

Resource Summary Report

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TarBase

RRID:SCR_010841

Type: Tool

Proper Citation

TarBase (RRID:SCR_010841)

Resource Information

URL: <http://diana.imis.athena-innovation.gr/DianaTools/index.php?r=tarbase/index>

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Description: Manually curated database of experimentally supported animal microRNA targets. Collection of experimentally supported miRNA gene interactions.

Abbreviations: DIANA-TarBase

Synonyms: DIANA-TarBase v7.0, DIANA-TarBase v.8, DIANA-TarBase v.6

Resource Type: database, data or information resource, service resource

Defining Citation: [PMID:22135297](#), [PMID:29156006](#)

Keywords: mirna-gene interaction

Funding Agency: Fondation Santé Grant , General Secretariat of Research and Technology, Greece Grant , Hellenic Foundation for Research and Innovation , IKY Foundation

Availability: Restricted

Resource Name: TarBase

Resource ID: SCR_010841

Alternate IDs: OMICS_00397

Alternate URLs: http://carolina.imis.athena-innovation.gr/diana_tools/web/index.php?r=tarbasev8%2Findex/

Ratings and Alerts

No rating or validation information has been found for TarBase.

No alerts have been found for TarBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 562 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Skoufos G, et al. (2024) TarBase-v9.0 extends experimentally supported miRNA-gene interactions to cell-types and virally encoded miRNAs. *Nucleic acids research*, 52(D1), D304.

Wan Y, et al. (2024) Identification of the role of pyroptosis-related genes in chronic rhinosinusitis based on WGCNA. *Heliyon*, 10(1), e22944.

Gaspari L, et al. (2024) Transgenerational Transmission of 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) Effects in Human Granulosa Cells: The Role of MicroRNAs. *International journal of molecular sciences*, 25(2).

Saranya I, et al. (2024) Circ_ST6GAL1-mediated competing endogenous RNA network regulates TGF- β 1-stimulated matrix Metalloproteinase-13 expression via Runx2 acetylation in osteoblasts. *Non-coding RNA research*, 9(1), 153.

Song S, et al. (2024) Identification of the shared genes in type 2 diabetes mellitus and osteoarthritis and the role of quercetin. *Journal of cellular and molecular medicine*, 28(4), e18127.

Sun R, et al. (2024) Transcriptome Sequencing Identifies Abnormal lncRNAs and mRNAs and Reveals Potentially Hub Immune-Related mRNA in Osteoporosis with Vertebral Fracture. *Clinical interventions in aging*, 19, 203.

Liao W, et al. (2024) MiR-150-5p contributes to unexplained recurrent spontaneous abortion by targeting VEGFA and downregulating the PI3K/AKT/mTOR signaling pathway. *Journal of assisted reproduction and genetics*, 41(1), 63.

Lawarde A, et al. (2024) ExpIORNet: An interactive web tool to explore stage-wise miRNA

expression profiles and their interactions with mRNA and lncRNA in human breast and gynecological cancers. *Non-coding RNA research*, 9(1), 125.

Gutierrez-Tordera L, et al. (2024) Exploring small non-coding RNAs as blood-based biomarkers to predict Alzheimer's disease. *Cell & bioscience*, 14(1), 8.

Liu M, et al. (2024) Regulatory function and mechanism research for m6A modification WTAP via SUCLG2-AS1- miR-17-5p-JAK1 axis in AML. *BMC cancer*, 24(1), 98.

Liu XS, et al. (2024) METTL3 as a novel diagnosis and treatment biomarker and its association with glycolysis, cuproptosis and ceRNA in oesophageal carcinoma. *Journal of cellular and molecular medicine*, 28(6), e18195.

Bryant CJ, et al. (2024) Discovery of novel microRNA mimic repressors of ribosome biogenesis. *Nucleic acids research*, 52(4), 1988.

Sasso CV, et al. (2024) Modulation of miR-29a and miR-29b Expression and Their Target Genes Related to Inflammation and Renal Fibrosis by an Oral Nutritional Supplement with Probiotics in Malnourished Hemodialysis Patients. *International journal of molecular sciences*, 25(2).

Guo Z, et al. (2024) Identification of mitophagy-related hub genes during the progression of spinal cord injury by integrated multinomial bioinformatics analysis. *Biochemistry and biophysics reports*, 38, 101654.

Mbeje M, et al. (2023) In Silico Bioinformatics Analysis on the Role of Long Non-Coding RNAs as Drivers and Gatekeepers of Androgen-Independent Prostate Cancer Using LNCaP and PC-3 Cells. *Current issues in molecular biology*, 45(9), 7257.

Latimer MN, et al. (2023) Cardiomyocyte-specific disruption of the circadian BMAL1-REV-ERB α regulatory network impacts distinct miRNA species in the murine heart. *Communications biology*, 6(1), 1149.

Li MK, et al. (2023) Integrative bioinformatics analysis to screen key genes and signalling pathways related to ferroptosis in obesity. *Adipocyte*, 12(1), 2264442.

Yu C, et al. (2023) Comparison of miRNA transcriptome of exosomes in three categories of somatic cells with derived iPSCs. *Scientific data*, 10(1), 616.

Ou-Yang Y, et al. (2023) Screening for genes, miRNAs and transcription factors of adipogenic differentiation and dedifferentiation of mesenchymal stem cells. *Journal of orthopaedic surgery and research*, 18(1), 46.

Colantoni A, et al. (2023) FUS Alters circRNA Metabolism in Human Motor Neurons Carrying the ALS-Linked P525L Mutation. *International journal of molecular sciences*, 24(4).