

Resource Summary Report

Generated by [kravitz2](#) on Aug 25, 2026

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: 20260821T194222+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 21 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Al Souz J, et al. (2026) Organ injury in systemic autoimmunity is mediated by stem-like CD8+ T cells arising from tissue-draining lymph nodes. *Immunity*, 59(6), 1667.

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.

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.

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.

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.

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.

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.

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

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).

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

Zhang YW, et al. (2023) Metabolic and transcriptomic analyses elucidate a novel insight into the network for biosynthesis of carbohydrate and secondary metabolites in the stems of a medicinal orchid *Dendrobium nobile*. Plant diversity, 45(3), 326.