**BEAST**

**RRID:** SCR_010228  
**Type:** Tool

**Proper Citation**

BEAST (RRID:SCR_010228)

**Resource Information**

**URL:** [http://beast.bio.ed.ac.uk/](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 suite of programs for analysing the results.

**Synonyms:** BEaST Segmentation Library, Beast Software

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

**Defining Citation:** DOI: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

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 5512 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Marquine S, et al. (2024) Sequence Data From a Travel-Associated Case of Microcephaly Highlight a Persisting Risk due to Zika Virus Circulation in Thailand. The Journal of infectious diseases, 229(2), 443.

Xing X, et al. (2024) Evolution and biological characterization of H5N1 influenza viruses bearing the clade 2.3.2.1 hemagglutinin gene. Emerging microbes & infections, 13(1), 2284294.


Ye Y, et al. (2024) Robust expansion of phylogeny for fast-growing genome sequence data.

Han Z, et al. (2024) Synergetic association between coxsackievirus A16 genotype evolution and recombinant form shifts. Virus evolution, 10(1), vead080.


de Campos GM, et al. (2024) Updated Insights into the Phylogenetics, Phylodynamics, and Genetic Diversity of Nipah Virus (NiV). Viruses, 16(2).


