Organization and Strategic Direction for the HUPO Human Proteome Project (HPP)

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Abstract

The HUPO Human Proteome Project announced in Sydney and launched in Geneva is now fully implemented. Many scientists are engaged with specific roles on the HPP-EC, Senior Scientific Advisory Board, Chromosome-centric C-HPP EC and Principal Investigators Council of 18 chromosome-specific teams, Biology and Disease-driven B/D-HPP EC and Principal Investigators Council of a dozen organ, biofluid, disease, model organism, and stem cell initiatives, and the Antibody-based, MS-based, and Knowledge-based resource pillar committees. A web portal has been established at www.thehpp.org, with a corresponding working group. Protein capture datasets will be organized along the lines of the Human Protein Atlas and Antibodypedia. Submission of MS-datasets is standardized through the ProteomeXchange, PRIDE, and PeptideAtlas, with reanalysis using TPP and stringent FDR (1% at the protein level). The PeptideAtlas for SRM Experimental Libraries has been launched, along with spectral libraries and peptide resources that facilitate and democratize SRM studies by groups worldwide. The C-HPP and B/D-HPP programs collaborate in building the parts list of proteins corresponding to the 20,300 protein-coding genes, plus PTMs, splice variants, and SNPs; the C-HPP aims to reveal co-expressed proteins of co-located genes; the B/D-HPP is defining a framework of protein networks and interactions. HPP investigators will analyze unusual specimens (nasal epithelium, placenta, fetus, brain regions) to detect “missing proteins”, use ultrasensitive methods for low-abundance proteins, identify and differentiate protein families, splice variants, and PTMs and deduce their functional features. Initial publications are Legrain et al, MCP 2011; Uhlen et al, MCP 2012; Paik et al, NBT 2012; and Paik et al, JPR 2012. The C-HPP is preparing a special issue of JPR for January 2013; the B/D-HPP will do so in coming years