

Resource Summary Report

Generated by T1D on Aug 1, 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 set, data or information resource

Resource Name: PITA

Resource ID: SCR_010853

Alternate IDs: OMICS_00412

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260801T042710+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 1047 mentions in open access literature.

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

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.

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.

Xin Q, et al. (2026) Novel miR-290 regulates melanogenesis in Liancheng white ducks via the PI3K/AKT signaling pathway. *Poultry science*, 105(1), 106216.

Wang Y, et al. (2025) Clinical significance and immune infiltration analyses of the coagulation factor V gene in brain lower grade glioma. *Discover oncology*, 16(1), 535.

Chiu Y, et al. (2025) Time-resolved miRNA-mRNA integrated analysis reveals the miRNA-mRNA networks underlying plasma membrane damage-dependent senescence and DNA damage response-dependent senescence in WI-38 normal human fibroblasts. *RNA biology*, 22(1), 1.

Zhao YQ, et al. (2025) A comprehensive pan-cancer analysis of the prognostic role and immunotherapy efficacy evaluation of Glyoxalase 1. *Discover oncology*, 16(1), 2326.

Sha M, et al. (2025) Integrated single-cell and bulk RNA sequencing to identify and validate prognostic genes related to T Cell senescence in acute myeloid leukemia. *Frontiers in bioinformatics*, 5, 1606284.

Ding B, et al. (2025) Resveratrol contributes to NK cell-mediated breast cancer cytotoxicity by upregulating ULBP2 through miR-17-5p downmodulation and activation of MINK1/JNK/c-Jun signaling. *Frontiers in immunology*, 16, 1515605.

Leung SY, et al. (2025) Nobiletin Modulates Adipocyte-Derived Exosomal miRNA to Improve Liver Lipid Metabolism in Obese Mice. *Journal of agricultural and food chemistry*, 73(35), 21959.

Hailati J, et al. (2025) Targeting PDCD4 in cancer and atrial fibrillation: mechanistic insights from integrated multi-omics and single-cell analysis. *Frontiers in oncology*, 15, 1593815.

Liu L, et al. (2025) Multi-omics dissection of CPNE1 reveals its prognostic value and immune-regulatory function in liver cancer. *Discover oncology*, 16(1), 1499.

Wang X, et al. (2025) hsa_circ_0002872 functions in lung cancer prognostic and tumorigenesis through regulating ZBTB46 via sponging hsa-miR-29b-1-5p. *Clinics (Sao*

Paulo, Brazil), 80, 100733.

Zhang J, et al. (2025) Helicobacter pylori induced miR-362-5p upregulation drives gastric cancer progression and links hepatocellular carcinoma through an exosome-dependent pathway. *Frontiers in cellular and infection microbiology*, 15, 1582131.

Yang J, et al. (2025) Exosomal miR-122-5p from tubular cells ameliorates renal interstitial fibrosis by regulating fibroblasts via HIF-1?. *Cell death discovery*, 11(1), 474.

Zeng Z, et al. (2025) Comprehensive analysis of LncRNA-miRNA-mRNA CeRNA network associated with umbilical cord blood PBMC in down syndrome. *Scientific reports*, 15(1), 36352.

McCusker P, et al. (2025) Polo-like kinase 1 regulates growth in juvenile *Fasciola hepatica*. *PLoS pathogens*, 21(12), e1013406.

Ma C, et al. (2025) Systems biology analysis of long non-coding RNAs and targets to identify key modules and biomarkers in breast cancer. *Discover oncology*, 16(1), 2325.

Liu FF, et al. (2025) The Abnormal ER?-miRNA Cross-Talk in AD-Affected Human Hippocampus: A Bioinformatics Perspective. *Molecular neurobiology*, 62(6), 7998.

Al-Abbas NS, et al. (2025) TRIM26 as a dual regulator of ferroptosis and chemoresistance in gastric cancer through HSF1 ubiquitination and exosomal miR-24-3p signaling. *Translational oncology*, 60, 102489.

Feng K, et al. (2025) Cuticle protein mediates the evolution of stress resistance by generating a decoy circular RNA in spider mite. *Science advances*, 11(25), eads3361.