

Resource Summary Report

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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 ;
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Availability: Free, Freely available

Resource Name: miRCode

Resource ID: SCR_023870

Record Creation Time: 20230725T050218+0000

Record Last Update: 20260805T044521+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 66 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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.

Mahmoud HS, et al. (2025) The diagnostic value of LncRNA NEAT1 targeting miR-129-5p in pancreatic cancer patients. Scientific reports, 15(1), 27638.

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.

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.

Liu Y, et al. (2025) Uncovering potential biomarkers of endometriosis: transcriptomic and single-cell analysis. Frontiers in medicine, 12, 1528434.

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.

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.

Salman A, et al. (2025) A comparison of the expression patterns and diagnostic capability of the ncRNAs NEAT1 and miR-34a in non-obstructive azoospermia and severe oligospermia. Human genomics, 19(1), 35.

Yang R, et al. (2025) Exploring the molecular mechanisms of comorbidity between thyroid cancer and breast cancer through multi-omics data. Scientific reports, 15(1), 23309.

Wu W, et al. (2025) HOTAIR, a ferroptosis-related gene, promotes malignant behavior of breast cancer via sponging miR-206. *Discover oncology*, 16(1), 948.

Zhang Y, et al. (2025) MT1JP/miR-103a-3p induce pyroptosis and regulate the tumor immune microenvironment in gastric cancer. *Scientific reports*, 15(1), 26799.

Tang J, et al. (2025) Neutrophil-related IL1R2 gene predicts the occurrence and early progression of myocardial infarction. *Frontiers in cardiovascular medicine*, 12, 1516043.

Ouyang ML, et al. (2025) Imaging and RNA sequencing-based radiogenomic analysis of occult lymph node metastasis and survival in lung adenocarcinoma staged non-metastatic. *Communications medicine*, 5(1), 517.

Zhu Y, et al. (2025) Development of a prognostic model based on the ceRNA network in Triple-Negative Breast cancer. *PeerJ*, 13, e19063.

Wang J, et al. (2025) Assessment of lncRNA biomarkers based on NETs for prognosis and therapeutic response in ovarian cancer. *Scientific reports*, 15(1), 13042.

Liu Y, et al. (2025) The comprehensive potential of AQP1 as a tumor biomarker: evidence from kidney neoplasm cohorts, cell experiments and pan-cancer analysis. *Human genomics*, 19(1), 15.

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.

Shimote K, et al. (2025) Upregulation of LINC02154 promotes esophageal cancer progression by enhancing cell cycling and epithelial-mesenchymal transition. *Non-coding RNA research*, 14, 107.

Wu Y, et al. (2025) Identification of the microglia-associated signature in experimental autoimmune encephalomyelitis. *Frontiers in immunology*, 16, 1581878.