

# Resource Summary Report

Generated by ASWG on Aug 3, 2026

## readxl

RRID:SCR\_018083

Type: Tool

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### Proper Citation

readxl (RRID:SCR\_018083)

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### 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 resource, data processing software, software application

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

**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:** 20260803T040745+0000

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### 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 27 mentions in open access literature.

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

Li Y, et al. (2025) Enhanced prognostic and immunomodulatory effects of novel cuproptosis-related long noncoding RNAs in wilms tumor. *Frontiers in molecular biosciences*, 12, 1566551.

Fuhrmann E, et al. (2025) Extended poly(A) tails are a shared feature of herpesvirus mRNAs. *bioRxiv : the preprint server for biology*.

Priego-Cubero S, et al. (2025) Evolution and diversification of the momilactone biosynthetic gene cluster in the genus *Oryza*. *The New phytologist*, 245(6), 2681.

Scial?? C, et al. (2025) Seeded aggregation of TDP-43 induces its loss of function and reveals early pathological signatures. *Neuron*, 113(10), 1614.

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.

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.

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

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.

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

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

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

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

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.

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