

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

miREval

RRID:SCR_010830

Type: Tool

Proper Citation

miREval (RRID:SCR_010830)

Resource Information

URL: <http://mimirna.centenary.org.au/mireval/>

Proper Citation: miREval (RRID:SCR_010830)

Description: A web tool for simple microRNA prediction in genome sequences.

Abbreviations: miREval

Resource Type: service resource, production service resource, analysis service resource, data analysis service

Defining Citation: [PMID:24048357](#)

Resource Name: miREval

Resource ID: SCR_010830

Alternate IDs: OMICS_00378

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260731T042836+0000

Ratings and Alerts

No rating or validation information has been found for miREval.

No alerts have been found for miREval.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Ahmed F, et al. (2023) Identification of conserved miRNAs and their targets in *Jatropha curcas*: an in silico approach. *Journal, genetic engineering & biotechnology*, 21(1), 43.

Ahsan MI, et al. (2021) In Silico Identification and Functional Characterization of Conserved miRNAs in the Genome of *Cryptosporidium parvum*. *Bioinformatics and biology insights*, 15, 11779322211027665.

Vizzini A, et al. (2021) Transcriptomic Analyses Reveal 2 and 4 Family Members of Cytochromes P450 (CYP) Involved in LPS Inflammatory Response in Pharynx of *Ciona robusta*. *International journal of molecular sciences*, 22(20).

Karimi E, et al. (2021) Interplay between SARS-CoV-2-derived miRNAs, immune system, vitamin D pathway and respiratory system. *Journal of cellular and molecular medicine*, 25(16), 7825.

Jalali-Qomi S, et al. (2021) Experimental validation of a predicted microRNA within human FVIII gene. *Molecular biology research communications*, 10(2), 45.

Ahmed M, et al. (2021) In silico identification of conserved miRNAs in the genome of fibre biogenesis crop *Corchorus capsularis*. *Heliyon*, 7(4), e06705.

Li C, et al. (2019) PCV2 Regulates Cellular Inflammatory Responses through Dysregulating Cellular miRNA-mRNA Networks. *Viruses*, 11(11).

Davoodi Mastakani F, et al. (2018) Identification and expression analysis of a microRNA cluster derived from pre-ribosomal RNA in *Papaver somniferum* L. and *Papaver bracteatum* L. *PloS one*, 13(8), e0199673.

Núñez-Hernández F, et al. (2018) African swine fever virus does not express viral microRNAs in experimentally infected pigs. *BMC veterinary research*, 14(1), 268.

Hussain K, et al. (2018) Identification, characterization and expression analysis of pigeonpea miRNAs in response to *Fusarium* wilt. *Gene*, 653, 57.

Kulkarni AP, et al. (2016) Sequence data mining in search of hookworm (*Necator americanus*) microRNAs. *Gene*, 590(2), 317.

Bai J, et al. (2015) NGSmirPlant: comprehensive characterization of the small RNA transcriptomes of plants. *Protein & cell*, 6(6), 397.

Jha A, et al. (2015) A legion of potential regulatory sRNAs exists beyond the typical microRNAs microcosm. *Nucleic acids research*, 43(18), 8713.

Khrustalev VV, et al. (2014) Intragenic isochores (intrachores) in the platelet phosphofructokinase gene of Passeriform birds. *Gene*, 546(1), 16.

Hansen TB, et al. (2014) miRdentity: high stringency miRNA predictor identifies several novel animal miRNAs. *Nucleic acids research*, 42(16), e124.

Zhang Y, et al. (2014) A novel HIV-1-encoded microRNA enhances its viral replication by targeting the TATA box region. *Retrovirology*, 11, 23.

Pani A, et al. (2013) Computational identification of microRNAs and their targets in *Catharanthus roseus* expressed sequence tags. *Genomics data*, 1, 2.

Pani A, et al. (2011) Computational identification of sweet wormwood (*Artemisia annua*) microRNA and their mRNA targets. *Genomics, proteomics & bioinformatics*, 9(6), 200.

Prabu GR, et al. (2010) Computational identification of miRNAs and their target genes from expressed sequence tags of tea (*Camellia sinensis*). *Genomics, proteomics & bioinformatics*, 8(2), 113.