

# Resource Summary Report

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## [microRNA.org](http://www.microrna.org)

RRID:SCR\_006997

Type: Tool

### Proper Citation

microRNA.org (RRID:SCR\_006997)

### Resource Information

**URL:** <http://www.microrna.org>

**Proper Citation:** microRNA.org (RRID:SCR\_006997)

**Description:** Database of microRNA target predictions and expression profiles. Target predictions are based on a development of the miRanda algorithm which incorporates current biological knowledge on target rules and on the use of an up-to-date compendium of mammalian microRNAs. MicroRNA expression profiles are derived from a comprehensive sequencing project of a large set of mammalian tissues and cell lines of normal and disease origin. This website enables users to explore: \* The set of genes that are potentially regulated by a particular microRNA. \* The implied cooperativity of multiple microRNAs on a particular mRNA. \* MicroRNA expression profiles in various mammalian tissues. The web resource provides users with functional information about the growing number of microRNAs and their interaction with target genes in many species and facilitates novel discoveries in microRNA gene regulation. The microRNA Target Detection Software, miRanda, is an algorithm for finding genomic targets for microRNAs. This algorithm has been written in C and is available as an open-source method under the GPL., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Abbreviations:** microRNA.org

**Synonyms:** microRNA.org - Targets and Expression

**Resource Type:** data or information resource, database, software resource

**Defining Citation:** [PMID:18158296](#)

**Keywords:** microrna, gene, expression, gene regulation, FASEB list

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

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** microRNA.org

**Resource ID:** SCR\_006997

**Alternate IDs:** nif-0000-03127, OMICS\_00402

**Record Creation Time:** 20220129T080239+0000

**Record Last Update:** 20260919T195122+0000

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## Ratings and Alerts

No rating or validation information has been found for microRNA.org.

No alerts have been found for microRNA.org.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2818 mentions in open access literature.

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

Zeng C, et al. (2026) Anti-Inflammatory and Protective Role of tiRNA-Glu-TTC-003 in Pediatric Sepsis Via TREM2/TLR4 Signaling Modulation. Inflammation, 49(1), 71.

Li J, et al. (2026) Mining Potential Therapeutic Targets for T Cell Exhaustion in Osteoarthritis by Integrating Mendelian Randomization and Single-Cell Sequencing. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(2), e71483.

Yang R, et al. (2026) Identification of Biomarkers Associated With Copper Metabolism in Ischemic Stroke Through Bulk RNA Sequencing and Mendelian Randomization Analysis. Cellular and molecular neurobiology, 46(1).

Chen YP, et al. (2026) miR-100-5p Enhances Cell Cycle-Mediated Chemoresistance by Modulating the CTDSPL/pRB/E2F1 Signaling Pathway in Oxaliplatin-Resistant Colorectal Cancer Cells. Oncology research, 34(4), 17.

Son HJ, et al. (2026) Therapeutic Potential of miR-196a in Protecting Corneal Endothelial Cells From Senescence Through Mitochondrial and TGF-? Signaling Modulation. Translational vision science & technology, 15(6), 23.

Aberuyi N, et al. (2026) Increased Expression of miR-326 Mediates Chemosensitivity in Pediatric Acute Lymphoblastic Leukemia Through ABCA2 and YY1 Downregulation: An

Observational and Experimental Study. Health science reports, 9(7), e72720.

Chen Y, et al. (2026) Identification of metabolism and inflammation-related biomarkers and potential drugs for schizophrenia based on comprehensive bioinformatics and machine learning. BMC psychiatry, 26(1).

Wu Y, et al. (2026) Identification and verification of biomarkers associated with integrated stress response in heart failure. Scientific reports, 16(1).

Song Y, et al. (2026) Electroacupuncture alleviates migraine through CXCL13/CXCR5-mediated communication. Chinese medicine, 21(1), 59.

Wang L, et al. (2026) Integrative Transcriptomic Signature of tRNA-Derived Fragment Targets and Lactylation-Related Genes for Prostate Cancer Diagnosis. Cancer medicine, 15(6), e71892.

Hu X, et al. (2026) Gene screening and immune phenotype shifts of osteoporosis. Scientific reports, 16(1), 3501.

Lin J, et al. (2026) Establishment of a microbial abundance prognostic model for colorectal cancer. BMC cancer, 26(1), 197.

Sugali CK, et al. (2026) TGF- $\beta$ 2/OPTN/FOXC1/miR-200 axis regulates actin dynamics in human trabecular meshwork cells. BBA advances, 9, 100177.

Xia C, et al. (2026) Circular RNA hsa\_circ\_0003472 Promotes Pancreatic Ductal Adenocarcinoma Progression and Gemcitabine Resistance Via the mir-1253/ERCC1 Axis. Biological procedures online, 28(1).

Yan W, et al. (2026) Dynamic miRNA-host gene co-expression and functional regulation in response to salinity fluctuations during biological invasions. Marine life science & technology, 8(2), 496.

Xu M, et al. (2026) Cation homeostasis-related prognostic genes uncovered by transcriptomic analysis in breast cancer. Translational cancer research, 15(5), 425.

Yu M, et al. (2026) Identification and validation of butyrate metabolism-related biomarkers for colorectal cancer diagnosis. PeerJ, 14, e20942.

Xu MR, et al. (2026) Alpinia zerumbet-Derived Extracellular Vesicles Protect Against UVB-Induced Photoaging by Enhancing Mitochondrial Bioenergetics and Skin Barrier Function. BioFactors (Oxford, England), 52(4), e70134.

Wu JS, et al. (2026) Hepatocyte-Derived Extracellular Vesicles Deliver miR-328-3p to Trigger PP2A-B56 $\gamma$ -Mediated p-NLRP3S295-Dependent Metaflammation in Macrophages upon Microcystin-LR Exposure. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(6), e07039.

Ni L, et al. (2026) MicroRNA transcriptome analysis reveals the potential role of miRNAs in regulating adipocyte hyperplasia and hypertrophy. Frontiers in genetics, 17, 1737852.