

Resource Summary Report

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TriTrypDB

RRID:SCR_007043

Type: Tool

Proper Citation

TriTrypDB (RRID:SCR_007043)

Resource Information

URL: <http://tritrypdb.org/tritrypdb/>

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Description: An integrated genomic and functional genomic database providing access to genome-scale datasets for kinetoplastid parasites, and supporting a variety of complex queries driven by research and development needs. Currently, TriTrypDB integrates datasets from *Leishmania braziliensis*, *L. infantum*, *L. major*, *L. tarentolae*, *Trypanosoma brucei* and *T. cruzi*. Users may examine individual genes or chromosomal spans in their genomic context, including syntenic alignments with other kinetoplastid organisms. Data within TriTrypDB can be interrogated utilizing a sophisticated search strategy system that enables a user to construct complex queries combining multiple data types. All search strategies are stored, allowing future access and integrated searches. "User Comments" may be added to any gene page, enhancing available annotation; such comments become immediately searchable via the text search, and are forwarded to curators for incorporation into the reference annotation when appropriate. TriTrypDB provides programmatic access to its searches, via REST Web Services. The result of a web service request is a list of records (genes, ESTs, etc) in either XML or JSON format. REST services can be executed in a browser by typing a specific URL. TriTrypDB and its continued development are possible through the collaborative efforts between EuPathDB, GeneDB and colleagues at the Seattle Biomedical Research Institute (SBRI).

Abbreviations: TriTrypDB

Resource Type: analysis service resource, data access protocol, data analysis service, data or information resource, database, production service resource, service resource, software resource, web service

Defining Citation: [PMID:19843604](#)

Keywords: kinetoplastid parasite, pathogen, genome, gene chromosome, annotation, trypanosomatidae, parasite, blast, bio.tools, FASEB list

Funding: Bill and Melinda Gates Foundation 50097;
Wellcome Trust WT085822MA;
Wellcome Trust WT085775/Z/08/Z

Availability: Public - please cite. Much of the data in TriTrypDB is provided by independent researchers. Please cite them if you use their data.

Resource Name: TriTrypDB

Resource ID: SCR_007043

Alternate IDs: nlx_152064, biotools:tritrypdb, r3d100011479

Alternate URLs: <https://bio.tools/tritrypdb>, <https://doi.org/10.17616/R3J05N>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260821T193817+0000

Ratings and Alerts

No rating or validation information has been found for TriTrypDB.

No alerts have been found for TriTrypDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 712 mentions in open access literature.

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

Carlioni R, et al. (2026) Defining the chromatin-associated protein landscapes on Trypanosoma brucei repetitive elements using synthetic TALE proteins. eLife, 14.

Stanojcic S, et al. (2026) Stranded short nascent strand sequencing reveals the topology of DNA replication origins in Trypanosoma brucei. eLife, 14.

Gutiérrez S, et al. (2026) Transcriptomic and ultrastructural responses to Amiodarone-Itraconazole in naturally benznidazole-resistant and -susceptible Trypanosoma cruzi strains. PLoS neglected tropical diseases, 20(1), e0013916.

Juez-Castillo G, et al. (2026) Heme limitation induces LHR2, an essential gene for Leishmania pathogenesis. PLoS pathogens, 22(2), e1013993.

Madan E, et al. (2026) Targeting Leishmania donovani Sphingosine Kinase 1 using PF-543 enhances immune response and limits parasite load. PLoS neglected tropical diseases, 20(3), e0013102.

Ridgway M, et al. (2026) Genetic origins and proteomic consequences of kinetoplast loss in trypanosomes. *PLoS pathogens*, 22(3), e1013846.

Lansink LIM, et al. (2026) Specialized RNA decay fine-tunes monogenic antigen expression in *Trypanosoma brucei*. *Nature microbiology*, 11(4), 1080.

Roson JN, et al. (2026) New Histone H4 variant and H2B variant Exhibits distinct genomic distributions, chromatin affinities, and dynamics throughout life and cell cycle of *Trypanosoma cruzi*. *PLoS pathogens*, 22(3), e1013310.

Silva-Espinoza JC, et al. (2026) Identification of *Leishmania* spp. and *Trypanosoma cruzi* in bats captured in El Paso County, Texas. *PLoS neglected tropical diseases*, 20(4), e0014169.

Yagoubat A, et al. (2026) The nuclear basket nucleoporin MLP1 is required to maintain nuclear integrity, and mitotic fidelity in *Trypanosoma brucei*. *PLoS neglected tropical diseases*, 20(6), e0013922.

Oliveira SSS, et al. (2026) The related EIF4G3 and EIF4G4 initiation factors from *Leishmania*: dissimilar modes of action during translation revealed by a comparative proteomic approach. *Parasites & vectors*, 19(1).

Kortbawi HM, et al. (2026) A *Trypanosoma cruzi* trans-sialidase peptide demonstrates high serological prevalence among infected populations across endemic regions. *The Journal of clinical investigation*, 136(6).

Dumetz F, et al. (2026) The UTRs of *Leishmania donovani* vary in length and are enriched in potential regulatory structures. *PLoS pathogens*, 22(3), e1013551.

Stettler P, et al. (2026) Kozak sequences regulate gene expression in *Trypanosoma brucei*. *Nucleic acids research*, 54(6).

Bertolini MS, et al. (2026) Composition and role of the vacuolar transporter chaperone complex in polyphosphate synthesis and infectivity in *Trypanosoma cruzi*. *mBio*, 17(6), e0037226.

Matsumoto H, et al. (2026) Distinct repeat architecture landscapes in the proteomes of protozoan parasites. *NAR genomics and bioinformatics*, 8(3), lqag061.

Banerjee S, et al. (2026) Cell surface localisation of GPI-anchored receptors in *Trypanosoma brucei*. *eLife*, 14.

Bose P, et al. (2026) Structural basis of secreted acid phosphatase polymerization in the *Leishmania* parasite. *Protein science : a publication of the Protein Society*, 35(5), e70591.

Ahmad R, et al. (2026) The EamA metabolite transporter does not affect antileishmanial drug susceptibility. *International journal for parasitology. Drugs and drug resistance*, 30, 100632.

Monti L, et al. (2026) Genome-wide mapping of DNA G-quadruplexes in *Trypanosoma brucei* chromatin reveals enrichment in coding regions and transcription start sites. *Nucleic acids research*, 54(12).