

Resource Summary Report

Generated by SPARC SAWG on Aug 8, 2026

miRCode

RRID:SCR_023870

Type: Tool

Proper Citation

miRCode (RRID:SCR_023870)

Resource Information

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

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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: web application, software resource

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: 20260808T190259+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 187 mentions in open access literature.

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

Chen J, et al. (2026) Multiomics combined drugs to explore the potential mechanism and treatment of ankylosing spondylitis. *Journal of orthopaedic surgery and research*, 21(1).

Bi Z, et al. (2026) Tiam1 up-regulation by long non-coding RNA ABHD11-AS1 sponging of miR-182-5p causes β -catenin pathway activation to promote hexavalent chromium lung carcinogenesis. *Journal of hazardous materials*, 501, 140697.

Zhou L, et al. (2026) The metastasis landscape of *Clonorchis sinensis*-associated hepatocellular carcinoma: an integrated multi-omics and clinical study. *Frontiers in immunology*, 17, 1723156.

Zhang Y, et al. (2026) LINC01996 suppresses non-small cell lung cancer proliferation and metastasis by orchestrating the miR-12115/CNRIP1/Ras signaling axis. *Clinical & experimental metastasis*, 43(2).

Wang H, et al. (2026) Revealing shared molecular markers and mechanisms in colorectal cancer and COVID-19 through bioinformatics and machine learning. *Briefings in bioinformatics*, 27(1).

Wei H, et al. (2026) Integrative multi-omics analysis identifies key ubiquitination regulators in prostate cancer. *Translational oncology*, 68, 102788.

Wang J, et al. (2026) Identification of shared biomarkers in obesity and non-alcoholic fatty liver disease: a comprehensive analysis of Mendelian randomization and transcriptomic data. *Frontiers in nutrition*, 13, 1780686.

Liang H, et al. (2026) Integrative Bioinformatics Analyses Reveal X Chromosome Inactivation Escape Genes Dosage Dysregulation Is the Primary Contributor to Turner Syndrome. *Iranian journal of biotechnology*, 24(2).

Chu C, et al. (2025) Bioinformatic analysis and retrospective clinical study identifying DNAJB4 as a pan-cancer biomarker with a highlight on kidney cancer. *Clinical and experimental medicine*, 25(1), 260.

- Bao J, et al. (2025) Application value of a prognostic risk model based on lactate-related genes in non-small cell lung cancer. *Translational cancer research*, 14(11), 8055.
- Zhang L, et al. (2025) Genetic evidence for amlodipine's protective role in gastroesophageal reflux disease: A focus on CACNB2. *PloS one*, 20(2), e0309805.
- Wang B, et al. (2025) Long noncoding RNA SNHG5 promotes 5-fluorouracil resistance in colorectal cancer by regulating miR-26b/p-glycoprotein axis. *World journal of gastrointestinal oncology*, 17(5), 102417.
- Liu Y, et al. (2025) Uncovering potential biomarkers of endometriosis: transcriptomic and single-cell analysis. *Frontiers in medicine*, 12, 1528434.
- Wei DP, et al. (2025) Identification and validation of autophagy-related genes in sepsis based on bioinformatics studies. *Virology journal*, 22(1), 81.
- Wei C, et al. (2025) The microRNA landscape and regulatory network in *Clonorchis sinensis*-infected hepatocellular carcinoma: implications for tumor progression. *Parasites & vectors*, 18(1), 68.
- Zhang L, et al. (2025) The LncRNA RMST-miR-4295-ITPR1 axis: a key mechanism in regulating autophagy in triple-negative breast cancer cells. *BMC cancer*, 25(1), 782.
- Mahmoud HS, et al. (2025) The diagnostic value of LncRNA NEAT1 targeting miR-129-5p in pancreatic cancer patients. *Scientific reports*, 15(1), 27638.
- Wang Y, et al. (2025) Investigating potential biomarkers associated with antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis using Mendelian randomization and transcriptomic analysis. *Arthritis research & therapy*, 27(1), 166.
- Liu S, et al. (2025) Identifying autophagy-related biomarkers in the treatment of renal interstitial fibrosis with Shen Fukang through network pharmacology. *Medicine*, 104(45), e45536.
- Wei J, et al. (2025) TLR4 identified as a major depressive disorder gene signature mediating effects through multiple immune cells. *Scientific reports*, 15(1), 12437.