

Resource Summary Report

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RAXML

RRID:SCR_006086

Type: Tool

Proper Citation

RAXML (RRID:SCR_006086)

Resource Information

URL: <https://github.com/stamatak/standard-RAXML>

Proper Citation: RAXML (RRID:SCR_006086)

Description: Software program for phylogenetic analyses of large datasets under maximum likelihood.

Abbreviations: RAXML

Synonyms: Randomized Axelerated Maximum Likelihood

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

Defining Citation: [PMID:24451623](#), [PMID:16928733](#), [PMID:15608047](#), [DOI:10.1093/bioinformatics/btu033](#)

Keywords: phylogeny, bio.tools

Availability: GNU General Public License

Resource Name: RAXML

Resource ID: SCR_006086

Alternate IDs: biotools:raxml, OMICS_02242

Alternate URLs: <https://bio.tools/raxml>, <https://sources.debian.org/src/raxml/>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260919T195104+0000

Ratings and Alerts

No rating or validation information has been found for RAxML.

No alerts have been found for RAxML.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12997 mentions in open access literature.

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

Telford MS, et al. (2026) Antibacterial microcins self-assemble to promote biofilm formation in *Acinetobacter baumannii*. *Cell reports*, 45(4), 117156.

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in *Mycobacterium tuberculosis* constitutively generates subpopulations with distinct clinical phenotypes. *iScience*, 29(5), 115045.

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology : CB*, 36(11), 2808.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Senti KA, et al. (2026) Co-evolving infectivity and expression patterns drive the diversification of endogenous retroviruses. *The EMBO journal*, 45(6), 1889.

Markkanen M, et al. (2026) Sulfonamide resistance gene *sul4* is hosted by common wastewater sludge bacteria and found in various newly described contexts and hosts. *Microbiology spectrum*, 14(1), e0085725.

Mungunkhuyag K, et al. (2026) Isolation and characterization of heavy metal tolerant microalgae from old mining areas of Saxony. *Scientific reports*, 16(1), 1337.

Sauerborn E, et al. (2026) Resolving plasmid-encoded carbapenem resistance dynamics and reservoirs in a hospital setting through nanopore sequencing. *Microbial genomics*, 12(2).

Liu MD, et al. (2026) Revisiting the phylogeny of *Conioselinum* (Apiaceae) by integrating nrDNA, plastomes and morphology evidence. *BMC plant biology*, 26(1).

Komoyo GF, et al. (2026) Influenza Surveillance in the Central African Republic From 2015 to 2018 to Inform Vaccination and Treatment Strategies. *Influenza and other respiratory viruses*, 20(1), e70221.

Sun Y, et al. (2026) Immunogenic relationship mapping supports a minimal-set trivalent vaccine strategy for broad sarbecovirus protection. *Signal transduction and targeted therapy*, 11(1), 48.

Bhattacharjee D, et al. (2026) Genomic insights into the functional and metabolic versatility of gut microbiome *Anaerostipes* species. *Microbial genomics*, 12(2).

Lee D, et al. (2026) Genomic Insights into Bacterioruberin and Halorhodopsin Biosynthetic Genes in 12 Halophilic Archaea Isolated from Korean Solar Salterns. *Journal of microbiology and biotechnology*, 36, e2601015.

Buczek DJ, et al. (2026) Sequence type and strain-level detection of *Klebsiella pneumoniae* in culture-enriched bacterial metagenomes: comparative performance of mSWEEP and StrainGE bioinformatic tools. *Microbial genomics*, 12(2).

Li Z, et al. (2026) Insight into the sulfate transporter gene family in *Nicotiana tabacum* and functional analysis of NtSULTR1;3 in response to salt stress. *BMC plant biology*, 26(1), 252.

Ajumobi V, et al. (2026) Population structure, antimicrobial resistance, and virulence factors of diabetic foot-associated *Escherichia coli*. *Microbiology spectrum*, 14(2), e0283725.

Li H, et al. (2026) Evolutionary dynamics of sex determination in *Branchiostoma belcheri* driven by repeated transposition of a single novel gene. *Nature communications*, 17(1), 1616.

Xie S, et al. (2026) Whole-genome resequencing reveals genetic divergence, local adaptation, and conservation priorities in three helmet catfishes (complex *Cranoglanis boudierius*). *BMC genomics*, 27(1).

Yamakawa S, et al. (2026) Multiple losses of ecdysone receptor genes in nematodes: an alternative evolutionary scenario of molting regulation. *Molecular biology and evolution*, 43(5).

Harmer CJ, et al. (2026) Mobilization of the AbGRI4 resistance island in *Acinetobacter baumannii*: IS26 action and homologous recombination both contribute. *Microbiology spectrum*, 14(6), e0038926.