

Resource Summary Report

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Full-Length cDNA Database

RRID:SCR_007666

Type: Tool

Proper Citation

Full-Length cDNA Database (RRID:SCR_007666)

Resource Information

URL: <http://fullmal.hgc.jp/>

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Description: Full-Length cDNA Database is a resource for cDNA libraries of arthropods and parasites. The arthropod species covered are *Anopheles stephensi*, *Glossina morsitans* (Tsetse fly), and *Dermatophagoides farinae* (House dust mite), while the parasitic species included are *Plasmodium falciparum* (Malaria), *Toxoplasma gondii*, *Cryptosporidium parvum*, *Babesia bovis* (Babesia), and *Echinococcus multilocularis*. A specialized database of each species is available as a link from the home page. This database has been constructed and maintained since 2001 by a Grant-in-Aid for Publication of Scientific Research Results from the Japan Society for the Promotion of Science. *Anopheles stephensi*, *Glossina morsitans*, Tsetse fly, *Dermatophagoides farinae*, House dust mite, *Plasmodium falciparum*, Malaria, *Toxoplasma gondii*, *Cryptosporidium parvum*, *Babesia bovis*, Babesia, *Echinococcus multilocularis*, cDNA, cDNA library, arthropod genome, parasite genome

Synonyms: Full-Length cDNA Database

Resource Type: data or information resource, database

Keywords: *echinococcus multilocularis*, *anopheles stephensi*, arthropod genome, babesia, *babesia bovis*, cDNA, cDNA library, *cryptosporidium parvum*, *dermatophagoides farinae*, *glossina morsitans*, house dust mite, malaria, parasite genome, *plasmodium falciparum*, *toxoplasma gondii*, tsetse fly, bio.tools

Resource Name: Full-Length cDNA Database

Resource ID: SCR_007666

Alternate IDs: biotools:full-parasites, nif-0000-02856

Alternate URLs: <https://bio.tools/full-parasites>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260821T193815+0000

Ratings and Alerts

No rating or validation information has been found for Full-Length cDNA Database.

No alerts have been found for Full-Length cDNA Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Karmodiya K, et al. (2015) A comprehensive epigenome map of Plasmodium falciparum reveals unique mechanisms of transcriptional regulation and identifies H3K36me2 as a global mark of gene suppression. Epigenetics & chromatin, 8, 32.

J?kalski M, et al. (2015) DB-AT: a 2015 update to the Full-parasites database brings a multitude of new transcriptomic data for apicomplexan parasites. Nucleic acids research, 43(Database issue), D631.

Yamagishi J, et al. (2014) Interactive transcriptome analysis of malaria patients and infecting Plasmodium falciparum. Genome research, 24(9), 1433.

Russell K, et al. (2013) Analysis of the spatial and temporal arrangement of transcripts over intergenic regions in the human malarial parasite Plasmodium falciparum. BMC genomics, 14, 267.

Tuda J, et al. (2011) Full-parasites: database of full-length cDNAs of apicomplexa parasites, 2010 update. Nucleic acids research, 39(Database issue), D625.

Yamagishi J, et al. (2010) High-resolution characterization of Toxoplasma gondii transcriptome with a massive parallel sequencing method. DNA research : an international journal for rapid publication of reports on genes and genomes, 17(4), 233.