

# Resource Summary Report

Generated by [nidm-terms](#) on Aug 9, 2026

## Human Proteomics Initiative

RRID:SCR\_002373

Type: Tool

### Proper Citation

Human Proteomics Initiative (RRID:SCR\_002373)

### Resource Information

**URL:** <http://www.ebi.ac.uk/swissprot/hpi/hpi.html>

**Proper Citation:** Human Proteomics Initiative (RRID:SCR\_002373)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented on August 03, 2011. IT HAS BEEN REPLACED BY A NEW UniProtKB/Swiss-Prot ANNOTATION PROGRAM CALLED UniProt Chordata protein annotation program. The Human Proteome Initiative (HPI) aims to annotate all known human protein sequences, as well as their orthologous sequences in other mammals, according to the quality standards of UniProtKB/Swiss-Prot. In addition to accurate sequences, we strive to provide, for each protein, a wealth of information that includes the description of its function, domain structure, subcellular location, similarities to other proteins, etc. Although as complete as currently possible, the human protein set they provide is still imperfect, it will have to be reviewed and updated with future research results. They will also create entries for newly discovered human proteins, increase the number of splice variants, explore the full range of post-translational modifications (PTMs) and continue to build a comprehensive view of protein variation in the human population. The availability of the human genome sequence has enabled the exploration and exploitation of the human genome and proteome to begin. Research has now focused on the annotation of the genome and in particular of the proteome. With expert annotation extracted from the literature by biologists as the foundation, it has been possible to expand into the areas of data mining and automatic annotation. With further development and integration of pattern recognition methods and the application of alignments clustering, proteome analysis can now be provided in a meaningful way. These various approaches have been integrated to attach, extract and combine as much relevant information as possible to the proteome. This resource should be valuable to users from both research and industry. We maintain a file containing all human UniProtKB/Swiss-Prot entries. This file is updated at every biweekly release of UniProt and can be downloaded by FTP download, HTTP download or by using a mirroring program which automatically retrieves the file at regular intervals.

**Abbreviations:** HPI

**Synonyms:** Human Proteome Initiative, UniProtKB/Swiss-Prot Human Proteome Initiative

**Resource Type:** database, data or information resource

**Defining Citation:** [PMID:11301130](#)

**Keywords:** function, gene, alignment, biologist, clustering, coding, development, genome, human, location, mammalian, modification, ortholog, population, post-translational, protein, proteome, proteomic, proteomics, sequence, splice, structure, subcellular, variant, variation, gold standard

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Human Proteomics Initiative

**Resource ID:** SCR\_002373

**Alternate IDs:** nif-0000-21199

**Record Creation Time:** 20220129T080213+0000

**Record Last Update:** 20260808T190353+0000

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## Ratings and Alerts

No rating or validation information has been found for Human Proteomics Initiative.

No alerts have been found for Human Proteomics Initiative.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.