

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

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

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: 20260725T191153+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 325 mentions in open access literature.

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

Costa VA, et al. (2025) Limited similarity in microbial composition among coral reef fishes from the Great Barrier Reef, Australia. *FEMS microbiology ecology*, 101(3).

Jaggi KE, et al. (2025) A pangenome reveals LTR repeat dynamics as a major driver of genome evolution in *Chenopodium*. *The plant genome*, 18(1), e70010.

Krishnakumar H, et al. (2025) Transcriptomic profiling to investigate the therapeutic potential and medicinal properties of *Momordica cymbalaria*. *Scientific reports*, 15(1), 33882.

Xiao Y, et al. (2025) Evolution of the Metazoan Protein Domain Repertoire Revealed by a Birth-Death-Gain Model. *Journal of molecular evolution*, 93(6), 777.

Liu S, et al. (2025) Discovery, structural characteristics and evolutionary analyses of functional domains in *Acinetobacter baumannii* phage tail fiber/spike proteins. *BMC microbiology*, 25(1), 73.

Costa VA, et al. (2025) Phylogenetic Diversity and Geographic Distribution of Atlantic Salmon Calicivirus in Major Salmon Farming Regions. *Journal of fish diseases*, 48(6), e14107.

Kuprina K, et al. (2025) How drought and ploidy level shape gene expression and DNA methylation in *Phragmites australis*. *Plant cell reports*, 44(9), 197.

Shukla S, et al. (2025) Intrinsic Disorder and Phase Separation Coordinate Exocytosis, Motility, and Chromatin Remodeling in the Human Acrosomal Proteome. *Proteomes*, 13(2).

Rao DM, et al. (2025) Systematic identification and characterization of eukaryotic and viral 2A peptide-bond-skipping sequences. *Cell reports*, 44(7), 115822.

Asghar R, et al. (2025) Computational studies reveal structural characterization and novel families of *Puccinia striiformis* f. sp. *tritici* effectors. *PLoS computational biology*, 21(3), e1012503.

Saeed H, et al. (2025) Characterization of holins, the membrane proteins of coliphage ASEC2201: a genomewide in silico approach. *Frontiers in microbiology*, 16, 1550594.

Lozada-Chavez AN, et al. (2025) Adaptive genomic signatures of globally invasive populations of the yellow fever mosquito *Aedes aegypti*. *Nature ecology & evolution*, 9(4), 652.

Guan DL, et al. (2025) Chromosome-level genome assembly and annotation of the predatory stink bug *Eocanthecona furcellata*. *Scientific data*, 12(1), 1920.

De La Forest Divonne S, et al. (2025) Diversity and functional specialization of oyster immune cells uncovered by integrative single-cell level investigations. *eLife*, 13.

Leavitt JS, et al. (2025) The Evolutionary Landscape of tRNA Modifications in Archaea: Insights from High-Throughput Sequencing. *bioRxiv : the preprint server for biology*.

Lipp NF, et al. (2025) An origin for a eukaryotic lipid transfer protein fold in Asgard archaea. *bioRxiv : the preprint server for biology*.

Sajic T, et al. (2025) Depletion-dependent activity-based protein profiling using SWATH/DIA-MS detects serine hydrolase lipid remodeling in lung adenocarcinoma progression. *Nature communications*, 16(1), 4889.

Boulton W, et al. (2025) Metagenome-assembled-genomes recovered from the Arctic drift expedition MOSAiC. *Scientific data*, 12(1), 204.

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. (2025) Small pangenome of *Candida parapsilosis* reflects overall low intraspecific diversity. *mBio*, 16(10), e0132025.