

# Resource Summary Report

Generated by [NIF](#) on Sep 3, 2026

## 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.