Resource Summary Report

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

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

Funding:

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: 20250501T081348+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 66 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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 terrestrialization toolkit from protein domains. Proceedings. Biological sciences, 291(2027), 20240985.

Bhosle A, et al. (2024) Integrated annotation prioritizes metabolites with bioactivity in inflammatory bowel disease. Molecular systems biology, 20(4), 338.

Zhou SO, et al. (2024) The evolution of constitutively active humoral immune defenses in Drosophila populations under high parasite pressure. PLoS pathogens, 20(1), e1011729.

Liu D, et al. (2024) Protocol for analyzing plasma cell-free DNA fragment end motifs from ultra-low-pass whole-genome sequencing. STAR protocols, 5(4), 103357.

Haimlich S, et al. (2024) Widespread horizontal gene transfer between plants and bacteria. ISME communications, 4(1), ycae073.

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.

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.

Hoyer MJ, et al. (2024) Combinatorial selective ER-phagy remodels the ER during neurogenesis. Nature cell biology, 26(3), 378.

Xu S, et al. (2024) Protocol to process crosslinking and immunoprecipitation data into annotated binding sites. STAR protocols, 5(2), 103040.

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).

Lehle JD, et al. (2024) An in vitro approach reveals molecular mechanisms underlying endocrine disruptor-induced epimutagenesis. eLife, 13.

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

Li C, et al. (2023) TimiGP: An R package to depict the tumor microenvironment from bulk transcriptomics. STAR protocols, 4(4), 102742.

Chuhma N, et al. (2023) The dopamine neuron synaptic map in the striatum. Cell reports, 42(3), 112204.

Álvarez-Prado ÁF, et al. (2023) Immunogenomic analysis of human brain metastases reveals diverse immune landscapes across genetically distinct tumors. Cell reports. Medicine, 4(1), 100900.

Lin YL, et al. (2023) Induced regeneration of articular cartilage - identification of a dormant regeneration program for a non-regenerative tissue. Development (Cambridge, England), 150(21).

Younginger BS, et al. (2023) Enrichment of oral-derived bacteria in inflamed colorectal tumors and distinct associations of Fusobacterium in the mesenchymal subtype. Cell reports. Medicine, 4(2), 100920.