

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## RColorBrewer

RRID:SCR\_016697

Type: Tool

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### Proper Citation

RColorBrewer (RRID:SCR\_016697)

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### 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:** software application, data visualization software, data processing software, 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:** 20260728T043521+0000

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### Ratings and Alerts

No rating or validation information has been found for RColorBrewer.

No alerts have been found for RColorBrewer.

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### Data and Source Information

## Usage and Citation Metrics

We found 80 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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

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

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

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

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.

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.

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.

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.

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

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.

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.

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

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.

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.

Chang T, et al. (2024) Genomic representativeness and chimerism in large collections of SAGs and MAGs of marine prokaryoplankton. *Microbiome*, 12(1), 126.

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.