

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 2026

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: 20260912T195635+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 [SPARC SAWG](#) .

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.

Gebert MJ, et al. (2026) A cross-environment comparison of nontuberculous mycobacterial diversity. *Applied and environmental microbiology*, 92(1), e0155225.

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

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.

Stephenson MJ, et al. (2026) Large-scale mining of plant genomes unlocks the diversity of oxidosqualene cyclases. *Nature chemical biology*, 22(2), 249.

Zhang Y, et al. (2026) Pivotal plasmids drive the global spread of CTX-M-27 in *Escherichia coli*. *Infection*, 54(1), 315.

Kon H, et al. (2026) Contribution of Fourier transform infrared spectroscopy for outbreak investigation of carbapenem-resistant *Acinetobacter baumannii*. *Microbiology spectrum*, 14(2), e0239225.

- Kaur A, et al. (2026) Phylogenetic insights derived from six *Xanthomonas* draft genome sequences associated with bacterial spot disease of tomato and pepper in Turkey. *Access microbiology*, 8(2).
- Liu MD, et al. (2026) Revisiting the phylogeny of *Conioselinum* (Apiaceae) by integrating nrDNA, plastomes and morphology evidence. *BMC plant biology*, 26(1).
- Liu H, et al. (2026) The first complete chloroplast genome sequence of an early spring flowering plant, *Corydalis repens*. *Mitochondrial DNA. Part B, Resources*, 11(3), 429.
- Wang D, et al. (2026) Mycorrhizal communities in Orchidaceae are likely shaped by plant trophic mode and biogeography but not phylogeny. *Plant diversity*, 48(1), 117.
- Regan MR, et al. (2026) Put your money where your mouth is: Surveillance of antibiotic resistance within the commensal *Neisseria*. *bioRxiv : the preprint server for biology*.
- Martins TW, et al. (2026) Sequencing of the invasive *E. coli* strain BEN2908 isolated from poultry: A comparative investigation of genomic regions shared with intestinal and extraintestinal model *E. coli* strains. *PloS one*, 21(2), e0342894.
- Avelar-Rivas JA, et al. (2026) Recurrent introgression and geographical stratification shape *Saccharomyces cerevisiae* in the Neotropics. *Nature communications*, 17(1).
- Thompson JB, et al. (2026) CactEcoDB: Trait, spatial, environmental, phylogenetic and diversification data for the cactus family. *Scientific data*, 13(1).
- Rembinski J, et al. (2026) Two Novel *Trichoderma* Species and their Antagonistic Activity against Sclerotia-producing Plant Pathogens. *Current microbiology*, 83(4).