

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 processing software, data analysis 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: 20260801T190304+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 12473 mentions in open access literature.

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

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.

Chen Z, et al. (2026) Evaluating Probe Design for Phylogenomics Across Taxonomic Scales: First Steps for Applying Ultraconserved Elements in an Understudied Class (Mollusca: Polyplacophora). *Molecular ecology resources*, 26(1), e70076.

Li C, et al. (2026) A cell-type-specific regulon controlling monoterpene indole alkaloid biosynthesis with feedback and feedforward activation loops. *The New phytologist*, 249(2), 945.

Cleveland ME, et al. (2026) Toward the Bioremediation of Nylon Waste Materials: Genome Mining Leads to the Identification of a Thermostable Laurolactamase From *Thermopolyspora flexuosa*. *ChemSusChem*, 19(1), e202501964.

Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.

Pourmahdi Borujeni M, et al. (2026) First Detection and Phylogenetic Analysis of Equine Hepacivirus (EqHV) in Iran. *Veterinary medicine and science*, 12(1), e70737.

Viruel J, et al. (2026) Phylogenomic Barcoding of Soil Seed Bank-Persistent and Wind-Dispersed Non-Native Plant Species in South Georgia. *Molecular ecology resources*, 26(1), e70068.

Stryko J, et al. (2026) Carbapenem-resistant *Acinetobacter baumannii* at a hospital in Botswana: detecting a protracted outbreak using whole genome sequencing. *Microbiology spectrum*, 14(1), e0176825.

Terpis KX, et al. (2025) Multiple plastid losses within photosynthetic stramenopiles revealed by comprehensive phylogenomics. *Current biology : CB*, 35(3), 483.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of

blue peafowl. GigaScience, 14.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. GigaScience, 14.

Yuan S, et al. (2025) Multiomic Analyses Reveal the Molecular Mechanisms of Arid Adaptation in a Desert Rodent Species. Molecular biology and evolution, 42(10).

Ren L, et al. (2025) Genomes reveal pervasive distant hybridization in nature among cyprinid fishes. GigaScience, 14.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. GigaScience, 14.

Záhonová K, et al. (2025) Diplonemid protists possess exotic endomembrane machinery, impacting models of membrane trafficking in modern and ancient eukaryotes. Current biology : CB, 35(7), 1508.

Cuevas Zuviría B, et al. (2025) Structural evolution of nitrogenase over 3 billion years. eLife, 14.

Unitt A, et al. (2025) *Neisseria gonorrhoeae* LIN codes provide a robust, multi-resolution lineage nomenclature. eLife, 14.

Kariyayama H, et al. (2025) Hagfish olfactory repertoire illuminates lineage-specific diversification of olfaction in basal vertebrates. iScience, 28(12), 114118.

Scadden J, et al. (2025) The nisin O cluster: species dissemination, candidate leader peptide proteases and the role of regulatory systems. Microbiology (Reading, England), 171(2).

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. GigaScience, 14.