

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 29, 2026

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: 20260729T044104+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 15523 mentions in open access literature.

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

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).

Jin S, et al. (2026) Microbial collagenase activity is linked to oral-gut translocation in advanced chronic liver disease. *Nature microbiology*, 11(1), 211.

Marks RA, et al. (2026) The architecture of resilience: a genome assembly of *Myrothamnus flabellifolia* sheds light on desiccation tolerance and sex determination. *The New phytologist*, 249(2), 1063.

Li Z, et al. (2026) Phylogenetic and functional characterization of Asgard primases. *Molecular biology and evolution*, 43(1).

Tominaga T, et al. (2026) OmpA_C-Like Domain of PorE Is Essential for PorE Function in the Type IX Secretion System (T9SS) of *Porphyromonas gingivalis* and Some T9SS Cargo Proteins Are Secreted in a PorE-Independent Manner. *Microbiology and immunology*, 70(1), 15.

- García JF, et al. (2026) Intraspecies sequence-graph analysis of the *Phytophthora theobromicola* genome reveals a dynamic structure and variable effector repertoires. *G3* (Bethesda, Md.), 16(1).
- Sun T, et al. (2026) Conserved spatial patterning of gene expression in independent lineages of C4 plants. *The New phytologist*, 249(1), 24.
- Markkanen M, et al. (2026) Sulfonamide resistance gene *sul4* is hosted by common wastewater sludge bacteria and found in various newly described contexts and hosts. *Microbiology spectrum*, 14(1), e0085725.
- Song LCT, et al. (2026) Identification of proteins influencing CRISPR-associated transposases for enhanced genome editing. *Science advances*, 12(1), eaea1429.
- Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.
- Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).
- Zhao Q, et al. (2025) The unique architecture of umbrella toxins permits a two-tiered molecular bet-hedging strategy for interbacterial antagonism. *Cell*.
- Sullivan AE, et al. (2025) The Panoptes system uses decoy cyclic nucleotides to defend against phage. *Nature*, 647(8091), 988.
- Guest SL, et al. (2025) Myosin 2 drives actin contractility in fast-crawling species outside of the amorphean lineage. *Current biology : CB*, 35(23), 5696.
- Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.
- Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.
- Conn T, et al. (2025) Genome assembly and annotation of *Acropora pulchra* from Mo'orea French Polynesia. *GigaByte* (Hong Kong, China), 2025, gigabyte153.
- Turner LA, et al. (2025) Differences in gene expression between high and low tolerance rainbow trout (*Oncorhynchus mykiss*) to acute thermal stress. *PloS one*, 20(1), e0312694.
- Sivakumar P, et al. (2025) Sporophyte-directed gametogenesis in *Arabidopsis*. *Nature plants*, 11(3), 398.
- Guang X, et al. (2025) Telomere-to-telomere African wild rice (*Oryza longistaminata*) reference genome reveals segmental and structural variation. *GigaScience*, 14.