

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

Defining Citation: [PMID:30958812](#)

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

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

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: 20260829T182558+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 211 mentions in open access literature.

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

Jia C, et al. (2026) Distinct genomic trajectory among invasive Salmonella Typhimurium ST313 infections. Nature communications, 17(1).

Bazyar K, et al. (2026) Mechanistic and clinical insights into a PmrB mutation driving colistin resistance and virulence in Acinetobacter baumannii. Scientific reports, 16(1), 4348.

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in Neisseria gonorrhoeae. bioRxiv : the preprint server for biology.

Gewecke A, et al. (2026) Environmental and Phylogenetic Investigations of Aspergillus flavus Outbreak Linked to Contaminated Building Materials, Denmark, 2025. Emerging infectious diseases, 32(3), 376.

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in Neisseria gonorrhoeae. PLoS pathogens, 22(5), e1013962.

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).

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.

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.

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).

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).

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.

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.

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.

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.

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

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

Maldonado-Barrueco A, et al. (2025) Genomic analysis of carbapenem resistant *Acinetobacter baumannii* outbreak in a burn intensive care unit of a tertiary-care hospital in Madrid, Spain. Antimicrobial resistance and infection control, 14(1), 124.

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.

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