Resource Summary Report

Generated by T1D on Aug 3, 2026

Proteomics Identifications (PRIDE)

RRID:SCR_003411
Type: Tool

Proper Citation

Proteomics Identifications (PRIDE) (RRID:SCR_003411)

Resource Information

URL: http://www.ebi.ac.uk/pride/

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Description: Centralized, standards compliant, public data repository for proteomics data, including protein and peptide identifications, post-translational modifications and supporting spectral evidence. Originally it was developed to provide a common data exchange format and repository to support proteomics literature publications. This remit has grown with PRIDE, with the hope that PRIDE will provide a reference set of tissue-based identifications for use by the community. The future development of PRIDE has become closely linked to HUPO PSI. PRIDE encourages and welcomes direct user submissions of protein and peptide identification data to be published in peer-reviewed publications. Users may Browse public datasets, use PRIDE BioMart for custom queries, or download the data directly from the FTP site. PRIDE has been developed through a collaboration of the EMBL-EBI, Ghent University in Belgium, and the University of Manchester.

Abbreviations: PRIDE

Synonyms: PRoteomics IDEntifications database, PRIDE Archive - proteomics data repository, PRIDE Archive, PRIDE, Proteomics Identifications, Proteomics Identifications (PRIDE), PRoteomics IDEntifications database (PRIDE)

Resource Type: data or information resource, database, data repository, service resource, storage service resource

Defining Citation: PMID:23203882, PMID:19662629

Keywords: proteomics, protein, peptide, mass spectrometry, annotation, standard, spectra, protein-protein interaction, amino acid, amino acid sequence, post-translational modification, biomart, bio.tools

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BBSRC BB/I024204/1

Availability: Free, Available for download, Freely available

Resource Name: Proteomics Identifications (PRIDE)

Resource ID: SCR_003411

Alternate IDs: nif-0000-03336, biotools:pride, r3d100011515

Alternate URLs: https://www.ebi.ac.uk/pride/archive/, https://bio.tools/pride, https://doi.org/10.17616/R3F330

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260803T040344+0000

Ratings and Alerts

No rating or validation information has been found for Proteomics Identifications (PRIDE).

No alerts have been found for Proteomics Identifications (PRIDE).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 642 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Renaud EA, et al. (2025) The HCF101 protein is an important component of the cytosolic iron-sulfur synthesis pathway in Toxoplasma gondii. PLoS biology, 23(2), e3003028.

Roumbo L, et al. (2025) The MAST kinase KIN-4 carries out mitotic entry functions of Greatwall in C. elegans. The EMBO journal, 44(7), 1943.

Zavadil F, et al. (2025) Translation of bi-directional transcripts enhances MHC-I peptide diversity. Frontiers in immunology, 16, 1554561.

Luklov?? M, et al. (2025) Light Quantity Impacts Early Response to Cold and Cold Acclimation in Young Leaves of Arabidopsis. Plant, cell & environment, 48(7), 5030.

Raja R, et al. (2025) Interferon-induced PARP14-mediated ADP-ribosylation in p62 bodies requires the ubiquitin-proteasome system. The EMBO journal, 44(10), 2741.

You Y, et al. (2025) Reduction of Chemokine CXCL9 Expression by Omega-3 Fatty Acids via ADP-Ribosylhydrolase ARH3 in MIN6 Insulin-Producing Cells. Proteomics, 25(3), e202400053.

Kok G, et al. (2025) Isoleucine-to-valine substitutions support cellular physiology during isoleucine deprivation. Nucleic acids research, 53(1).

Bendig TAL, et al. (2025) Alkaline pH-Driven Metabolic Plasticity of Lactococcus lactis FM03. Environmental microbiology, 27(11), e70200.

Yan M, et al. (2025) Lactylated Proteomic Analysis Reveals Functional Implications of Lysine Lactylation In Asthenozoospermia. Molecular & cellular proteomics : MCP, 24(12), 101439.

Zhou S, et al. (2025) The S-depalmitoylase ABHD10 is essential for sperm mitochondrial sheath formation and male fertility. Nature communications, 16(1), 10334.

Zhang N, et al. (2025) UBD-mediated glycolytic reprogramming promotes M2 macrophage polarization in ovarian cancer immune evasion. Journal of cell communication and signaling, 19(3), e70034.

Bartmanski BJ, et al. (2025) Multi-omics profiling of cross-resistance between ceftazidime-avibactam and meropenem identifies common and strain-specific mechanisms in Pseudomonas aeruginosa clinical isolates. mBio, 16(7), e0389624.

Lee JW, et al. (2025) Control of flagellar gene expression by a chemotaxis receptor-like regulator in pathogenic Escherichia coli. The EMBO journal, 44(22), 6675.

Hagemeier B, et al. (2025) The serine protease HTRA1 targets tau fibrils and provides a proteolytic barrier against pathogenic protein conformations. The Journal of biological chemistry, 301(10), 110729.

Yosef O, et al. (2025) Metabolic reprogramming driven by Ant2 deficiency augments T Cell function and anti-tumor immunity in mice. Nature communications, 16(1), 4292.

Zheng H, et al. (2025) In situ valence-transited arsenic nanosheets for multi-modal therapy of colorectal cancer. Nature communications, 16(1), 2088.

Lin H, et al. (2025) Mitochondrial fatty acid oxidation as the target for blocking therapy-resistance and inhibiting tumor recurrence: The proof-of-principle model demonstrated for ovarian cancer cells. Journal of advanced research.

Yin Z, et al. (2025) Exosomal integrin alpha 3 promotes epithelial ovarian cancer cell migration via the S100A7/p-ERK signaling pathway. Acta biochimica et biophysica Sinica, 57(6), 1006.

Goldberg N, et al. (2025) The RNA-binding protein PRRC2B preserves 5' TOP mRNA during starvation to maintain ribosome biogenesis during nutrient recovery. Nucleic acids research, 53(22).

Ries F, et al. (2025) A truncated variant of the ribosome-associated trigger factor specifically contributes to plant chloroplast ribosome biogenesis. Nature communications, 16(1), 629.