**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/)

**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.

**Resource Name:** BEAST  
**Proper Citation:** BEAST (RRID:SCR_010228)  
**Resource Type:** Resource, data analysis software, data processing software, software application, sequence analysis software, software repository, software resource  
**Resource ID:** SCR_010228  
**Parent Organization:** University of Edinburgh; Scotland; United Kingdom  
**Related resources:** TempEst, BEAST2  
**Website Status:** Last checked down  
**Alternate IDs:** nlx_156859, SCR_015988  
**Alternate URLs:** [http://www.nitrc.org/projects/beast-library](http://www.nitrc.org/projects/beast-library)
Old URLs: http://beast.bio.ed.ac.uk/Main_Page

Mentions Count: 3101

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 3101 mentions in open access literature.

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


Oswald JA, et al. (2020) Ancient DNA and high-resolution chronometry reveal a long-term human role in the historical diversity and biogeography of the Bahamian hutia. Scientific reports, 10(1), 1373.


Perdigão J, et al. (2020) Using genomics to understand the origin and dispersion of multidrug and extensively drug resistant tuberculosis in Portugal. Scientific reports, 10(1), 2600.


