

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

BEAST

RRID:SCR_010228

Type: Tool

Proper Citation

BEAST (RRID:SCR_010228)

Resource Information

URL: <http://beast.bio.ed.ac.uk/>

Proper Citation: BEAST (RRID:SCR_010228)

Description: A cross-platform software program for Bayesian MCMC analysis of molecular sequences. It is entirely orientated towards rooted, time-measured phylogenies inferred using strict or relaxed molecular clock models. It can be used as a method of reconstructing phylogenies but is also a framework for testing evolutionary hypotheses without conditioning on a single tree topology. BEAST uses MCMC to average over tree space, so that each tree is weighted proportional to its posterior probability. We include a simple to use user-interface program for setting up standard analyses and a suit of programs for analysing the results.

Synonyms: BEaST Segmentation Library, Beast Software

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

Defining Citation: [DOI:10.1186/1471-2148-7-214](https://doi.org/10.1186/1471-2148-7-214)

Keywords: bio.tools

Resource Name: BEAST

Resource ID: SCR_010228

Alternate IDs: nlx_156859, OMICS_04233, biotools:beast, SCR_015988

Alternate URLs: <http://www.nitrc.org/projects/beast-library>, <https://bio.tools/beast>, <https://sources.debian.org/src/beast-mcmc/>

Old URLs: http://beast.bio.ed.ac.uk/Main_Page

Record Creation Time: 20220129T080257+0000

Ratings and Alerts

No rating or validation information has been found for BEAST.

No alerts have been found for BEAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6460 mentions in open access literature.

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

Monteiro AC, et al. (2026) OPG-Producing B Cells and RANKL-Expressing T Cells Define Immune Signatures Predictive of Bone Metastases in Breast Cancer. *Cancer research communications*, 6(1), 85.

Frajman B, et al. (2026) Multiple long-distance dispersals accompanied by reduction of body size shaped the evolutionary history of four spurges (*Euphorbia*) endemic to Mediterranean islands. *Plant biology (Stuttgart, Germany)*, 28(1), 178.

Shi M, et al. (2026) Genomic architecture and evolution of heterostyly: new insights from *Cordia subcordata* (Boraginaceae). *Molecular biology and evolution*, 43(1).

Nguyen HH, et al. (2025) WaveSeekerNet: accurate prediction of influenza A virus subtypes and host source using attention-based deep learning. *GigaScience*, 14.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

Schenk JJ, et al. (2025) Comparative diversification analyses of Hydrangeaceae and Loasaceae reveal complex evolutionary history as species disperse out of Mesoamerica. *American journal of botany*, 112(1), e16455.

Veytsel G, et al. (2025) Molecular epidemiology, evolution, and transmission dynamics of raccoon rabies virus in Connecticut. *Virus evolution*, 11(1), veae114.

Foerster SÍA, et al. (2025) Body size prediction in scorpions: a phylogenetic comparative examination of linear measurements of individual body parts. *PeerJ*, 13, e18621.

Nicholls JA, et al. (2025) Continuous colonization of the Atlantic coastal rain forests of South America from Amazônia. *Proceedings. Biological sciences*, 292(2039), 20241559.

Dang Y, et al. (2025) Temperature-dependent variations in under-canopy herbaceous foliar diseases following shrub encroachment in grasslands. *Nature communications*, 16(1), 1131.

Zang G, et al. (2025) Identifications of Common Species and Descriptions of Two New Species of Siphonaria (Mollusca: Gastropoda) in China. *Biology*, 14(1).

Mendonça P, et al. (2025) The influence of the forest corridors to the north of the Andes on the diversification of the bright-rumped Attila, *Attila spadiceus* (Passeriformes, Tyrannidae), during the climatic oscillations of the middle Pleistocene. *Ecology and evolution*, 15(1), e70331.

Pang X, et al. (2025) HIV molecular transmission networks among students in Guangxi: unraveling the dynamics of student-driven HIV epidemic. *Emerging microbes & infections*, 14(1), 2459142.

Morey-León G, et al. (2025) Global epidemiology of *Mycobacterium tuberculosis* lineage 4 insights from Ecuadorian genomic data. *Scientific reports*, 15(1), 3823.

Lou Y, et al. (2025) Detection and Whole Genome Amplification of the 4d Type of Porcine Hepatitis E Virus in Eastern Tibet, China. *Veterinary medicine and science*, 11(1), e70194.

Zhu W, et al. (2025) Origin, pathogenicity, and transmissibility of a human isolated influenza A(H10N3) virus from China. *Emerging microbes & infections*, 14(1), 2432364.

Witharana EP, et al. (2025) Subfamily evolution analysis using nuclear and chloroplast data from the same reads. *Scientific reports*, 15(1), 687.

Zamunér CFC, et al. (2025) Evolution and spread of *Xanthomonas citri* subsp. *citri* in the São Paulo, Brazil, citrus belt inferred from 758 novel genomes. *Microbial genomics*, 11(1).

Dufresnes C, et al. (2025) Speciation and historical invasions of the Asian black-spined toad (*Duttaphrynus melanostictus*). *Nature communications*, 16(1), 298.