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.

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

Keywords: bio.tools

Parent Organization: University of Edinburgh; Scotland; United Kingdom

Related resources: TempEst, BEAST2, PhyDyn

Website Status: Last checked down

Resource Name: BEAST

Resource ID: SCR_010228

Alternate IDs: nlx_156859, biotools:beast, SCR_015988
**Alternate URLs:** http://www.nitrc.org/projects/beast-library, https://bio.tools/beast

**Old URLs:** http://beast.bio.ed.ac.uk/Main_Page

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**Ratings and Alerts**

No rating or validation information has been found for BEAST.

No alerts have been found for BEAST.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 3754 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](http://www.scicrunch.org).


Yang H, et al. (2020) Microevolution and Gain or Loss of Mobile Genetic Elements of Outbreak-Related in Food Processing Environments Identified by Whole Genome


Boschin F, et al. (2020) The first evidence for Late Pleistocene dogs in Italy. Scientific reports, 10(1), 13313.


