Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 3, 2025

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: database, data or information resource

Defining Citation: PMID:24288371, PMID:19920124

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

Funding: EMBL core funds ;
Howard Hughes Medical Institute ;
BBSRC BB/L024136/1;

Wellcome Trust 108433/Z/15/Z

Availability: Acknowledgement requested, Available via FTP

Resource Name: Pfam

Resource ID: SCR_004726

Alternate IDs: biotools:pfam, OMICS_01696, nlx_72111

Alternate URLs: https://bio.tools/pfam

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

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Record Creation Time: 20220129T080226+0000

Record Last Update: 20250403T060349+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 14123 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Cui Y, et al. (2025) Microbial community structure and functional traits involved in the adaptation of culturable bacteria within the gut of amphipods from the deepest ocean. Microbiology spectrum, 13(1), e0072324.

Gomaa F, et al. (2025) Array of metabolic pathways in a kleptoplastidic foraminiferan protist supports chemoautotrophy in dark, euxinic seafloor sediments. The ISME journal, 19(1).

Hemara LM, et al. (2025) Identification and Characterization of Innate Immunity in Actinidia melanandra in Response to Pseudomonas syringae pv. actinidiae. Plant, cell & environment, 48(2), 1037.

Zhou X, et al. (2025) LncPepAtlas: a comprehensive resource for exploring the translational landscape of long non-coding RNAs. Nucleic acids research, 53(D1), D468.

Yu C, et al. (2025) A novel Alteromonas phage with tail fiber containing six potential iron-binding domains. Microbiology spectrum, 13(1), e0093424.

Tangpranomkorn S, et al. (2025) A land plant-specific VPS13 mediates polarized vesicle trafficking in germinating pollen. The New phytologist, 245(3), 1072.

Hsieh LC, et al. (2025) Transcriptomic and enzymatic analysis of peroxidase families at the early growth stage of halophyte ice plant (Mesembryanthemum crystallinum L.) under salt stress. Botanical studies, 66(1), 5.

Liu S, et al. (2025) Chromosome-level genome assembly and annotation of Japanese anchovy (Engraulis japonicus). Scientific data, 12(1), 134.

Van Goethem MW, et al. (2025) Novel adaptive immune systems in pristine Antarctic soils. Scientific reports, 15(1), 2368.

Ghelfi A, et al. (2025) Hayai-Annotation: A functional gene prediction tool that integrates orthologs and gene ontology for network analysis in plant species. Computational and structural biotechnology journal, 27, 117.

Inskeep WP, et al. (2025) Respiratory processes of early-evolved hyperthermophiles in sulfidic and low-oxygen geothermal microbial communities. Nature communications, 16(1), 277.

Wang Y, et al. (2025) Identification of the CaCRT gene family and function of CaCRT1 under low-temperature stress in pepper (Capsicum annuum L.). Scientific reports, 15(1), 90.

An M, et al. (2025) Chromosome-Level Genome Assembly and Annotation of the Highly Heterozygous Phallus echinovolvatus Provide New Insights into Its Genetics. Journal of fungi (Basel, Switzerland), 11(1).

Pozdnyakov IR, et al. (2025) Gene Expression in Aphelid Zoospores Reveals Their Transcriptional and Translational Activity and Alacrity for Invasion. Journal of fungi (Basel, Switzerland), 11(1).

Islam MSU, et al. (2025) Genome-wide identification and characterization of cation-proton antiporter (CPA) gene family in rice (Oryza sativa L.) and their expression profiles in response to phytohormones. PloS one, 20(1), e0317008.

Zhou W, et al. (2025) Comparative transcriptome and metabolome analysis reveals the differential response to salinity stress of two genotypes brewing sorghum. Scientific reports, 15(1), 3365.

Vysakh VG, et al. (2025) De novo transcriptome assembly of the Perna viridis: A novel invertebrate model for ecotoxicological studies. Scientific data, 12(1), 147.

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (Eleusine indica). Scientific data, 12(1), 156.

Roshka YA, et al. (2025) Antimicrobial Potential of Secalonic Acids from Arctic-Derived Penicillium chrysogenum INA 01369. Antibiotics (Basel, Switzerland), 14(1).

Pozzobon D, et al. (2025) Pan-Cancer Upregulation of the FOXM1 Transcription Factor. Genes, 16(1).