

Resource Summary Report

Generated by T1D on Aug 2, 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 visualization software, software application, 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: 20260801T190550+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 80 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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.