# The methods involved in the human proteomic analysis.

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## Description

The availability of human genome sequences has revolutionized biomedical research in the last decade. However, there is not yet an equivalent map of human proteomes that directly measured proteins and peptides. Here is a draft map of the human proteome using high resolution fourier transform mass spectrometry. Detailed proteomics profiling of 30 histologically normal human specimens, including 17 adult tissues, 7 fetal tissues, and 6 purified primary hematopoietic cells, identified proteins encoded by 17,294 genes. It accounted for about 84% of all annotated proteins. Coding human genes is important. A unique and comprehensive strategy for proteogenomic analysis has allowed us to discover many new protein coding regions, including translated pseudogenes, non-coding RNAs, and upstream open reading frames. This extensive human proteome catalog complements the available human genome and transcriptome data to accelerate biomedical research in health and illness. Human Proteome Organization (HUPO) launched the Human Proteome Project (HPP) in 2010, an international framework for global collaboration, data exchange, quality assurance, and improved accurate annotation of genome-encoded proteomes. Over the next decade, HPP has established collaborations, developed guidelines and metrics, and reanalyzed previously stored community data to continually increase coverage of human proteomes. To commemorate the 10th anniversary of HPP, here we report on a 90.4% complete, very rigorous blueprint for the human proteome.

This knowledge is essential to understanding the molecular processes of health and disease, as demonstrated by highlighting the potential role of the human proteome in understanding, diagnosing and treating cancer, cardiovascular disease and infectious diseases. A decade after the release of the draft Human Genome Project (HGP), the Human Proteome Organization (HUPO) leveraged this genomic encyclopedia to launch a visionary international scientific collaboration called the Human Proteome Project. Utilizing substantial community data, the HPP connects scientists, clinicians, industry, institutions and knowledgebase partners to create a framework for collaboration, data sharing and quality assurance all targeted at discovering incredible evidence for the entire complement of human genome coded proteins. The HPP mission is to assemble and analyze community data, bringing increased granularity to our molecular understanding of the dynamic nature of the proteome, its modifications and relationships to human biology and disease. This aligns closely with HUPO`s aim of `translating the code of life`, providing crucial biochemical and cell biological information that genomics per se cannot deliver, while laying better foundations for diagnostic, prognostic, therapeutic and precision medicine applications. Comparisons with the HGP are numerous. Both global projects are ambitious collaborative projects that seek to explore how genes (HGPs) or proteins (HPPs) can help define the underlying molecular mechanisms of health and disease. Both groups have extensive data sharing and rigorous quality control efforts. However, today it is known that sequencing the human genome is necessary, but not enough to understand the complexity of human biology and pathology. Knowledge of expressed proteins, including concentrations, spatiotemporal positions, activity, protease treatment forms, transport, interactions, splice isoforms, PTMs, and many proteome-derived proteoforms cannot be predicted by genomic sequencing alone. Future successes in the study of the human proteome use bioinformatics techniques to elucidate existing protein species and provide high-performance algorithms for MS analysis, high-throughput measurements, and de novo assembly of protein sequences based on MS results. It depends on the availability. In addition, increasing the sensitivity of analytical techniques increases access to ultra-low copy proteins, expanding detection and analysis possibilities. In this regard, the theoretical prediction of the number of proteome forms (estimation of proteome width) and their distribution over the dynamic range.

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