

# Resource Summary Report

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## TDR Targets Database

RRID:SCR\_007963

Type: Tool

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### Proper Citation

TDR Targets Database (RRID:SCR\_007963)

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### Resource Information

**URL:** <http://tdrtargets.org/>

**Proper Citation:** TDR Targets Database (RRID:SCR\_007963)

**Description:** This database functions both as a website where researchers can look for information on their targets of interest; and as a tool for prioritization of targets in whole genomes. Using the database as a tool, researchers can quickly prioritize a genome of interest by performing any number of individual queries on a species of interest, then assigning numerical weights to each query (in the history page) to finally obtain a ranked list of genes by combining the weighted queries. This site is part of a WHO/TDR project seeking to exploit the availability of diverse datasets to facilitate the identification and prioritization of drug targets in pathogens causing neglected diseases.

**Synonyms:** TDR Targets

**Resource Type:** data or information resource, database

**Keywords:** bio.tools, FASEB list

**Resource Name:** TDR Targets Database

**Resource ID:** SCR\_007963

**Alternate IDs:** nif-0000-03542, biotools:tdr\_targets

**Alternate URLs:** [https://bio.tools/tdr\\_targets](https://bio.tools/tdr_targets)

**Record Creation Time:** 20220129T080244+0000

**Record Last Update:** 20260919T195713+0000

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### Ratings and Alerts

No rating or validation information has been found for TDR Targets Database.

No alerts have been found for TDR Targets Database.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 46 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

Bhattacharyya A, et al. (2025) The potential of Leishmania donovani Aurora kinase in the diagnosis of Indian and Brazilian visceral leishmaniasis patients. Microbiology spectrum, 13(6), e0324724.

Mogire RM, et al. (2024) Protein target similarity is positive predictor of in vitro antipathogenic activity: a drug repurposing strategy for Plasmodium falciparum. Journal of cheminformatics, 16(1), 63.

Ren X, et al. (2023) Comprehensive survey of target prediction web servers for Traditional Chinese Medicine. Heliyon, 9(8), e19151.

Knoll KE, et al. (2022) In Silico Drug Discovery Strategies Identified ADMET Properties of Decoquinone RMB041 and Its Potential Drug Targets against Mycobacterium tuberculosis. Microbiology spectrum, 10(2), e0231521.

Wu L, et al. (2022) Machine learning methods, databases and tools for drug combination prediction. Briefings in bioinformatics, 23(1).

Galán-Vásquez E, et al. (2022) A landscape of gene regulation in the parasitic amoebozoan Entamoeba spp. PLoS one, 17(8), e0271640.

Aguoru NA, et al. (2022) Molecular insights into the heat shock proteins of the human parasitic blood fluke Schistosoma mansoni. Parasites & vectors, 15(1), 365.

Melo MCR, et al. (2021) Accelerating antibiotic discovery through artificial intelligence. Communications biology, 4(1), 1050.

Peixoto JF, et al. (2021) In Silico Insights into the Mechanism of Action of Epoxy-?-Lapachone and Epoxymethyl-Lawsone in Leishmania spp. Molecules (Basel, Switzerland), 26(12).

Silva SF, et al. (2020) Structural features and development of an assay platform of the parasite target deoxyhypusine synthase of Brugia malayi and Leishmania major. PLoS neglected tropical diseases, 14(10), e0008762.

Hirst NL, et al. (2020) Deep phosphoproteome analysis of *Schistosoma mansoni* leads development of a kinomic array that highlights sex-biased differences in adult worm protein phosphorylation. *PLoS neglected tropical diseases*, 14(3), e0008115.

Urán Landaburu L, et al. (2020) TDR Targets 6: driving drug discovery for human pathogens through intensive chemogenomic data integration. *Nucleic acids research*, 48(D1), D992.

Camargo de Lima J, et al. (2020) Dynamics of protein synthesis in the initial steps of strobilation in the model cestode parasite *Mesocotyle colubriformis* (syn. *vogae*). *Journal of proteomics*, 228, 103939.

Mansoldo FRP, et al. (2020) Chagas Disease: Perspectives on the Past and Present and Challenges in Drug Discovery. *Molecules (Basel, Switzerland)*, 25(22).

Nunes RR, et al. (2019) Brazilian malaria molecular targets (BraMMT): selected receptors for virtual high-throughput screening experiments. *Memorias do Instituto Oswaldo Cruz*, 114, e180465.

Singh SK, et al. (2019) Investigation of hub genes and their nonsynonymous single nucleotide polymorphism analysis in *Plasmodium falciparum* for designing therapeutic methodologies using next-generation sequencing approach. *Indian journal of pharmacology*, 51(6), 389.

Osorio-Méndez JF, et al. (2018) Discovery and Genetic Validation of Chemotherapeutic Targets for Chagas' Disease. *Frontiers in cellular and infection microbiology*, 8, 439.

da Silva RA, et al. (2018) Mining of potential drug targets through the identification of essential and analogous enzymes in the genomes of pathogens of *Glycine max*, *Zea mays* and *Solanum lycopersicum*. *PloS one*, 13(5), e0197511.

Wu Z, et al. (2018) Network-Based Methods for Prediction of Drug-Target Interactions. *Frontiers in pharmacology*, 9, 1134.

Katiyar A, et al. (2018) Identification of Missing Carbon Fixation Enzymes as Potential Drug Targets in *Mycobacterium Tuberculosis*. *Journal of integrative bioinformatics*, 15(3).