

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

Protein Information Resource

RRID:SCR_008229

Type: Tool

Proper Citation

Protein Information Resource (RRID:SCR_008229)

Resource Information

URL: <https://proteininformationresource.org/>

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Description: Integrated databases and bioinformatics tools to support genomic, proteomic and systems biology research. PIR maintains the Protein Sequence Database (PSD), an annotated protein database containing over 283 000 sequences covering the entire taxonomic range. Family classification is used for sensitive identification, consistent annotation, and detection of annotation errors. The superfamily curation defines signature domain architecture and categorizes memberships to improve automated classification. To increase the amount of experimental annotation, the PIR has developed a bibliography system for literature searching, mapping, and user submission, and has conducted retrospective attribution of citations for experimental features. PIR also maintains NREF, a non-redundant reference database, and iProClass, an integrated database of protein family, function, and structure information. PIR is a member of the UniProt Consortium that provides the central international resource on protein sequence and function. Located both at the University of Delaware and Georgetown University, PIR conducts research in biomedical text mining and ontology, computational systems biology, and bioinformatics cyberinfrastructure. The PIR web sites are freely accessible by researchers worldwide with over 4 million hits per month from over 100,000 unique sites.

Abbreviations: PIR

Synonyms: MIRROR: Protein Information Resource

Resource Type: data or information resource, database

Keywords: family, function, annotation, bioinformatic, biomedical, computational systems biology, cyberinfrastructure, database, genomic, mining, protein, protein bioinformatics, proteomic, research, scientific, sequence, structure, systems biology, taxonomic, tool, ontology, text, bio.tools, FASEB list

Funding: NLM P41 LM05978

Resource Name: Protein Information Resource

Resource ID: SCR_008229

Alternate IDs: biotools:pir, nif-0000-21327

Alternate URLs: <https://bio.tools/pir>, <http://pir.georgetown.edu/>

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260903T234953+0000

Ratings and Alerts

No rating or validation information has been found for Protein Information Resource.

No alerts have been found for Protein Information Resource.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

De-Simone SG, et al. (2023) High-Throughput IgG Epitope Mapping of Tetanus Neurotoxin: Implications for Immunotherapy and Vaccine Design. *Toxins*, 15(4).

Lu H, et al. (2021) iTRAQ-BASED Proteomic Analysis of the Mechanism of Fructose on Improving Fengycin Biosynthesis in *Bacillus Amyloliquefaciens*. *Molecules (Basel, Switzerland)*, 26(20).

Syifa N, et al. (2020) Phosphoproteomics and Bioinformatics Analyses Reveal Key Roles of GSK-3 and AKAP4 in Mouse Sperm Capacitation. *International journal of molecular sciences*, 21(19).

Bryant JA, et al. (2020) Structure of dual BON-domain protein DoIP identifies phospholipid binding as a new mechanism for protein localisation. *eLife*, 9.

Li M, et al. (2019) Genome structure and evolution of *Antirrhinum majus* L. *Nature plants*, 5(2), 174.

Kundu S, et al. (2018) Origin, evolution, and divergence of plant class C GH9 endoglucanases. *BMC evolutionary biology*, 18(1), 79.

Li G, et al. (2018) A study on screening and antitumor effect of CD55-specific ligand peptide in cervical cancer cells. *Drug design, development and therapy*, 12, 3899.

Ling HQ, et al. (2018) Genome sequence of the progenitor of wheat A subgenome *Triticum urartu*. *Nature*, 557(7705), 424.

Henneman B, et al. (2018) Structure and function of archaeal histones. *PLoS genetics*, 14(9), e1007582.

E Y, et al. (2017) PGPR strain *Paenibacillus polymyxa* SQR-21 potentially benefits watermelon growth by re-shaping root protein expression. *AMB Express*, 7(1), 104.

Wang C, et al. (2017) High-Salt Diet Has a Certain Impact on Protein Digestion and Gut Microbiota: A Sequencing and Proteome Combined Study. *Frontiers in microbiology*, 8, 1838.

Han J, et al. (2017) iTRAQ-based proteomic analysis of LI-F type peptides produced by *Paenibacillus polymyxa* JSa-9 mode of action against *Bacillus cereus*. *Journal of proteomics*, 150, 130.

Galperin MY, et al. (2017) The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes. *Nucleic acids research*, 45(D1), D1.

Hajjari M, et al. (2016) Tissue Specific Expression Levels of Apoptosis Involved Genes Have Correlations with Codon and Amino Acid Usage. *Genomics & informatics*, 14(4), 234.

Ma R, et al. (2016) Proteomic Analyses Provide Novel Insights into Plant Growth and Ginsenoside Biosynthesis in Forest Cultivated *Panax ginseng* (F. Ginseng). *Frontiers in plant science*, 7, 1.

Zhao K, et al. (2016) Edible Safety Assessment of Genetically Modified Rice T1C-1 for Sprague Dawley Rats through Horizontal Gene Transfer, Allergenicity and Intestinal Microbiota. *PloS one*, 11(10), e0163352.

Bhawna , et al. (2016) PvTFDB: a *Phaseolus vulgaris* transcription factors database for expediting functional genomics in legumes. *Database : the journal of biological databases and curation*, 2016.

Wu X, et al. (2016) Proteomic analysis of changes in mitochondrial protein expression during peach fruit ripening and senescence. *Journal of proteomics*, 147, 197.

Loginov D, et al. (2016) Proteomics of survival structures of fungal pathogens. *New biotechnology*, 33(5 Pt B), 655.

Thakur S, et al. (2016) A De-Novo Genome Analysis Pipeline (DeNoGAP) for large-scale comparative prokaryotic genomics studies. *BMC bioinformatics*, 17(1), 260.