

Resource Summary Report

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ProteomicsDB

RRID:SCR_015562

Type: Tool

Proper Citation

ProteomicsDB (RRID:SCR_015562)

Resource Information

URL: <https://www.proteomicsdb.org/>

Proper Citation: ProteomicsDB (RRID:SCR_015562)

Description: Database for the identification of the human proteome and its use across the scientific community. Users can browse proteins and chromosomes and contribute to the data repository.

Resource Type: data or information resource, database

Defining Citation: [PMID:24870543](#)

Keywords: human proteome, human proteomics, proteomics database, human proteomics database, bio.tools, FASEB list

Availability: The research community can contribute to this resource

Resource Name: ProteomicsDB

Resource ID: SCR_015562

Alternate IDs: r3d100013408, biotools:proteomicsdb

Alternate URLs: <https://bio.tools/proteomicsdb>, <https://doi.org/10.17616/R31NJMU8>

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260905T133212+0000

Ratings and Alerts

No rating or validation information has been found for ProteomicsDB.

No alerts have been found for ProteomicsDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 180 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Goo S, et al. (2026) Proteolysis-targeting Chimera efficacy prediction using a deep-learning-QSP model. Journal of cheminformatics, 18(1), 19.

Picciani M, et al. (2026) Mapping drug mechanisms with ProteomicsDB: unified omics and cell sensitivity data at scale. Nucleic acids research, 54(D1), D470.

Schilling V, et al. (2026) The State of Peptide Detectability in Computational Proteomics and Guidelines for AI Applications. Computational and structural biotechnology journal, 35(1), 0037.

Feinberg D, et al. (2026) Oncostatin-M ligand-based CAR-T therapy displays robust anti-tumor activity against osteosarcoma. BMC medicine, 24(1).

Kumar V, et al. (2026) Domain architecture of plant eukaryotic translation initiation factor 3 subunit E governs interaction with translational cis-elements to regulate pollen tube growth. The Plant cell, 38(2).

Balasubramaniam AM, et al. (2026) Decoding the therapeutic promise of Solanum trilobatum in oral submucous fibrosis: a network pharmacology, docking, and bioactivity study. Scientific reports, 16(1).

Kumar S, et al. (2026) Pan-cancer analysis reveals differential PERK expression across tumour types and its potential as a therapeutic target. Discover oncology, 17(1).

Murr J, et al. (2026) The Protein Phosphatase Inhibitor LB100 Targets the Mesenchymal Lineage of Pancreatic Ductal Adenocarcinoma. MedComm, 7(6), e70794.

Khan NM, et al. (2026) Chondrogenic potential of mesenchymal progenitors from somatic and cartilage-derived iPSCs is predicted by their transcriptomic signatures. Genes & diseases, 13(2), 101730.

Zheng J, et al. (2026) PMADS: an integrated database of curated and proteomics-inferred associations between protein post-translational modifications and drug sensitivity. Nucleic acids research, 54(D1), D1569.

Bang IH, et al. (2026) PAK4 in metabolic diseases: regulation by nutrient signals and therapeutic implications. Experimental & molecular medicine, 58(2), 416.

Cortés A, et al. (2025) In-depth mass-spectrometry reveals phospho-RAB12 as a blood biomarker of G2019S LRRK2-driven Parkinson's disease. Brain : a journal of neurology, 148(6), 2075.

Jana M, et al. (2025) Chemically Synthesized LRAD3-D1 Interacts with N-Terminal Domain of SARS-CoV-2 Spike Protein. *Chembiochem : a European journal of chemical biology*, 26(22), e202500403.

Stojanov R, et al. (2025) Applicability Assessment of Technologies for Predictive and Prescriptive Analytics of Nephrology Big Data. *Proteomics*, 25(11-12), e202400135.

Kasmaeifar V, et al. (2025) Computational design and evaluation of optimal bait sets for scalable proximity proteomics. *Nature communications*, 16(1), 9333.

Zhang N, et al. (2025) Integration of multi-omics data accelerates molecular analysis of common wheat traits. *Nature communications*, 16(1), 2200.

Nomura N, et al. (2025) γ -Lipoic acid increases phagocytosis of some lactic acid bacteria via modulation of CD36 expression. *Bioscience of microbiota, food and health*, 44(1), 43.

Abdul-Khalek N, et al. (2025) To Fly, or Not to Fly, That Is the Question: A Deep Learning Model for Peptide Detectability Prediction in Mass Spectrometry. *Journal of proteome research*, 24(6), 2709.

Shaheed SU, et al. (2025) Comprehensive proteome profiling of cytochrome P450 isoforms in cancer models. *Clinical proteomics*, 22(1), 41.

Abele M, et al. (2025) Proteomic Diversity in Bacteria: Insights and Implications for Bacterial Identification. *Molecular & cellular proteomics : MCP*, 24(3), 100917.