

Resource Summary Report

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Transporter Classification Database

RRID:SCR_004490

Type: Tool

Proper Citation

Transporter Classification Database (RRID:SCR_004490)

Resource Information

URL: <http://www.tcdb.org/>

Proper Citation: Transporter Classification Database (RRID:SCR_004490)

Description: Curated, relational database containing sequence, classification, structural, functional and evolutionary information about transport systems from variety of living organisms based on IUBMB-approved transporter classification (TC) system. Descriptions, TC numbers, and examples of over 600 families of transport proteins are provided. TC system is analogous to Enzyme Commission (EC) system for classification of enzymes, except that it incorporates both functional and phylogenetic information. TCDB users may submit their own sequenced proteins and descriptions for inclusion into database. The software tools used are all freely available for download. These programs are used for analysis of Protein and DNA sequences. Programs require UNIX server to run.

Abbreviations: TCDB, TC

Synonyms: Transporter Classification Database

Resource Type: data or information resource, data processing software, data repository, source code, software application, data analysis software, storage service resource, software resource, database, data analysis service, production service resource, service resource, analysis service resource

Defining Citation: [PMID:19022853](#), [PMID:16381841](#)

Keywords: membrane transport, protein sequence, transporter, bio.tools, FASEB list

Funding: NIGMS GM1077402

Availability: Free, Freely available

Resource Name: Transporter Classification Database

Resource ID: SCR_004490

Alternate IDs: nlx_47724, biotools:tcdB

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

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260806T054403+0000

Ratings and Alerts

No rating or validation information has been found for Transporter Classification Database.

No alerts have been found for Transporter Classification Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 311 mentions in open access literature.

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

Xiao H, et al. (2025) Covariation MS uncovers a protein that controls cysteine catabolism. *Nature*.

Pereira LMS, et al. (2025) Advances in fungal sugar transporters: unlocking the potential of second-generation bioethanol production. *Applied microbiology and biotechnology*, 109(1), 19.

Perveen A, et al. (2025) Integrative physiological, biochemical, and proteomic analysis of the leaves of two cotton genotypes under heat stress. *PloS one*, 20(1), e0316630.

Wang Q, et al. (2025) A stacked ensemble classifier for the discovery of prokaryotic efflux proteins based on sequence information. *BMC genomics*, 26(1), 851.

Bai R, et al. (2025) Whole-Genome Characterization of *Inonotus hispidus* from *Ulmus macrocarpa* and Its Comparative Genomics with Strains from *Morus alba* and *Acer truncatum*. *Journal of fungi (Basel, Switzerland)*, 11(5).

Gu T, et al. (2025) *Faucicola mancuniensis* isolated from human respiratory tract and its genomic characteristics. *BMC microbiology*, 25(1), 587.

Deng K, et al. (2025) Decoding Pecan's Fungal Foe: A Genomic Insight into *Colletotrichum plurivorum* Isolate W-6. *Journal of fungi (Basel, Switzerland)*, 11(3).

Yang Y, et al. (2025) A Chromosome-Scale Genome of *Trametes versicolor* and Transcriptome-Based Screening for Light-Induced Genes That Promote Triterpene

Biosynthesis. *Journal of fungi* (Basel, Switzerland), 11(1).

Wang N, et al. (2025) Structural basis and evolutionary pathways of glycerol-1-phosphate transport in marine bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, 122(50), e2524546122.

Fan Q, et al. (2025) Whole-Genome Sequence Analysis, Probiotic Potential, and Safety Assessment of the Marine Bacterium *Paraliobacillus zengyii* CGMCC1.16464. *Marine drugs*, 23(5).

Castelli M, et al. (2024) Host association and intracellularity evolved multiple times independently in the Rickettsiales. *Nature communications*, 15(1), 1093.

Vasylyshyn R, et al. (2024) Engineering of *Ogataea polymorpha* strains with ability for high-temperature alcoholic fermentation of cellobiose. *FEMS yeast research*, 24.

Coles DW, et al. (2024) Functional genomics identifies a small secreted protein that plays a role during the biotrophic to necrotrophic shift in the root rot pathogen *Phytophthora medicaginis*. *Frontiers in plant science*, 15, 1439020.

Yu L, et al. (2024) Antimicrobial resistance and virulence factors analysis of a multidrug-resistant *Acinetobacter baumannii* isolated from chickens using whole-genome sequencing. *BMC microbiology*, 24(1), 526.

Verstraeten S, et al. (2024) *Faecalibacterium duncaniae* A2-165 regulates the expression of butyrate synthesis, ferrous iron uptake, and stress-response genes based on acetate consumption. *Scientific reports*, 14(1), 987.

Barraco-Vega M, et al. (2024) Mutational analysis of *Phanerochaete chrysosporium*'s purine transporter. *PloS one*, 19(10), e0313174.

Zhu Q, et al. (2024) Highly flexible cell membranes are the key to efficient production of lipophilic compounds. *Journal of lipid research*, 65(8), 100597.

Fang Y, et al. (2024) Whole-genome sequencing and comparative genomic analyses of the medicinal fungus *Sanguinoderma infundibulare* in Ganodermataceae. *G3* (Bethesda, Md.), 14(4).

Wilhelm J, et al. (2024) Molecular insights into the determinants of substrate specificity and efflux inhibition of the RND efflux pumps AcrB and AdeB. *Microbiology* (Reading, England), 170(2).

Sugimoto TN, et al. (2024) Search for genes gained by horizontal gene transfer in an entomopoxvirus, with special reference to the analysis of the transfer of an ABC transporter gene. *Virus research*, 347, 199418.