

Resource Summary Report

Generated by PRECISE-TBI on Aug 26, 2026

PITA

RRID:SCR_010853

Type: Tool

Proper Citation

PITA (RRID:SCR_010853)

Resource Information

URL: http://genie.weizmann.ac.il/pubs/mir07/mir07_data.html

Proper Citation: PITA (RRID:SCR_010853)

Description: Catalogs of predicted microRNA targets in worm (based on ce6 genome assembly), fly (dm3), mouse (mm9) and human (hg18). We follow standard seed parameter settings and consider seeds of length 6-8 bases, beginning at position 2 of the microRNA. No mismatches or loops are allowed, but a single G:U wobble is allowed in 7- or 8-mers. In genes missing a 3' UTR annotation, 500 bp (fly), 800 bp (human and mouse) or 300 bp (worm) downstream of the annotated end of the coding sequence were used as the predicted UTR. For each organism, a catalog with zero flank and with a flank of 3 and 15 bases upstream and downstream.

Abbreviations: PITA

Resource Type: data or information resource, data set

Resource Name: PITA

Resource ID: SCR_010853

Alternate IDs: OMICS_00412

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260821T193926+0000

Ratings and Alerts

No rating or validation information has been found for PITA.

No alerts have been found for PITA.

Data and Source Information

Usage and Citation Metrics

We found 1079 mentions in open access literature.

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

Yu X, et al. (2026) miR-339-5p impairs myogenic proliferation and differentiation by repressing contractile gene programs in skeletal muscle. *American journal of physiology. Cell physiology*, 331(2), C425.

Wang J, et al. (2026) Bioinformatics analyses of a potential miRNA-mRNA regulatory axis in lumbar degenerative disc disease. *BMC medical genomics*, 19(1).

Liu Z, et al. (2026) miR-34 regulates cuticle pigmentation by targeting Bm-iAANAT and Bmserpin3 in *Bombyx mori*. *RNA biology*, 23(1), 1.

Shrestha A, et al. (2026) Sperm RNA landscape during sexual maturation in Duroc boars. *BMC genomics*, 27(1), 197.

Yao Y, et al. (2026) *Eriocheir sinensis* PI3K-mediated 14-3-3 phosphorylation at a conserved tyrosine residue enhances ROS production to defend against *Spiroplasma eriocheiris* infection. *Cell communication and signaling : CCS*, 24(1).

Zhao W, et al. (2026) C1RL-AS1/microRNA-424-5p/adrenoceptor $\alpha 2$ axis: A novel regulatory mechanism in lung adenocarcinoma associated with immune infiltration and prognosis. *PloS one*, 21(3), e0343805.

Yao H, et al. (2026) Hub genes and molecular mechanisms related to hypospadias based on transcriptome sequencing data and bioinformatics analysis. *BMC medical genomics*, 19(1).

Shi W, et al. (2026) Melanin Deposition and Screening of Melanogenesis-Related Differential RNAs and Construction of ceRNA Regulatory Network in Liancheng White Ducks. *Animals : an open access journal from MDPI*, 16(12).

Chen S, et al. (2026) Engineered bone-targeting *Lycium barbarum* L.-derived extracellular vesicle-like nanoparticles deliver miR167a-5p to regulate mitochondrial dynamics and metabolic reprogramming in alleviating osteoporosis. *Materials today. Bio*, 38, 103312.

Zhang X, et al. (2026) Identification and Analysis of Biomarkers Associated With Lipid Metabolism and Ferroptosis in Ulcerative Colitis. *Journal of immunology research*, 2026(1), e9283449.

Dong R, et al. (2026) Exploring Biomarkers and Regulatory Mechanisms Associated with Lytic Cell Death in Allergic Rhinitis Based on Transcriptome Analysis. *Biomedicines*, 14(6).

Chitre S, et al. (2026) *Campylobacter jejuni* infection impacts host-derived miRNAs targeting bacterial and host genes. *Microbiology spectrum*, 14(3), e0318425.

Liang Z, et al. (2026) Identification of key ferroptosis-related targets in colorectal cancer: A transcriptomics-driven study via machine learning and AUCell analysis of single-cell RNA-sequencing. *Journal of Cancer*, 17(1), 32.

Kim M, et al. (2026) Prognostic Implications of Exosomal miRNA Networks Regulating TGF β 1-induced Epithelial-Mesenchymal Transition Signature in Oral Squamous Cell Carcinoma. *Cancer genomics & proteomics*, 23(1), 50.

He Y, et al. (2026) Identification of susceptibility modules and genes through WGCNA and ceRNA network analysis in neuropathic pain-induced anxiodepression. *Translational psychiatry*, 16(1).

Chandra H, et al. (2026) Exosomal microRNAs from Alveolar Macrophages Reveal a Protective Role of the Lung Microbiome Against Oncogenic Signaling During PAH Exposure. *Cells*, 15(8).

Soliman B, et al. (2026) Let-7a and miR-34a Interplay Potent Suppressive Roles in Hepatocellular Carcinoma via Co-Targeting FNDC3B, IGF2 and SOX4. *International journal of molecular sciences*, 27(4).

Luo S, et al. (2026) Identification of prognostic genes associated with tolerogenic dendritic cells in gastric cancer based on transcriptomic data. *PloS one*, 21(3), e0343688.

Kyritsis A, et al. (2026) Mutual feedback regulation between Poly(A)-specific ribonuclease (PARN) and cognate microRNAs. *Life science alliance*, 9(5).

Wang H, et al. (2026) Identification and regulatory mechanism analysis of macrophage-related key genes in diabetic nephropathy. *Diabetology & metabolic syndrome*, 18(1).