.proteored.org	June 16-17, 2018 Santiago de Compotela	Fernando J. Corrales fcorrales@cnb.csic.es Centro Nacional de Biotecnología (CSIC) Darwin 3, 28049, Madrid Tel: (34) 91 585 4696 Fax: (34) 91 585 4506
20th C-HPP Workshop www.c-hpp.org (jointly with HPP Workshop)	Sept 30 and Oct 4, 2018 Loews Royal Pacific (Universal Studios) in Orlando, FL [As a part of HUPO Congress]	HPP Workshop Planning Team paikyk@gmail.com fcorrales@cnb.csic.es
21st C-HPP Workshop	May 13-14, 2019 St. Malo, France	Charles Pineau charles.pineau@inserm.fr Inserm Irset - Inserm U1085 TEL: +33 (0)2 2323 5279 FAX: +33 (0)2 2323 5282
22nd C-HPP Workshop	June 1-3, 2020 (tentative) St.-Petersburg–Moscow, Russia (on the Boat along the river from St. Petersburg to Moscow)	Alexander Archakov alexander.archakov@ibmc.msk.ru RHUPO

C-HPP Leadership

Update on the C-HPP Leadership and Membership

Election of the C-HPP Co-Chair: Lydie Lane was re-elected as Co-Chair of the C-HPP Consortium by PIC Members. Her second term will run from Jan 1, 2018 until Dec 31, 2020. The rest of EC members are listed below.

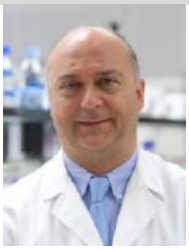
Young-Ki Paik
Chair

Lydie Lane
Co-Chair

Christopher Overall
Co-Chair

Peter Horvatovich
Secretary General

Gilberto B. Domont
MAL



Fernando Corrales
MAL

Ping Xu
MAL

Position	Name	Affiliation	Term Ends	Remarks
Chair	Young-Ki Paik (Asia Oceania)	Yonsei Univ., Seoul, Korea	Dec 31, 2019	PI, Chr 13
Co-Chairs	Lydie Lane (Europe)	SIB, Univ. of Geneva, Switzerland	Dec 31, 2020	PI, Chr 2
	Christopher Overall (America)	UBC, Vancouver, Canada.	Dec 31, 2018	PI, Chr 6
Secretary General	Peter Horvatovich (Europe)	Univ. Groningen, Groningen, Netherlands	Dec 31, 2019	PI, Chr 5 WiKi Manager
Members -at-Large	Gilberto B. Domont (America)	Federal University of Rio de Jeneiro, Brazil	Dec 31, 2018	PI, Chr 15
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	Ping Xu (Asia Oceania)	Beijing Proteome Research Center (BPRC), China	Dec 31, 2018	PI, Chr 1

C-HPP Principal Investigators Council (PIC)

The current members of PIC are listed below. Note that PIs of Chr 3, 6, 19, 21 and X are newly joined the C-HPP in 2017. (see also next page for details).

Chr. 1	Chr. 2	Chr. 3	Chr. 4	Chr. 5	Chr. 6	Chr. 7
						
Ping Xu	**Lydie Lane**	**Takeshi Kawamura**	**Yu-Ju Chen**	**Peter Horvatovich**	**Christoph H. Borchers**	**Edouard Nice**
Chr. 8	**Chr. 9**	**Chr. 10**	**Chr. 11**	**Chr. 12**	**Chr. 13**	**Chr. 14**
						
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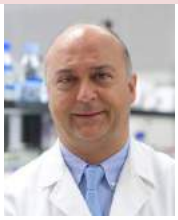
Chr. 15	**Chr. 16**	**Chr. 17**	**Chr. 18**	**Chr. 19**	**Chr. 20**	**Chr. 21**
						
Gilberto B. Domont	**Fernando J. Corrales**	**Gilbert S. Omenn**	**Alexander Archakov**	**Sergio Encarnación-Guevara**	**Siqi Liu**	**Albert Sickmann**
Chr. 22	**Chr. X**	**Chr. Y**	**Mitochondria**			
						
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| **Newsletter Editor:**
Young-Ki Paik

| **Editorial Staff:**
Peter Horvatovich
Jin-Young Cho

| **HQ Office:**
Yonsei Proteome Research Center, Yonsei University
50 Yonsei-ro Seodaemoon-gu, Seoul, 120-740, Korea
(www.c-hpp.org)

| **Chair:** Young-Ki Paik
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