

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: 20250430T055843+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 [dkNET](#).

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

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

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

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.

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.

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.

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.

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.

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.

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 ^{11}C -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.