

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 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: 20260919T195013+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 [PRECISE-TBI](#) .

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).