

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, software application, analysis service resource, storage service resource, software resource, data analysis software, data repository, database, production service resource, data processing software, service resource, source code, data analysis service

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: 20260819T044114+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 343 mentions in open access literature.

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

Scharff-Poulsen P, et al. (2026) Structural bases of signal generation and transduction by the SPS amino acid sensor of *Saccharomyces cerevisiae*. *G3* (Bethesda, Md.), 16(3).

Zhao G, et al. (2026) Improved Longan Genome Assembly Reveals Insights Into Flowering Mechanisms. *Plant biotechnology journal*, 24(3), 1678.

Chen J, et al. (2026) Septic Shock Caused by Coinfection of *Shewanella* algae Bloodstream Infection and Epstein-Barr Virus: Clinical Characteristics and Genomic Analysis. *MicrobiologyOpen*, 15(1), e70221.

Zhen Z, et al. (2026) Genome-wide characteristics, antibiotic resistance, and pathogenicity analysis of *Streptococcus parasuis* strains isolated from diseased pigs. *BMC microbiology*, 26(1).

Cai R, et al. (2026) Genomic Analysis Reveals Diversified and Stress-Responsive Transport Repertoire in *Candidozyma* (*Candida*) *auris*. *Journal of fungi* (Basel, Switzerland), 12(3).

Chen YZ, et al. (2026) Whole-Genome Sequencing of Pathogenic *Nigrospora musae* ST1 Causing Leaf Spot Disease in *Idesia polycarpa*. *Journal of fungi* (Basel, Switzerland), 12(3).

Pereira MF, et al. (2026) Genomics of Hospital-Associated Brazilian Multidrug-Resistant *Klebsiella pneumoniae*: Abundance of Resistance and Virulence Genes and Mosaicism of

the blaKPC-2 Genetic Context Among Enterobacterales. *Current microbiology*, 83(8).

Sun J, et al. (2026) Safety and probiotic characterization of *Lactocaseibacillus rhamnosus* SAL2: insights from integrated genomics and functional validation. *Frontiers in microbiology*, 17, 1767191.

Deng T, et al. (2026) A trimeric architecture reveals the glucitol PTS transporter as a distinct superfamily. *Communications biology*, 9(1).

Sun W, et al. (2026) Comparative Genomics Reveals Host-Specific Adaptation of *Pyricularia oryzae* Strains Isolated from Rice and Barnyard Grass. *Journal of fungi (Basel, Switzerland)*, 12(2).

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.

Ding X, et al. (2025) Whole-Genome Analysis of a Novel Multidrug-Resistant *Escherichia coli* Strain from Dairy Calves in Northeast China: Mechanisms of Antibiotic Resistance and Biofilm Formation. *Biology*, 14(9).

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.

Vazquez-Ortiz K, et al. (2025) Comparative genomics of dominant members of the gut core microbiome of the bark beetle, *Dendroctonus rhizophagus* (Curculionidae: Scolytinae) reveals potential functional complementarity in the detoxification process. *BMC genomics*, 26(1), 1064.

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

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).

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).