Most recent update on the Human Proteome Project

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A systematic effort to organize and map the entire human proteome will enhance our understanding of human biology at the protein level and accelerate diagnostic, prognostic, therapeutic, and preventive medical applications. In early 2010, we proposed a gene-centric approach to generate a human proteome map with an information backbone about the proteins expressed from each gene locus. A working group for a Human Proteome Project (HPP) created in October 2009 has worked toward an international consensus and a coherent proposal for this project. We have concluded that recent substantial advances in proteomics methods specifically related to quantitative mass spectrometry, protein capture with antibodies, and global exchange of large primary datasets and databases make the generation of such a human proteome map feasible, even without further paradigm shifts in technology. A HPP consortium was formally created at the HPP workshop in Busan (Korea) in March 2011. It is composed of two wings: on one side, the Chromosome-centered Consortium (C-HPP) will help map and annotate subsets of the human proteome; on the other side Biology and Disease-driven projects (B/D-HPP) will populate the Human proteome knowledge base with information on proteins in their biological and pathological context. The HPP consortium is currently working on guidelines for operational approaches, data submission, and information sharing. A HPP portal will be built to offer access to all potentially available databases and datasets on Human proteins.

The most recent development of national and local initiatives in the HPP will be presented in order to prepare the future HPP workshop that will take place in Geneva at the HUPO annual congress.

\textbf{Keywords}: Human proteome, Chromosome-centered projects, Biology/disease driven projects, knowledge base, HPP