

Resource Summary Report

Generated by [dkNET](#) on Aug 27, 2026

[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 [dkNET](#) .

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

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.

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.

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.

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.

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

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

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

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.

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

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

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

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.

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.

Amsalu A, et al. (2026) Characterisation of the wound microbiome and antimicrobial resistance profiles in clinical isolates from epidermolysis bullosa patients. Orphanet journal of rare diseases, 21(1).

Sujeeth NK, et al. (2026) Microbiome signatures of mangroves and salt marsh halophyte rhizosphere soil sediments: a metagenomic approach. Scientific reports, 16(1).

Kim H, et al. (2026) Exploratory randomized trial of Weissella cibaria CMU and oral microbiome changes in peri implant mucositis. Scientific reports, 16(1).

Asiloglu R, et al. (2026) Predator-mediated local convergence fosters global microbial community divergence. Nature communications, 17(1).

Lee SC, et al. (2026) Functional divergence of the gut microbiome associated with lifestyle and helminth infection in Indigenous Peninsular Malaysian. Research square.

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.