

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

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/>

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

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: 20260729T044034+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 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Zou Z, et al. (2025) Characterization of Caleosin Genes in Carica papaya and Insights into Lineage-Specific Family Evolution in Brassicales. Plants (Basel, Switzerland), 14(21).

Wu X, et al. (2025) Genome-wide identification, phylogenetic analysis and expression pattern study of trihelix transcription factors in Pisum sativum L. Scientific reports, 15(1), 37699.

Zhang P, et al. (2025) NY-ESO-1 facilitates anoikis resistance and tumor metastasis by hijacking deubiquitinase OTUB1 to stabilize PP1??. Cell death & disease, 16(1), 682.

Mi X, et al. (2025) Aquilaria sinensis MYB-Like Transcription Factor AsMYB1 Promotes 2-(2-Phenylethyl)Chromone Biosynthesis Through Interacting With 14-3-3 Family Protein AsGRF1. Plant biotechnology journal, 23(12), 5800.

Bardhan K, et al. (2025) Regulation of the activity of a tetra-modular lytic polysaccharide monooxygenase from Enterobacter cloacae by inter-domain copper coordination. The Journal of biological chemistry, 302(1), 110964.

Khan F, et al. (2025) Functional Division of Insect Blood Cells by Single-Cell RNA-Sequencing and Cell-Type-Specific FISH Markers. Cells, 14(23).

Sevgen E, et al. (2025) ProT-VAE: Protein Transformer Variational AutoEncoder for functional protein design. Proceedings of the National Academy of Sciences of the United States of America, 122(41), e2408737122.

Yang X, et al. (2025) Transcription-metabolism association analysis of molecular mechanisms in sweet orange plants in response to boron deficiency. BMC genomics, 26(1), 1136.

Aloryi KD, et al. (2025) Genome landscape of the universal stress protein gene family in lettuce and expression profile in response to heat stress. BMC plant biology, 25(1), 1636.

Bellay J, et al. (2011) Bringing order to protein disorder through comparative genomics and genetic interactions. Genome biology, 12(2), R14.