

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

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 analysis software, data processing 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: 20260821T194221+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 354 mentions in open access literature.

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

Din NS, et al. (2026) Dynamics of a large multidrug-resistant plasmid encoding New Delhi metallo- β -lactamase-1 and oxacillinase-58 carbapenemases in *Acinetobacter baumannii* clinical isolates from a tertiary hospital in Malaysia. *Microbial genomics*, 12(2).

Luo L, et al. (2026) Paternal genomic history and Y-chromosome phylogeny from the Chengdu Plain reveal multiple Indigenous East Asian farmer contributions to ancient Shu and their descendants. *BMC biology*, 24(1).

Guan J, et al. (2026) Emergence of a high-risk multidrug-resistant *Acinetobacter baumannii* clone ST697 in nosocomial settings. *Microbiology spectrum*, 14(6), e0229325.

Tomomatsu K, et al. (2026) Double flower is associated with defects in a *Phantastica*-like gene in *Catharanthus roseus*. *Scientific reports*, 16(1).

Zhao Z, et al. (2026) Comparative genomics of different haplotypes in *Ditylenchus destructor* provides insights into their host preferences. *Communications biology*, 9(1).

Zou Y, et al. (2026) *Mycobacterium nanjing* sp. nov. Isolated from Cutaneous Infection, China. *Emerging infectious diseases*, 32(3), 452.

Thivolle A, et al. (2026) Genomic insights into antagonistic coevolution: collagen-like protein expansion and genome plasticity in the *Daphnia* parasite *Pasteuria ramosa*. *G3 (Bethesda, Md.)*, 16(6).

Choi N, et al. (2026) Novel mechanisms of chemosensory adaptation to the cave environment. *bioRxiv : the preprint server for biology*.

Ketchum RN, et al. (2026) Genomic signatures of speciation and adaptation in the ctenophore *Mnemiopsis*. *BMC biology*, 24(1).

Lebreton F, et al. (2026) Preferred evolutionary routes of convergence in *Klebsiella pneumoniae* favor siderophore acquisition over hypervirulence. *Research square*.

Pouga L, et al. (2026) Genomic and patient epidemiology of *Streptococcus dysgalactiae* subspecies *equisimilis* in Houston, Texas. *Microbiology spectrum*, 14(4), e0368325.

Hourigan D, et al. (2026) The Hungate1000 prokaryotic culture collection encodes a wide variety of bacteriocins. *mSystems*, 11(6), e0019526.

Jiu S, et al. (2026) Pangenome and resequencing analyses reveal flowering evolution and genetic control in *Cerasus*. *Nature communications*, 17(1).

Garcia-Candela E, et al. (2026) Phylogenomic and comparative genomic analyses of *Aeromonas* spp. from South American aquatic systems reveal extensive genomic diversity, antimicrobial resistance, and predicted human pathogenicity. *Frontiers in microbiology*, 17, 1823138.

Arp G, et al. (2026) SpiR is a gut microbial enzyme that drives cholesterol conversion. *Nature communications*, 17(1).

Chrudinová M, et al. (2026) Evolution of Insulin, Insulin-like Growth Factors, and Their Cognate Receptors in Vertebrates, Invertebrates, and Viruses. *Molecular biology and evolution*, 43(1).

Zhai J, et al. (2026) Genomic characteristics and risk factor analysis of carbapenem-non-susceptible *Pseudomonas aeruginosa* causing bacteremia in a tertiary hospital (2014-2023). *BMC microbiology*, 26(1).

Choung S, et al. (2026) Chemically guided single-cell transcriptomics reveals sulfotransferase-mediated scaffold remodeling in securinine biosynthesis. *Nature communications*, 17(1).

Wei YM, et al. (2026) Comparative Chloroplast Genome Analyses Reveal a Fine-Scale Phylogenetic Framework and Cryptic Diversity in the *Fagopyrum dibotrys* Complex (Polygonaceae). *Genes*, 17(2).

Totikov AA, et al. (2026) Comparative Genomics and Phylogenomics of the Mustelinae Lineage (Mustelidae, Carnivora). *Genome biology and evolution*, 18(3).