

Resource Summary Report

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Protein families database of alignments and HMMs

RRID:SCR_002115

Type: Tool

Proper Citation

Protein families database of alignments and HMMs (RRID:SCR_002115)

Resource Information

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

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. iPfam is a resource that describes physical interactions between those Pfam domains that have a representative structure in the Protein DataBank (PDB). When two or more domains occur within a single structure, the domains are analysed to see if they form an interaction. If the domains are close enough to form an interaction, the bonds that play a role in that interaction are determined. The goal has been to re-calculate iPfam interaction data for each new Pfam release, so that, as Pfam changes, the information within iPfam remains up to date.

Synonyms: iPfam

Resource Type: data or information resource, database

Defining Citation: [PMID:9223186](#), [PMID:18819075](#)

Keywords: bond, pfam, physical interaction, protein

Availability: Free, Freely available

Resource Name: Protein families database of alignments and HMMs

Resource ID: SCR_002115

Alternate IDs: nif-0000-20898

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

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260829T182921+0000

Ratings and Alerts

No rating or validation information has been found for Protein families database of alignments and HMMs.

No alerts have been found for Protein families database of alignments and HMMs.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 307 mentions in open access literature.

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

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.

Sun Y, et al. (2026) A Dynamic Gate Enables Regioselective Hydroxylation of Free Arginine by a Non-Canonical Heme Enzyme. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(6), e13032.

Tang X, et al. (2026) PfTALE5 Acts as a hub for multi-stress resilience: a genome-wide study of the TALE family in *Paulownia fortunei*. *BMC plant biology*, 26(1), 255.

Guan Y, et al. (2026) Genomic survey and expression analysis of the CDPK genes in *Liriodendron Chinense* to explore their potential functions under multiple abiotic stresses. *BMC genomics*, 27(1), 198.

Liu J, et al. (2026) Genome-wide identification and immunological expression analysis of the C3HC4-type zinc finger protein genes in the silkworm, *Bombyx Mori*. *BMC genomics*, 27(1).

Zhang X, et al. (2026) The mechanism of dynamic equilibrium of ascorbate redox status mediated by PbrDHAR5 during scald development in pear fruit. *Molecular horticulture*, 6(1).

Dai H, et al. (2026) Genome-wide identification of the UMAMIT gene family in *Medicago sativa* L. and analysis of the response of umamits mutant to abiotic stress. *BMC plant biology*, 26(1).

Wang YD, et al. (2026) Characterization of the full-length transcriptome of female *Eucoleus annulatus* and comparative transcriptomic analysis of its head, middle, and tail body sections. *Parasites & vectors*, 19(1).

Li Q, et al. (2026) Genome-wide unraveling of the AUX/IAA family in *Avena sativa* L. with observations on seedling root growth and stress resilience. *Frontiers in plant science*, 17,

1836152.

Ma Y, et al. (2026) Genome-Wide Characterization and Expression Profiling of Putative m6A Methylation Regulatory Proteins (Writers and Erasers) in *Ginkgo biloba*. *Biology*, 15(12).

Chen Y, et al. (2026) *Fusarium sacchari* 14-3-3 Protein FsBmh1 Sequesters a Novel Elicitor FsEcm33 to Evade Host Immunity. *Molecular plant pathology*, 27(7), e70309.

Bian Y, et al. (2026) Genome-wide characterization and adaptive evolution of favorable gibberellin 2-oxidase alleles contributing to wheat agronomic traits. *Journal of advanced research*, 83, 65.

Fan Z, et al. (2026) Genome-wide identification and expression profiling of the CoVQ gene family in *Camellia Oleifera*. *BMC plant biology*, 26(1).

Shuvo MNH, et al. (2026) Genome-wide identification and characterization of argonaute, dicer-like, and RNA-dependent RNA polymerase gene families in potato (*Solanum tuberosum*): Advancing RNA interference-based crop enhancement. *PloS one*, 21(2), e0339021.

Lv G, et al. (2026) Genome-wide characterization of the PHT gene family in *Uncaria rhynchophylla* identified UrPHT1;11 as a key regulator to low phosphorus response. *BMC plant biology*, 26(1).

Long Y, et al. (2026) Genome-wide identification of the GRF gene family and response to cold stress in *Astragalus membranaceus*. *BMC genomics*, 27(1).

Zhang Z, et al. (2026) Identification of BvUGT90 Family Members and Analysis of Drought Resistance Gene Screening in Sugar Beet. *Plants (Basel, Switzerland)*, 15(5).

Li Y, et al. (2026) Analysis of BpbHLH Gene Family Responsive to MeJA Signalling in *Betula platyphylla* Suk. and Functional Mechanisms of BpbHLH42/44 in Genetic Improvement and Triterpenoid Biosynthesis. *Plant biotechnology journal*, 24(6), 4342.

Panahi B, et al. (2026) Genome-wide identification and functional characterisation of the EDS1 gene family reveals evolutionary conservation and stress-responsive regulatory roles in barley. *Scientific reports*, 16(1).

Fan Y, et al. (2026) Identification of SmNAC28 Transcription Factor and Its Mechanism of Regulating Salt Tolerance in Eggplant via S-Palmitoylation. *Current issues in molecular biology*, 48(4).