Resource Summary Report

Generated by dkNET on May 8, 2025

readxl

RRID:SCR_018083
Type: Tool

Proper Citation

readxl (RRID:SCR_018083)

Resource Information

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

Proper Citation: readxl (RRID:SCR_018083)

Description: Software R package to import excel files into R. Has no external dependencies for easy installment and use on all operating systems. Designed to work with tabular data.

Synonyms: Read Excel Files into R

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

Keywords: Import excel files, tabular data, data processing, excel file into R

Funding:

Availability: Free, Available for download, Freely available

Resource Name: readxl

Resource ID: SCR_018083

Alternate URLs: https://readxl.tidyverse.org/, https://github.com/tidyverse/readxl

License: GNU GPL

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250508T065817+0000

Ratings and Alerts

No rating or validation information has been found for readxl.

No alerts have been found for readxl.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Lykke-Andersen S, et al. (2024) Protocol for generating customizable and reproducible plots of sequencing coverage data using the seqNdisplayR package. STAR protocols, 5(2), 102960.

Kerstens M, et al. (2024) PLETHORA transcription factors promote early embryo development through induction of meristematic potential. Development (Cambridge, England), 151(12).

Perkins MA, et al. (2024) Protocol for programing a degree-to-careers dashboard in R using Posit and Shiny. STAR protocols, 5(1), 102902.

Ruehrmund L, et al. (2024) Protocol for visualizing complex volatile metabolomics data in clinical setups using EDaViS software. STAR protocols, 5(1), 102808.

Giovannetti M, et al. (2024) SIN-3 transcriptional coregulator maintains mitochondrial homeostasis and polyamine flux. iScience, 27(5), 109789.

Blaszczak W, et al. (2024) Protocol for separating cancer cell subpopulations by metabolic activity using flow cytometry. STAR protocols, 5(2), 103105.

Spiegelhalder RP, et al. (2024) Dual role of BdMUTE during stomatal development in the model grass Brachypodium distachyon. Development (Cambridge, England), 151(20).

Fuchs Wightman F, et al. (2024) Influence of RNA circularity on Target RNA-Directed MicroRNA Degradation. Nucleic acids research, 52(6), 3358.

Yuan Z, et al. (2024) Longitudinal cohort study highlights cancer-preventive benefits of lipid-lowering drugs. iScience, 27(9), 110680.

House RRJ, et al. (2024) ceas: an R package for Seahorse data analysis and visualization. Bioinformatics (Oxford, England), 40(8).

Carrick BH, et al. (2024) PUF partner interactions at a conserved interface shape the RNA-

binding landscape and cell fate in Caenorhabditis elegans. Developmental cell, 59(5), 661.

Reynolds RH, et al. (2023) Local genetic correlations exist among neurodegenerative and neuropsychiatric diseases. NPJ Parkinson's disease, 9(1), 70.

Nolden KA, et al. (2023) Human Fis1 directly interacts with Drp1 in an evolutionarily conserved manner to promote mitochondrial fission. The Journal of biological chemistry, 299(12), 105380.

Tsuyuzaki K, et al. (2023) Non-negative tensor factorization workflow for time series biomedical data. STAR protocols, 4(3), 102318.

Vannetti SM, et al. (2023) Amoeba species colonizing the gills of rainbow trout (Oncorhynchus mykiss) in Swiss aquaculture. Journal of fish diseases, 46(9), 987.

Larkins-Ford J, et al. (2022) Design principles to assemble drug combinations for effective tuberculosis therapy using interpretable pairwise drug response measurements. Cell reports. Medicine, 3(9), 100737.

Ahmaderaghi B, et al. (2022) Molecular Subtyping Resource: a user-friendly tool for rapid biological discovery from transcriptional data. Disease models & mechanisms, 15(3).

Okoh OS, et al. (2022) Epidemiology and genetic diversity of SARS-CoV-2 lineages circulating in Africa. iScience, 25(3), 103880.

Esposito E, et al. (2022) Mitotic checkpoint gene expression is tuned by codon usage bias. The EMBO journal, 41(15), e107896.

Wu S, et al. (2021) Deep computational analysis details dysregulation of eukaryotic translation initiation complex eIF4F in human cancers. Cell systems, 12(9), 907.