

Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

miRecords

RRID:SCR_013021

Type: Tool

Proper Citation

miRecords (RRID:SCR_013021)

Resource Information

URL: <http://c1 accurascience.com/miRecords/>

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Description: A resource for animal miRNA-target interactions consisting of the Validated Targets component, a large, high-quality database of experimentally validated miRNA targets resulting from meticulous literature curation, and the Predicted Targets component, an integration of predicted miRNA targets produced by 11 established miRNA target prediction programs. April 27, 2013, the Validated Targets component of miRecords hosts 2705 records of interactions between 644 miRNAs and 1901 target genes in 9 animal species. Among these records, 2028 were curated from low throughput experiments. The Predicted Targets component of miRecords integrates the predicted targets of the following miRNA target prediction tools: DIANA-microT, MicroInspector, miRanda, MirTarget2, miTarget, NBmiRTar, PicTar, PITA, RNA22, RNAhybrid, and TargetScan/TargertScanS. We would be glad to include your experimentally validated miRNA target data (published or unpublished) into miRecords., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: miRecords

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

Defining Citation: [PMID:18996891](#)

Keywords: FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: miRecords

Resource ID: SCR_013021

Alternate IDs: OMICS_00405

Alternate URLs: <https://omictools.com/mirecords-tool>

Old URLs: <http://mirecords.umn.edu/miRecords/>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260821T193954+0000

Ratings and Alerts

No rating or validation information has been found for miRecords.

No alerts have been found for miRecords.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 452 mentions in open access literature.

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

Yu X, et al. (2026) Evaluating the Diagnostic Value and Molecular Mechanism of Energy Metabolism-Related Gene PEA15 in Sepsis. Journal of inflammation research, 19, 556793.

Zhang T, et al. (2026) Identification of key genes in the pathogenesis of hepatic ischemia-reperfusion injury based on bioinformatics and experimental verification. Scientific reports, 16(1).

Xu M, et al. (2026) Identification of key miRNAs and target genes in psoriasis vulgaris and obesity co-morbidity. European journal of medical research, 31(1), 247.

Zheng F, et al. (2026) Transcriptome data combined with two-sample Mendelian randomization reveal IRF1 and PRKD1 as UPR-related key regulators in intervertebral disc degeneration. Medicine, 105(14), e48213.

Chiu Y, et al. (2025) Time-resolved miRNA-mRNA integrated analysis reveals the miRNA-mRNA networks underlying plasma membrane damage-dependent senescence and DNA damage response-dependent senescence in WI-38 normal human fibroblasts. RNA biology, 22(1), 1.

Lin S, et al. (2025) Predicting microRNA target genes using pan-cancer correlation patterns. BMC genomics, 26(1), 77.

Liu J, et al. (2025) A novel stemness-related lncRNA signature predicts prognosis, immune infiltration and drug sensitivity of clear cell renal cell carcinoma. *Journal of translational medicine*, 23(1), 238.

Mechelli R, et al. (2025) A disease-specific convergence of host and Epstein-Barr virus genetics in multiple sclerosis. *Proceedings of the National Academy of Sciences of the United States of America*, 122(14), e2418783122.

Wei W, et al. (2025) Deciphering the role of lncRNA-mediated ceRNA network in disuse osteoporosis: insights from bone marrow mesenchymal stem cells under simulated microgravity. *Frontiers in medicine*, 12, 1444165.

Weich A, et al. (2025) Repurposed clindamycin suppresses pyroptosis in tumor-associated macrophages through Inhibition of caspase-1. *Journal of experimental & clinical cancer research : CR*, 44(1), 225.

Vaz C, et al. (2025) Short-term diet intervention comprising of olive oil, vitamin D, and omega-3 fatty acids alters the small non-coding RNA (sncRNA) landscape of human sperm. *Scientific reports*, 15(1), 7790.

Liu L, et al. (2025) Bioinformatic Analysis of Apoptosis-Related Genes in Preeclampsia Using Public Transcriptomic and Single-Cell RNA Sequencing Datasets. *Journal of inflammation research*, 18, 4785.

Z??rate-Segura PB, et al. (2025) Changes in miRNA Pattern Expression Associated With COVID-19 Severity. *In vivo (Athens, Greece)*, 39(1), 482.

Lawarde A, et al. (2025) Tumor tissue-of-origin classification using miRNA-mRNA-lncRNA interaction networks and machine learning methods. *Frontiers in bioinformatics*, 5, 1571476.

Sunnetci-Akkoyunlu D, et al. (2025) Identification of Common miRNAs Differentially Expressed in Periodontitis and Pancreatic Cancer. *In vivo (Athens, Greece)*, 39(3), 1422.

Wei X, et al. (2024) Exploration of a miRNA-mRNA network shared between acute pancreatitis and Epstein-Barr virus infection by integrated bioinformatics analysis. *PloS one*, 19(11), e0311130.

Ge J, et al. (2024) New HCC Subtypes Based on CD8 Tex-Related lncRNA Signature Could Predict Prognosis, Immunological and Drug Sensitivity Characteristics of Hepatocellular Carcinoma. *Journal of hepatocellular carcinoma*, 11, 1331.

Yuan Y, et al. (2024) Astragali radix vesicle-like nanoparticles improve energy metabolism disorders by repairing the intestinal mucosal barrier and regulating amino acid metabolism in sleep-deprived mice. *Journal of nanobiotechnology*, 22(1), 768.

Wu J, et al. (2024) ID MIR: identification of dysregulated miRNAs associated with disease based on a miRNA-miRNA interaction network constructed through gene expression data. *Briefings in bioinformatics*, 25(4).

Sultana T, et al. (2024) Computational exploration of SLC14A1 genetic variants through structure modeling, protein-ligand docking, and molecular dynamics simulation. *Biochemistry and biophysics reports*, 38, 101703.