



The Chromosome Centric Human Proteome Project (C-HPP) Annual Report 2020-2021 prepared for the 2021 HUPO Council

Presented on September 27, 2021, by:

Christopher M. Overall Chair, Young-Ki Paik Co-Chair and Lydie Lane, Co-Chair
On behalf of the C-HPP Executive Committee

1. Name of Initiative: Chromosome-Centric Human Proteome Project (C-HPP)

2. Name of Committee Chair: Chair: **Christopher M. Overall,**
Co-Chairs: **Young-Ki Paik, Lydie Lane**

3. Names of Committee Members:

C-HPP Executive Committee (EC):

Chair: Christopher M. Overall	Canada	to Dec 31, 2021
Co-Chair: Lydie Lane	Switzerland	to Dec 31, 2023
Co-Chair: Young-Ki Paik	Korea	to Dec 31, 2021
Secretary General: Peter Horatovich	The Netherlands	to Dec 31, 2022
Member-at-Large: Pengyuan Yang	China	to Dec 31, 2021
Member-at-Large: Fernando Corrales	Spain	to Dec 31, 2022
Member-at-Large: Gilberto Domont	Brazil	to Dec 31, 2021

Principal Investigators Council (PIC):

Chromosome 1: Ping Xu	China	Chromosome 15: Gilberto Domont	Brazil
Chromosome 2: Lydie Lane	Switzerland	Chromosome 16: Fernando Corrales	Spain
Chromosome 3: Takeshi Kawamura	Japan	Chromosome 17: Gilbert S. Omenn	USA
Chromosome 4: Yu Ju Chen	Taiwan	Chromosome 18: Alexander Archakov	Russia
Chromosome 5: Peter Horvatovich	The Netherlands	Chromosome 19: Sergio Encarnacion	Mexico
Chromosome 6: Rob Moritz	USA/Canada	Chromosome 20: Siqi Liu	China
Chromosome 7: Edouard Nice	Australia	Chromosome 21: OPEN	
Chromosome 8: Pengyuan Yang	China	Chromosome 22: OPEN	
Chromosome 9: Je-Yoel Cho	Korea	Chromosome X: Yasushi Ishihama	Japan
Chromosome 10: Josh Labaer	USA	Chromosome Y: Ghasem Hoeissini	
Chromosome 11: Jong Shin Yoo	Korea	Salekdeh	Iran
Chromosome 12: Ravi Siredeshmukh	India	Mitochondrial: Andrea Urbani	Italy
Chromosome 13: Young-Ki Paik	Korea		
Chromosome 14: Charles Pineau	France		

4. C-HPP Mission and Objectives

The mission of the C-HPP is to map and annotate the entire human proteome comprising the individual proteins encoded by each chromosome, their primary splice forms, mature N- and C-termini, and their major protein post-translational modifications (PTMs) (see hupo.org/C-HPP). In the C-HPP, this is accomplished by directed studies initiated by the 25-international chromosome + mitochondrial DNA teams. Effective collaborations exist between the chromosome teams and other members of HUPO within the 19 B/D-HPP initiatives and the 4 HPP Pillars.

Phase 1 of the HPP project is focused on identifying by mass spectrometry all human proteins, presently estimated in the human genome to be 19,778 (neXtProt 2021-01). Those proteins confidently identified by protein existence (PE) information number 18,357, an increase of 483 from 17,874 PE1 proteins in 2020, with 1,421 PE2 – 4 proteins “missing proteins” remaining to be detected at the protein level. At the Santiago C-HPP-2018 workshop, the C-HPP resolved to complete the human functional proteome. To start this project, the neXt-CP50 Challenge was launched to functionalize proteins in the “Dark Proteome” with no known function, whether predicted or described. To tackle the Challenge with realistic goals, only those uncharacterized (u) proteins that have already been identified at the protein level (PE1) are being analyzed. In 2021 these represent 1,273, reduced from 1,254 proteins in 2020.

Phase 2 Future Plans: The C-HPP will focus on identifying the remaining ~9% of the human protein, on reducing the number of PE1 proteins that lack MS evidence (nonMS-PE1 proteins) for their existence, and the neXt-CP50+ to functionalize all uPE1s, ~5 PTMs/PE1 protein, and splice forms.

5. Summary of Recent Accomplishments, Current Activities, and Tasks

Progress was slow due to the pandemic in 2020 and 2021. The 22nd C-HPP Workshop in Busan, South Korea, June 28 – 30, 2021, was cancelled, and we are waiting to see how the vaccination and infections rates stabilize before announcing the next C-HPP workshop in 2022. The C-HPP is seeking new teams and leaders to adopt Chromosomes 21 and 22 to renew their activities.

A. neXt-MP50 and neXt-CP50: The decreasing numbers of MPs found each year reflect both the increasing difficulty in devising and executing deep discovery of MPs in the human proteome and some realignment of protein-encoding gene numbers and PE identifications occurring from time to time by database curators. To address this, the neXt-MP50 Challenge was launched at Sun Moon Lake C-HPP-2015 to encourage the Chr teams to identify 50 new MPs each from 2,949 MPs (2016) and to devise and employ innovative approaches to uncover MPs. Many teams have completed the initial goal, and all teams are moving well to achieve this and the remaining 9% of the human proteome—the pandemic notwithstanding. Annual reports from each chromosome and CP50 teams are posted on the [C-HPP Wiki](http://c-hpp.web.rug.nl/tiki-index.php) (<http://c-hpp.web.rug.nl/tiki-index.php>), and the most recent report from October 2021 will be available on here and on the C-HPP pages of the HUPO/HPP website by HUPO-RECONNECT.

B. Publication of the Journal of Proteome Research Virtual Issue.

On the 19th October, 2020, the Journal of Proteome Research compiled and published online a virtual issue (<https://pubs.acs.org/page/jprobs/vi/humanproteome>) of 60 key papers with an Editorial (<https://dx.doi.org/10.1021/acs.jproteome.0c00794>) to coincide with the publication of the high stringency draft of the human proteome and to celebrate 10 years of the HPP and the C-HPP.

C. 8th Special Issue of the HPP in the Journal of Proteome Research.

The C-HPP and B/D-HPP teams, sometimes in collaboration, published 15 papers in the 2020 Journal of Proteome Research 8th HPP Special Issue (Journal of Proteome Research (2020) 19, issue 12, 4,731 – 4,912), with a similar number in consideration for the 2021 9th HPP Special Issue of the Journal of Proteome Research.

The Special Issue Associate Editor is Christopher M. Overall, with Guest Editors: Young-Ki Paik, Eric Deutsch, Fernando Corrales, Lydie Lane, Robert Moritz, and Gil Omenn. Except for the COVID-19 pandemic years, SI submissions steadily increased and tracked consistently two years after publication. They maintain higher, or not significantly different, citation rates versus the standard JPR Issues and maintain a consistent average download rate.

