

Resource Summary Report

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HOCTAR

RRID:SCR_010842

Type: Tool

Proper Citation

HOCTAR (RRID:SCR_010842)

Resource Information

URL: <http://hoctar.tigem.it/>

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Description: Database serving as a tool for microRNA target prediction. The HOCTAR procedure is based on the integration of expression profiling and sequence-based miRNA target recognition softwares. HOCTAR database (db) is the first and unique database to use transcriptomic data to score putative miRNA targets looking at the expression behaviour of their host genes, and it includes and re-analyzes all miRNA target predictions generated by softwares such as miRanda, TargetScan and PicTar. The HOCTARdb contains the prediction target lists for 290 human intragenic miRNAs and also provides tentative assignments of miRNA function based on Gene Ontology analyses of their predicted targets. There are two ways to interrogate HOCTARdb: (i) by selecting a miRNA using either an alphabetically sorted pull-down menu in the microRNA query, or (ii) by typing a target gene symbol (HUGO Gene Name-approved) in the Target Gene Name query.

Abbreviations: HOCTAR

Synonyms: Host gene Opposite Correlated TARgets, HOCTARdb, HOCTAR database

Resource Type: data or information resource, database

Defining Citation: [PMID:21435384](#), [PMID:19088304](#)

Keywords: microrna, target prediction.

Availability: Public

Resource Name: HOCTAR

Resource ID: SCR_010842

Alternate IDs: OMICS_00398

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260729T044256+0000

Ratings and Alerts

No rating or validation information has been found for HOCTAR.

No alerts have been found for HOCTAR.

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 [kravitz2](#) .

Huang L, et al. (2020) CircRNA_000864 Upregulates B-cell Translocation Gene 2 Expression and Represses Migration and Invasion in Pancreatic Cancer Cells by Binding to miR-361-3p. *Frontiers in oncology*, 10, 547942.

Hernandez-Romero IA, et al. (2019) The Regulatory Roles of Non-coding RNAs in Angiogenesis and Neovascularization From an Epigenetic Perspective. *Frontiers in oncology*, 9, 1091.

Yang Z, et al. (2019) Elevated Plasma microRNA-105-5p Level in Patients With Idiopathic Parkinson's Disease: A Potential Disease Biomarker. *Frontiers in neuroscience*, 13, 218.

Lin Y, et al. (2018) Biomarker microRNAs for prostate cancer metastasis: screened with a network vulnerability analysis model. *Journal of translational medicine*, 16(1), 134.

Zhang H, et al. (2017) Biomarker MicroRNAs for Diagnosis of Oral Squamous Cell Carcinoma Identified Based on Gene Expression Data and MicroRNA-mRNA Network Analysis. *Computational and mathematical methods in medicine*, 2017, 9803018.

Zhu Y, et al. (2017) Identification of biomarker microRNAs for predicting the response of colorectal cancer to neoadjuvant chemoradiotherapy based on microRNA regulatory network. *Oncotarget*, 8(2), 2233.

Ehya F, et al. (2017) Identification of miR-24 and miR-137 as novel candidate multiple sclerosis miRNA biomarkers using multi-staged data analysis protocol. *Molecular biology research communications*, 6(3), 127.

Shen S, et al. (2016) Biomarker MicroRNAs for Diagnosis, Prognosis and Treatment of Hepatocellular Carcinoma: A Functional Survey and Comparison. *Scientific reports*, 6, 38311.

Tarang S, et al. (2014) Macros in microRNA target identification: a comparative analysis of in silico, in vitro, and in vivo approaches to microRNA target identification. *RNA biology*, 11(4), 324.

Hamam D, et al. (2014) microRNA-320/RUNX2 axis regulates adipocytic differentiation of human mesenchymal (skeletal) stem cells. *Cell death & disease*, 5(10), e1499.

Gennarino VA, et al. (2011) HOCTAR database: a unique resource for microRNA target prediction. *Gene*, 480(1-2), 51.