

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

phylobase

RRID:SCR_024292

Type: Tool

Proper Citation

phylobase (RRID:SCR_024292)

Resource Information

URL: <https://cran.r-project.org/package=phylobase>

Proper Citation: phylobase (RRID:SCR_024292)

Description: Software R package provides base S4 class for comparative methods, incorporating one or more trees and trait data. Used for phylogenetic analysis.

Resource Type: software resource, software toolkit

Keywords: associate, manipulate, explore, plot, phylogenetic trees and data, phylogenetic analysis,

Availability: Free, Available for download, Freely available,

Resource Name: phylobase

Resource ID: SCR_024292

Alternate URLs: <https://sources.debian.org/src/r-cran-phylobase/>

License: GPL-2 | GPL-3 [expanded from: GPL (? 2)]

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260919T195622+0000

Ratings and Alerts

No rating or validation information has been found for phylobase.

No alerts have been found for phylobase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Chaguza C, et al. (2023) The population-level impact of Enterococcus faecalis genetics on intestinal colonization and extraintestinal infection. Microbiology spectrum, 11(6), e0020123.

Chaguza C, et al. (2022) Population genomics of Group B Streptococcus reveals the genetics of neonatal disease onset and meningeal invasion. Nature communications, 13(1), 4215.