

Resource Summary Report

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[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

Availability: Free, Available for download, Freely available

Resource Name: reshape2

Resource ID: SCR_022679

License: MIT

Record Creation Time: 20220817T050143+0000

Record Last Update: 20260801T042854+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 19 mentions in open access literature.

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

Meghdadi B, et al. (2026) Digital twins for in vivo metabolic flux estimations in patients with brain cancer. *Cell metabolism*, 38(1), 228.

Zeng D, et al. (2025) Evaluation of seven fermentation methods for enhancing the fertilizer potential of the liquid fraction of cow manure. *Scientific reports*, 15(1), 36537.

Landi D, et al. (2025) A Checkpoint Reversal Receptor Mediates Bipartite Activation and Enhances CAR T-cell Function. *Cancer research communications*, 5(3), 527.

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.

Hu Q, et al. (2025) Circulating tumor DNA monitoring detects minimal residual disease and predicts outcomes in patients with esophageal adenocarcinoma or squamous cell carcinoma after esophagectomy. *BJC reports*, 3(1), 52.

Ackermann RE, et al. (2025) Temporal changes in the bacterial microbiome of the salivary gland and midgut tissues of *Rhipicephalus sanguineus* (s.l.) ticks in South Africa. *Scientific reports*, 15(1), 17434.

Wagoner ZW, et al. (2025) Systems immunology analysis of human immune organoids identifies host-specific correlates of protection to different influenza vaccines. *Cell stem cell*, 32(4), 529.

Sureshchandra S, et al. (2025) Deep profiling of human T cells defines compartmentalized clones and phenotypic trajectories across blood and tonsils. *Immunity*, 58(12), 3130.

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.

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

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

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.

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.

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

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.

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).

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

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

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