Resource Summary Report

Generated by RRID on Apr 28, 2025

omiRas

RRID:SCR_010833
Type: Tool

Proper Citation

omiRas (RRID:SCR_010833)

Resource Information

URL: http://tools.genxpro.net/omiras/

Proper Citation: omiRas (RRID:SCR_010833)

Description: A web server for the annotation, comparison and visualization of interaction networks of non-coding RNAs derived from small RNA-Sequencing experiments of two different conditions.

Abbreviations: omiRas

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

Defining Citation: PMID:23946503

Keywords: bio.tools

Funding:

Resource Name: omiRas

Resource ID: SCR_010833

Alternate IDs: biotools:omiras, OMICS_00383

Alternate URLs: https://bio.tools/omiras

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250428T053624+0000

Ratings and Alerts

No rating or validation information has been found for omiRas.

No alerts have been found for omiRas.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Smith AO, et al. (2024) The Tumor-Associated Calcium Signal Transducer 2 (TACSTD2) oncogene is upregulated in cystic epithelial cells revealing a potential new target for polycystic kidney disease. PLoS genetics, 20(12), e1011510.

Kenneweg F, et al. (2024) Circulating miR-let7a levels predict future diagnosis of chronic thromboembolic pulmonary hypertension. Scientific reports, 14(1), 4514.

Postel MD, et al. (2022) Transcriptome analysis provides critical answers to the "variants of uncertain significance" conundrum. Human mutation, 43(11), 1590.

Lipps C, et al. (2019) Non-Invasive Approach for Evaluation of Pulmonary Hypertension Using Extracellular Vesicle-Associated Small Non-Coding RNA. Biomolecules, 9(11).

Zhang H, et al. (2018) miRDis: a Web tool for endogenous and exogenous microRNA discovery based on deep-sequencing data analysis. Briefings in bioinformatics, 19(3), 415.

Liamina D, et al. (2017) Radiation-Induced Changes of microRNA Expression Profiles in Radiosensitive and Radioresistant Leukemia Cell Lines with Different Levels of Chromosome Abnormalities. Cancers, 9(10).

Bottini S, et al. (2017) From benchmarking HITS-CLIP peak detection programs to a new method for identification of miRNA-binding sites from Ago2-CLIP data. Nucleic acids research, 45(9), e71.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Mansur F, et al. (2016) Gld2-catalyzed 3' monoadenylation of miRNAs in the hippocampus has no detectable effect on their stability or on animal behavior. RNA (New York, N.Y.), 22(10), 1492.

Fell LH, et al. (2016) Impact of individual intravenous iron preparations on the differentiation of monocytes towards macrophages and dendritic cells. Nephrology, dialysis, transplantation : official publication of the European Dialysis and Transplant Association - European Renal Association, 31(11), 1835.

Satoh J, et al. (2015) MicroRNA-Seq Data Analysis Pipeline to Identify Blood Biomarkers for Alzheimer's Disease from Public Data. Biomarker insights, 10, 21.

Müller S, et al. (2015) Next-generation sequencing reveals novel differentially regulated mRNAs, lncRNAs, miRNAs, sdRNAs and a piRNA in pancreatic cancer. Molecular cancer, 14, 94.

Bokszczanin KL, et al. (2015) Identification of novel small ncRNAs in pollen of tomato. BMC genomics, 16(1), 714.

Zawada AM, et al. (2014) Massive analysis of cDNA Ends (MACE) and miRNA expression profiling identifies proatherogenic pathways in chronic kidney disease. Epigenetics, 9(1), 161.