

# Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

## SUPFAM

RRID:SCR\_005304

Type: Tool

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### Proper Citation

SUPFAM (RRID:SCR\_005304)

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### Resource Information

**URL:** <http://supfam.mbu.iisc.ernet.in/index.html>

**Proper Citation:** SUPFAM (RRID:SCR\_005304)

**Description:** SUPFAM is a database that consists of clusters of potentially related homologous protein domain families, with and without three-dimensional structural information, forming superfamilies. The present release (Release 3.0) of SUPFAM uses homologous families in Pfam (Version 23.0) and SCOP (Release 1.69) which are examples of sequence -alignment and structure classification databases respectively. The two steps involved in setting up of SUPFAM database are \* Relating Pfam and SCOP families using a new profile-profile alignment algorithm AlignHUSH. This results in identifying many Pfam families which could be related to a family or superfamily of known structural information. \* An all-against-all match among Pfam families with yet unknown structure resulting in identification of related Pfam families forming new potential superfamilies. The SUPFAM database can be used in either the Browse mode or Search mode. In Browse mode you can browse through the Superfamilies, Pfam families or SCOP families. In each of these modes you will be presented with a full list which can be easily browsed. In Search mode, you can search for Pfam families, SCOP families or Superfamilies based on keywords or SCOP/Pfam identifiers of families and superfamilies., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Abbreviations:** SUPFAM

**Resource Type:** database, data or information resource

**Defining Citation:** [PMID:15113407](#), [PMID:11752317](#)

**Keywords:** duf/upf connections, 3-d structure, alignment, amino acid sequence, bioinformatics, clustering, homologous protein family, multiple sequence alignment, nmr, pali, pfam, phylogeny, protein classification, protein domain database, protein families, protein sequence database, rps\_blast, scop, structural genomics, structure determination, superfamily, three-dimensional, x-ray crystallography

**Funding:** Council of Scientific and Industrial Research New Delhi ;  
Wellcome Trust

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** SUPFAM

**Resource ID:** SCR\_005304

**Alternate IDs:** nif-0000-03517

**Old URLs:** <http://pauling.mbu.iisc.ernet.in/~supfam>

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260805T044120+0000

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## Ratings and Alerts

No rating or validation information has been found for SUPFAM.

No alerts have been found for SUPFAM.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 13 mentions in open access literature.

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

van der Meij A, et al. (2025) Streptomyces venezuelae uses secreted chitinases and a designated ABC transporter to support the competitive saprophytic catabolism of chitin. PLoS biology, 23(8), e3003292.

Durai P, et al. (2023) Iterative machine learning-based chemical similarity search to identify novel chemical inhibitors. Journal of cheminformatics, 15(1), 86.

Kader MA, et al. (2022) Hypothetical protein predicted to be tumor suppressor: a protein functional analysis. Genomics & informatics, 20(1), e6.

Lithgow KV, et al. (2022) Protease activities of vaginal Porphyromonas species disrupt coagulation and extracellular matrix in the cervicovaginal niche. NPJ biofilms and microbiomes, 8(1), 8.

Ghorbel M, et al. (2022) Identification and Expression Profiling of Two Saudi Arabia Catalase Genes from Wheat and Barley in Response to Abiotic and Hormonal Stresses. Antioxidants (Basel, Switzerland), 11(11).

Simpson J, et al. (2022) Cross-species transmission of an ancient endogenous retrovirus and convergent co-option of its envelope gene in two mammalian orders. *PLoS genetics*, 18(10), e1010458.

Shim H, et al. (2021) Diverse ATPase Proteins in Mobilomes Constitute a Large Potential Sink for Prokaryotic Host ATP. *Frontiers in microbiology*, 12, 691847.

Kanade M, et al. (2020) A Distinct Motif in a Prokaryotic Small Ras-Like GTPase Highlights Unifying Features of Walker B Motifs in P-Loop NTPases. *Journal of molecular biology*, 432(20), 5544.

Machulin AV, et al. (2019) The number of domains in the ribosomal protein S1 as a hallmark of the phylogenetic grouping of bacteria. *PloS one*, 14(8), e0221370.

Ramakrishnan G, et al. (2016) Computational recognition and analysis of hitherto uncharacterized nucleotide cyclase-like proteins in bacteria. *Biology direct*, 11, 27.

Yue J, et al. (2016) PTIR: Predicted Tomato Interactome Resource. *Scientific reports*, 6, 25047.

Yue J, et al. (2015) FR database 1.0: a resource focused on fruit development and ripening. *Database : the journal of biological databases and curation*, 2015.

Yue J, et al. (2015) Kiwifruit Information Resource (KIR): a comparative platform for kiwifruit genomics. *Database : the journal of biological databases and curation*, 2015.