Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 16, 2025

Structure-function linkage database

RRID:SCR_001375
Type: Tool

Proper Citation

Structure-function linkage database (RRID:SCR_001375)

Resource Information

URL: http://sfld.rbvi.ucsf.edu/

Proper Citation: Structure-function linkage database (RRID:SCR_001375)

Description: A database of hierarchical classification of enzymes that relates specific sequence-structure features to specific chemical capabilities. The SFLD classifies evolutionarily related enzymes according to shared chemical functions and maps these shared functions to conserved active site features. The classification is hierarchical, where broader levels encompass more distantly related proteins with fewer shared features. It thus serves as the analysis and archive site for superfamilies targeted by the Enzyme Function Initiative, and is developed by the Babbitt Laboratory in collaboration with the UCSF Resource for Biocomputing, Visualization, and Informatics. The resource also provides a collection of tools and data for investigating sequence-structure-function relationships and hypothesizing function.

Abbreviations: SFLD

Resource Type: database, data analysis service, data or information resource, service resource, analysis service resource, production service resource

Defining Citation: PMID:18428763, PMID:16489747

Keywords: software, enzyme, structure-function relationship, blast, reaction, superfamily, hidden markov model, sequence alignment, protein similarity network, sequence, structure, function

Funding: NIGMS R01GM60595;
NIGMS P01GM071790;
NIGMS U54GM093342

Resource Name: Structure-function linkage database

Resource ID: SCR_001375

Alternate IDs: nlx_152532

Record Creation Time: 20220129T080207+0000

Record Last Update: 20250416T063234+0000

Ratings and Alerts

No rating or validation information has been found for Structure-function linkage database.

No alerts have been found for Structure-function linkage database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zamarreño Beas J, et al. (2023) In Campylobacter jejuni, a new type of chaperone receives heme from ferrochelatase. Frontiers in genetics, 14, 1199357.

Miller J, et al. (2022) Chromosome-level genome and the identification of sex chromosomes in Uloborus diversus. GigaScience, 12.

Lesk AM, et al. (2020) Not Enough Natural Data? Sequence and Ye Shall Find. Frontiers in molecular biosciences, 7, 65.

Holliday GL, et al. (2020) A strategy for large-scale comparison of evolutionary- and reaction-based classifications of enzyme function. Database : the journal of biological databases and curation, 2020.

Louro B, et al. (2019) A haplotype-resolved draft genome of the European sardine (Sardina pilchardus). GigaScience, 8(5).

Holliday GL, et al. (2018) Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a "Plug and Play" Domain. Methods in enzymology, 606, 1.

Knutson ST, et al. (2017) An approach to functionally relevant clustering of the protein universe: Active site profile-based clustering of protein structures and sequences. Protein science : a publication of the Protein Society, 26(4), 677.

Holliday GL, et al. (2017) Biocuration in the structure-function linkage database: the anatomy of a superfamily. Database : the journal of biological databases and curation, 2017(1).

Benjdia A, et al. (2017) Radical SAM Enzymes in the Biosynthesis of Ribosomally Synthesized and Post-translationally Modified Peptides (RiPPs). Frontiers in chemistry, 5, 87.

Lee SH, et al. (2017) Cyclosporine Sparing Effect of Enteric-Coated Mycophenolate Sodium in De Novo Kidney Transplantation. Yonsei medical journal, 58(1), 217.

Holliday GL, et al. (2017) Evaluating Functional Annotations of Enzymes Using the Gene Ontology. Methods in molecular biology (Clifton, N.J.), 1446, 111.

Gerlt JA, et al. (2017) Genomic Enzymology: Web Tools for Leveraging Protein Family Sequence-Function Space and Genome Context to Discover Novel Functions. Biochemistry, 56(33), 4293.

Holliday GL, et al. (2015) Key challenges for the creation and maintenance of specialist protein resources. Proteins, 83(6), 1005.

Mashiyama ST, et al. (2014) Large-scale determination of sequence, structure, and function relationships in cytosolic glutathione transferases across the biosphere. PLoS biology, 12(4), e1001843.

Fernández-Suárez XM, et al. (2014) The 2014 Nucleic Acids Research Database Issue and an updated NAR online Molecular Biology Database Collection. Nucleic acids research, 42(Database issue), D1.

Wichelecki DJ, et al. (2014) Discovery of function in the enolase superfamily: D-mannonate and d-gluconate dehydratases in the D-mannonate dehydratase subgroup. Biochemistry, 53(16), 2722.

Zhao S, et al. (2013) Discovery of new enzymes and metabolic pathways by using structure and genome context. Nature, 502(7473), 698.