

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, software application, software resource, data analysis software

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/>

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 10546 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Pu Y, et al. (2024) A high-quality chromosomal genome assembly of the sea cucumber *Chiridota heheva* and its hydrothermal adaptation. *GigaScience*, 13.

Guedes JG, et al. (2024) The leaf idioblastome of the medicinal plant *Catharanthus roseus* is associated with stress resistance and alkaloid metabolism. *Journal of experimental botany*, 75(1), 274.

Zhang H, et al. (2024) The haplotype-resolved genome assembly of autotetraploid rhubarb *Rheum officinale* provides insights into its genome evolution and massive accumulation of anthraquinones. *Plant communications*, 5(1), 100677.

Sundermann AJ, et al. (2024) Two Artificial Tears Outbreak-Associated Cases of Extensively Drug-Resistant *Pseudomonas aeruginosa* Detected Through Whole Genome Sequencing-Based Surveillance. *The Journal of infectious diseases*, 229(2), 517.

Zhernakova DV, et al. (2024) Host genetic regulation of human gut microbial structural variation. *Nature*, 625(7996), 813.

Bergman I, et al. (2024) Ciliate Grazing on the Bloom-Forming Microalga *Gonyostomum* semen. *Microbial ecology*, 87(1), 33.

Chavarro-Carrero EA, et al. (2024) The soil-borne white root rot pathogen *Rosellinia necatrix* expresses antimicrobial proteins during host colonization. *PLoS pathogens*, 20(1), e1011866.

Feng YY, et al. (2024) Reciprocal expression of MADS-box genes and DNA methylation reconfiguration initiate bisexual cones in spruce. *Communications biology*, 7(1), 114.

Sun BJ, et al. (2024) Genetically Encoded Lizard Color Divergence for Camouflage and Thermoregulation. *Molecular biology and evolution*, 41(2).

Wang X, et al. (2024) De novo chromosome-level genome assembly of Chinese motherwort (*Leonurus japonicus*). *Scientific data*, 11(1), 55.

Yun BH, et al. (2024) The characteristics and phylogenetic relationship of two complete mitochondrial genomes of *Cottus pollux* (scorpaeniformes: cottidae). *Mitochondrial DNA. Part B, Resources*, 9(1), 55.

Harrison LB, et al. (2024) An imputed ancestral reference genome for the *Mycobacterium tuberculosis* complex better captures structural genomic diversity for reference-based alignment workflows. *Microbial genomics*, 10(1).

Vázquez-López M, et al. (2024) ?Biogeographic factors contributing to the diversification of Euphoniinae (Aves, Passeriformes, Fringillidae): a phylogenetic and ancestral areas analysis. *ZooKeys*, 1188, 169.

Ocejo M, et al. (2024) Whole-genome long-read sequencing to unveil *Enterococcus* antimicrobial resistance in dairy cattle farms exposed a widespread occurrence of *Enterococcus lactis*. *Microbiology spectrum*, 12(2), e0367223.

Dvorak M, et al. (2024) Molecular and morphological characterisation of larvae of the genus *Diamesa* Meigen, 1835 (Diptera: Chironomidae) in Alpine streams (Ötztal Alps, Austria). *PloS one*, 19(2), e0298367.

Combosch DJ, et al. (2024) Barcoding and mitochondrial phylogenetics of *Porites* corals. *PloS one*, 19(2), e0290505.

López-Sánchez R, et al. (2024) Metagenomic analysis of carbohydrate-active enzymes and their contribution to marine sediment biodiversity. *World journal of microbiology & biotechnology*, 40(3), 95.

Hofstaedter CE, et al. (2024) Divergent *Pseudomonas aeruginosa* LpxO enzymes perform site-specific lipid A 2-hydroxylation. *mBio*, 15(2), e0282323.

Carruthers T, et al. (2024) Repeated upslope biome shifts in *Saxifraga* during late-Cenozoic climate cooling. *Nature communications*, 15(1), 1100.

Chaowvieng A, et al. (2024) ?Molecular phylogeny and taxonomic position of *Macrobrachium lancesteri* (De Man, 1911), with descriptions of two new species from Thailand (Decapoda, Caridea, Palaemonidae). *ZooKeys*, 1190, 163.