

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 [Kravitz](#) .

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.

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.

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

Arai N, et al. (2026) Transmission of Salmonella clones between different animal species in a horse and cattle breeding region in Japan. Scientific reports, 16(1).

Jiang X, et al. (2026) Maternal genetic structure and population affinities of the Sichuan Han Chinese based on whole mitochondrial genomes. BMC genomics, 27(1).

Cunha MS, et al. (2026) Yellow fever virus resurgence in Sao Paulo State, Brazil, 2024-2025. Revista do Instituto de Medicina Tropical de Sao Paulo, 68, e13.

Ali RLMN, et al. (2026) Evidence of a putative new species Haemagogus 'Trinidad sp. A' from the Caribbean sharing mitogenome lineages with species endemic to the Amazon. Scientific reports, 16(1).

- 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.
- Chang W, et al. (2026) Identification of a novel second-generation HIV-1 circulating recombinant form, CRF182_0708, in Yunnan, China. *BMC infectious diseases*, 26(1).
- Zuza AM, et al. (2026) Temporal genomic dynamics of sequence type 39 *Klebsiella pneumoniae* in a neonatal unit in Blantyre, Malawi. *Microbial genomics*, 12(4).
- Campbell AKO, et al. (2026) Genomic epidemiology of the 2025 mpox epidemic in Sierra Leone. *Nature medicine*, 32(5), 1917.
- 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).
- 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.
- Li B, et al. (2026) Phylogenomics, ecomorphological evolution, and historical biogeography in *Deuterocohnia* (Bromeliaceae: Pitcairnioideae). *American journal of botany*, 113(2), e70153.
- 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.
- Ralph DK, et al. (2026) Inference of germinal center evolutionary dynamics via simulation-based deep learning. *eLife*, 14.
- 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).
- Baca M, et al. (2026) The evolutionary history of the field vole species complex revealed by modern and ancient genomes. *Genome biology*, 27(1).