

Resource Summary Report

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PIRSF

RRID:SCR_003352

Type: Tool

Proper Citation

PIRSF (RRID:SCR_003352)

Resource Information

URL: <http://pir.georgetown.edu/pirwww/dbinfo/pirsf.shtml>

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Description: A SuperFamily classification system, with rules for functional site and protein name, to facilitate the sensible propagation and standardization of protein annotation and the systematic detection of annotation errors. The PIRSF concept is being used as a guiding principle to provide comprehensive and non-overlapping clustering of UniProtKB sequences into a hierarchical order to reflect their evolutionary relationships. The PIRSF classification system is based on whole proteins rather than on the component domains; therefore, it allows annotation of generic biochemical and specific biological functions, as well as classification of proteins without well-defined domains. There are different PIRSF classification levels. The primary level is the homeomorphic family, whose members are both homologous (evolved from a common ancestor) and homeomorphic (sharing full-length sequence similarity and a common domain architecture). At a lower level are the subfamilies which are clusters representing functional specialization and/or domain architecture variation within the family. Above the homeomorphic level there may be parent superfamilies that connect distantly related families and orphan proteins based on common domains. Because proteins can belong to more than one domain superfamily, the PIRSF structure is formally a network. The FTP site provides free download for PIRSF.

Abbreviations: PIRSF

Synonyms: PIR SuperFamily, Protein Information Resource SuperFamily

Resource Type: data or information resource, database, narrative resource, standard specification

Defining Citation: [PMID:19455212](#), [PMID:14681371](#)

Keywords: protein annotation, classification, protein, superfamily, functional site, protein name, bio.tools

Funding: NHGRI U01-HG02712;
NSF DBI-0138188;
NSF ITR-0205470

Availability: Free, Freely available

Resource Name: PIRSF

Resource ID: SCR_003352

Alternate IDs: biotools:pirsf, OMICS_01697, nif-0000-03294

Alternate URLs: <https://bio.tools/pirsf>

Old URLs: <http://pir.georgetown.edu/pirsf/>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260829T182131+0000

Ratings and Alerts

No rating or validation information has been found for PIRSF.

No alerts have been found for PIRSF.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

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

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).

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

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.

- 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.
- 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.
- Shuang H, et al. (2025) A High-quality chromosome-level genome assembly of *Swertia przewalskii* Pissjauk. *Scientific data*, 12(1), 2026.
- Puginier C, et al. (2024) Phylogenomics reveals the evolutionary origins of lichenization in chlorophyte algae. *Nature communications*, 15(1), 4452.
- Wang Y, et al. (2023) Time-ordering japonica/geng genomes analysis indicates the importance of large structural variants in rice breeding. *Plant biotechnology journal*, 21(1), 202.
- Ribeiro AJM, et al. (2023) Enzyme function and evolution through the lens of bioinformatics. *The Biochemical journal*, 480(22), 1845.
- Lima-Cabello E, et al. (2023) α -Conglutins' Unique Mobile Arm Is a Key Structural Domain Involved in Molecular Nutraceutical Properties of Narrow-Leafed Lupin (*Lupinus angustifolius* L.). *International journal of molecular sciences*, 24(8).
- Yang Y, et al. (2022) Chromosome-level genome assembly of the shuttles hopppfish, *Periophthalmus modestus*. *GigaScience*, 11(1).
- Miller J, et al. (2022) Chromosome-level genome and the identification of sex chromosomes in *Uloborus diversus*. *GigaScience*, 12.
- Vázquez-Campos X, et al. (2021) Genomic Insights Into the Archaea Inhabiting an Australian Radioactive Legacy Site. *Frontiers in microbiology*, 12, 732575.
- Van Dam MH, et al. (2021) The Easter Egg Weevil (*Pachyrhynchus*) genome reveals syntenic patterns in Coleoptera across 200 million years of evolution. *PLoS genetics*, 17(8), e1009745.
- Charon J, et al. (2020) Metatranscriptomic Identification of Diverse and Divergent RNA Viruses in Green and Chlorarachniophyte Algae Cultures. *Viruses*, 12(10).
- Li H, et al. (2020) A High-Quality Genome Sequence of Model Legume *Lotus japonicus* (MG-20) Provides Insights into the Evolution of Root Nodule Symbiosis. *Genes*, 11(5).
- Struck AK, et al. (2020) A structural UGDH variant associated with standard Munchkin cats. *BMC genetics*, 21(1), 67.
- Vicente I, et al. (2020) Combined Comparative Genomics and Gene Expression Analyses Provide Insights into the Terpene Synthases Inventory in *Trichoderma*. *Microorganisms*, 8(10).
- Wang C, et al. (2020) Donkey genomes provide new insights into domestication and selection for coat color. *Nature communications*, 11(1), 6014.