

Resource Summary Report

Generated by [Kravitz](#) on Sep 11, 2026

miRBase

RRID:SCR_003152

Type: Tool

Proper Citation

miRBase (RRID:SCR_003152)

Resource Information

URL: <http://www.mirbase.org/>

Proper Citation: miRBase (RRID:SCR_003152)

Description: Central online repository for microRNA nomenclature, sequence data, annotation and target prediction. Collection of published miRNA sequences and annotation.

Abbreviations: miRBase

Synonyms: microRNA database

Resource Type: data or information resource, data repository, database, naming service, service resource, storage service resource

Defining Citation: [PMID:24275495](#), [PMID:21037258](#), [PMID:20205188](#), [PMID:17991681](#), [PMID:16957372](#), [PMID:16381832](#), [PMID:14681370](#)

Keywords: gene, annotation, hairpin, microrna, nomenclature, rna, sequence, target, transcript, unique name, mirna registry, genetics, bio.tools, FASEB list

Funding: BBSRC ;
Wellcome Trust Sanger Institute

Availability: Free, Available for download, Freely available

Resource Name: miRBase

Resource ID: SCR_003152

Alternate IDs: SCR_017497, r3d100010670, nif-0000-03134, biotools:mirbase

Alternate URLs: <http://microrna.sanger.ac.uk/>, <https://bio.tools/mirbase>, <https://doi.org/10.17616/R3VG8D>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132458+0000

Ratings and Alerts

No rating or validation information has been found for miRBase.

No alerts have been found for miRBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10387 mentions in open access literature.

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

Lee SM, et al. (2026) Host microRNA-31-5p regulates KHDRBS3 expression and modulates viral gene expression during KSHV lytic reactivation. Cell reports, 45(4), 117160.

Ning B, et al. (2026) Upregulation of an Epithelial miRNA Is Associated with Immune Evasion in Progressive Bronchial Premalignant Lesions. Cancer immunology research, 14(4), 689.

Kärkkäinen M, et al. (2026) Integrative omics approaches to uncover liquid-based cancer-predicting biomarkers in Lynch syndrome. International journal of cancer, 158(1), 243.

Xiao Y, et al. (2026) RNAi Regulator C3PO Promotes Arbovirus Infection in Insect Vectors. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(4), e15869.

Zhai B, et al. (2026) Dynamic landscape of microRNA expression in the feline small intestine during Toxoplasma gondii infection. Parasites & vectors, 19(1).

Morini M, et al. (2026) Evolution in metazoans of the TRPM channel family involves multiple gains and losses of genes and domains. Molecular biology and evolution, 43(5).

Podraza J, et al. (2026) Negative correlation between microRNA and insulin sensitivity gene expression in adipose tissue: potential implications for diabetes and neurodegenerative diseases. Nutrition & metabolism, 23(1).

Jones G, et al. (2026) Comprehensive profiling of the human tear fluid miRNome using small RNA sequencing. The ocular surface, 40, 133.

Shen Z, et al. (2026) Identification of potential biomarkers related to the Bitong mixture in osteoarthritis based on bioinformatics and network pharmacology, and exploration of the mechanism involved. Frontiers in immunology, 17, 1739355.

- Lee HJ, et al. (2026) Differential microRNA Expression Profiles in Girls with Idiopathic Central Precocious Puberty and Premature Thelarche. *International journal of molecular sciences*, 27(4).
- Déctor MA, et al. (2026) An Exploratory Biomarker Study of First-Trimester Circulating miRNAs Associated with Later Gestational Diabetes Mellitus. *International journal of molecular sciences*, 27(4).
- Tastsoglou S, et al. (2026) Estrogen receptor β target gene expression reveals novel repressive functions in aggressive breast cancer. *NPJ breast cancer*, 12(1).
- Rasmussen AM, et al. (2026) bayesReact: expression-coupled regulatory motif analysis detects microRNA activity across cancers, tissues, and at the single-cell level. *Nucleic acids research*, 54(4).
- Ma H, et al. (2026) Transcriptome profiling indicates varied gene responses to *Pasteurella multocida* mutant infections in cattle. *PloS one*, 21(1), e0341813.
- Kawamoto Y, et al. (2026) Functional properties of skeletal myotube-derived extracellular vesicles based on microRNA profiles: a comparative analysis with mesenchymal stem cell-derived extracellular vesicles. *Scientific reports*, 16(1).
- Kanno S, et al. (2026) Comparative analysis of microRNA expression in serum-derived extracellular vesicles from sudden infant death syndrome cases. *Scientific reports*, 16(1).
- Rosell-Moll E, et al. (2026) Analyzing the transcriptomic diversity in isolated mature adipocytes from the major fat depots in rainbow trout (*Oncorhynchus mykiss*). *BMC genomics*, 27(1).
- Zhu Z, et al. (2026) A Multi-Tissue Yak (*Bos grunniens*) ceRNA Atlas with Ribo-Seq-Informed lncRNA Curation and Candidate Prioritization. *Animals : an open access journal from MDPI*, 16(4).
- Gao L, et al. (2026) Transcriptome Sequencing Unveils a Novel Mechanism Underlying Breed Distinctions Between Thin- and Fat-Tailed Sheep. *Genes*, 17(2).
- Pyrkova A, et al. (2026) Regulatory Potential of piRNAs Targeting Klotho and Other Genes. *Genes*, 17(2).