

Resource Summary Report

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Megadepth

RRID:SCR_022779

Type: Tool

Proper Citation

Megadepth (RRID:SCR_022779)

Resource Information

URL: <https://github.com/ChristopherWilks/megadepth>

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Description: Software tool for quantifying alignments and coverage for BigWig and BAM/CRAM input files. Quantifies number of RNA-seq reads assigned to gene in BAM file, successor of bamcounts.

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

Defining Citation: [PMID:33693500](#)

Keywords: quantifying alignments, BigWig and BAM/CRAM input files, RNA-seq reads assigned to gene in BAM file quantification,

Funding: NIGMS R01GM118568;
NIGMS R01GM121459;
UK Medical Research Council

Availability: Free, Available for download, Freely available

Resource Name: Megadepth

Resource ID: SCR_022779

Alternate URLs: <https://bioconductor.org/packages/megadepth>

License: MIT License

Record Creation Time: 20220923T050148+0000

Record Last Update: 20260829T182809+0000

Ratings and Alerts

No rating or validation information has been found for Megadepth.

No alerts have been found for Megadepth.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

García-Ruiz S, et al. (2025) Splicing accuracy varies across human introns, tissues, age and disease. Nature communications, 16(1), 1068.

García-Ruiz S, et al. (2023) Splicing accuracy varies across human introns, tissues and age. bioRxiv : the preprint server for biology.