

Resource Summary Report

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PAXdb

RRID:SCR_018910

Type: Tool

Proper Citation

PAXdb (RRID:SCR_018910)

Resource Information

URL: <https://pax-db.org/>

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Description: Database of protein abundance averages across all three domains of life. Protein abundance database, which contains whole genome protein abundance information across organisms and tissues. Publicly available experimental data are imported and mapped onto common name space and, in case of tandem mass spectrometry data, re-processed using in-house standardized spectral counting pipeline. All datasets in are scored and ranked by importing protein network information. Orthology relations at various hierarchy levels are pre-computed for each protein.

Synonyms: PaxDb version 4.0

Resource Type: data or information resource, database

Defining Citation: [DOI:10.1002/pmic.201400441](https://doi.org/10.1002/pmic.201400441), [PMID:22535208](https://pubmed.ncbi.nlm.nih.gov/22535208/)

Keywords: Protein abundance database, whole genome protein data, organisms protein data, tissues protein data, experimental data protein orthology relation

Funding: Swiss National Science Foundation ;
University of Zurich

Availability: Free, Freely available

Resource Name: PAXdb

Resource ID: SCR_018910

License URLs: <https://pax-db.org/license>

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260729T044447+0000

Ratings and Alerts

No rating or validation information has been found for PAXdb.

No alerts have been found for PAXdb.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Chagoyen M, et al. (2025) Disentangling protein metabolic costs in human cells and tissues. PNAS nexus, 4(1), pgaf008.

Liu T, et al. (2025) Effective Gene Expression Prediction and Optimization from Protein Sequences. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(8), e2407664.

Hogan PG, et al. (2025) TOX, through a glass, darkly. Frontiers in immunology, 16, 1576468.

Liu J, et al. (2025) Structural insights into the dual Ca²⁺-sensor-mediated activation of the PPEF phosphatase family. Nature communications, 16(1), 3120.

Abdullah HQ, et al. (2025) When less is more: Counterintuitive stoichiometries and cellular abundances are essential for ABC transporters' function. Science advances, 11(21), eadq7470.

Takeuchi K, et al. (2025) PI5P4K inhibitors: promising opportunities and challenges. The FEBS journal, 292(17), 4446.

Rivas-Santisteban J, et al. (2025) Cell Compartment is a Predictor of Protein Rate of Evolution, but not in the Manner Expected: Evidence Against the Extended Complexity Hypothesis. Genome biology and evolution, 17(7).

Gary CR, et al. (2024) Kinase-catalyzed biotinylation for discovery and validation of substrates to multispecificity kinases NME1 and NME2. The Journal of biological chemistry, 300(8), 107588.

Terui R, et al. (2024) Single-Molecule Imaging Reveals the Mechanism of Bidirectional Replication Initiation in Metazoa. bioRxiv : the preprint server for biology.

Moon SJ, et al. (2024) Identification of high sugar diet-induced dysregulated metabolic pathways in muscle using tissue-specific metabolic models in Drosophila. bioRxiv : the preprint server for biology.

Wang S, et al. (2024) Integrated Proteomics Analysis of Baseline Protein Expression in Pig Tissues. *Journal of proteome research*, 23(6), 1948.

Zarin S, et al. (2024) Rv2231c, a unique histidinol phosphate aminotransferase from *Mycobacterium tuberculosis*, supports virulence by inhibiting host-directed defense. *Cellular and molecular life sciences : CMLS*, 81(1), 203.

Mi??cicka A, et al. (2024) Ribosomal collision is not a prerequisite for ZNF598-mediated ribosome ubiquitination and disassembly of ribosomal complexes by ASCC. *Nucleic acids research*, 52(8), 4627.

Badonyi M, et al. (2023) Buffering of genetic dominance by allele-specific protein complex assembly. *Science advances*, 9(22), eadf9845.

Huang Q, et al. (2023) PaxDb 5.0: Curated Protein Quantification Data Suggests Adaptive Proteome Changes in Yeasts. *Molecular & cellular proteomics : MCP*, 22(10), 100640.

Skinninger MA, et al. (2023) Mapping protein states and interactions across the tree of life with co-fractionation mass spectrometry. *Nature communications*, 14(1), 8365.

Phillips NJ, et al. (2023) Capture, Release, and Identification of Newly Synthesized Proteins for Improved Profiling of Functional Translatomes. *Molecular & cellular proteomics : MCP*, 22(3), 100497.

Lignieres L, et al. (2023) Extending the Range of SLIM-Labeling Applications: From Human Cell Lines in Culture to *Caenorhabditis elegans* Whole-Organism Labeling. *Journal of proteome research*, 22(3), 996.

Sindram E, et al. (2023) ARPC5 deficiency leads to severe early-onset systemic inflammation and mortality. *Disease models & mechanisms*, 16(7).

Zhao Z, et al. (2023) A Peptidisc-Based Survey of the Plasma Membrane Proteome of a Mammalian Cell. *Molecular & cellular proteomics : MCP*, 22(8), 100588.