

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: 20260801T190721+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 [RRID](#) .

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.