

Resource Summary Report

Generated by [NIF](#) on Aug 20, 2026

Myrna

RRID:SCR_006951

Type: Tool

Proper Citation

Myrna (RRID:SCR_006951)

Resource Information

URL: <http://bowtie-bio.sourceforge.net/myrna/index.shtml>

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Description: A cloud computing tool for calculating differential gene expression in large RNA-seq datasets. It uses Bowtie for short read alignment and R/Bioconductor for interval calculations, normalization, and statistical testing. These tools are combined in an automatic, parallel pipeline that runs in the cloud (Elastic MapReduce in this case) on a local Hadoop cluster, or on a single computer, exploiting multiple computers and CPUs wherever possible.

Abbreviations: Myrna

Synonyms: Myrna: Cloud-scale differential gene expression for RNA-seq

Resource Type: software resource

Defining Citation: [PMID:20701754](#)

Keywords: mapreduce, hadoop, cloud computing, differential expression, gene expression, rna-seq, bio.tools

Availability: Artistic License

Resource Name: Myrna

Resource ID: SCR_006951

Alternate IDs: OMICS_01310, biotools:myrna

Alternate URLs: <https://github.com/BenLangmead/myrna>, <https://bio.tools/myrna>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260815T182330+0000

Ratings and Alerts

No rating or validation information has been found for Myrna.

No alerts have been found for Myrna.

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 [NIF](#) .

Arya A, et al. (2025) Navigating single-cell RNA-sequencing: protocols, tools, databases, and applications. Genomics & informatics, 23(1), 13.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.