

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, software application, data analysis software, 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: 20260731T043101+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 [kravitz2](#) .

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.

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.

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.

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.

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.

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.

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).

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.

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.

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

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.

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

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

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.

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.

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.

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.

Hill R, et al. (2025) Starship giant transposable elements cluster by host taxonomy using k-mer-based phylogenetics. *G3 (Bethesda, Md.)*, 15(6).

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.

Nagpala MJM, et al. (2025) Genomic characterization of antimicrobial-resistant *Salmonella enterica* in chicken meat from wet markets in Metro Manila, Philippines. *Frontiers in microbiology*, 16, 1496685.