Resource Summary Report

Generated by NIF on Apr 21, 2025

devtools

RRID:SCR_016961
Type: Tool

Proper Citation

devtools (RRID:SCR_016961)

Resource Information

URL: https://cran.r-project.org/web/packages/devtools/index.html

Proper Citation: devtools (RRID:SCR_016961)

Description: Software tools to make developing R packages easier by providing R functions that simplify and expedite common tasks.

Resource Type: software toolkit, software resource

Keywords: make, developing, R, package, easier

Funding:

Availability: Free, Available for download, Freely available

Resource Name: devtools

Resource ID: SCR_016961

License: GPL 3

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250420T015818+0000

Ratings and Alerts

No rating or validation information has been found for devtools.

No alerts have been found for devtools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Hargadon AC, et al. (2024) An acidic microenvironment produced by the V-type ATPase of Euprymna scolopes promotes specificity during Vibrio fischeri recruitment. Communications biology, 7(1), 1642.

Bai W, et al. (2024) Protocol to detect immune levels, abnormal metabolism, and signaling pathways in tumor tissue based on scRNA-seq obtained from patient databases. STAR protocols, 5(2), 103065.

Chen Z, et al. (2024) Protocol for directly selecting cell type marker genes for single-cell clustering analyses by Festem. STAR protocols, 6(1), 103514.

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

Agarwala S, et al. (2023) Enrichment of carcinogen-driven "mitochondria-primed" human skin stem cells and their identification using single-cell analyses. STAR protocols, 4(3), 102545.

Alfonso-Gonzalez C, et al. (2023) Identification of regulatory links between transcription and RNA processing with long-read sequencing. STAR protocols, 4(4), 102505.

Li C, et al. (2023) TimiGP: Inferring cell-cell interactions and prognostic associations in the tumor immune microenvironment through gene pairs. Cell reports. Medicine, 4(7), 101121.

Zhong X, et al. (2023) Disturbance of skin sensation and autism spectrum disorder: A bidirectional Mendelian randomization study. Brain and behavior, 13(11), e3238.

Takada H, et al. (2023) Single-cell transcriptomics uncovers EGFR signaling-mediated gastric progenitor cell differentiation in stomach homeostasis. Nature communications, 14(1), 3750.

Guthrie L, et al. (2022) Impact of a 7-day homogeneous diet on interpersonal variation in human gut microbiomes and metabolomes. Cell host & microbe, 30(6), 863.

Xi NM, et al. (2021) Protocol for executing and benchmarking eight computational doublet-detection methods in single-cell RNA sequencing data analysis. STAR protocols, 2(3), 100699.

Wastyk HC, et al. (2021) Gut-microbiota-targeted diets modulate human immune status.

Cell, 184(16), 4137.

Wogsland CE, et al. (2021) High-dimensional immunotyping of tumors grown in obese and non-obese mice. Disease models & mechanisms, 14(4).

Sabik OL, et al. (2021) A computational approach for identification of core modules from a co-expression network and GWAS data. STAR protocols, 2(3), 100768.

Ghandikota S, et al. (2021) Computational workflow for functional characterization of COVID-19 through secondary data analysis. STAR protocols, 2(4), 100873.

Sardiu ME, et al. (2020) Generating topological protein interaction scores and data visualization with TopS. Methods (San Diego, Calif.), 184, 13.