Resource Summary Report

Generated by dkNET on Apr 29, 2025

vegan

RRID:SCR_011950
Type: Tool

Proper Citation

vegan (RRID:SCR_011950)

Resource Information

URL: http://cran.r-project.org/web/packages/vegan/index.html

Proper Citation: vegan (RRID:SCR_011950)

Description: Ordination methods, diversity analysis and other functions for community and vegetation ecologists.

Abbreviations: vegan

Synonyms: vegan: Community Ecology Package

Resource Type: software resource

Funding:

Resource Name: vegan

Resource ID: SCR_011950

Alternate IDs: OMICS_01523

Alternate URLs: https://sources.debian.org/src/r-cran-vegan/

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014602+0000

Ratings and Alerts

No rating or validation information has been found for vegan.

No alerts have been found for vegan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5420 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Wyatt NJ, et al. (2025) Evaluation of intestinal biopsy tissue preservation methods to facilitate large-scale mucosal microbiota research. EBioMedicine, 112, 105550.

Srinivas M, et al. (2025) Evaluating the efficiency of 16S-ITS-23S operon sequencing for species level resolution in microbial communities. Scientific reports, 15(1), 2822.

Calderón-Osorno M, et al. (2025) The influence of depth on the global deep-sea plasmidome. Scientific reports, 15(1), 2959.

Dobrzy?ski J, et al. (2025) Non-native PGPB consortium consisting of Pseudomonas sp. G31 and Azotobacter sp. PBC2 promoted winter wheat growth and slightly altered the native bacterial community. Scientific reports, 15(1), 3248.

Li HR, et al. (2025) Differential responses of root and leaf-associated microbiota to continuous monocultures. Environmental microbiome, 20(1), 13.

Özcan E, et al. (2025) Dietary fiber content in clinical ketogenic diets modifies the gut microbiome and seizure resistance in mice. Nature communications, 16(1), 987.

Beghini F, et al. (2025) Gut microbiome strain-sharing within isolated village social networks. Nature, 637(8044), 167.

Lalli MK, et al. (2025) Associations between dietary fibers and gut microbiome composition in the EDIA longitudinal infant cohort. The American journal of clinical nutrition, 121(1), 83.

Blattner LA, et al. (2025) Sediment Core DNA-Metabarcoding and Chitinous Remain Identification: Integrating Complementary Methods to Characterise Chironomidae Biodiversity in Lake Sediment Archives. Molecular ecology resources, 25(1), e14035.

Alam Y, et al. (2025) Variation in human gut microbiota impacts tamoxifen pharmacokinetics. mBio, 16(1), e0167924.

Dimpor JJ, et al. (2025) Identifying spatiotemporal patterns and drivers of fecal indicator

bacteria in an urban lake for water quality assessment and management. Heliyon, 11(1), e40955.

Chan DTC, et al. (2025) Fine-Tuning Genetic Circuits via Host Context and RBS Modulation. ACS synthetic biology, 14(1), 193.

Battistolli M, et al. (2025) The circadian clock gene period regulates the composition and daily bacterial load of the gut microbiome in Drosophila melanogaster. Scientific reports, 15(1), 1016.

Feng Y, et al. (2025) Regional antimicrobial resistance gene flow among the One Health sectors in China. Microbiome, 13(1), 3.

Guan W, et al. (2025) Signature of pre-pregnancy microbiome in infertile women undergoing frozen embryo transfer with gestational diabetes mellitus. NPJ biofilms and microbiomes, 11(1), 6.

Bromaghin JF, et al. (2025) The importance of method selection when estimating diet composition with quantitative fatty acid signature analysis. PloS one, 20(1), e0308283.

Hussain U, et al. (2025) Peptide nucleic acid (PNA) clamps reduce amplification of host chloroplast and mitochondria rRNA gene sequences and increase detected diversity in 16S rRNA gene profiling analysis of oak-associated microbiota. Environmental microbiome, 20(1), 14.

Defendini H, et al. (2025) The release of sexual conflict after sex loss is associated with evolutionary changes in gene expression. Proceedings. Biological sciences, 292(2039), 20242631.

Biguenet A, et al. (2025) Genomic epidemiology of third-generation cephalosporin-resistant Escherichia coli from companion animals and human infections in Europe. One health (Amsterdam, Netherlands), 20, 100971.

Wang M, et al. (2025) Fecal Microbiome and Metabolomic Profiles of Mixed-Fed Infants Are More Similar to Formula-Fed than Breastfed Infants. Microorganisms, 13(1).