

Resource Summary Report

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ComiR

RRID:SCR_013023

Type: Tool

Proper Citation

ComiR (RRID:SCR_013023)

Resource Information

URL: <http://www.benoslab.pitt.edu/comir/>

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Description: Data analysis service that predicts whether a given mRNA is targeted by a set of miRNAs. ComiR uses miRNA expression to improve and combine multiple miRNA targets for each of the four prediction algorithms: miRanda, PITA, TargetScan and mirSVR. The composite scores of the four algorithms are then combined using a support vector machine trained on Drosophila Ago1 IP data.

Abbreviations: ComiR

Synonyms: Combinatorial miRNA targeting, ComiR: Combinatorial miRNA target prediction tool, ComiR - Combinatorial miRNA target prediction tool

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:23703208](#), [PMID:23284279](#)

Keywords: mirna, bio.tools

Funding: NLM ;
Fondazione RiMED

Availability: Acknowledgement requested

Resource Name: ComiR

Resource ID: SCR_013023

Alternate IDs: OMICS_00395, biotools:comir

Alternate URLs: <https://bio.tools/comir>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260821T042831+0000

Ratings and Alerts

No rating or validation information has been found for ComiR.

No alerts have been found for ComiR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Menzies JAC, et al. (2024) A microRNA that controls the emergence of embryonic movement. *eLife*, 13.

Grexa I, et al. (2024) SuperCUT, an unsupervised multimodal image registration with deep learning for biomedical microscopy. *Briefings in bioinformatics*, 25(2).

Breznik E, et al. (2024) Cross-modality sub-image retrieval using contrastive multimodal image representations. *Scientific reports*, 14(1), 18798.

Guo Y, et al. (2021) The plasma exosomal miR-1180-3p serves as a novel potential diagnostic marker for cutaneous melanoma. *Cancer cell international*, 21(1), 487.

Rajan C, et al. (2021) MiRNA expression profiling and emergence of new prognostic signature for oral squamous cell carcinoma. *Scientific reports*, 11(1), 7298.

Bertolazzi G, et al. (2020) An improvement of ComiR algorithm for microRNA target prediction by exploiting coding region sequences of mRNAs. *BMC bioinformatics*, 21(Suppl 8), 201.

Boström AE, et al. (2020) Hypermethylation-associated downregulation of microRNA-4456 in hypersexual disorder with putative influence on oxytocin signalling: A DNA methylation analysis of miRNA genes. *Epigenetics*, 15(1-2), 145.

Li Y, et al. (2020) Metabolic syndrome increases senescence-associated micro-RNAs in extracellular vesicles derived from swine and human mesenchymal stem/stromal cells. *Cell communication and signaling : CCS*, 18(1), 124.

Bertolazzi G, et al. (2020) miR-1207-5p Can Contribute to Dysregulation of Inflammatory Response in COVID-19 via Targeting SARS-CoV-2 RNA. *Frontiers in cellular and infection microbiology*, 10, 586592.

Zhao B, et al. (2019) Significant improvement of miRNA target prediction accuracy in large datasets using meta-strategy based on comprehensive voting and artificial neural networks. *BMC genomics*, 20(1), 158.

Zhang W, et al. (2019) MicroRNA-153 Decreases Tryptophan Catabolism and Inhibits Angiogenesis in Bladder Cancer by Targeting Indoleamine 2,3-Dioxygenase 1. *Frontiers in oncology*, 9, 619.

Seong KM, et al. (2019) Impacts of Sub-lethal DDT Exposures on microRNA and Putative Target Transcript Expression in DDT Resistant and Susceptible *Drosophila melanogaster* Strains. *Frontiers in genetics*, 10, 45.

Jerez S, et al. (2019) Extracellular vesicles from osteosarcoma cell lines contain miRNAs associated with cell adhesion and apoptosis. *Gene*, 710, 246.

Zhang J, et al. (2019) MicroRNA-154 functions as a tumor suppressor in bladder cancer by directly targeting ATG7. *Oncology reports*, 41(2), 819.

Meng Y, et al. (2018) Obesity-induced mitochondrial dysfunction in porcine adipose tissue-derived mesenchymal stem cells. *Journal of cellular physiology*, 233(8), 5926.

Bagla S, et al. (2018) A distinct microRNA expression profile is associated with [¹¹C]-methyl-L-tryptophan (AMT) PET uptake in epileptogenic cortical tubers resected from patients with tuberous sclerosis complex. *Neurobiology of disease*, 109(Pt A), 76.

Agarwal V, et al. (2018) Predicting microRNA targeting efficacy in *Drosophila*. *Genome biology*, 19(1), 152.

Seong KM, et al. (2018) Differentially expressed microRNAs associated with changes of transcript levels in detoxification pathways and DDT-resistance in the *Drosophila melanogaster* strain 91-R. *PloS one*, 13(4), e0196518.

Eirin A, et al. (2017) Integrated transcriptomic and proteomic analysis of the molecular cargo of extracellular vesicles derived from porcine adipose tissue-derived mesenchymal stem cells. *PloS one*, 12(3), e0174303.

Akhtar MM, et al. (2016) Bioinformatic tools for microRNA dissection. *Nucleic acids research*, 44(1), 24.