

Resource Summary Report

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TAM

RRID:SCR_023800

Type: Tool

Proper Citation

TAM (RRID:SCR_023800)

Resource Information

URL: <http://www.lirmed.com/tam2/>

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Description: Web server for miRNA set enrichment analysis. TAM 2.0 is updated version of this web server. Allows to test functional and disease annotations of miRNAs by overrepresentation analysis and to compare input de-regulated miRNAs with those de-regulated in other disease conditions via correlation analysis.

Synonyms: TAM 2.0

Resource Type: software resource, data access protocol, web service

Defining Citation: [PMID:29878154](#), [PMID:20696049](#)

Keywords: miRNA set enrichment analysis, functional and disease annotations testing, miRNAs, overrepresentation analysis,

Funding: National Natural Science Foundation of China ;
Fundamental Research Funds for Central Universities of China ;
Natural Science Foundation of Hebei Province ;
Doctoral Fund of Ministry of Education of China

Availability: Free, Freely available

Resource Name: TAM

Resource ID: SCR_023800

Record Creation Time: 20230719T050218+0000

Record Last Update: 20260818T043728+0000

Ratings and Alerts

No rating or validation information has been found for TAM.

No alerts have been found for TAM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Ronchi J, et al. (2026) Multi-Omics Analysis in Autoimmunity: Identification of MicroRNA Regulatory Networks and Cell-Type-Specific Dysregulations in Multiple Sclerosis and Type 1 Diabetes. *MedComm*, 7(4), e70647.

Huang Q, et al. (2025) Bio-engineered microRNA-7 effectively interferes with the Akt3/p53 axis to suppress human non-small cell lung cancer. *Cancer cell international*, 25(1), 250.

Sessa F, et al. (2025) MiRNA Dysregulation in Brain Injury: An In Silico Study to Clarify the Role of a MiRNA Set. *Current neuropharmacology*, 23(2), 209.

Abu-Toamih Atamni HJ, et al. (2025) Circulating microRNA signatures as potential biomarkers differentiating diabetic, prediabetic, and healthy individuals. *Frontiers in endocrinology*, 16, 1699100.

Lei H, et al. (2023) Exploration of the underlying comorbidity mechanism in psoriasis and periodontitis: a bioinformatics analysis. *Hereditas*, 160(1), 7.

Zhong B, et al. (2023) Identification and Analysis of Sex-Biased MicroRNAs in Human Diseases. *Genes*, 14(9).

Wang B, et al. (2023) IDH1 K224 acetylation promotes colorectal cancer via miR-9-5p/NHE1 axis-mediated regulation of acidic microenvironment. *iScience*, 26(7), 107206.

Xian N, et al. (2023) Bioinformatics analysis to reveal the potential comorbidity mechanism in psoriasis and nonalcoholic steatohepatitis. *Skin research and technology : official journal of International Society for Bioengineering and the Skin (ISBS) [and] International Society for Digital Imaging of Skin (ISDIS) [and] International Society for Skin Imaging (ISSI)*, 29(9), e13457.

Sessa F, et al. (2023) New Insight into Mechanisms of Cardiovascular Diseases: An Integrative Analysis Approach to Identify TheraNoMiRNAs. *International journal of molecular sciences*, 24(7).

Gayt??n-Pacheco N, et al. (2022) miR-146a, miR-221, and miR-155 are Involved in Inflammatory Immune Response in Severe COVID-19 Patients. *Diagnostics (Basel, Switzerland)*, 13(1).

Tang C, et al. (2022) Improving the prediction for the response to radiotherapy of clinical tumor samples by using combinatorial model of MicroRNA expression. *Frontiers in genetics*, 13, 1069112.