

Resource Summary Report

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GeneDB Tbrucei

RRID:SCR_004786

Type: Tool

Proper Citation

GeneDB Tbrucei (RRID:SCR_004786)

Resource Information

URL: <http://www.genedb.org/Homepage/Tbruceibrucei927>

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Description: Database of the most recent sequence updates and annotations for the *T. brucei* genome. New annotations are constantly being added to keep up with published manuscripts and feedback from the Trypanosomatid research community. You may search by Protein Length, Molecular Mass, Gene Type, Date, Location, Protein Targeting, Transmembrane Helices, Product, GO, EC, Pfam ID, Curation and Comments, and Dbxrefs. BLAST and other tools are available. *T. brucei* possesses a two-unit genome, a nuclear genome and a mitochondrial (kinetoplast) genome with a total estimated size of 35Mb/haploid genome. The nuclear genome is split into three classes of chromosomes according to their size on pulsed-field gel electrophoresis, 11 pairs of megabase chromosomes (0.9-5.7 Mb), intermediate (300-900 kb) and minichromosomes (50-100 kb). The *T. brucei* genome contains a ~0.5Mb segmental duplication affecting chromosomes 4 and 8, which is responsible for some 75 gene duplicates unique to this species. A comparative chromosome map of the duplicons can be accessed here (PubMedID 18036214). Protozoan parasites within the species *Trypanosoma brucei* are the etiological agent of human sleeping sickness and Nagana in animals. Infections are limited to patches of sub-Saharan Africa where insects vectors of the *Glossina* genus are endemic. The most recent estimates indicate between 50,000 - 70,000 human cases currently exist, with 17 000 new cases each year (WHO Factsheet, 2006). In collaboration with GeneDB, the EuPathDB genomic sequence data and annotations are regularly deposited on TriTrypDB where they can be integrated with other datasets and queried using customized queries.

Abbreviations: GeneDB_Tbrucei, GeneDB Tbrucei, GeneDB *T. brucei*

Synonyms: Trypanosoma brucei TREU927 homepage on GeneDB, Trypanosoma brucei TREU927 on GeneDB

Resource Type: analysis service resource, production service resource, database, data or information resource, service resource, data analysis service

Defining Citation: [PMID:16020726](#)

Keywords: blast, sequence, annotation, genome

Funding: Wellcome Trust

Resource Name: GeneDB Tbrucei

Resource ID: SCR_004786

Alternate IDs: nlx_78417

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250522T060218+0000

Ratings and Alerts

No rating or validation information has been found for GeneDB Tbrucei.

No alerts have been found for GeneDB Tbrucei.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Sheikh S, et al. (2023) A Novel Group of Dynamin-Related Proteins Shared by Eukaryotes and Giant Viruses Is Able to Remodel Mitochondria From Within the Matrix. Molecular biology and evolution, 40(6).

Pyrih J, et al. (2023) Comprehensive sub-mitochondrial protein map of the parasitic protist Trypanosoma brucei defines critical features of organellar biology. Cell reports, 42(9), 113083.

- Jaskolowski M, et al. (2020) Structural Insights into the Mechanism of Mitochondrial Large Subunit Biogenesis. *Molecular cell*, 79(4), 629.
- Currier RB, et al. (2018) Decoding the network of *Trypanosoma brucei* proteins that determines sensitivity to apolipoprotein-L1. *PLoS pathogens*, 14(1), e1006855.
- Kaurov I, et al. (2018) The Diverged Trypanosome MICOS Complex as a Hub for Mitochondrial Cristae Shaping and Protein Import. *Current biology : CB*, 28(21), 3393.
- Ponte-Sucre A, et al. (2016) An Overview of *Trypanosoma brucei* Infections: An Intense Host-Parasite Interaction. *Frontiers in microbiology*, 7, 2126.
- Swann J, et al. (2015) Systems analysis of host-parasite interactions. *Wiley interdisciplinary reviews. Systems biology and medicine*, 7(6), 381.
- Fernández-Moya SM, et al. (2014) Depletion of the RNA-binding protein RBP33 results in increased expression of silenced RNA polymerase II transcripts in *Trypanosoma brucei*. *PloS one*, 9(9), e107608.
- Singh A, et al. (2014) Trypanosome MKT1 and the RNA-binding protein ZC3H11: interactions and potential roles in post-transcriptional regulatory networks. *Nucleic acids research*, 42(7), 4652.
- Alsford S, et al. (2014) Cathepsin-L can resist lysis by human serum in *Trypanosoma brucei*. *PLoS pathogens*, 10(5), e1004130.
- Cross GA, et al. (2014) Capturing the variant surface glycoprotein repertoire (the VSGnome) of *Trypanosoma brucei* Lister 427. *Molecular and biochemical parasitology*, 195(1), 59.
- Capewell P, et al. (2013) Regulation of *Trypanosoma brucei* Total and Polysomal mRNA during Development within Its Mammalian Host. *PloS one*, 8(6), e67069.
- Ramírez CA, et al. (2013) Identification of proteins interacting with HSP70 mRNAs in *Leishmania braziliensis*. *Journal of proteomics*, 94, 124.
- Savage AF, et al. (2012) Transcript expression analysis of putative *Trypanosoma brucei* GPI-anchored surface proteins during development in the tsetse and mammalian hosts. *PLoS neglected tropical diseases*, 6(6), e1708.
- Mercer L, et al. (2011) 2,4-Diaminopyrimidines as potent inhibitors of *Trypanosoma brucei* and identification of molecular targets by a chemical proteomics approach. *PLoS neglected tropical diseases*, 5(2), e956.
- Inoue M, et al. (2010) Phosphorylation-dependent protein interaction with *Trypanosoma brucei* 14-3-3 proteins that display atypical target recognition. *PloS one*, 5(12), e15566.

Cooper A, et al. (2008) Genetic analysis of the human infective trypanosome *Trypanosoma brucei gambiense*: chromosomal segregation, crossing over, and the construction of a genetic map. *Genome biology*, 9(6), R103.