

Resource Summary Report

Generated by [NIF](#) on Apr 29, 2025

[miRCode](#)

RRID:SCR_023870

Type: Tool

Proper Citation

miRCode (RRID:SCR_023870)

Resource Information

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

Proper Citation: miRCode (RRID:SCR_023870)

Description: Web tool for transcriptome wide microRNA target prediction including lncRNAs. Used for whole transcriptome human microRNA target predictions based on the comprehensive GENCODE gene annotation, including long non-coding RNA genes. Coding genes are also covered, including atypical regions such as 5'UTRs and CDS. MicroRNA family definitions and names are consistent with TargetScan. Site conservation is evaluated based on 46 vertebrates species. Map of putative microRNA target sites in the long non-coding transcriptome.

Resource Type: software resource, web application

Defining Citation: [PMID:22718787](#)

Keywords: microRNA target sites, target prediction, transcriptome wide microRNA target prediction, lncRNAs, whole transcriptome human microRNA,

Funding: Swedish Medical Research Council ;
Assar Gabrielsson Foundation ;
Magnus Bergvall Foundation ;
Lars Hierta Memorial Foundation

Availability: Free, Freely available

Resource Name: miRCode

Resource ID: SCR_023870

Record Creation Time: 20230725T050218+0000

Record Last Update: 20250429T060300+0000

Ratings and Alerts

No rating or validation information has been found for miRCode.

No alerts have been found for miRCode.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Shi J, et al. (2025) Integrated Mendelian Randomization and Single-Cell Transcriptomics Analysis Identifies Critical Blood Biomarkers and Potential Mechanisms in Epilepsy. *CNS neuroscience & therapeutics*, 31(1), e70172.

Wang L, et al. (2025) Differential mRNA and lncRNA Expression Profiles Associated with Early Pregnancy Loss in ART Patients. *Reproductive sciences* (Thousand Oaks, Calif.), 32(1), 229.

Wang J, et al. (2024) Comprehensive characterization of small noncoding RNA profiles in hypoxia-induced pulmonary hypertension (HPH) rat tissues. *iScience*, 27(2), 108815.

Chen Z, et al. (2024) Construction and analysis of competitive endogenous RNA networks and prognostic models associated with ovarian cancer based on the exoRBase database. *PloS one*, 19(4), e0291149.

Berenji E, et al. (2024) Discovering therapeutic possibilities for polycystic ovary syndrome by targeting XIST and its associated ceRNA network through the analysis of transcriptome data. *Scientific reports*, 14(1), 6180.

Hu F, et al. (2024) Single-Cell Sequencing Combined with Transcriptome Sequencing Constructs a Predictive Model of Key Genes in Multiple Sclerosis and Explores Molecular Mechanisms Related to Cellular Communication. *Journal of inflammation research*, 17, 191.

Lian Z, et al. (2024) Long noncoding RNA MEG3 regulates cell proliferation and apoptosis by disrupting microRNA-9-5p-mediated inhibition of NDRG1 in prostate cancer. *Aging*, 16(2), 1938.

Zhang M, et al. (2024) KLK10/LIPH/PARD6B/SLC52A3 are promising molecular biomarkers for the prognosis of pancreatic cancer through a ceRNA network. *Heliyon*, 10(1), e24287.

Norouzi R, et al. (2024) In-silico and in-vitro evidence suggest LINC01405 as a sponge for miR-29b and miR-497-5p, and a potential regulator of Wnt, PI3K, and TGFB signaling pathways in breast carcinoma. *Cancer reports (Hoboken, N.J.)*, 7(2), e1972.

Ren S, et al. (2024) Constructing lncRNA-miRNA-mRNA networks specific to individual cancer patients and finding prognostic biomarkers. *BMC genomic data*, 25(Suppl 1), 67.

Yan Q, et al. (2024) Roles of long non-coding RNAs in esophageal cell squamous carcinoma (Review). *International journal of molecular medicine*, 54(2).

Guan J, et al. (2024) Role of N6-methyladenosine-related lncRNAs in pseudoexfoliation glaucoma. *Epigenetics*, 19(1), 2348840.

Zhu R, et al. (2024) Identification of immune-related hub genes and potential molecular mechanisms involved in COVID-19 via integrated bioinformatics analysis. *Scientific reports*, 14(1), 29964.

Tang Y, et al. (2024) Shared and specific competing endogenous RNAs network mining in four digestive system tumors. *Computational and structural biotechnology journal*, 23, 4271.

Zhang M, et al. (2024) Comprehensive analysis of immune-related lncRNAs in AML patients uncovers potential therapeutic targets and prognostic biomarkers. *Heliyon*, 10(9), e30616.

Liu Z, et al. (2024) Uncovering the ceRNA Network Related to the Prognosis of Stomach Adenocarcinoma Among 898 Patient Samples. *Biochemical genetics*, 62(6), 4770.

Zhang C, et al. (2024) Long non-coding RNA HOTTIP promotes renal cell carcinoma progression through the regulation of the miR-506 pathway. *Aging*, 16(13), 10832.

Senousy MA, et al. (2024) Serum lncRNAs TUG1, H19, and NEAT1 and their target miR-29b/SLC3A1 axis as possible biomarkers of preeclampsia: Potential clinical insights. *Non-coding RNA research*, 9(4), 995.

Li Y, et al. (2024) Male breast cancer differs from female breast cancer in molecular features that affect prognoses and drug responses. *Translational oncology*, 45, 101980.

Zheng S, et al. (2024) Bioinformatics analysis and validation of mesenchymal stem cells related gene MT1G in osteosarcoma. *Aging*, 16(9), 8155.