

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: 20260821T194054+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 [NIF](#) .

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).

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.

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).

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).

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

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.

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.

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

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

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.

Müller J, et al. (2025) PTMNavigator: interactive visualization of differentially regulated post-translational modifications in cellular signaling pathways. *Nature communications*, 16(1), 510.