

Resource Summary Report

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TransportDB

RRID:SCR_005643

Type: Tool

Proper Citation

TransportDB (RRID:SCR_005643)

Resource Information

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

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Description: TransportDB is a relational database describing the predicted cytoplasmic membrane transport protein complement for organisms whose complete genome sequence are available. For each organism, its complete membrane transport complement was identified, classified into protein families according to the TC classification system, and functional predictions are provided. For each organism, a summary page is available, overviewing the whole transporter system, including transporter types and individual transporter families. For individual transporter types, a detailed list of transporters with their possible substrates is shown with links to individual protein page which contains protein sequence and annotation information. You can also compare the transporter system from two or more different organisms. A search engine is set up for easy search in our transporter database for transporter type, family, individual proteins and their substrates. You can also blast search your protein sequence against our transporter database. With the rapid development of genomic sequencing both in TIGR and in other institutes, more and more genomes are available for the analysis of their transporter system. We will keep updating this site with the newly published genomes. If you have any suggestions, corrections, or comments on our site, please contact us. We are currently working on providing additional functionality for this database.

Synonyms: TransportDB

Resource Type: database, data or information resource

Keywords: FASEB list

Resource Name: TransportDB

Resource ID: SCR_005643

Alternate IDs: nif-0000-03581

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260803T040429+0000

Ratings and Alerts

No rating or validation information has been found for TransportDB.

No alerts have been found for TransportDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 138 mentions in open access literature.

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

Albuquerque-Wendt A, et al. (2025) TransLeish: Identification of membrane transporters essential for survival of intracellular Leishmania parasites in a systematic gene deletion screen. Nature communications, 16(1), 299.

Zhang Z, et al. (2025) Construction of a Plasmid-Free Escherichia coli Strain with Enhanced Heme Supply to Produce Active Hemoglobins. Metabolites, 15(3).

Kotsovolos N, et al. (2025) Sequence- and structure-based bioinformatic screening for potential Theileria parva transport-related proteins. Computational biology and chemistry, 120(Pt 1), 108653.

Naeij HB, et al. (2025) Unraveling the metabolic landscape of Exophiala spinifera strain FM: Model reconstruction, insights into biodesulfurization and beyond. PloS one, 20(1), e0317796.

Tec-Campos D, et al. (2025) A genome-scale metabolic model for the denitrifying bacterium Thauera sp. MZ1T accurately predicts degradation of pollutants and production of polymers. PLoS computational biology, 21(1), e1012736.

Campbell BC, et al. (2024) Krumholzibacteriota and Deltaproteobacteria contain rare genetic potential to liberate carbon from monoaromatic compounds in subsurface coal seams. mBio, 15(3), e0173523.

Zhang RY, et al. (2024) Metagenomic characterization of a novel non-ammonia-oxidizing Thaumarchaeota from hadal sediment. Microbiome, 12(1), 7.

Clifton BE, et al. (2024) The ultra-high affinity transport proteins of ubiquitous marine bacteria. Nature, 634(8034), 721.

Chen J, et al. (2024) Transcriptomic insights into the shift of trophic strategies in mixotrophic dinoflagellate *Lepidodinium* in the warming ocean. *ISME communications*, 4(1), ycae087.

Chen J, et al. (2024) Chemosynthetic alphaproteobacterial diazotrophs reside in deep-sea cold-seep bottom waters. *mSystems*, 9(9), e0017624.

Casey J, et al. (2024) Transporter annotations are holding up progress in metabolic modeling. *Frontiers in systems biology*, 4, 1394084.

Valentin-Alvarado LE, et al. (2024) Complete genomes of Asgard archaea reveal diverse integrated and mobile genetic elements. *Genome research*, 34(10), 1595.

Lenferink WB, et al. (2024) Hydroxylamine production by *Alcaligenes faecalis* challenges the paradigm of heterotrophic nitrification. *Science advances*, 10(23), eadl3587.

Chanket W, et al. (2024) The complete catalog of antimicrobial resistance secondary active transporters in *Clostridioides difficile*: evolution and drug resistance perspective. *Computational and structural biotechnology journal*, 23, 2358.

Bodilis J, et al. (2024) HME, NFE, and HAE-1 efflux pumps in Gram-negative bacteria: a comprehensive phylogenetic and ecological approach. *ISME communications*, 4(1), ycad018.

Veshkini A, et al. (2024) *Cryptosporidium parvum* infection alters the intestinal mucosa transcriptome in neonatal calves: impacts on epithelial barriers and transcellular transport systems. *Frontiers in cellular and infection microbiology*, 14, 1495309.

Liu Y, et al. (2023) The Phylogeny, Metabolic Potentials, and Environmental Adaptation of an Anaerobe, *Abyssolibacter* sp. M8S5, Isolated from Cold Seep Sediments of the South China Sea. *Microorganisms*, 11(9).

Dittmer J, et al. (2023) The terrestrial isopod symbiont '*Candidatus Hepatincola porcellionum*' is a potential nutrient scavenger related to Holosporales symbionts of protists. *ISME communications*, 3(1), 18.

Semenec L, et al. (2023) Cross-protection and cross-feeding between *Klebsiella pneumoniae* and *Acinetobacter baumannii* promotes their co-existence. *Nature communications*, 14(1), 702.

Li S, et al. (2023) Genomic Analysis of the Deep-Sea Bacterium *Shewanella* sp. MTB7 Reveals Backgrounds Related to Its Deep-Sea Environment Adaptation. *Microorganisms*, 11(3).