

Resource Summary Report

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[phyloseq](#)

RRID:SCR_013080

Type: Tool

Proper Citation

phyloseq (RRID:SCR_013080)

Resource Information

URL: <http://www.bioconductor.org/packages/2.12/bioc/html/phyloseq.html>

Proper Citation: phyloseq (RRID:SCR_013080)

Description: Software for handling and analysis of high-throughput microbiome census data.

Abbreviations: phyloseq

Resource Type: software resource

Defining Citation: [DOI:10.1371/journal.pone.0061217](https://doi.org/10.1371/journal.pone.0061217)

Keywords: bio.tools

Resource Name: phyloseq

Resource ID: SCR_013080

Alternate IDs: OMICS_01520, biotools:phyloseq

Alternate URLs: <https://bio.tools/phyloseq>, <https://sources.debian.org/src/r-bioc-phyloseq/>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260821T193943+0000

Ratings and Alerts

No rating or validation information has been found for phyloseq.

No alerts have been found for phyloseq.

Data and Source Information

Usage and Citation Metrics

We found 3080 mentions in open access literature.

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

Deng S, et al. (2026) Repurposing of the Macrolide Antibiotic Clarithromycin for the Prevention of Lung Cancer. *Molecular cancer therapeutics*, 25(2), 283.

Hussain U, et al. (2026) Microbial communities in semi-mature oak trees are resilient to drought, nutrient limitation, and pathogen challenge. *Cell host & microbe*, 34(2), 344.

Fields BC, et al. (2026) High dietary fiber is associated with improved outcomes in patients with melanoma and sarcoma treated with immunotherapy regardless of gut microbiome dysbiosis and social vulnerability. *Cancer*, 132(6), e70335.

Chen S, et al. (2026) Diversity-triggered 2-naphthoic acid exudation recruits keystone microbial taxa to promote soybean drought tolerance. *Cell host & microbe*, 34(5), 844.

Parween S, et al. (2026) Host genome and bacterial taxa shape the Arabidopsis seed microbiome. *EMBO reports*, 27(1), 122.

Lobel L, et al. (2026) Dietary sulfur amino acids enhance anti-tumor immunity in colon cancer via an NKT cell-XCL1-cDC1 circuit. *Immunity*, 59(6), 1708.

Sinha A, et al. (2026) Prophage induction contributes to alterations in the gut phageome during intestinal inflammation. *Cell reports*, 45(7), 117491.

Estensmo EL, et al. (2026) Cecal microbiota and *Clostridium perfringens* in broilers fed barley-based diets: Effects of enzyme supplementation and degree of grinding. *Poultry science*, 105(4), 106543.

Lhoste E, et al. (2026) Seasons and vertical dynamics influence community composition in a flooded and abandoned mica mine. *FEMS microbiology ecology*, 102(2).

Li X, et al. (2026) Metabarcoding-based characterization of the boxwood root-zone soil microbiome. *BMC plant biology*, 26(1), 276.

Jacob SM, et al. (2026) The Oral Microbiome in Amyotrophic Lateral Sclerosis Shows Differentially Abundant Organisms in Limb Versus Bulbar Onset Disease: A Binational Study. *Journal of clinical neurology (Seoul, Korea)*, 22(1), 66.

Dalmasso M, et al. (2026) Plant species, metabolites, and environmental factors shape the phyllosphere microbiota of grazed grasslands. *Applied and environmental microbiology*, 92(2), e0128925.

Murdoch B, et al. (2026) Microbiota discovered in scorpion venom. *PloS one*, 21(1), e0328427.

Shubaita M, et al. (2026) Diet-responsive genetic determinants of intestinal colonization in the yeast *Candida albicans*. *mBio*, 17(1), e0243025.

Lien HM, et al. (2026) Anisomeles indica enriched with ovatodiolide protects against aspirin-induced gastric ulcers through gut microbiota modulation. *Biomedical journal*, 49(2), 100893.

Kato H, et al. (2026) Higher-dimensional ordination analysis teases out impacts of *Bradyrhizobium* bioaugmentation on native soil microbial communities. *Microbiology spectrum*, 14(4), e0288025.

Evenepoel M, et al. (2026) The role of the oxytocinergic system in oral microbiome composition in children with autism: evidence from a randomized controlled trial of intranasal oxytocin. *Translational psychiatry*, 16(1).

Mortensen GA, et al. (2026) Metagenomic profiling and predictive modeling of the gut microbiome reveal signatures of gestational disease. *Microbiology spectrum*, 14(5), e0315525.

Rahman FA, et al. (2026) Longitudinal analysis of broiler cecal microbiome: unraveling the species level dynamics across age and sex. *Poultry science*, 105(7), 106911.

Bian K, et al. (2026) Quantitative metagenomics using a portable protocol. *Applied and environmental microbiology*, 92(3), e0217925.