# Resource Summary Report

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# 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:** service resource, storage service resource, data or information resource, data repository, database

**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:** Public, Acknowledgement requested

**Resource Name:** Proteomics Identifications (PRIDE)

**Resource ID:** SCR_003411

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

**Alternate URLs:** https://www.ebi.ac.uk/pride/archive/, https://bio.tools/pride

**Record Creation Time:** 20220129T080218+0000

**Record Last Update:** 20250426T055623+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 559 mentions in open access literature.

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

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

Subramanian V, et al. (2025) Long-Term Effects of Radiation Therapy on Cerebral Microvessel Proteome: A Six-Month Post-Exposure Analysis. bioRxiv : the preprint server for biology.

Perez-Riverol Y, et al. (2025) The PRIDE database at 20 years: 2025 update. Nucleic acids

research, 53(D1), D543.

Tyl MD, et al. (2025) Infection-induced lysine lactylation enables herpesvirus immune evasion. Science advances, 11(2), eads6215.

Rani P, et al. (2025) Elucidation of peptide screen for targeted identification of Yersinia pestis by nano-liquid chromatography tandem mass spectrometry. Scientific reports, 15(1), 1096.

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.

Kulow VA, et al. (2025) Beyond hemoglobin: Critical role of 2,3-bisphosphoglycerate mutase in kidney function and injury. Acta physiologica (Oxford, England), 241(1), e14242.

Liu YC, et al. (2025) Targeting the ERK1/2 and p38 MAPK pathways attenuates Golgi tethering factor golgin-97 depletion-induced cancer progression in breast cancer. Cell communication and signaling : CCS, 23(1), 22.

Yang J, et al. (2025) VSTM2L protects prostate cancer cells against ferroptosis via inhibiting VDAC1 oligomerization and maintaining mitochondria homeostasis. Nature communications, 16(1), 1160.

Wang X, et al. (2025) Construction of functional tissue-engineered microvasculatures using circulating fibrocytes as mural cells. Journal of tissue engineering, 16, 20417314251315523.

Petibon C, et al. (2025) Transcription factors induce differential splicing of duplicated ribosomal protein genes during meiosis. Nucleic acids research, 53(2).

Aghila Rani KG, et al. (2025) Medwakh smoking induces alterations in salivary proteins and cytokine expression: a clinical exploratory proteomics investigation. Clinical proteomics, 22(1), 2.

Pastor F, et al. (2024) Deciphering the phospho-signature induced by hepatitis B virus in primary human hepatocytes. Frontiers in microbiology, 15, 1415449.

Kahnert K, et al. (2024) Proteomics couples electrical remodelling to inflammation in a murine model of heart failure with sinus node dysfunction. Cardiovascular research, 120(8), 927.

Solari CA, et al. (2024) Riboproteome remodeling during quiescence exit in Saccharomyces cerevisiae. iScience, 27(1), 108727.

Giannangelo C, et al. (2024) Chemoproteomics validates selective targeting of Plasmodium M1 alanyl aminopeptidase as an antimalarial strategy. eLife, 13.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. GigaScience, 13.

Parsons JD, et al. (2024) Factors governing attachment of Rhizobium leguminosarum to legume roots at acid, neutral, and alkaline pHs. mSystems, 9(9), e0042224.

Tirado TC, et al. (2024) A peptide dataset for target analysis of human complement system proteins. Data in brief, 53, 110217.

Volkov M, et al. (2024) Acetylated bacterial proteins as potent antigens inducing an anti-modified protein antibody response. RMD open, 10(3).