

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

Funding: EMBL core funds ;
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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: 20260905T133126+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 [Kravitz](#) .

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.
- Du L, et al. (2026) Cell-Type-Specific and Variety-Specific Responses to Salt Stress in Wheat Root Revealed by Single-Cell Transcriptomics. *Plant biotechnology journal*, 24(3), 1446.
- Guo X, et al. (2026) Diversity and Ecological Potentials of Marine Viruses Inhabiting Continental Shelf Seas. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e11707.
- Liu T, et al. (2026) Chromosome-level genome assembly and annotation of the endangered plant *Primula kwangtungensis* (Primulaceae). *Scientific data*, 13(1), 212.
- Luo Y, et al. (2026) A chromosome-level genome assembly and multi-omics analyses provide insights into the biosynthesis of piperlongumine in *Piper sarmentosum*. *Communications biology*, 9(1), 170.
- Zhao G, et al. (2026) Improved Longan Genome Assembly Reveals Insights Into Flowering Mechanisms. *Plant biotechnology journal*, 24(3), 1678.
- Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.
- Ji Y, et al. (2026) Unveiling Global Diversity of Patescibacteriota and Functional Interactions with Host Microbes. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(11), e09416.
- Jin S, et al. (2026) Microbial collagenase activity is linked to oral-gut translocation in advanced chronic liver disease. *Nature microbiology*, 11(1), 211.
- Luo Z, et al. (2026) Host adaptation and genome evolution of the broad host range fungal rust pathogen, *Austropuccinia psidii*. *G3* (Bethesda, Md.), 16(1).
- Wang J, et al. (2026) Comparative Genomics of Viral Genomes and Identification of Three Novel Viroporin-Like Superfamilies. *Microbial physiology*, 36(1), 19.
- Wong ELY, et al. (2026) Historical comparative genomics to track the evolution of fungal pathogens: a proof of concept. *BMC genomics*, 27(1), 164.
- Sun W, et al. (2026) The RcMYB308-RcEGL1 module regulates cyanidin accumulation by targeting the RcF3'H promoter in pink roses. *BMC plant biology*, 26(1), 254.
- Lei FL, et al. (2026) Chromosome-level genome assembly of *Nemipterus japonicus* based on PacBio sequencing and Hi-C technology. *Scientific data*, 13(1), 218.
- Mishra R, et al. (2026) Gut plasma membrane proteomes reflect the distinct feeding strategies of *Nezara viridula* and *Diaphorina citri*. *Scientific reports*, 16(1), 4130.