

Resource Summary Report

Generated by [dkNET](#) on Apr 25, 2025

reshape2

RRID:SCR_022679

Type: Tool

Proper Citation

reshape2 (RRID:SCR_022679)

Resource Information

URL: <https://cran.r-project.org/web/packages/reshape2/index.html>

Proper Citation: reshape2 (RRID:SCR_022679)

Description: Software R package to flexible rearrange, reshape and aggregate data. Reshape2 is reboot of reshape package.

Resource Type: software resource, software toolkit

Keywords: flexible rearrange data, reshape data, aggregate data

Funding:

Availability: Free, Available for download, Freely available

Resource Name: reshape2

Resource ID: SCR_022679

License: MIT

Record Creation Time: 20220817T050143+0000

Record Last Update: 20250422T060259+0000

Ratings and Alerts

No rating or validation information has been found for reshape2.

No alerts have been found for reshape2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 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.

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.

Najafi A, et al. (2024) Protocol for inferring epithelial-to-mesenchymal transition trajectories from single-cell RNA sequencing data using R. *STAR protocols*, 5(1), 102819.

Hodonsky CJ, et al. (2024) Multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci. *Cell genomics*, 4(1), 100465.

Liu G, et al. (2024) Identification of mitochondria-related gene biomarkers associated with immune infiltration in acute myocardial infarction. *iScience*, 27(7), 110275.

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.

Rietz M, et al. (2024) Facilitating ambulatory heart rate variability analysis using accelerometry-based classifications of body position and self-reported sleep. *Physiological measurement*, 45(5).

Ascenção C, et al. (2024) A TOPBP1 allele causing male infertility uncouples XY silencing dynamics from sex body formation. *eLife*, 12.

Nodari R, et al. (2023) Computational protocol to perform a spatiotemporal reconstruction of an epidemic. *STAR protocols*, 4(4), 102548.

Berard AR, et al. (2023) Vaginal epithelial dysfunction is mediated by the microbiome, metabolome, and mTOR signaling. *Cell reports*, 42(5), 112474.