

# Resource Summary Report

Generated by [dkNET](#) on Aug 31, 2026

## [miRNet](#)

RRID:SCR\_024567

Type: Tool

### Proper Citation

miRNet (RRID:SCR\_024567)

### Resource Information

**URL:** <https://www.mirnet.ca/>

**Proper Citation:** miRNet (RRID:SCR\_024567)

**Description:** Web based tool that offers statistical, visual and network based approaches to understand miRNAs functions and regulatory mechanisms. Used for dissecting miRNA-target interactions and functional associations through network-based visual analysis. miRNet 2.0 is network based visual analytics for miRNA functional analysis and systems biology.

**Synonyms:** miRNet 2.0

**Resource Type:** software resource, web application

**Defining Citation:** [PMID:27105848](#), [PMID:30421406](#), [DOI:10.1093/nar/gkaa467](#)

**Keywords:** network based visual analytics, dissecting miRNA-target interactions and functional associations, network-based visual analysis, miRNA functional analysis,

**Funding:** Canadian Institute for Health Research ;  
Genome Canada ;  
Genome Quebec and Canada Research Chairs ;  
McGill Startup Fund ;  
Natural Sciences and Engineering Research Council of Canada

**Availability:** Free, Freely available

**Resource Name:** miRNet

**Resource ID:** SCR\_024567

**Alternate URLs:** <https://github.com/xia-lab/miRNetR>

**License:** GNU GPL v3

**Record Creation Time:** 20231017T050222+0000

**Record Last Update:** 20260829T182829+0000

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## Ratings and Alerts

No rating or validation information has been found for miRNet.

No alerts have been found for miRNet.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 384 mentions in open access literature.

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

Pasbola K, et al. (2026) Transcriptome profiling reveals the role of XIST/miR-335-5p regulatory axis as a crucial mediator of chemoresistance in esophageal cancer by influencing EMT and Ferroptosis. Functional & integrative genomics, 26(1).

Shi X, et al. (2026) Specific GPCRs elicit unique extracellular vesicle miRNA array signatures. eLife, 14.

He M, et al. (2026) Identify Diagnostic Biomarkers Related to Taurine Metabolism in Diabetic Foot Ulcers Using Bulk RNA-seq and ScRNA-seq Analysis. Journal of diabetes, 18(1), e70166.

Peng Q, et al. (2026) Identification and Mechanism Research of Oxidative Stress-Related Biomarkers in Oral Lichen Planus. Biomedicines, 14(2).

Ahmadizad Firouzjaei A, et al. (2026) Regulation of ferroptosis in colorectal cancer through therapeutic modulation and miRNA targeting. Biochemistry and biophysics reports, 45, 102444.

He J, et al. (2026) Identification of common genes associated with diabetic nephropathy and diabetic retinopathy. Frontiers in cell and developmental biology, 14, 1808941.

Popovic-Vukovic M, et al. (2026) Circulating EV miRNA Cargo in Glioblastoma Patients Is Associated with Distinct Gene Expression Signatures in Peripheral Immune Cells, Suggesting an Early, Compartment-Specific Immune Priming State. Biomedicines, 14(3).

Nikezi?? A, et al. (2026) Bioinformatics Analysis of microRNAs Associated with Metastatic Potential in Breast Cancer. Biology, 15(8).

Luo T, et al. (2026) Integrative multi-omics and network analysis identify potential targets of Chaihu Shugan Xiaozheng Formula in breast cancer. Translational oncology, 70,

102829.

Yang L, et al. (2026) Bioinformatics analysis identifies biomarkers associated with T-cell depletion in systemic lupus erythematosus. *Medicine*, 105(22), e49016.

Lin Y, et al. (2026) Mendelian randomization identifies circulating miRNAs as causal mediators of gastric cancer susceptibility and survival outcomes. *Medicine*, 105(1), e46833.

Cai H, et al. (2026) The role of PLOD family genes in liver hepatocellular carcinoma: from mechanisms to therapeutic potential. *BMC cancer*, 26(1), 172.

Cai S, et al. (2026) Identification and validation of novel inflammatory response-related diagnostic biomarkers in diabetic foot ulcers. *Journal of diabetes investigation*, 17(1), 103.

Qin H, et al. (2026) Cuproptosis-associated PDHA1 promotes sarcoma progression and immunotherapy responsiveness via the E2F1-PD-L1 axis: a multi-omics and clinical validation study. *NPJ precision oncology*, 10(1).

Chen Y, et al. (2026) Identification of metabolism and inflammation-related biomarkers and potential drugs for schizophrenia based on comprehensive bioinformatics and machine learning. *BMC psychiatry*, 26(1).

Tang D, et al. (2026) Functional network analysis in hepatolithiasis: identifying novel therapeutic targets through whole-exome sequencing. *PeerJ*, 14, e21059.

Li S, et al. (2026) Identification of a Diagnostic Gene Signature Associated with Centrosome Amplification in Pressure Injuries: A Cross-Sectional Transcriptome and Machine Learning Study. *Journal of inflammation research*, 19, 580289.

Wang Y, et al. (2026) Exploring Immune-Related Gene and Mechanisms in Rosacea Through Transcriptome Analysis and Mendelian Randomization. *BioMed research international*, 2026(1), e7294117.

Yang Q, et al. (2026) Identification and mechanistic exploration of VEGFA and CALML3 as calcium channel-related prognostic genes in cervical cancer. *Discover oncology*, 17(1).

Alrefaey AI, et al. (2026) MicroRNAs as Diagnostic and Therapeutic Biomarkers in Childhood Asthma: A Systematic Review with Bioinformatics Analysis. *Journal of personalized medicine*, 16(4).