Resource Summary Report

Generated by dkNET on Apr 28, 2025

Max Planck Unified Proteome Database

RRID:SCR_007771
Type: Tool

Proper Citation

Max Planck Unified Proteome Database (RRID:SCR_007771)

Resource Information

URL: http://www.mapuproteome.com

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Description: Database containing several body fluid proteomes, including plasma, urine, and cerebrospinal fluid. Cell lines have been mapped to a depth of several thousand proteins and the red blood cell proteome has also been analyzed in depth. The liver proteome is represented with 3200 proteins. By employing high resolution MS and stringent validation criteria, false positive identification rates in MAPU are lower than 1:1000. Thus MAPU datasets can serve as reference proteomes in biomarker discovery. MAPU contains the peptides identifying each protein, measured masses, scores and intensities using a clickable interface of cell or body parts. Proteome data can be queried across proteomes by protein name, accession number, sequence similarity, peptide sequence and annotation information. More than 4500 mouse and 2500 human proteins have already been identified in at least one proteome. Basic annotation information and links to other public databases are provided in MAPU and we plan to add further analysis tools.

Synonyms: MAPU

Resource Type: data or information resource, database

Keywords: proteome, protein, blood, plasma, urine, cerebral spinal fluid

Funding:

Resource Name: Max Planck Unified Proteome Database

Resource ID: SCR_007771

Alternate IDs: nif-0000-03102

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250426T055956+0000

Ratings and Alerts

No rating or validation information has been found for Max Planck Unified Proteome Database.

No alerts have been found for Max Planck Unified Proteome Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Leng W, et al. (2017) Proof-of-Concept Workflow for Establishing Reference Intervals of Human Urine Proteome for Monitoring Physiological and Pathological Changes. EBioMedicine, 18, 300.

Kalantari S, et al. (2015) Human Urine Proteomics: Analytical Techniques and Clinical Applications in Renal Diseases. International journal of proteomics, 2015, 782798.