

Resource Summary Report

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Protein Information Resource

RRID:SCR_002837

Type: Tool

Proper Citation

Protein Information Resource (RRID:SCR_002837)

Resource Information

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

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Description: Integrated public bioinformatics resource to support genomic, proteomic and systems biology research and scientific studies. Provides databases and protein sequence analysis tools to scientific community, including Protein Sequence Database which grew out from the Atlas of Protein Sequence and Structure. Conducts research in biomedical text mining and ontology, computational systems biology, and bioinformatics cyberinfrastructure. In 2002 PIR, along with its international partners, EBI (European Bioinformatics Institute) and SIB (Swiss Institute of Bioinformatics), were awarded a grant from NIH to create UniProt, a single worldwide database of protein sequence and function, by unifying the PIR-PSD, Swiss-Prot, and TrEMBL databases. Currently, PIR major activities include: i) UniProt (Universal Protein Resource) development, ii) iProClass protein data integration and ID mapping, iii) PRO protein ontology, and iv) iProLINK protein literature mining and ontology development. The FTP site provides free download for iProClass, PIRSF, and PRO.

Abbreviations: PIR

Synonyms: PIR - Protein Information Resource

Resource Type: topical portal, data or information resource, portal

Defining Citation: [PMID:12520019](#)

Keywords: annotation, genomic, mining, protein, protein bioinformatics, proteomic, research, sequence, structure, systems biology, gold standard, bio.tools, FASEB list

Funding: NLM P41 LM05798

Availability: Free, Freely available

Resource Name: Protein Information Resource

Resource ID: SCR_002837

Alternate IDs: biotools:pir, nif-0000-21327, nif-0000-00143, SCR_008229

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

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260731T042636+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 83 mentions in open access literature.

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

Mora-Márquez F, et al. (2025) gymnotoa-db: a database and application to optimize functional annotation in gymnosperms. Database : the journal of biological databases and curation, 2025.

Meng Y, et al. (2025) Protein structure prediction via deep learning: an in-depth review. Frontiers in pharmacology, 16, 1498662.

Ozkan-Nikitaras T, et al. (2024) N-SREBP2 Provides a Mechanism for Dynamic Control of Cellular Cholesterol Homeostasis. Cells, 13(15).

Peng P, et al. (2024) Transcriptome Analysis of the Harmful Dinoflagellate Heterocapsa bohaiensis Under Varied Nutrient Stress Conditions. Microorganisms, 12(12).

Zhao MX, et al. (2024) Nphos: Database and Predictor of Protein N-phosphorylation. Genomics, proteomics & bioinformatics, 22(3).

Kraemer AI, et al. (2023) The immunopeptidome landscape associated with T cell infiltration, inflammation and immune editing in lung cancer. Nature cancer, 4(5), 608.

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

Müller-Dott S, et al. (2023) Expanding the coverage of regulons from high-confidence prior knowledge for accurate estimation of transcription factor activities. *Nucleic acids research*, 51(20), 10934.

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).

Hou X, et al. (2021) Autophagy deficiency downregulates O6methylguanine-DNA methyltransferase and increases chemosensitivity of liver cancer cells. *Aging*, 13(10), 14289.

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.

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

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.

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

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.

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.

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.