

Resource Summary Report

Generated by RRID on Aug 15, 2026

tibble

RRID:SCR_026493

Type: Tool

Proper Citation

tibble (RRID:SCR_026493)

Resource Information

URL: <https://tibble.tidyverse.org/>

Proper Citation: tibble (RRID:SCR_026493)

Description: Software package for modern re-imagining of data frame. Provides 'tbl_df' class with stricter checking and better formatting than traditional data frame.

Resource Type: software toolkit, source code, software resource

Keywords: modern re-imagining of data frame, modern data frame, data frame,

Availability: Free, Available for download, Freely available

Resource Name: tibble

Resource ID: SCR_026493

Alternate URLs: <https://github.com/tidyverse/tibble>

License: MIT license

Record Creation Time: 20250305T060325+0000

Record Last Update: 20260815T042917+0000

Ratings and Alerts

No rating or validation information has been found for tibble.

No alerts have been found for tibble.

Data and Source Information

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Clemens E, et al. (2026) Cap-adjacent 2'-O-ribose methylation of RNA in *C. elegans* is required for postembryonic growth and germline development in the presence of the decapping exonuclease EOL-1. *Nucleic acids research*, 54(8).

Allen AM, et al. (2026) Differential neuronal survival defines a novel axis of sexual dimorphism in the *Drosophila* brain. *Cell genomics*, 101125.

Clemens E, et al. (2025) Cap-adjacent 2'-O-ribose methylation of RNA in *C. elegans* is required for postembryonic growth and germline development in the presence of the decapping exonuclease EOL-1. *bioRxiv : the preprint server for biology*.

Stefanatos R, et al. (2025) Developmental mitochondrial complex I activity determines lifespan. *EMBO reports*, 26(8), 1957.

Allen AM, et al. (2025) A high-resolution atlas of the brain predicts lineage and birth order underlying neuronal identity. *Cell genomics*, 101103.

Specker F, et al. (2024) Treemendous: an R package for integrating taxonomic information across backbones. *PeerJ*, 12, e16896.

Han J, et al. (2023) AmpSeqR: an R package for amplicon deep sequencing data analysis. *F1000Research*, 12, 327.