

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: 20260729T044405+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 149 mentions in open access literature.

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

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.

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.

Prakash A, et al. (2025) Integrated View of Baseline Protein Expression in Human Tissues Using Public Data Independent Acquisition Data Sets. *Journal of proteome research*, 24(2), 685.

Islam F, et al. (2025) Insights into the cellular function and mechanism of action of quinone reductase 2 (NQO2). *The Biochemical journal*, 482(6), 309.

Vagiona AC, et al. (2025) Prediction of protein interactions with function in protein (de-)phosphorylation. *PloS one*, 20(3), e0319084.

Ivanisenko NV, et al. (2025) Oligomerised RIPK1 is the main core component of the CD95 necrosome. *The EMBO journal*, 44(11), 3231.

Federspiel JD, et al. (2024) Differential Analysis of Cereblon Neosubstrates in Rabbit Embryos Using Targeted Proteomics. *Molecular & cellular proteomics : MCP*, 23(7), 100797.

Phung TK, et al. (2024) CURTAIN-A unique web-based tool for exploration and sharing of MS-based proteomics data. *Proceedings of the National Academy of Sciences of the United States of America*, 121(7), e2312676121.

Zhang G, et al. (2024) Spi1 regulates the microglial/macrophage inflammatory response via the PI3K/AKT/mTOR signaling pathway after intracerebral hemorrhage. *Neural regeneration research*, 19(1), 161.

Williams G, et al. (2024) Use of Nonhuman Sera as a Highly Cost-Effective Internal Standard for Quantitation of Multiple Human Proteins Using Species-Specific Tryptic Peptides: Applicability in Clinical LC-MS Analyses. *Journal of proteome research*, 23(8), 3052.

Waury K, et al. (2024) Proteome encoded determinants of protein sorting into extracellular vesicles. *Journal of extracellular biology*, 3(1), e120.

O'Donoghue L, et al. (2024) Roles of G proteins and their GTPase-activating proteins in platelets. *Bioscience reports*, 44(5).

Reinecke M, et al. (2024) Chemical proteomics reveals the target landscape of 1,000 kinase inhibitors. *Nature chemical biology*, 20(5), 577.

Schneider C, et al. (2024) A Novel AMPK Inhibitor Sensitizes Pancreatic Cancer Cells to Ferroptosis Induction. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(31), e2307695.

Lee CY, et al. (2024) Illuminating phenotypic drug responses of sarcoma cells to kinase inhibitors by phosphoproteomics. *Molecular systems biology*, 20(1), 28.