

Resource Summary Report

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BEAST2

RRID:SCR_017307

Type: Tool

Proper Citation

BEAST2 (RRID:SCR_017307)

Resource Information

URL: <https://www.beast2.org/>

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Description: Software package for advanced Bayesian evolutionary analysis by sampling trees. Used for phylogenetics, population genetics and phylodynamics. Program for Bayesian phylogenetic analysis of molecular sequences. Estimates rooted, time measured phylogenies using strict or relaxed molecular clock models. Framework can be extended by third parties. Comprised of standalone programs including BEAUti, BEAST, MASTER, RBS, SNAPP, MultiTypeTree, BDSKY, LogAnalyser, LogCombiner, TreeAnnotator, DensiTree and package manager.

Synonyms: , Beast 2.5

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

Defining Citation: [PMID:30958812](#)

Keywords: Bayesian, evolutionary, sampling, tree, phylogenic, analysis, Markov, chain, monte carlo, phylogenetic, population, genetic, phylodynamic, sequence

Funding: Royal Society of New Zealand Marsden award ;
European Research Council ;
NIGMS U01 GM110749;
Swiss National Science foundation ;
Max Planck Society ;
EMBL

Availability: Free, Available for download, Freely available

Resource Name: BEAST2

Resource ID: SCR_017307

License: GNU GPL v2

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260729T044433+0000

Ratings and Alerts

No rating or validation information has been found for BEAST2.

No alerts have been found for BEAST2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 194 mentions in open access literature.

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

Ma Y, et al. (2025) Epidemic dynamics and clinical characteristics of HIV-1 CRF07_BC_N and CRF07_BC_O in Shanghai, 2017-2023. *Virulence*, 16(1), 2554301.

White RT, et al. (2025) 20 years later: unravelling the genomic success of New Zealand's home-grown AK3 community-associated methicillin-resistant *Staphylococcus aureus*. *Microbial genomics*, 11(7).

Jeon JH, et al. (2025) Chloroplast genome and haplotype relationships unravel the genetic introgression and complex evolutionary history of East Asian *Rosa* section *Synstylae* roses (Rosaceae). *Botanical studies*, 66(1), 17.

Lambisia AW, et al. (2025) Genomic and clinical epidemiology of SARS-CoV-2 in coastal Kenya: insights into variant circulation, reinfection, and multiple lineage importations during a post-pandemic wave. *BMC global and public health*, 3(1), 80.

Iqbal BN, et al. (2025) Molecular Epidemiology of SARS-CoV-2 Detected from Different Areas of the Kandy District of Sri Lanka from November 2020-March 2022. *Viruses*, 17(9).

Islam MA, et al. (2025) Complete mitogenomes of two major dengue vectors *Aedes aegypti* and *Aedes albopictus* from Bangladesh: Insights from comparative genomics with global mitogenome diversity and phylogenetics. *PloS one*, 20(9), e0333693.

Zhu ZX, et al. (2025) Discovery of an ancient Himalayan birch mouse lineage illuminates the evolution of the family Sicistidae (Rodentia: Dipodoidea), with descriptions of a new genus and two new species. *Zoological research*, 46(4), 921.

Borja-Martínez G, et al. (2025) Evolutionary and Ecological Drivers of Gut Microbiota in Wild Rodent Species from the Yucatán Peninsula. *Microbial ecology*, 88(1), 100.

Dehasque M, et al. (2025) Genomic and morphological analysis reveals long-term mammoth hybridization in British Columbia, Canada. *Biology letters*, 21(9), 20250305.

Da Silva KE, et al. (2025) Comparison of phylogenetic metrics of transmission in symptomatic and asymptomatic tuberculosis. *medRxiv : the preprint server for health sciences*.

Brocklebank JW, et al. (2025) Maternal origins and genetic diversity of Sabahan swamp buffalo using mitochondrial cytochrome b gene. *Scientific reports*, 15(1), 33685.

Fu J, et al. (2025) Increased GII.3[P12] norovirus outbreaks and viral whole genome analysis in Beijing, China during 2021 and 2023. *Gut pathogens*, 17(1), 76.

Salman M, et al. (2025) Evolutionary dynamics of repetitive elements and genome size in Tetrigidae (Orthoptera: Caelifera). *Scientific reports*, 15(1), 34509.

Strydom H, et al. (2025) Temporal reconstruction of a *Salmonella* Enteritidis ST11 outbreak in New Zealand. *Microbial genomics*, 11(10).

Segawa T, et al. (2025) Colonization history of snow algae on Hawai'i island. *The ISME journal*, 19(1).

Paulino Monteiro SR, et al. (2025) Efficiency of the cytochrome c oxidase subunit II gene for the delimitation of termite species (Blattodea: Isoptera) in the state of Paraíba, northeastern Brazil. *PloS one*, 20(9), e0328685.

Goya S, et al. (2025) Distinct Evolutionary Signatures of Human Parainfluenza Viruses 2 and 4 Reveal Host Antagonism Divergence and Phylogenetic Discordance. *Molecular biology and evolution*, 42(10).

Fusca DD, et al. (2025) Phylogenomic timetree-calibrated speciation clocks for *Caenorhabditis* nematodes reveal slow but disproportionate accumulation of post-zygotic reproductive isolation. *PLoS genetics*, 21(9), e1011852.

Ding W, et al. (2025) The asynchronous rise of Northern Hemisphere alpine floras reveals general responses of biotic assembly to orogeny and climate change. *Science advances*, 11(51), eadz1888.

Frade PR, et al. (2025) Hybridization as driving force for cryptic species diversity in the Caribbean coral genus *Madracis*. *Scientific reports*, 15(1), 33359.