

Resource Summary Report

Generated by ASWG on Aug 9, 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: software resource, software application, data analysis software, data processing software

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: 20260808T190100+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 [ASWG](#) .

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.

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.

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.

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.