

# Resource Summary Report

Generated by [ASWG](#) on Sep 1, 2026

## Myrna

RRID:SCR\_006951

Type: Tool

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### Proper Citation

Myrna (RRID:SCR\_006951)

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### Resource Information

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

**Proper Citation:** Myrna (RRID:SCR\_006951)

**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:** 20260829T182248+0000

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## Ratings and Alerts

No rating or validation information has been found for Myrna.

No alerts have been found for Myrna.

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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 [ASWG](#) .

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.