Resource Summary Report

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GeneDB Lmajor

RRID:SCR_004613
Type: Tool

Proper Citation

GeneDB Lmajor (RRID:SCR_004613)

Resource Information

URL: http://www.genedb.org/Homepage/Lmajor

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Description: Database of the most recent sequence updates and annotations for the L. major 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. Leishmania species cause a spectrum of human diseases in tropical and subtropical regions of the world. We have sequenced the 36 chromosomes of the 32.8-megabase haploid genome of Leishmania major (Friedlin strain) and predict 911 RNA genes, 39 pseudogenes, and 8272 protein-coding genes, of which 36% can be ascribed a putative function. These include genes involved in host-pathogen interactions, such as proteolytic enzymes, and extensive machinery for synthesis of complex surface glycoconjugates. The Pathogen Genomics group at the Wellcome Trust Sanger Institute played a major role in sequencing the genome of Leishmania major (see Ivens et al.) Details of the centres involved and which chromosomes they sequenced, are given. The sequence data were obtained by adopting several parallel approaches, including complete cosmid sequencing, whole chromosome shotguns and/or BAC sequencing/skimming. The Leishmania parasite is an intracellular pathogen of the immune system targeting macrophages and dendritic cells. The disease Leishmaniasis affects the populations of 88 counties worldwide with symptoms ranging from disfiguring cutaneous and muco-cutaneous lesions that can cause widespread destruction of mucous membranes to visceral disease affecting the haemopoetic organs. 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_Lmajor, GeneDB Lmajor, GeneDB L. major,

Synonyms: Leishmania major strain Friedlin, Leishmania major strain Friedlin homepage on GeneDB, GeneDB Leishmania major, Leishmania major strain Friedlin on GeneDB

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

Defining Citation: PMID:16020728

Keywords: genome, gene, rna gene, rna, pseudogene, protein-coding, function, host-pathogen interaction, interaction, proteolytic enzyme, glycoconjugate, sequence annotation

Funding: Wellcome Trust

Resource Name: GeneDB Lmajor

Resource ID: SCR_004613

Alternate IDs: nlx_60997

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250524T060018+0000

Ratings and Alerts

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

No alerts have been found for GeneDB Lmajor.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Morea EGO, et al. (2017) A calmodulin-like protein (LCALA) is a new Leishmania amazonensis candidate for telomere end-binding protein. Biochimica et biophysica acta. General subjects, 1861(11 Pt A), 2583.

Chavali AK, et al. (2012) Metabolic network analysis predicts efficacy of FDA-approved

drugs targeting the causative agent of a neglected tropical disease. BMC systems biology, 6, 27.

Gannavaram S, et al. (2011) Mitochondrial associated ubiquitin fold modifier-1 mediated protein conjugation in Leishmania donovani. PloS one, 6(1), e16156.

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.

Flórez AF, et al. (2010) Protein network prediction and topological analysis in Leishmania major as a tool for drug target selection. BMC bioinformatics, 11, 484.

Silverman JM, et al. (2008) Proteomic analysis of the secretome of Leishmania donovani. Genome biology, 9(2), R35.

Johner A, et al. (2006) Cyclic nucleotide specific phosphodiesterases of Leishmania major. BMC microbiology, 6, 25.