Resource Summary Report

Generated by dkNET on May 19, 2025

BLAST Similarity Search

RRID:SCR_008419
Type: Tool

Proper Citation

BLAST Similarity Search (RRID:SCR_008419)

Resource Information

URL: http://www.broad.mit.edu/cgi-bin/annotation/disease_vector/aedes_aegypti/blast_page.cgi, http://www.broadinstitute.org/cgi-bin/annotation/disease_vector/aedes_aegypti/blast_page.cgi

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Description: The goals of this sequencing effort are to produce and publicly release a whole-genome assembly and auto-annotation of the Aedes genome representing 8X sequence coverage. In collaboration, these centers have delivered the target 8X draft coverage of the disease vector genome. Assembly of the genome was performed using the Broad''s whole genome assembly package ARACHNE (Batzoglou et al., 2002 and Jaffe et al., 2003). The Aedes genome will be annotated in a collaborative effort involving both MSCs and Vectorbase, which is a bioinformatics resource center at the University of Notre Dame. Sponsor: This resource is supported by the National Institute of Allergy and Infectious Diseases. Keywords: Genome, BLAST, Similarity, Search, Engine, Sequence, Bioinformatics, Resource,

Synonyms: BLAST

Resource Type: data or information resource, topical portal, portal

Funding:

Resource Name: BLAST Similarity Search

Resource ID: SCR_008419

Alternate IDs: nif-0000-30152

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250516T053911+0000

Ratings and Alerts

No rating or validation information has been found for BLAST Similarity Search.

No alerts have been found for BLAST Similarity Search.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Pu Y, et al. (2024) A high-quality chromosomal genome assembly of the sea cucumber Chiridota heheva and its hydrothermal adaptation. GigaScience, 13.

D'Adamo GL, et al. (2023) Bacterial clade-specific analysis identifies distinct epithelial responses in inflammatory bowel disease. Cell reports. Medicine, 4(7), 101124.

Ntefidou M, et al. (2023) Physcomitrium patens PpRIC, an ancestral CRIB-domain ROP effector, inhibits auxin-induced differentiation of apical initial cells. Cell reports, 42(2), 112130.

Zhang Y, et al. (2022) Improved microbial genomes and gene catalog of the chicken gut from metagenomic sequencing of high-fidelity long reads. GigaScience, 11.

Alvarez F, et al. (2022) Genome mining of Burkholderia ambifaria strain T16, a rhizobacterium able to produce antimicrobial compounds and degrade the mycotoxin fusaric acid. World journal of microbiology & biotechnology, 38(7), 114.

Salazar G, et al. (2019) Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 179(5), 1068.

Kinjo S, et al. (2018) Maser: one-stop platform for NGS big data from analysis to visualization. Database : the journal of biological databases and curation, 2018.

Sørhus E, et al. (2017) Novel adverse outcome pathways revealed by chemical genetics in a developing marine fish. eLife, 6.

Velmurugan G, et al. (2017) Gut microbial degradation of organophosphate insecticides-induces glucose intolerance via gluconeogenesis. Genome biology, 18(1), 8.

Winter F, et al. (2007) Anopheles gambiae miRNAs as actors of defence reaction against Plasmodium invasion. Nucleic acids research, 35(20), 6953.