

Resource Summary Report

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

miRanda

RRID:SCR_017496

Type: Tool

Proper Citation

miRanda (RRID:SCR_017496)

Resource Information

URL: <http://www.mirtoolsgallery.org/miRToolsGallery/node/1055>

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Description: Comprehensive resource of microRNA target predictions and expression profiles. Used for whole genome prediction of miRNA target genes. For each miRNA, target genes are selected on basis of sequence complementarity using position weighted local alignment algorithm, free energies of RNA-RNA duplexes, and conservation of target sites in related genomes. Provides information about set of genes potentially regulated by particular microRNA, co-occurrence of predicted target sites for multiple microRNAs in mRNA and microRNA expression profiles in tissues. Users are allowed to customize algorithm, numerical parameters, and position-specific rules., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: MicroRNA.org. microrna.org

Resource Type: data or information resource, database, service resource

Defining Citation: [PMID:18158296](#)

Keywords: Whole, genome, prediction, miRNA, target, gene, expression, profile, data, FASEB list

Funding: NIGMS ;
Atlantic Philanthropies ;
Alfred W. Bressler Scholars Endowment Fund

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: miRanda

Resource ID: SCR_017496

Alternate URLs: <http://www.microrna.org/microrna/home.do>

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260731T043011+0000

Ratings and Alerts

No rating or validation information has been found for miRanda.

No alerts have been found for miRanda.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 210 mentions in open access literature.

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

Cheng J, et al. (2025) MiR- 146b-5p inhibits Candida albicans-induced inflammatory response through targeting HMGB1 in mouse primary peritoneal macrophages. Heliyon, 11(1), e41464.

Zhang Y, et al. (2025) Integrated bioinformatics identifies ferroptosis biomarkers and therapeutic targets in idiopathic pulmonary arterial hypertension. Scientific reports, 15(1), 25187.

Wu X, et al. (2025) Genome-wide identification of WRKY gene family and expression analysis of key WRKY genes in response to Fusarium solani infection in Lycium barbarum. Frontiers in plant science, 16, 1543373.

Mi Y, et al. (2025) circEFR3A promotes breast cancer progression by sponging miR-590-3p to upregulate androgen receptor expression. Oncology letters, 30(3), 446.

Ding B, et al. (2025) Resveratrol contributes to NK cell-mediated breast cancer cytotoxicity by upregulating ULBP2 through miR-17-5p downmodulation and activation of MINK1/JNK/c-Jun signaling. Frontiers in immunology, 16, 1515605.

Zhi Y, et al. (2025) Screening and validation of key microRNAs regulating muscle development in Hanper sheep. PloS one, 20(6), e0325054.

Mai W, et al. (2025) Expression regulation network in papillae of sea cucumbers: Whole-transcriptome and DNA methylation datasets. Scientific data, 12(1), 1231.

Liu C, et al. (2025) Identification and characterization of signature genes related to fetoplacental vascular endothelial cell programming in gestational diabetes mellitus using bioinformatics analysis. Frontiers in genetics, 16, 1600756.

Ge J, et al. (2025) Identification of tRF-29-79MP9P9NH525 as a biomarker and tumor suppressor of gastric cancer via regulating KIF14/AKT pathway. *Cell death discovery*, 11(1), 238.

Ma C, et al. (2025) Systems biology analysis of long non-coding RNAs and targets to identify key modules and biomarkers in breast cancer. *Discover oncology*, 16(1), 2325.

Deng Z, et al. (2025) sdRNA-D43 derived from small nucleolar RNA snoRD43 improves chondrocyte senescence and osteoarthritis progression by negatively regulating PINK1/Parkin-mediated mitophagy pathway via dual-targeting NRF1 and WIPI2. *Cell communication and signaling : CCS*, 23(1), 77.

Peng F, et al. (2025) IKZF1 as a potential therapeutic target for dendritic cell-mediated immunotherapy in IgA nephropathy. *Cell communication and signaling : CCS*, 23(1), 216.

Dametto S, et al. (2025) Unveiling the hemolymphatic miRNome composition of the schistosomiasis vector snail *Biomphalaria glabrata*. *Current research in parasitology & vector-borne diseases*, 7, 100262.

Huang S, et al. (2025) hsa_circ_0008305 facilitates the malignant progression of hepatocellular carcinoma by regulating AKR1C3 expression and sponging miR-379-5p. *Scientific reports*, 15(1), 1309.

Luo M, et al. (2025) The interplay between epigenomic and transcriptomic variation during ecotype divergence in stickleback. *BMC biology*, 23(1), 70.

Huang J, et al. (2025) Comprehensive analysis of tRNA-derived fragment expression in endometriosis using PANDORA-seq technology. *RNA biology*, 22(1), 1.

Yue X, et al. (2025) Increased expression of RIPOR1 predicts the poor prognosis of colorectal cancer patients. *Translational cancer research*, 14(5), 2707.

Sheng B, et al. (2025) Exosomes-mediated delivery of miR-486-3p alleviates neuroinflammation via SIRT2-mediated inhibition of mitophagy after subarachnoid hemorrhage. *Stroke and vascular neurology*, 10(3), 335.

Ullah K, et al. (2025) Target miRNA identification for the LPL gene in large yellow croaker (*Larimichthys crocea*). *Scientific reports*, 15(1), 4164.

Abudoureyimu M, et al. (2025) Aurora-A promotes lenvatinib resistance experimentally through hsa-circ-0058046/miR-424-5p/FGFR1 axis in hepatocellular carcinoma. *International journal of immunopathology and pharmacology*, 39, 3946320251316692.