

Resource Summary Report

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parallel-fastq-dump

RRID:SCR_024150

Type: Tool

Proper Citation

parallel-fastq-dump (RRID:SCR_024150)

Resource Information

URL: <https://github.com/rvalieris/parallel-fastq-dump>

Proper Citation: parallel-fastq-dump (RRID:SCR_024150)

Description: Software wrapper to speed up downloading process by dividing the work into multiple threads.

Resource Type: software library, software resource, software toolkit

Keywords: wrapper, speed up downloading process, dividing the work into multiple threads,

Availability: Free, Available for download, Freely available,

Resource Name: parallel-fastq-dump

Resource ID: SCR_024150

Alternate URLs: <https://sources.debian.org/src/parallel-fastq-dump/>

License: MIT License

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260919T195619+0000

Ratings and Alerts

No rating or validation information has been found for parallel-fastq-dump.

No alerts have been found for parallel-fastq-dump.

Data and Source Information

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Yao L, et al. (2026) Comprehensive analysis and validation of m6A-G4 colocalization and its regulatory role in Marek's disease virus infection. BMC veterinary research, 22(1).

Gooden C, et al. (2026) The gene-like promoter and transcription of LTR retrotransposons. bioRxiv : the preprint server for biology.

Li T, et al. (2026) TriticeaeExpDB: a centralized transcriptomic resource for Triticeae research. BMC genomics, 27(1).

Zheng M, et al. (2026) huSA: a comprehensive database for multi-dimensional resolution of bulk, single cell and spatial transcription profiles in skin diseases. Database : the journal of biological databases and curation, 2026.

King A, et al. (2026) Endothelial Adgrl2 Expression and Alternative Splicing Controls the Cerebrovasculature. The Journal of neuroscience : the official journal of the Society for Neuroscience, 46(16).

Montero H, et al. (2025) Convergent losses of arbuscular mycorrhizal symbiosis in carnivorous plants. The New phytologist, 248(4), 2040.

Fuma K, et al. (2025) Prenatal inflammation impairs early CD11c-positive microglia induction and delays myelination in neurodevelopmental disorders. Communications biology, 8(1), 75.

Cullen JN, et al. (2025) Charting the equine miRNA landscape: An integrated pipeline and browser for annotating, quantifying, and visualizing expression. PLoS genetics, 21(9), e1011835.

Zhang J, et al. (2025) Exploration of RNA-binding proteins identified RPS27 as a potential regulator associated with Kaposi's sarcoma development. BMC cancer, 25(1), 362.

Hoetzing M, et al. (2024) Geographic population structure and distinct intra-population dynamics of globally abundant freshwater bacteria. The ISME journal, 18(1).

Hwang W, et al. (2024) The Rice Online Expression Profiles Array Database Version 2 (ROADv2): An Interactive Atlas for Rice Functional Genomics. Rice (New York, N.Y.), 17(1), 75.

Li R, et al. (2024) Genome-wide characterization and evolution analysis of miniature inverted-repeat transposable elements in Barley (*Hordeum vulgare*). Frontiers in plant science, 15, 1474846.

Mokrousov I, et al. (2023) Insight into pathogenomics and phylogeography of hypervirulent and highly-lethal Mycobacterium tuberculosis strain cluster. BMC infectious diseases, 23(1), 426.

Padwal MK, et al. (2023) Application of Machine Learning in Predicting Hepatic Metastasis or Primary Site in Gastroenteropancreatic Neuroendocrine Tumors. Current oncology (Toronto, Ont.), 30(10), 9244.

Novella-Rausell C, et al. (2023) A comprehensive mouse kidney atlas enables rare cell population characterization and robust marker discovery. iScience, 26(6), 106877.

Maia Falc o R, et al. (2022) The Expression of the Immunoproteasome Subunit PSMB9 Is Related to Distinct Molecular Subtypes of Uterine Leiomyosarcoma. Cancers, 14(20).