

Resource Summary Report

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SYSTERS

RRID:SCR_007955

Type: Tool

Proper Citation

SYSTERS (RRID:SCR_007955)

Resource Information

URL: <http://systers.molgen.mpg.de/>

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Description: SYSTERS is a database of protein sequences grouped into homologous families and superfamilies. The SYSTERS project aims to provide a meaningful partitioning of the whole protein sequence space by a fully automatic procedure. A refined two-step algorithm assigns each protein to a family and a superfamily. The sequence data underlying SYSTERS release 4 now comprise several protein sequence databases derived from completely sequenced genomes (ENSEMBL, TAIR, SGD and GeneDB), in addition to the comprehensive Swiss-Prot/TrEMBL databases. To augment the automatically derived results, information from external databases like Pfam and Gene Ontology are added to the web server. Furthermore, users can retrieve pre-processed analyses of families like multiple alignments and phylogenetic trees. New query options comprise a batch retrieval tool for functional inference about families based on automatic keyword extraction from sequence annotations. A new access point, PhyloMatrix, allows the retrieval of phylogenetic profiles of SYSTERS families across organisms with completely sequenced genomes. Gene, Human, Vertebrate, Genome, Human ORFs

Synonyms: SYSTERS

Resource Type: data or information resource, database

Keywords: family, gene, genome, human, human orfs, protein, superfamily, vertebrate

Resource Name: SYSTERS

Resource ID: SCR_007955

Alternate IDs: nif-0000-03528

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260829T183016+0000

Ratings and Alerts

No rating or validation information has been found for SYSTERS.

No alerts have been found for SYSTERS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Polyanovsky V, et al. (2020) The ranging of amino acids substitution matrices of various types in accordance with the alignment accuracy criterion. BMC bioinformatics, 21(Suppl 11), 294.

Naqvi AA, et al. (2015) Identification of functional candidates amongst hypothetical proteins of *Treponema pallidum* ssp. *pallidum*. PloS one, 10(4), e0124177.

Shahbaaz M, et al. (2013) Functional annotation of conserved hypothetical proteins from *Haemophilus influenzae* Rd KW20. PloS one, 8(12), e84263.

Hoshino T, et al. (2012) Evolution of cariogenic character in *Streptococcus* mutans: horizontal transmission of glycosyl hydrolase family 70 genes. Scientific reports, 2, 518.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Krause A, et al. (2005) Large scale hierarchical clustering of protein sequences. BMC bioinformatics, 6, 15.

Mulder NJ, et al. (2002) Tools and resources for identifying protein families, domains and motifs. Genome biology, 3(1), REVIEWS2001.