

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

Defining Citation: [PMID:11535656](#), [PMID:28379490](#), [PMID:23564938](#), [PMID:29669107](#)

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

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

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: 20260821T194133+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 12 mentions in open access literature.

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

Zheng H, et al. (2026) Identification of Significant Genomic Changes and Compartmentalization of Simian Foamy Virus in a Human Zoonotically Infected by a Chimpanzee (*Pan troglodytes troglodytes*). *Viruses*, 18(2).

Shankar A, et al. (2026) Molecular Characterization of Complete Simian Foamy Virus Genomes from Three Colobine Monkeys Reveals Highly Divergent Evolutionary Trajectories and Identifies Transmission to Humans. *Viruses*, 18(3).

Gu X, et al. (2026) The Emerging JEV Genotype 5 Exhibits Distinct Codon Usage Characteristics. *Pathogens (Basel, Switzerland)*, 15(1).

Winn JC, et al. (2025) Annotated Bioinformatic Pipelines for Phylogenomic Placement of Mitochondrial Genomes. *Bio-protocol*, 15(5), e5232.

Pimvichai P, et al. (2025) Morphological and DNA sequence data uncover a new millipede species in the *Thyropygus opinatus* subgroup and assign *T. peninsularis* to this subgroup (Diplopoda: Spirostreptida: Harpagophoridae). *PeerJ*, 13, e19277.

Winn JC, et al. (2025) Annotated Bioinformatic Pipelines for Genome Assembly and Annotation of Mitochondrial Genomes. *Bio-protocol*, 15(5), e5231.

Shao R, et al. (2025) ZAP inhibits double-stranded RNA virus infection by degrading negative-strand RNA and blocking the elongation phase of viral protein synthesis. *Cell reports*, 45(1), 116742.

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.