

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: data analysis software, data processing software, sequence analysis software, software application, 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 6777 mentions in open access literature.

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

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.

Dai Q, et al. (2026) Comparative Population Genetics of Two Alvinocaridid Shrimp Species in Chemosynthetic Ecosystems of the Western Pacific. *Integrative zoology*, 21(2), 291.

Fourment M, et al. (2026) torchtree: Flexible Phylogenetic Model Development and Inference Using PyTorch. *Systematic biology*, 75(1), 39.

Li B, et al. (2026) Phylogenomics, ecomorphological evolution, and historical biogeography in Deuterocohnia (Bromeliaceae: Pitcairnioideae). *American journal of botany*, 113(2), e70153.

Bourgikos E, et al. (2026) Evolutionary history of Jamestown Canyon virus disentangles complex multi-vector ecology. *bioRxiv : the preprint server for biology*.

She Q, et al. (2026) Rapid dissemination of *Staphylococcus aureus* in the neonatal intensive care unit is associated with invasive infection. *Nature communications*, 17(1).

Riutord-Fe C, et al. (2026) Transmission of MPXV from fire-footed rope squirrels to sooty mangabeys. *Nature*, 651(8104), 185.

Ranaivoson RM, et al. (2026) Plastid and nuclear phylogenomics of *Cyphostemma* (Vitaceae) provide new insights into genome size evolution across sub-Saharan Africa. *Journal of integrative plant biology*, 68(5), 1399.

López-Astacio RA, et al. (2026) Distinct evolutionary patterns of endemic and emerging parvoviruses and the origin of a new pandemic virus. *Proceedings of the National Academy of Sciences of the United States of America*, 123(16), e2515274123.

Li X, et al. (2026) Clinical characteristics and molecular epidemiology of KPC-NDM co-producing carbapenem-resistant *Klebsiella pneumoniae* in China: a multicentre retrospective case-control study. *EBioMedicine*, 126, 106222.

Leng Y, et al. (2026) Molecular evolution and spatial transmission of severe fever with thrombocytopenia syndrome virus. *Nature communications*, 17(1).

Ogrzewalska M, et al. (2026) Genomic analysis of high pathogenicity avian influenza viruses from Antarctica reveals multiple introductions from South America. *Nature communications*, 17(1).

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.

Smith AN, et al. (2026) Body Size Evolution in Burying Beetles (Staphylinidae: Silphinae: Nicrophorus). *Ecology and evolution*, 16(3), e73012.

Cho AY, et al. (2026) Wild birds drive the introduction, maintenance, and spread of H5N1 clade 2.3.4.4b high pathogenicity avian influenza viruses in Spain, 2021-2022. *Virus evolution*, 12(1), veag006.

Wang N, et al. (2026) Biogeography and Climate Drive Population Divergence and Genomic Vulnerability in High Altitude Endemic Bird. *Molecular ecology*, 35(4), e70274.

Mason LCE, et al. (2026) The natural history of the emergence of sexually transmissible shigellosis. *Microbial genomics*, 12(1).

Shirai T, et al. (2026) Molecular Evolution of the Fusion (F) Genes in Human Metapneumovirus Genotype B. *Microorganisms*, 14(2).

Shan CB, et al. (2026) Diverse mitogenomic variations contribute to population differentiation in Eurasian tree sparrows (*Passer montanus*). *Zoological research*, 47(1), 101.

Mkpuma N, et al. (2026) Molecular characterization and phylogeography of equine influenza virus H3N8 detected in donkeys in Nigeria 2022-2023. *BMC veterinary research*, 22(1).