

Resource Summary Report

Generated by [dkNET](#) on Aug 25, 2026

PAXdb

RRID:SCR_018910

Type: Tool

Proper Citation

PAXdb (RRID:SCR_018910)

Resource Information

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

Proper Citation: PAXdb (RRID:SCR_018910)

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: 20260821T194136+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 69 mentions in open access literature.

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

Larrea-Sebal A, et al. (2026) Blood proteomics: insights from public data. *Genome biology*, 27(1).

Sauer T, et al. (2026) Impact of single freeze-thaw cycles on human serum proteins: Implications for mass spectrometry biomarker validation. *iScience*, 29(6), 115934.

Hsu HC, et al. (2026) Mycobacterium tuberculosis assembles a unique hexameric E2p core of the pyruvate dehydrogenase complex. *The Journal of biological chemistry*, 302(4), 111284.

Yan Y, et al. (2026) Functional DNAzyme-Guided Target Identification and Portable Detection of Colorectal Cancer. *JACS Au*, 6(6), 3506.

Huang Q, et al. (2026) PaxDb v6.0: reprocessed, LLM-selected, curated protein abundance data across organisms. *Nucleic acids research*, 54(D1), D427.

Hajnal ÁB, et al. (2026) The non-catalytic binding of auxin, cytokinin and salicylic acid by tomato Phi class glutathione transferases: insights from computational modelling. *Plant molecular biology*, 116(2), 17.

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).

Eldin P, et al. (2025) tRNA Modifications: A Tale of Two Viruses-SARS-CoV-2 and ZIKV. *International journal of molecular sciences*, 26(15).

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

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

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

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

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.

Cao H, et al. (2025) Genome-Wide Identification and Expression Profiling of SIGeBP Gene Family in Response to Hormone and Abiotic Stresses in Solanum lycopersicum L. International journal of molecular sciences, 26(13).

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).

Chérot H, et al. (2025) In-Cell Residue-Resolved NMR of Micromolar α -Synuclein and Tau at 310 K. Journal of the American Chemical Society, 147(50), 46259.

Ayoubi R, et al. (2025) A consensus platform for antibody characterization. Nature protocols, 20(6), 1509.

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.

Eldin P, et al. (2024) SARS-CoV-2 Displays a Suboptimal Codon Usage Bias for Efficient Translation in Human Cells Diverted by Hijacking the tRNA Epitranscriptome. International journal of molecular sciences, 25(21).