

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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: data or information resource, database

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: 20260905T133148+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 345 mentions in open access literature.

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

Grudman S, et al. (2026) Conservation of Human IgSF Proteins Throughout Eukaryotic Evolution. *Genome biology and evolution*, 18(6).

Wang KT, et al. (2026) RoboA reinforces planarian stem cell fate through FoxA and Anosmin1a. *Nature communications*, 17(1).

Stilwell PA, et al. (2026) The genome of *Istocheta aldrichi* (Diptera: Tachinidae), a parasitoid of the Japanese beetle, *Popillia japonica* (Coleoptera: Scarabaeidae). *G3 (Bethesda, Md.)*, 16(4).

Bortoletto E, et al. (2026) Chromosome-level genome assembly of the striped venus clam *Chamelea gallina*. *Scientific data*, 13(1).

Lin X, et al. (2026) An integrated fine-mapping, re-sequencing and transcriptome analysis provides further insights and candidate genes for silique number in oilseed rape (*Brassica napus* L.). *BMC plant biology*, 26(1).

Köstlbacher S, et al. (2026) Prediction of eukaryotic cellular complexity in Asgard archaea using structural modelling. *Nature microbiology*, 11(3), 747.

Wang K, et al. (2026) Melatonin Enhances Thermal Resilience and Extends Worker Lifespan in *Apis cerana* via Redox-Metabolic Reprogramming. *Insects*, 17(4).

Liang M, et al. (2026) IVCDB: a comprehensive database of iridoviruses for epidemiology, genetic evolution, and disease management. *Nucleic acids research*, 54(D1), D790.

Machado V, et al. (2026) An integrative bioinformatics framework for functional annotation and prioritization of hypothetical proteins in *Bacillus thuringiensis* relevant to biological pest control. *Brazilian journal of microbiology : [publication of the Brazilian Society for Microbiology]*, 57(1).

Marcheschi AK, et al. (2026) Chromosome-level genome assembly of the Australian *Chenopodium trigonon* reveals a new subgenome type. *Frontiers in plant science*, 17, 1841078.

Alfaro C, et al. (2026) Stage-specific impacts of a simulated natural heatwave on *Aedes albopictus*. *BMC biology*, 24(1).

Nalça AR, et al. (2026) Evolutionary Patterns of the Genes Involved in the Integrity and Segregation of Chromosomes in Sawflies (Hymenoptera: Symphyta). *Ecology and evolution*, 16(6), e73748.

Montes-Ortiz Z, et al. (2026) Comparative genomics reveal signatures of ecological specialization in the striped ambrosia beetle *Trypodendron lineatum*. *BMC genomics*, 27(1).

Xu S, et al. (2026) A Chemoenzymatic Method To Systematically Quantify Core Fucosylation Stoichiometry of Glycoproteins and Reveal Its Roles in EMT and Embryonic Development. *Analytical chemistry*, 98(4), 2968.

Hu QL, et al. (2026) Chromosome-level genome assembly of the predatory stink bug, *Eocanthecona furcellata* (Wolff). *Scientific data*, 13(1), 6.

Ajmera S, et al. (2026) Curation of the *Fasciola hepatica* kinome as a resource for drug target discovery. *BMC genomics*, 27(1), 98.

Saenko S, et al. (2026) Annotation of 200 Insect Genomes with BRAKER for Consistent Comparisons across Species. *Scientific data*, 13(1).

Nuzzo G, et al. (2026) Jorumycidine, a hexacyclic bis-tetrahydroisoquinoline alkaloid from marine symbiosis reveals new biosynthetic logic for anticancer design. *Communications chemistry*, 9(1).

Elrashedy A, et al. (2026) Immunoinformatics-based design of artificial chimeric proteins as universal vaccine candidates against foot-and-mouth disease virus serotypes A, O, and SAT2. *Scientific reports*, 16(1).

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.