## **Resource Summary Report**

Generated by <u>dkNET</u> on Apr 30, 2025

# **SUPERFAMILY**

RRID:SCR\_007952 Type: Tool

**Proper Citation** 

SUPERFAMILY (RRID:SCR\_007952)

#### **Resource Information**

URL: http://supfam.org/SUPERFAMILY/

Proper Citation: SUPERFAMILY (RRID:SCR\_007952)

**Description:** SUPERFAMILY is a database of structural and functional protein annotations for all completely sequenced organisms. The SUPERFAMILY annotation is based on a collection of hidden Markov models, which represent structural protein domains at the SCOP superfamily level. A superfamily groups together domains which have an evolutionary relationship. The annotation is produced by scanning protein sequences from over 1,700 completely sequenced genomes against the hidden Markov models.

Synonyms: Superfamily - HMM library and genome assignments server

Resource Type: database, data or information resource

Defining Citation: PMID:11697912

**Keywords:** protein, hmm, hidden markov model, genome, structure, homology, model, FASEB list

Funding:

Resource Name: SUPERFAMILY

Resource ID: SCR\_007952

Alternate IDs: nif-0000-03511

Old URLs: http://supfam.org, http://stash.mrc-lmb.cam.ac.uk/SUPERFAMILY

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250430T055542+0000

### **Ratings and Alerts**

No rating or validation information has been found for SUPERFAMILY.

No alerts have been found for SUPERFAMILY.

#### Data and Source Information

Source: SciCrunch Registry

#### **Usage and Citation Metrics**

We found 302 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Mughal F, et al. (2025) Evolution of intrinsic disorder in the structural domains of viral and cellular proteomes. Scientific reports, 15(1), 2878.

Ryan AP, et al. (2024) Genome Analysis of a Newly Discovered Yeast Species, Hanseniaspora menglaensis. Journal of fungi (Basel, Switzerland), 10(3).

Elrashedy A, et al. (2024) Bioinformatics approach for structure modeling, vaccine design, and molecular docking of Brucella candidate proteins BvrR, OMP25, and OMP31. Scientific reports, 14(1), 11951.

C?rulis A, et al. (2024) Sex-limited experimental evolution drives transcriptomic divergence in a hermaphrodite. Genome biology and evolution, 16(1).

Carr CM, et al. (2024) Identification and expression of MarCE, a marine carboxylesterase with synthetic ester-degrading activity. Microbial biotechnology, 17(6), e14479.

Jebastin T, et al. (2024) Unveiling the mysteries: Functional insights into hypothetical proteins from Bacteroides fragilis 638R. Heliyon, 10(11), e31713.

Salgado JFM, et al. (2024) Unveiling lignocellulolytic potential: a genomic exploration of bacterial lineages within the termite gut. Microbiome, 12(1), 201.

Ma X, et al. (2024) Seagrass genomes reveal ancient polyploidy and adaptations to the marine environment. Nature plants, 10(2), 240.

Yadav DK, et al. (2024) Proteome-wide analysis reveals G protein-coupled receptor-like

proteins in rice (Oryza sativa). Plant signaling & behavior, 19(1), 2365572.

Liu F, et al. (2024) Niche-dependent sponge hologenome expression profiles and the hostmicrobes interplay: a case of the hawaiian demosponge Mycale Grandis. Environmental microbiome, 19(1), 22.

Peters DL, et al. (2024) Functional domains of Acinetobacter bacteriophage tail fibers. Frontiers in microbiology, 15, 1230997.

Hesketh-Best PJ, et al. (2024) Dominance of recombinant DWV genomes with changing viral landscapes as revealed in national US honey bee and varroa mite survey. Communications biology, 7(1), 1623.

Puginier C, et al. (2024) Phylogenomics reveals the evolutionary origins of lichenization in chlorophyte algae. Nature communications, 15(1), 4452.

Frey B, et al. (2024) Searching for new plastic-degrading enzymes from the plastisphere of alpine soils using a metagenomic mining approach. PloS one, 19(4), e0300503.

Xu X, et al. (2024) Systematic Investigation of the Trafficking of Glycoproteins on the Cell Surface. Molecular & cellular proteomics : MCP, 23(5), 100761.

Promubon K, et al. (2024) Computational-guided discovery of UDP-glycosyltransferases for lauryl glucoside production using engineered E. coli. Bioresources and bioprocessing, 11(1), 103.

Mifsud JCO, et al. (2024) Mapping glycoprotein structure reveals Flaviviridae evolutionary history. Nature, 633(8030), 695.

Bai Y, et al. (2023) Multi-omic insights into the formation and evolution of a novel shell microstructure in oysters. BMC biology, 21(1), 204.

Farlow AJ, et al. (2023) Rosenbergiella meliponini D21B Isolated from Pollen Pots of the Australian Stingless Bee Tetragonula carbonaria. Microorganisms, 11(4).

Prajapati MR, et al. (2023) De novo transcriptome analysis and identification of defensive genes in garlic (Allium sativum L.) using high-throughput sequencing. Journal, genetic engineering & biotechnology, 21(1), 56.