

Resource Summary Report

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BEAST

RRID:SCR_010228

Type: Tool

Proper Citation

BEAST (RRID:SCR_010228)

Resource Information

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

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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).

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

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

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

Huang J, et al. (2025) Genomic survey of multidrug resistant *Salmonella enterica* serovar Minnesota clones in chicken products. *npj antimicrobials and resistance*, 3(1), 10.

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

Tee HS, et al. (2025) Host-Calibrated Time Tree Caps the Age of Giant Viruses. *Molecular biology and evolution*, 42(2).

Wangui J, et al. (2025) Molecular Analysis of Human Respiratory Syncytial Virus Group B Strains Isolated in Kenya Before and During the Emergence of Pandemic Influenza A/H1N1. *Influenza and other respiratory viruses*, 19(2), e70082.

Guo D, et al. (2025) Cryptic diversity, phenotypic congruence, and evolutionary history of the *Leptobotia citraurata* complex (Pisces: Botiidae) within subtropical eastern China. *BMC ecology and evolution*, 25(1), 23.

Kniha E, et al. (2025) Combining phylogeography and climate models to track the diversification and spread of *Phlebotomus simici*. *Scientific reports*, 15(1), 10188.

Hisatsune J, et al. (2025) *Staphylococcus aureus* ST764-SCCmecII high-risk clone in bloodstream infections revealed through national genomic surveillance integrating clinical data. *Nature communications*, 16(1), 2698.

Wardani RK, et al. (2025) Unraveling the Evolutionary Patterns of Genus *Frontonia*: An Integrative Approach with Morphological and Molecular Data. *Biology*, 14(3).

McLean BS, et al. (2025) Integrative species delimitation reveals an Idaho-endemic ground squirrel, *Urocitellus idahoensis* (Merriam 1913). *Journal of mammalogy*, 106(2), 406.

Wang T, et al. (2025) Evolutionary analysis and population dynamics in the global transmission of Kaposi's sarcoma-associated herpesvirus. *Archives of virology*, 170(5), 92.

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.

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

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

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