Resource Summary Report

Generated by RRID on Apr 17, 2025

TM Function Database

RRID:SCR_007058
Type: Tool

Proper Citation

TM Function Database (RRID:SCR_007058)

Resource Information

URL: http://tmbeta-genome.cbrc.jp/TMFunction/

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Description: A database of functional residues in alpha-helical and beta-barrel membrane proteins. Each protein is identified with its name and source alongwith the Uniprot code. The protein data bank (PDB) codes are also given for available proteins. Different methods and experimental parameters, for example, affinity, dissociation constant, IC50, activity etc. are given in the database. Further, the database provides the numerical experimental value for each residue (or mutant) in a protein. The experimental data are collected from the literature both by searching the journals as well as with the keyword search at PUBMED. In addition, complete reference is given with journal citation and PMID number. TNFunction is cross-linked with the sequence database, Uniprot, structural database, PDB, and literature database, PubMed. The WWW interface enables users to search data based on various terms with different display options for outputs.

Synonyms: TMFunction Database

Resource Type: database, data or information resource

Keywords: functional residue, active sites, binding affinity, dissociation constant, membrane protein, protein data bank, protein sequence database, protein sequence motif, protein uniprot, sequence structure function relationship of membrane proteins, maximal velocity of transport

Funding:

Resource Name: TM Function Database

Resource ID: SCR_007058

Alternate IDs: nif-0000-08632, nif-0000-06665, SCR_007057

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250412T055145+0000

Ratings and Alerts

No rating or validation information has been found for TM Function Database.

No alerts have been found for TM Function Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Gromiha MM, et al. (2015) Mutational studies to understand the structure-function relationship in multidrug efflux transporters: applications for distinguishing mutants with high specificity. International journal of biological macromolecules, 75, 218.