

Resource Summary Report

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RAXML Next Generation

RRID:SCR_022066

Type: Tool

Proper Citation

RAXML Next Generation (RRID:SCR_022066)

Resource Information

URL: <https://github.com/amkozlov/raxml-ng>

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Description: Software phylogenetic tree inference tool which uses maximum likelihood optimality criterion. Used for maximum likelihood phylogenetic inference. Offers improved accuracy, flexibility, speed, scalability, and usability compared with RAXML/ExaML.

Abbreviations: RAXML-NG

Synonyms: Randomized Axelerated Maximum Likelihood Next Generation

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

Defining Citation: [DOI:10.1093/bioinformatics/btz305](https://doi.org/10.1093/bioinformatics/btz305)

Keywords: phylogenetic tree inference, maximum likelihood optimality criterion, maximum likelihood phylogenetic inference

Funding: Klaus Tschira Foundation

Availability: Free, Available for download, Freely available

Resource Name: RAXML Next Generation

Resource ID: SCR_022066

Alternate URLs: <https://sources.debian.org/src/raxml-ng/>

License: GNU Affero General Public License v3.0

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260801T042846+0000

Ratings and Alerts

No rating or validation information has been found for RAxML Next Generation.

No alerts have been found for RAxML Next Generation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 273 mentions in open access literature.

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

Xu ZS, et al. (2025) High-throughput analysis of microbiomes in a meat processing facility: are food processing facilities an establishment niche for persisting bacterial communities? Microbiome, 13(1), 25.

Fujii A, et al. (2025) Comprehensive analysis of bacteriocins produced by clinical enterococcal isolates and their antibacterial activity against Enterococci including VRE. Scientific reports, 15(1), 4846.

Krutova M, et al. (2025) Genomic islands and molecular mechanisms relating to drug-resistance in Clostridioides (Clostridium) difficile PCR ribotype 176. Emerging microbes & infections, 14(1), 2482698.

Dantas K, et al. (2025) Emergent Escherichia coli of the highly virulent B2-ST1193 clone producing KPC-2 carbapenemase in ready-to-eat vegetables. Journal of global antimicrobial resistance, 41, 105.

Gillet L, et al. (2025) Resistome and virulome determination in Helicobacter pylori using next-generation sequencing with target-enrichment technology. Microbiology spectrum, 13(4), e0329824.

Kong Y, et al. (2025) Investigation of an outbreak of carbapenem resistant Acinetobacter baumannii in an intensive care unit during the COVID-19 epidemic. Antimicrobial resistance and infection control, 14(1), 30.

Marik T, et al. (2025) Novel peptaibiotics identified from Trichoderma clade Viride. Natural products and bioprospecting, 15(1), 48.

Ross TA, et al. (2025) Enterococcus lactis is ecologically and genetically distinct from the major opportunistic pathogen Enterococcus faecium. Microbial genomics, 11(6).

Perreau C, et al. (2025) Molecular investigation of unexpected Helicobacter pylori bacteremia. European journal of clinical microbiology & infectious diseases : official publication of the European Society of Clinical Microbiology, 44(10), 2421.

Xiang R, et al. (2025) Comparative chloroplast genomes and phylogenetic analysis of the *Phlegmariurus* (Lycopodiaceae) from China and neighboring regions. *Frontiers in plant science*, 16, 1543431.

Rusinko J, et al. (2025) PickMe: Sample Selection for Species Tree Reconstruction using Coalescent Weighted Quartets. *Systematic biology*, 74(4), 656.

Jeon D, et al. (2025) A Draft Genome Assembly of the Antarctic Springtail *Cryptopygus antarcticus* and Diversity of Glycoside Hydrolase Genes. *Genome biology and evolution*, 17(12).

Solis-Ponce L, et al. (2025) Genotype distribution and molecular characterization of HPV in the Peruvian amazon: insights into prevalence, lineage diversity, and viral integration. *Scientific reports*, 15(1), 32535.

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Li T, et al. (2025) Adaptive evolution of extensive drug resistance and persistence in epidemic ST11 KPC-producing *Klebsiella pneumoniae* during antimicrobial chemotherapy. *Antimicrobial agents and chemotherapy*, 69(1), e0123524.

Jorquera J, et al. (2025) Genomic Introgression and Adaptation of Southern Seabird Species Facilitate Recent Polar Colonization. *Molecular biology and evolution*, 42(3).

Hill R, et al. (2025) Evolutionary genomics reveals variation in structure and genetic content implicated in virulence and lifestyle in the genus *Gaeumannomyces*. *BMC genomics*, 26(1), 239.

Hisatsune J, et al. (2025) *Staphylococcus aureus* ST764-SCCmecII high-risk clone in bloodstream infections revealed through national genomic surveillance integrating clinical data. *Nature communications*, 16(1), 2698.

Zilov D, et al. (2025) Genome structure and molecular phylogeny of the only Eurasian *Boechera* species, *Boechera falcata* (Brassicaceae). *G3 (Bethesda, Md.)*, 15(7).

Verrett TB, et al. (2025) *Borrelia* Lineages Adjacent to Zoonotic Clades in Black Flying Foxes (*Pteropus alecto*), Australia, 2018-2020. *Emerging infectious diseases*, 31(7), 1415.