Resource Summary Report

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DAMBE

RRID:SCR_018528
Type: Tool

Proper Citation

DAMBE (RRID:SCR_018528)

Resource Information

URL: http://dambe.bio.uottawa.ca/DAMBE/dambe.aspx

Proper Citation: DAMBE (RRID:SCR_018528)

Description: Software package for data analysis in molecular biology and evolution. Integrated software package for converting, manipulating, statistically and graphically describing, and analyzing molecular sequence data. Used for genomic and phylogenetic data analysis on Windows, Linux, and Macintosh computers.

Synonyms: DAMBE6, DAMBE5, DAMBE7, Data Analysis in Molecular Biology and Evolution

Resource Type: software application, data processing software, software resource, data analysis software, sequence analysis software

Defining Citation: PMID:11535656, PMID:28379490, PMID:23564938, PMID:29669107

Keywords: Data analysis, molecular sequence data, genomic data, phylogenetic data, data, anaysis, sequence analysis, bio.tools

Funding: Natural Science and Engineering Research Council of Canada ;
University of Hong Kong ;
Hong Kong Research Grant Council

Availability: Free, Available for download, Freely available

Resource Name: DAMBE

Resource ID: SCR_018528

Alternate IDs: biotools:dampe

Alternate URLs: https://bio.tools/dambe

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250410T071023+0000

Ratings and Alerts

No rating or validation information has been found for DAMBE.

No alerts have been found for DAMBE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Li J, et al. (2023) High subtelomeric GC content in the genome of a zoonotic Cryptosporidium species. Microbial genomics, 9(7).

Lu JH, et al. (2023) De Novo Assembly and Characterization of the Transcriptome of an Omnivorous Camel Cricket (Tachycines meditationis). International journal of molecular sciences, 24(4).

Xiang Y, et al. (2021) Mitochondrial Genomes of the Genus Claassenia (Plecoptera: Perlidae) and Phylogenetic Assignment to Subfamily Perlinae. Genes, 12(12).

Bhattacharjee A, et al. (2020) Machine learning based imputation techniques for estimating phylogenetic trees from incomplete distance matrices. BMC genomics, 21(1), 497.

Sarkar I, et al. (2020) Turdoides affinis mitogenome reveals the translational efficiency and importance of NADH dehydrogenase complex-I in the Leiothrichidae family. Scientific reports, 10(1), 16202.