Resource Summary Report

Generated by RRID on Aug 2, 2026

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: data analysis service, data or information resource, data access protocol, database, service resource, production service resource, software resource, analysis service 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;
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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: 20260801T190326+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 670 mentions in open access literature.

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

Gómez-Liñán C, et al. (2025) Role of the nucleotide excision repair endonuclease XPF in the kinetoplastid parasite Trypanosoma brucei. Scientific reports, 15(1), 23579.

Aminzadeh M, et al. (2025) Unraveling Leishmania major Metacyclogenesis: A Comprehensive Analysis of Transcriptomic and Metabolomic Profiles. Iranian biomedical journal, 29(1 & 2), 68.

Quilles JC, et al. (2025) A short ncRNA modulates gene expression and affects stress response and parasite differentiation in Leishmania braziliensis. Frontiers in cellular and infection microbiology, 15, 1513908.

Barrinha A, et al. (2025) Endosymbiosis in trypanosomatids: the bacterium regulates the intermediate and oxidative metabolism of the host cell. mSphere, 10(11), e0045725.

de Almeida RF, et al. (2025) Histone post-translational modifications of Leishmania braziliensis. Scientific data, 12(1), 1899.

Ahmed M, et al. (2025) Cyclic AMP compartmentalization drives signal specificity to control vector colonization and mammalian host infection by American trypanosomes. bioRxiv : the preprint server for biology.

Herrmann May N, et al. (2025) Improved base editing and functional screening in Leishmania via co-expression of the AsCas12a ultra variant, a T7 RNA polymerase, and a cytosine base editor. eLife, 13.

Rojas-Sánchez S, et al. (2025) Deep mutational scanning of the Trypanosoma brucei developmental regulator RBP6 reveals an essential disordered region influenced by positive residues. Nature communications, 16(1), 1168.

Gabiatti BP, et al. (2025) Detailed characterisation of the trypanosome nuclear pore architecture reveals conserved asymmetrical functional hubs that drive mRNA export. PLoS biology, 23(2), e3003024.

de Oliveira B, et al. (2025) Characterization of a novel Leishmania antigen containing a repetitive domain and its potential use as a prophylactic and therapeutic vaccine. mSphere, 10(5), e0009725.

Kashyap S, et al. (2025) CryoEM structure of the Trypanosoma brucei flagellum central apparatus. bioRxiv : the preprint server for biology.

Díaz-Viraqué F, et al. (2025) Genomic Organization of Trypanosoma cruzi tRNA Genes. Genome biology and evolution, 17(6).

Ros-Lucas A, et al. (2025) Identification of novel compounds against Trypanosoma cruzi using AlphaFold structures. Computational and structural biotechnology journal, 27, 1838.

Thiam R, et al. (2025) A novel Leishmania infantum reference strain for gene editing and the study of visceral leishmaniasis. PloS one, 20(9), e0327390.

Zavrelova A, et al. (2025) The trypanosome vault particle is composed of multiple major vault protein paralogs and harbors vault RNA. The Journal of biological chemistry, 301(10), 110706.

Gutierrez Guarnizo SA, et al. (2025) A specific, stable, and accessible LAMP assay targeting the HSP70 gene of Trypanosoma cruzi. Microbiology spectrum, 13(11), e0017225.

Honorato NRM, et al. (2025) K-mer-based approach for serodiagnostic antigen discovery in Chagas disease using unassembled sequencing reads. PLoS neglected tropical diseases, 19(12), e0013835.

Bhattarai NR, et al. (2025) Can cutaneous leishmaniasis provoke a resurgence of kala-azar in the Indian subcontinent? BMC infectious diseases, 25(1), 281.

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.

Doran MH, et al. (2025) Evolutionary adaptations of doublet microtubules in trypanosomatid parasites. Science (New York, N.Y.), 387(6739), eadr5507.