Resource Summary Report

Generated by NIF on Apr 9, 2025

FunTree

RRID:SCR_006014
Type: Tool

Proper Citation

FunTree (RRID:SCR_006014)

Resource Information

URL: http://www.ebi.ac.uk/thornton-srv/databases/FunTree/

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Description: FunTree provides a range of data resources to detect the evolution of enzyme function within distant structurally related clusters within domain super families as determined by CATH. To access the resource enter a specific CATH superfamily code or search for a structure / sequence / function (either via a EC code or KEGG ligand / reaction ID, PDB ID or UniProtKB ID). Or browse the resource via superfamily / function / structure / metabolites & reactions via the menu on the left panel. FunTree is a new resource that brings together sequence, structure, phylogenetic, chemical and mechanistic information for structurally defined enzyme superfamilies. Gathering together this range of data into a single resource allows the investigation of how novel enzyme functions have evolved within a structurally defined superfamily as well as providing a means to analyse trends across many superfamilies. This is done not only within the context of an enzyme""s sequence and structure but also the relationships of their reactions. Developed in tandem with the CATH database, it currently comprises 276 superfamilies covering 1800 (70%) of sequence assigned enzyme reactions. Central to the resource are phylogenetic trees generated from structurally informed multiple sequence alignments using both domain structural alignments supplemented with domain sequences and whole sequence alignments based on commonality of multi-domain architectures. These trees are decorated with functional annotations such as metabolite similarity as well as annotations from manually curated resources such the catalytic site atlas and MACiE for enzyme mechanisms.

Abbreviations: FunTree

Resource Type: database, data or information resource

Defining Citation: PMID:22006843

Keywords: enzyme function, enzyme superfamily, enzyme, sequence, structure, phylogenetic, chemical, mechanistic, functional annotation, superfamily, gold standard, bio.tools

Funding: European Molecular Biology Laboratory; Heidelberg; Germany ;
BBSRC ;
Wellcome Trust 081989/Z/07/A;
DOE contract DE-AC02-06CH11357

Availability: Free

Resource Name: FunTree

Resource ID: SCR_006014

Alternate IDs: biotools:funtree, nlx_151402

Alternate URLs: https://bio.tools/funtree

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250409T060501+0000

Ratings and Alerts

No rating or validation information has been found for FunTree.

No alerts have been found for FunTree.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Giuliani S, et al. (2018) Computationally-guided drug repurposing enables the discovery of kinase targets and inhibitors as new schistosomicidal agents. PLoS computational biology, 14(10), e1006515.

Valasatava Y, et al. (2018) To what extent do structural changes in catalytic metal sites

affect enzyme function? Journal of inorganic biochemistry, 179, 40.

Pavli?ev M, et al. (2016) Development Shapes a Consistent Inbreeding Effect in Mouse Crania of Different Line Crosses. Journal of experimental zoology. Part B, Molecular and developmental evolution, 326(8), 474.

Furnham N, et al. (2016) Large-Scale Analysis Exploring Evolution of Catalytic Machineries and Mechanisms in Enzyme Superfamilies. Journal of molecular biology, 428(2 Pt A), 253.