

Resource Summary Report

Generated by SPARC SAWG on Aug 6, 2026

miR2Disease

RRID:SCR_007792

Type: Tool

Proper Citation

miR2Disease (RRID:SCR_007792)

Resource Information

URL: <http://www.mir2disease.org/>

Proper Citation: miR2Disease (RRID:SCR_007792)

Description: A manually curated database, aims at providing a comprehensive resource of miRNA deregulation in various human diseases. Each entry in the miR2Disease contains detailed information on a miRNA-disease relationship, including miRNA ID, disease name, a brief description of the miRNA-disease relationship, miRNA expression pattern in the disease state, detection method for miRNA expression, experimentally verified miRNA target gene(s), and literature reference . All entries can be retrieved by miRNA ID, disease name or target gene. miR2Disease will be updated bimonthly. miR2Disease sincerely looks forward to recently established relationship between miRNA and human diseases to be submitted.

Synonyms: miR2Disease

Resource Type: data or information resource, database

Keywords: FASEB list

Resource Name: miR2Disease

Resource ID: SCR_007792

Alternate IDs: nif-0000-03133

Old URLs: <http://mlg.hit.edu.cn:8080/miR2Disease>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260806T054448+0000

Ratings and Alerts

No rating or validation information has been found for miR2Disease.

No alerts have been found for miR2Disease.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 102 mentions in open access literature.

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

Yuan M, et al. (2025) Exploring molecular and modular insights into space ionizing radiation effects through heterogeneous gene regulatory networks. NPJ microgravity, 11(1), 44.

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

Chang M, et al. (2025) Unbiased microRNA-Disease Association Prediction Using ICD-11 Codes and Negative Sampling. Pharmacology research & perspectives, 13(6), e70192.

Hu C, et al. (2024) Optimizing drug combination and mechanism analysis based on risk pathway crosstalk in pan cancer. Scientific data, 11(1), 74.

Abdallah HY, et al. (2023) Expression Signature of Immune-Related MicroRNAs in Autoimmune Skin Disease: Psoriasis and Vitiligo Insights. Molecular diagnosis & therapy, 27(3), 405.

Abdallah HY, et al. (2023) Introducing Circulating Vasculature-Related Transcripts as Biomarkers in Coronary Artery Disease. Molecular diagnosis & therapy, 27(2), 243.

Loganathan T, et al. (2023) Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. Functional & integrative genomics, 23(1), 33.

Garcia-Vallicrosa C, et al. (2023) The Role of Longevity Assurance Homolog 2/Ceramide Synthase 2 in Bladder Cancer. International journal of molecular sciences, 24(21).

Huan S, et al. (2023) Dihydroartemisinin inhibits the activation and proliferation of hepatic stellate cells by regulating miR-29b-3p. International journal of molecular medicine, 51(5).

Abdallah HY, et al. (2022) The lncRNA PRINS-miRNA-mRNA Axis Gene Expression Profile as a Circulating Biomarker Panel in Psoriasis. Molecular diagnosis & therapy, 26(4), 451.

Wang L, et al. (2022) Prediction of lncRNA-disease association based on a Laplace normalized random walk with restart algorithm on heterogeneous networks. BMC

bioinformatics, 23(1), 5.

Sun Q, et al. (2021) Current Status of MicroRNAs that Target the Wnt Signaling Pathway in Regulation of Osteogenesis and Bone Metabolism: A Review. Medical science monitor : international medical journal of experimental and clinical research, 27, e929510.

Prashanth G, et al. (2021) Potential Molecular Mechanisms and Remdesivir Treatment for Acute Respiratory Syndrome Corona Virus 2 Infection/COVID 19 Through RNA Sequencing and Bioinformatics Analysis. Bioinformatics and biology insights, 15, 11779322211067365.

Bo C, et al. (2021) Construction of a TF-miRNA-gene feed-forward loop network predicts biomarkers and potential drugs for myasthenia gravis. Scientific reports, 11(1), 2416.

Zhuang M, et al. (2021) The circular RNA expression profile in ovarian serous cystadenocarcinoma reveals a complex circRNA-miRNA regulatory network. BMC medical genomics, 14(Suppl 2), 276.

Cai C, et al. (2021) Identification of novel transcription factor-microRNA-mRNA co-regulatory networks in pulmonary large-cell neuroendocrine carcinoma. Annals of translational medicine, 9(2), 133.

Liu B, et al. (2021) Comprehensive characterization of a drug-resistance-related ceRNA network across 15 anti-cancer drug categories. Molecular therapy. Nucleic acids, 24, 11.

Zhou X, et al. (2020) Regulatory Network Analysis to Reveal Important miRNAs and Genes in Non-Small Cell Lung Cancer. Cell journal, 21(4), 459.

Sun YM, et al. (2020) Principles and innovative technologies for decrypting noncoding RNAs: from discovery and functional prediction to clinical application. Journal of hematology & oncology, 13(1), 109.

Zhang L, et al. (2020) Identification of Differentially Expressed Genes and miRNAs Associated with Esophageal Squamous Cell Carcinoma by Integrated Analysis of Microarray Data. BioMed research international, 2020, 1980921.