

Resource Summary Report

Generated by [dkNET](#) on Aug 27, 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: 20260821T193655+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 [dkNET](#) .

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.

Yue L, et al. (2026) Transcriptome and proteome combined analysis of wool fiber diameter regulation mechanism. Animal bioscience, 39(2), 250378.

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.

Zhai SN, et al. (2026) CIRCpedia v3: an interactive database for circular RNA characterization and functional exploration. Nucleic acids research, 54(D1), D78.

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

Du Y, et al. (2026) Whole-transcriptome sequencing revealed the ceRNA regulatory network of stable knockdown of the CD8A gene in chicken T lymphocytes. Poultry science, 105(2), 106318.

Cao Y, et al. (2026) The Zma-miRNA319-ZmMYB74 Module Regulates Maize Resistance to Stalk Rot Disease by Modulating Lignin Deposition. Plant biotechnology journal, 24(3), 1598.

Choudhary A, et al. (2026) Identification of novel exosomal miRNAs and their role in diagnosis and prognosis of triple negative breast cancer. BMC cancer, 26(1), 210.

Liang J, et al. (2026) The Novel ROCK Inhibitor Fasudil Derivative Fasudil-D-6h Prevents Tumour Progression by Regulating the Adherens Junction Signalling Pathway in Triple-Negative Breast Cancer. *Breast cancer* (Dove Medical Press), 18, 547003.

Green A, et al. (2026) GOFLOWLLM-curating miRNA literature with large language models and flowcharts. *Bioinformatics* (Oxford, England), 42(1).

Zhang D, et al. (2026) ASTRO: Automated Spatial-Transcriptome whole RNA Output. *Bioinformatics* (Oxford, England), 42(2).

Wang M, et al. (2026) MicroRNA dysregulation in cow's jejunum, jejunal lymph node, and caecal Peyer's patch during *Mycobacterium avium* subsp. *paratuberculosis* infection. *BMC genomics*, 27(1), 25.

Chen QY, et al. (2026) Analysis and identification of circRNA-regulated ceRNA networks associated with the virulence differences between PRV FA and FB strains. *BMC veterinary research*, 22(1), 106.

Park S, et al. (2026) JULGI coordinates vascular development and leaf patterning through non-cell-autonomous regulation of miR165/166. *Nature communications*, 17(1), 684.

Córdoba-Caballero J, et al. (2026) An integrative approach to identify novel miRNA-mRNA interaction networks in LMNA-cardiomyopathy. *Scientific reports*, 16(1), 6110.

Lyu S, et al. (2026) Identification of candidate microRNA biomarkers of endometriosis in different bodily fluids. *Scientific reports*, 16(1), 6218.

Dautt-Castro M, et al. (2026) Genome-wide analysis of conserved and novel miRNAs in mango mesocarp reveals early regulatory networks involved in postharvest heat stress response. *Scientific reports*, 16(1).

Malkoc Z, et al. (2026) Sub-Neuronal Network Profiling of Extracellular Vesicle Release Using a Compartmentalized Neurofluidic Platform. *Advanced biology*, 10(2), e00381.

Cui H, et al. (2026) The consensus molecular subtypes of esophageal squamous cell carcinoma. *Signal transduction and targeted therapy*, 11(1), 65.