

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

rsync

RRID:SCR_003113

Type: Tool

Proper Citation

rsync (RRID:SCR_003113)

Resource Information

URL: <http://rsync.samba.org/>

Proper Citation: rsync (RRID:SCR_003113)

Description: Software that provides rapid incremental file transfer.

Resource Type: software resource, source code

Keywords: file transfer

Availability: Free, Available for download, Freely available

Resource Name: rsync

Resource ID: SCR_003113

Alternate IDs: nlx_156711

License: GNU General Public License

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260731T042648+0000

Ratings and Alerts

No rating or validation information has been found for rsync.

No alerts have been found for rsync.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Fraga-González G, et al. (2025) Affording reusable data: recommendations for researchers from a data-intensive project. *Scientific data*, 12(1), 258.

B?inda K, et al. (2023) Efficient and Robust Search of Microbial Genomes via Phylogenetic Compression. *bioRxiv : the preprint server for biology*.

Julian AT, et al. (2021) 3DFI: a pipeline to infer protein function using structural homology. *Bioinformatics advances*, 1(1).

Blondel L, et al. (2021) Evolution of a Cytoplasmic Determinant: Evidence for the Biochemical Basis of Functional Evolution of the Novel Germ Line Regulator Oskar. *Molecular biology and evolution*, 38(12), 5491.

Lee V, et al. (2020) Evaluation of a digital triage platform in Uganda: A quality improvement initiative to reduce the time to antibiotic administration. *PloS one*, 15(10), e0240092.

Turnbull MG, et al. (2018) Related Endogenous Retrovirus-K Elements Harbor Distinct Protease Active Site Motifs. *Frontiers in microbiology*, 9, 1577.

Lampa S, et al. (2013) Lessons learned from implementing a national infrastructure in Sweden for storage and analysis of next-generation sequencing data. *GigaScience*, 2(1), 9.