

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

RColorBrewer

RRID:SCR_016697

Type: Tool

Proper Citation

RColorBrewer (RRID:SCR_016697)

Resource Information

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

Proper Citation: RColorBrewer (RRID:SCR_016697)

Description: Software tool to provide color schemes for maps and other graphics. R package to create colorful graphs with pre-made color palettes that visualize data.

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

Keywords: color, palette, scheme, map, graph, visualize, data

Availability: Free, Available for download, Freely available

Resource Name: RColorBrewer

Resource ID: SCR_016697

Alternate URLs: <http://colorbrewer2.org/#type=sequential&scheme=BuGn&n=3>

License: Apache licence 2.0

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260912T195843+0000

Ratings and Alerts

No rating or validation information has been found for RColorBrewer.

No alerts have been found for RColorBrewer.

Data and Source Information

Usage and Citation Metrics

We found 85 mentions in open access literature.

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

Schulz A, et al. (2026) LAMA5 links extracellular matrix organization to a candidate WNT-associated endothelial signaling niche during human chondrogenesis. *iScience*, 29(8), 116687.

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

Alvaro-Espinosa L, et al. (2026) MIF-Induced CD74+ Microglia and Macrophages Promote Progression of Brain Metastasis and Are Clinically Relevant across Central Nervous System Disorders. *Cancer research*, 86(13), 3249.

Cao T, et al. (2026) Astrocyte-microglia crosstalk via CSF1 and IFN- γ promotes central nervous system repair. *Cell reports*, 45(6), 117418.

Kondi T, et al. (2025) ShinyScreen: mass spectrometry data inspection and quality checking utility. *Journal of cheminformatics*, 17(1), 98.

Stefanatos R, et al. (2025) Developmental mitochondrial complex I activity determines lifespan. *EMBO reports*, 26(8), 1957.

Berger AH, et al. (2025) High-resolution transcriptional impact of AIRE: effects of pathogenic variants p.Arg257Ter, p.Cys311Tyr, and polygenic risk variant p.Arg471Cys. *Frontiers in immunology*, 16, 1572789.

Mondragon-Estrada E, et al. (2025) Protocol to analyze deep-learning-predicted functional scores for noncoding de novo variants and their correlation with complex brain traits. *STAR protocols*, 6(2), 103738.

Maneiro R, et al. (2025) Application of association rules to ball possessions in professional men's football. *Frontiers in psychology*, 16, 1527437.

Ellegaard KM, et al. (2025) SARS-CoV-2 sequencing artifacts associated with targeted PCR enrichment and read mapping. *PloS one*, 20(10), e0334009.

Xiong EH, et al. (2025) Protocol to identify genes important for *Candida albicans* fitness in diverse environmental conditions using pooled bar-seq screening approach. *STAR protocols*, 6(1), 103645.

Vandana JJ, et al. (2025) ChemPerturb-seq screen identifies a small molecule cocktail enhancing human beta cell survival after subcutaneous transplantation. *Cell stem cell*, 32(8), 1299.

Lall D, et al. (2025) An organ-chip model of sporadic ALS using iPSC-derived spinal cord motor neurons and an integrated blood-brain-like barrier. *Cell stem cell*, 32(7), 1139.

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. *Nature*, 643(8070), 252.

Okoye GD, et al. (2025) Single-cell map of innate-like lymphocyte response to *Francisella tularensis* infection reveals interleukin-17-dependent protection by MAIT cells. *iScience*, 28(3), 111810.

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. *Cell reports*, 45(1), 116748.

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.

Lanciano S, et al. (2024) Locus-level L1 DNA methylation profiling reveals the epigenetic and transcriptional interplay between L1s and their integration sites. *Cell genomics*, 4(2), 100498.

Liu Y, et al. (2024) Protocol for using scCURE to construct an immunotherapy outcome prediction model. *STAR protocols*, 5(4), 103476.

Dhabalia Ashok A, et al. (2024) Evolutionary assembly of the plant terrestriallization toolkit from protein domains. *Proceedings. Biological sciences*, 291(2027), 20240985.