

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>

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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: software resource, data or information resource, database

Defining Citation: [PMID:18158296](#)

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

Funding: NIGMS ;
Atlantic Philanthropies ;
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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: 20260801T190321+0000

Ratings and Alerts

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

No alerts have been found for microRNA.org.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2648 mentions in open access literature.

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

Qiu AW, et al. (2025) Retinal Müller Cell-Released Exosomal MiR-92a-3p Delivers Interleukin-17A Signal by Targeting Notch-1 to Promote Diabetic Retinopathy. Investigative ophthalmology & visual science, 66(1), 1.

Zhou H, et al. (2025) Hsa-miR-532-3p protects human decidual mesenchymal stem cells from oxidative stress in recurrent spontaneous abortion via targeting KEAP1. Redox biology, 80, 103508.

Chen S, et al. (2025) Urinary exosomal lnc-TAF12-2:1 promotes bladder cancer progression through the miR-7847-3p/ASB12 regulatory axis. Genes & diseases, 12(4), 101384.

Lee CJ, et al. (2025) MicroRNA-1912 regulates cholesterol homeostasis by targeting PCSK9. Molecular therapy. Nucleic acids, 36(3), 102589.

Lin F, et al. (2025) Topical application of Tea leaf-derived nanovesicles reduce melanogenesis by modulating the miR-828b/MYB4 axis: better permeability and therapeutic efficacy than conventional tea extracts. Materials today. Bio, 34, 102108.

Zheng B, et al. (2025) Identification of potential biomarkers and mechanisms for keloid disorder based on comprehensive bioinformatics analysis and machine learning algorithms. BMC medical genomics, 18(1), 108.

Ma L, et al. (2025) Bone marrow mesenchymal stem cell-derived exosomes attenuate hepatic stellate cell activation through miR-223-3p-mediated mitophagy. *BMC medical genomics*, 18(1), 148.

Chen R, et al. (2025) Comprehensive analysis of disulfidptosis-related genes in pulmonary hypertension through machine learning and immune infiltration: Spotlight on USP32 and ZNF655 as key regulators. *PloS one*, 20(9), e0330832.

Ji Y, et al. (2025) Kaempferol regulates Ewing sarcoma progression via miR-26b-5p-mediated expression of the family with sequence similarity 98 member A. *BMC pharmacology & toxicology*, 26(1), 167.

Hou Y, et al. (2025) Comprehensive high-throughput sequencing analysis and verification of miRNAs isolated from bronchial epithelial cells undergoing radiation-induced epithelial-mesenchymal transition. *Science progress*, 108(3), 368504251362376.

Cheng S, et al. (2025) Identification and characterization of microRNAs in the liver of yak (*Bos grunniens*) associated with energy deficiency at high-altitude. *Animal bioscience*, 38(7), 1372.

Cao X, et al. (2025) Branched-Chain Amino Acids Target miR-203a/fosb Axis to Promote Skeletal Muscle Growth in Common Carp (*Cyprinus carpio*). *Aquaculture nutrition*, 2025, 9406490.

Zeng B, et al. (2025) Roles of MARCKSL1, MCM6, RFC4, and PLAU genes in esophageal cancer and their association with radiotherapy response. *Scientific reports*, 15(1), 23559.

Du J, et al. (2025) Exploring the association between circadian rhythms and osteoporosis: new diagnostic and therapeutic targets identified via machine learning. *Frontiers in molecular biosciences*, 12, 1614221.

Liu S, et al. (2025) Erythropoietin-Stimulated Macrophage-Derived Extracellular Vesicles in Chitosan Hydrogel Rescue BMSCs Fate by Targeting EGFR to Alleviate Inflammatory Bone Loss in Periodontitis. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(23), e2500554.

Meng X, et al. (2025) A novel tsRNA signature -tRF-58:76-Tyr-GTA-2-M3 as potential biomarker and therapeutic target for duodenal atresia. *Cell biology and toxicology*, 41(1), 88.

He Y, et al. (2025) Identification and validation of SQLE in steroid-induced osteonecrosis of the femoral head: a bioinformatics and experimental study. *Journal of orthopaedic surgery and research*, 20(1), 894.

Yang X, et al. (2025) Identification and external validation of a prognostic signature based on N6-methyladenosine- and tertiary lymphoid structures-related genes to evaluate survival prognosis and treatment efficacy in lung adenocarcinoma. *Discover oncology*, 16(1), 2265.

Chen Y, et al. (2025) Overexpression of miR-516a-5p Promotes Erosive Oral Lichen Planus: In Vitro Study Based on Bioinformatics Analyses. *Clinical and experimental dental research*, 11(6), e70270.

Li H, et al. (2025) Exosomes derived from hypoxia-preconditioned M2 macrophages alleviate degeneration in knee osteoarthritis through the miR-124/STAT3 axis. *Journal of translational medicine*, 23(1), 772.