Resource Summary Report

Generated by dkNET on Apr 24, 2025

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

Proper Citation: dplyr (RRID:SCR_016708)

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, filer, summerise, arrange.

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

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

Funding:

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: 20250423T060930+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 140 mentions in open access literature.

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

Santo B, et al. (2025) Exploring the utility of snRNA-seq in profiling human bladder tissue: A comprehensive comparison with scRNA-seq. iScience, 28(1), 111628.

Olweny G, et al. (2025) Protocol for identifying Mycobacterium tuberculosis infection status through airway microbiome profiling. STAR protocols, 6(1), 103574.

Soni J, et al. (2025) Protocol for investigating intracellular microbial diversity using single-cell RNA-seq in immune cells of SARS-CoV-2-positive and recovered patients. STAR protocols, 6(1), 103546.

Allman A, et al. (2025) Splenic fibroblasts control marginal zone B cell movement and function via two distinct Notch2-dependent regulatory programs. Immunity, 58(1), 143.

Delalay G, et al. (2025) The use of scenario tree models in support of animal health surveillance: A scoping review. Preventive veterinary medicine, 234, 106371.

Liao K, et al. (2024) Spatial and single-nucleus transcriptomics decoding the molecular landscape and cellular organization of avian optic tectum. iScience, 27(2), 109009.

Hoersten J, et al. (2024) Engineering spacer specificity of the Cre/loxP system. Nucleic acids research, 52(13), 8017.

Borgmästars E, et al. (2024) Multi-omics profiling to identify early plasma biomarkers in pre-diagnostic pancreatic ductal adenocarcinoma: a nested case-control study. Translational oncology, 48, 102059.

Garschall K, et al. (2024) The cellular basis of feeding-dependent body size plasticity in sea anemones. Development (Cambridge, England), 151(20).

Wang K, et al. (2024) Protocol for fast clonal family inference and analysis from large-scale B cell receptor repertoire sequencing data. STAR protocols, 5(2), 102969.

Haimlich S, et al. (2024) Widespread horizontal gene transfer between plants and bacteria. ISME communications, 4(1), ycae073.

Mozin E, et al. (2024) Dystrophin deficiency impairs cell junction formation during embryonic myogenesis from pluripotent stem cells. iScience, 27(7), 110242.

Sharker Y, et al. (2024) Pairwise Accelerated Failure Time Regression Models for Infectious Disease Transmission in Close-Contact Groups With External Sources of Infection. Statistics in medicine, 43(27), 5138.

Golov AK, et al. (2024) A genome-wide nucleosome-resolution map of promoter-centered interactions in human cells corroborates the enhancer-promoter looping model. eLife, 12.

Klooster IT, et al. (2024) A systematic review on eHealth technology personalization approaches. iScience, 27(9), 110771.

Alahdab F, et al. (2024) Development and validation of a machine learning model to predict myocardial blood flow and clinical outcomes from patients' electrocardiograms. Cell reports. Medicine, 5(10), 101746.

Sun N, et al. (2024) Establishing a 3D culture system for early organogenesis of monkey embryos ex vivo and single-cell transcriptome analysis of cultured embryos. STAR protocols, 5(1), 102835.

Kerzel T, et al. (2024) VisualZoneR: A computational protocol to identify compartmental zones from single-cell spatial transcriptomics using R. STAR protocols, 5(3), 103196.

Muse VP, et al. (2024) Protocol for EHR laboratory data preprocessing and seasonal adjustment using R and RStudio. STAR protocols, 5(1), 102912.

Kirk AM, et al. (2024) DNAJB1-PRKACA fusion neoantigens elicit rare endogenous T cell responses that potentiate cell therapy for fibrolamellar carcinoma. Cell reports. Medicine, 5(3), 101469.