

Resource Summary Report

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Pfam

RRID:SCR_004726

Type: Tool

Proper Citation

Pfam (RRID:SCR_004726)

Resource Information

URL: <http://pfam.xfam.org/>

Proper Citation: Pfam (RRID:SCR_004726)

Description: A database of protein families, each represented by multiple sequence alignments and hidden Markov models (HMMs). Users can analyze protein sequences for Pfam matches, view Pfam family annotation and alignments, see groups of related families, look at the domain organization of a protein sequence, find the domains on a PDB structure, and query Pfam by keywords. There are two components to Pfam: Pfam-A and Pfam-B. Pfam-A entries are high quality, manually curated families that may automatically generate a supplement using the ADDA database. These automatically generated entries are called Pfam-B. Although of lower quality, Pfam-B families can be useful for identifying functionally conserved regions when no Pfam-A entries are found. Pfam also generates higher-level groupings of related families, known as clans (collections of Pfam-A entries which are related by similarity of sequence, structure or profile-HMM).

Synonyms: Pfam Database, Protein Families Database, PFAM, Pfam protein families database

Resource Type: data or information resource, database

Defining Citation: [PMID:24288371](#), [PMID:19920124](#)

Keywords: database, clan, structure, sequence, protein family, domain, bio.tools, FASEB list

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Availability: Acknowledgement requested, Available via FTP

Resource Name: Pfam

Resource ID: SCR_004726

Alternate IDs: biotools:pfam, OMICS_01696, r3d100012850, nlx_72111

Alternate URLs: <https://bio.tools/pfam>, <https://doi.org/10.17616/R3QV4F>

Old URLs: <http://pfam.sanger.ac.uk/>

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Record Creation Time: 20220129T080226+0000

Record Last Update: 20260821T193727+0000

Ratings and Alerts

No rating or validation information has been found for Pfam.

No alerts have been found for Pfam.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17424 mentions in open access literature.

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

Wu X, et al. (2026) Locus-Specific Human Endogenous Retrovirus ERVK18 Expression Indicates an Inflamed Microenvironment and Favorable Immunotherapy Outcome in Small Cell Lung Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(11), 2214.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Yu L, et al. (2026) Systematic characterization of PBP2 as the primary siderophore recognizer in Actinomycetes and other Gram-positive bacteria. *Microbial genomics*, 12(4).

Black JJ, et al. (2026) The *Legionella pneumophila* effector SidL is an adenylyltransferase that modifies the glycolytic intermediate 3-phosphoglycerate. *Molecular cell*.

Yan L, et al. (2026) A NACHT domain-containing protein Ncp is required for appendage-associated unconventional protein secretion in the fungus *Penicillium herquei*. *iScience*, 29(7), 116464.

Chasapi MN, et al. (2026) metagRoot: a comprehensive database of protein families associated with plant root microbiomes. *Nucleic acids research*, 54(D1), D1733.

Liu D, et al. (2026) Transcriptome Analysis Revealed Potential Regulatory Networks Underlying Corolla Movement in *Mirabilis jalapa* (Nyctaginaceae). *Biology*, 15(7).

Zhao Z, et al. (2026) From Molecular Perturbations to Functional Decline: Multi-Omics Reveals Sperm Cryodamage in Sichuan Bream (*Sinibrama taeniatus*). *Animals : an open access journal from MDPI*, 16(7).

Gao J, et al. (2026) Genome-wide identification of the GATA transcription factor family in ten Cucurbitaceae species and expression analysis of CIGATA genes in watermelon stress responses. *BMC genomics*, 27(1).

Tong Y, et al. (2026) Genome-wide identification and expression analysis of stress-associated proteins (SAPs) containing A20/AN1 Zinc finger in *Dendrobium officinale*. *BMC plant biology*, 26(1).

Zhang X, et al. (2026) Genome-wide identification and characterization of the RPA gene family in maize. *BMC plant biology*, 26(1).

Liu WZ, et al. (2026) Genomic insights into the broad-spectrum antifungal activity of a novel *Paenibacillus polymyxa* strain X-11. *BMC microbiology*, 26(1).

Aoyagi YB, et al. (2026) Chromosome-level genome assembly of the *Gerbera* (*Gerbera hybrida*) using HiFi long-read and Hi-C technologies. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Nishihara A, et al. (2026) Exploring the Diversity and Metabolic Potential of CO₂ fixation Mediated by RubisCO in Prokaryotes in the Japan Collection of Microorganisms. *Microbes and environments*, 41(1).

Xue T, et al. (2026) Pan-genomic analysis and abiotic stress expression of eight TPS gene families in *Brassica napus*. *BMC plant biology*, 26(1).

Han L, et al. (2026) Genome-Wide Identification and Characterization of Stress-Responsive SNARE Genes in Quinoa (*Chenopodium quinoa* Willd.). *Biology*, 15(5).

Duarte SA, et al. (2026) ET-Pfam: ensemble transfer learning for protein family prediction. *Bioinformatics (Oxford, England)*, 42(4).

Jiang Z, et al. (2026) Glycogen Synthase Kinase 3 (GSK3) Gene Family in *Glycine max* Under the Effect of Manganese Stress. *International journal of molecular sciences*, 27(5).

Xu Z, et al. (2026) Analysis of the TIL gene family in Brassicaceae species and functional study of BrTIL1 in cold tolerance. *Frontiers in plant science*, 17, 1794987.

Shen D, et al. (2026) Enhanced resistance to *Botryosphaeria dothidea* through upregulation of the lignin biosynthesis regulator WRKY11 in poplar. *Frontiers in plant science*, 17, 1737207.