

Resource Summary Report

Generated by PRECISE-TBI on Sep 18, 2026

dplyr

RRID:SCR_016708

Type: Tool

Proper Citation

dplyr (RRID:SCR_016708)

Resource Information

URL: <https://cran.r-project.org/web/packages/dplyr/index.html>

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Description: Software tool for working with data frame like objects, both in memory and out of memory. It is a grammar of data manipulation, providing a consistent set of verbs that help you solve the most common data manipulation challenges: mutate, select, filter, summarise, arrange.

Resource Type: data analysis software, data processing software, software application, software resource

Keywords: data, frame, object, in and of memory, grammar, manipulation, set, verb, mutate, select, filter, summarise, arrange

Availability: Open Source, Available for download

Resource Name: dplyr

Resource ID: SCR_016708

Alternate URLs: <https://github.com/tidyverse/dplyr>, <https://dplyr.tidyverse.org/>

License: MIT

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T195843+0000

Ratings and Alerts

No rating or validation information has been found for dplyr.

No alerts have been found for dplyr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 264 mentions in open access literature.

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

Lee JB, et al. (2026) Lazertinib with stereotactic body radiotherapy in oligometastatic EGFR-mutant non-small-cell lung cancer. ESMO open, 11(2), 106057.

Tan K, et al. (2026) Protocol to produce and apply barcoded rabies virus for single-neuron input mapping in mice. STAR protocols, 7(2), 104537.

Murugu L, et al. (2026) Protocol for total internal reflection fluorescence microscopy image preprocessing and radial analysis of LFA-1 in T cell immune synapses. STAR protocols, 7(3), 104636.

Hassan AZ, et al. (2026) Orobas: A computational approach for scoring and analysis of quantitative chemical-genetic interactions from CRISPR-Cas9 screens. STAR protocols, 7(2), 104594.

Fei L, et al. (2026) barbieQ: an R software package for analysing barcode count data from clonal tracking experiments. Bioinformatics (Oxford, England), 42(6).

Bartenschlager F, et al. (2026) Proteomic profiling of equine airway mucus reveals compositional changes in asthmatic phenotypes. Scientific reports, 16(1), 5880.

Pachernegg S, et al. (2026) The emergence of multiple testicular cell lineages in human stem cell-derived testis-like organoids. Development (Cambridge, England), 153(5).

Scimone ML, et al. (2026) Single-cell transcriptomics and RNAi screening define a hierarchical program of planarian eye regeneration. Cell reports, 45(4), 117245.

Fuhrmann E, et al. (2026) Extended poly(A) tails are a shared feature of herpesvirus mRNAs. PLoS pathogens, 22(6), e1014341.

De Angelis F, et al. (2026) Temporal shifts in polygenic traits track major epidemics in Western Eurasia. bioRxiv : the preprint server for biology.

Oberg AL, et al. (2026) Pancreatic Cancer Detection Consortium Biomarker Bakeoff: A Phase II Blinded Biomarker Validation and Panel Discovery Study. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2438.

Gause EL, et al. (2026) Data needs for accelerating research at the intersection of climate stressors and health: an online survey. Environmental research, health : ERH, 4(1), 015007.

Honda T, et al. (2026) CRAGE-RB-PI-seq reveals transcriptional dynamics of plant-associated bacteria during root colonization. *Nature communications*, 17(1).

Khan MY, et al. (2026) Long non-coding RNA LINC00607 epigenetically regulates endothelial TSPAN18 to promote hypoxia-induced thromboinflammation. *The Journal of biological chemistry*, 302(3), 111186.

Mouli K, et al. (2026) SOD1 at the Crossroads: Co-Overexpression of Canonical Antioxidant Response and Noncanonical Hydrogen Sulfide Generation Pathways in Down Syndrome, With Immune Cell Implications. *Research square*.

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).

Pereus D, et al. (2026) Genetic metrics decode *Plasmodium falciparum* diversity: complexity of infection, parasite connectivity, and transmission intensity in Mainland Tanzania's diverse regions. *Frontiers in genetics*, 17, 1695073.

Ortega-Retuerta E, et al. (2026) Changes in DOM Quality Determine Prokaryotic Activities and Extracellular Release in the NW Mediterranean Sea: An Experimental Approach. *Environmental microbiology reports*, 18(3), e70288.

Walker MN, et al. (2026) Stepwise Protocol for Alternative Splicing Analysis in Single-Cell SMART-Seq2 RNA-Seq Data. *Bio-protocol*, 16(12), e5735.

Hall BL, et al. (2026) Changes in interlimb coordination induced by within-stride changes in treadmill speed. *Journal of neurophysiology*, 136(1), 48.