Resource Summary Report

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TDR Targets Database

RRID:SCR_007963
Type: Tool

Proper Citation

TDR Targets Database (RRID:SCR_007963)

Resource Information

URL: http://tdrtargets.org/

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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: database, data or information resource

Keywords: bio.tools, FASEB list

Funding:

Resource Name: TDR Targets Database

Resource ID: SCR_007963

Alternate IDs: nif-0000-03542, biotools:tdr_targets

Alternate URLs: https://bio.tools/tdr_targets

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250519T204749+0000

Ratings and Alerts

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

No alerts have been found for TDR Targets Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 42 mentions in open access literature.

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

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

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

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

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).

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

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 Mesocestoides corti (syn. vogae). Journal of proteomics, 228, 103939.

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.

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.

Calixto NM, et al. (2018) In silico repositioning of approved drugs against Schistosoma mansoni energy metabolism targets. PloS one, 13(12), e0203340.

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.

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

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

Catharina L, et al. (2017) A Computational Methodology to Overcome the Challenges Associated With the Search for Specific Enzyme Targets to Develop Drugs Against Leishmania major. Bioinformatics and biology insights, 11, 1177932217712471.

Abid H, et al. (2017) Leishmania infantum 5'-Methylthioadenosine Phosphorylase presents relevant structural divergence to constitute a potential drug target. BMC structural biology, 17(1), 9.

Chhajer R, et al. (2016) Leishmania donovani Aurora kinase: A promising therapeutic target against visceral leishmaniasis. Biochimica et biophysica acta, 1860(9), 1973.