

Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

[ape](#)

RRID:SCR_017343

Type: Tool

Proper Citation

ape (RRID:SCR_017343)

Resource Information

URL: <https://CRAN.R-project.org/package=ape>

Proper Citation: ape (RRID:SCR_017343)

Description: Software R package for analysis of phylogenetics and evolution. Environment for modern phylogenetics and evolutionary analyses in R.

Synonyms: ape 3.0, ape 5.0, Analysis of Phylogenetics and Evolution

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

Defining Citation: [PMID:30016406](#), [PMID:14734327](#), [PMID:22495750](#)

Keywords: analysis, phylogenetics, evolution, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: ape

Resource ID: SCR_017343

Alternate IDs: biotools:ape

Alternate URLs: <https://cran.r-project.org/web/packages/ape/ape.pdf>, <http://ape-package.ird.fr/>, <https://bio.tools/ape>

License: GPLv3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260801T042808+0000

Ratings and Alerts

No rating or validation information has been found for ape.

No alerts have been found for ape.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Ma H, et al. (2025) Microbial profile of the appendix niche in acute appendicitis: a novel sampling approach. FEBS open bio, 15(12), 2001.

Ma H, et al. (2025) Spatially Resolved Tumor Ecosystems and Cell States in Gastric Adenocarcinoma Progression and Evolution. Cancer discovery, 15(4), 767.

Moshiri N, et al. (2025) CompactTree: a lightweight header-only C++ library and Python wrapper for ultra-large phylogenetics. GigaByte (Hong Kong, China), 2025, gigabyte152.

Bertinetti C, et al. (2025) Phenotypic plasticity in visual opsin gene expression: a meta-analysis in teleost fish. The Journal of experimental biology, 228(13).

Dempsey E, et al. (2025) Protective Properties of the White Button Mushroom, *Agaricus bisporus*, in a Mouse Model of Colitis. Molecular nutrition & food research, e70133.

Christmas MJ, et al. (2025) Interpreting mammalian synonymous site conservation in light of the unwanted transcript hypothesis. Nature communications, 16(1), 2007.

Krueger ME, et al. (2025) Comparative analysis of Parkinson's and inflammatory bowel disease gut microbiomes reveals shared butyrate-producing bacteria depletion. NPJ Parkinson's disease, 11(1), 50.

Wilken AT, et al. (2025) Avian cranial kinesis is the result of increased encephalization during the origin of birds. Proceedings of the National Academy of Sciences of the United States of America, 122(13), e2411138122.

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

Menozzi E, et al. (2025) Exploring the relationship between GBA1 host genotype and gut microbiome in the GBA1 L444P/WT mouse model: implications for Parkinson's disease pathogenesis. Frontiers in neuroscience, 19, 1546203.

Youk J, et al. (2024) Quantitative and qualitative mutational impact of ionizing radiation on normal cells. Cell genomics, 4(2), 100499.

Wang M, et al. (2024) HIF α 1 and macrophage activation signalling pathways are potential biomarkers of invasive aspergillosis. *Experimental and therapeutic medicine*, 27(2), 86.

Weibel CA, et al. (2024) The protein domains of vertebrate species in which selection is more effective have greater intrinsic structural disorder. *eLife*, 12.

Tian WH, et al. (2024) Phylogenetic Insights Reveal New Taxa in Thyridariaceae and Massarinaceae. *Journal of fungi (Basel, Switzerland)*, 10(8).

Qin S, et al. (2024) Predicting the sequence-dependent backbone dynamics of intrinsically disordered proteins. *eLife*, 12.

Tian WH, et al. (2024) New and Interesting Pine-Associated Hyphomycetes from China. *Journal of fungi (Basel, Switzerland)*, 10(8).

Liu H, et al. (2024) Integrative molecular and spatial analysis reveals evolutionary dynamics and tumor-immune interplay of in situ and invasive acral melanoma. *Cancer cell*, 42(6), 1067.

Schall PZ, et al. (2023) Genome-wide methylation patterns from canine nanopore assemblies. *G3 (Bethesda, Md.)*, 13(11).

Olkkonen E, et al. (2023) Analysis of population structure and genetic diversity in low-variance Saimaa ringed seals using low-coverage whole-genome sequence data. *STAR protocols*, 4(4), 102567.

Turk Dermastia T, et al. (2023) Evaluation of the rbcL marker for metabarcoding of marine diatoms and inference of population structure of selected genera. *Frontiers in microbiology*, 14, 1071379.