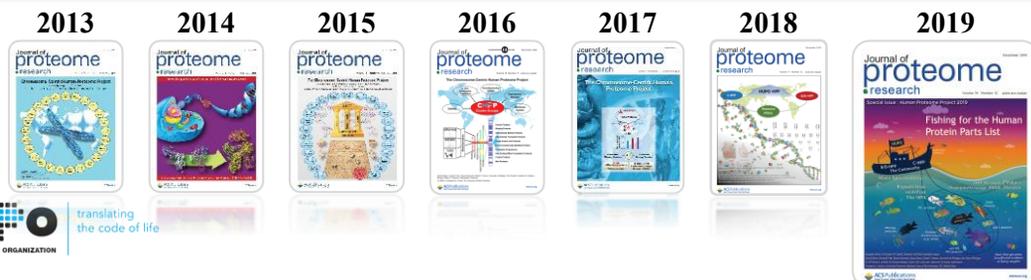




2020 JPR Special Issue Call for Papers

Submission Deadline: **June 30th, 2020**



CHIP

HUPO
HUMAN PROTEOME ORGANIZATION

translating
the code of life

The *Journal of Proteome Research* will publish its seventh annual Special Issue dedicated to highlight progress on the HUPO Human Proteome Project (HPP). 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 be 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.

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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
- ❖ Progress on the protein list of individual chromosomes and groups of chromosomes, annotating known proteins and their isoforms/proteofoms and/or credibly identifying missing proteins (PE2 – 4)
- ❖ Annotating proteins and their isoforms/proteofoms and/or identifying missing proteins found in rare or under explored cells and tissues, and protein lists of human cell types as a step in creating a human cell proteome atlas
- ❖ Produce and utilize “popular proteins” lists in B/D-HPP and contribute to the identification of missing proteins
- ❖ Proteomic studies of proteofoms produced by proteolytic processing, PTMs, alternative splicing (ASV), coding non-synonymous single nucleotide polymorphisms (cSNPs), or chromosome abnormalities

- ❖ 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
- ❖ New bioinformatic tools and approaches for annotating the human proteome
- ❖ Biological mechanistic analyses inspired from proteomics data in diseases or biological processes
- ❖ Biomarker discoveries based on the identification of novel ASVs, PTMs or cSNPs in proteomic studies

Submission Procedure

Manuscripts must be submitted by 30th June, 2020 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 and 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-2019. Due to the publication schedule, only papers that are accepted by September 31, 2019 will be published in the December 2019 HPP Special Issue. Papers requiring more time for revision or falling outside of the scope of the Special Issue will be published in 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 2019-01 and neXtProt release 2019-02. Papers not doing so will be returned without review.

