

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

miRanalyzer

RRID:SCR_000163

Type: Tool

Proper Citation

miRanalyzer (RRID:SCR_000163)

Resource Information

URL: <http://bioinfo5.ugr.es/miRanalyzer/miRanalyzer.php>

Proper Citation: miRanalyzer (RRID:SCR_000163)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 30,2023. A microRNA detection and analysis tool for next-generation sequencing experiments. The program uses a minimum match length of 17bp starting at the first base of the read. The maximum read length is set to 28bp. Reads with more than 5 matches to the genome are discarded, and if a read matches to more than 5 transcripts or Rfam entries it will be removed.

Resource Type: software resource, web application

Defining Citation: [PMID:21515631](#)

Keywords: mirna, microrna, next gen sequencing, analysis, next generation, next gen, detection tool, analysis tool

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: miRanalyzer

Resource ID: SCR_000163

Alternate IDs: OMICS_00361

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260912T195504+0000

Ratings and Alerts

No rating or validation information has been found for miRanalyzer.

No alerts have been found for miRanalyzer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wang J, et al. (2017) Non-coding RNAs and Their Roles in Stress Response in Plants. Genomics, proteomics & bioinformatics, 15(5), 301.

Snyman MC, et al. (2017) The use of high-throughput small RNA sequencing reveals differentially expressed microRNAs in response to aster yellows phytoplasma-infection in Vitis vinifera cv. 'Chardonnay'. PloS one, 12(8), e0182629.

Shriram V, et al. (2016) MicroRNAs As Potential Targets for Abiotic Stress Tolerance in Plants. Frontiers in plant science, 7, 817.

Doubi-Kadmiri S, et al. (2016) Substantial and robust changes in microRNA transcriptome support postnatal development of the hypothalamus in rat. Scientific reports, 6, 24896.

Duffy DJ, et al. (2015) Integrative omics reveals MYCN as a global suppressor of cellular signalling and enables network-based therapeutic target discovery in neuroblastoma. Oncotarget, 6(41), 43182.

Tripathi A, et al. (2015) Role of bioinformatics in establishing microRNAs as modulators of abiotic stress responses: the new revolution. Frontiers in physiology, 6, 286.

Kim KH, et al. (2015) ?Np63 intronic miR-944 is implicated in the ?Np63-mediated induction of epidermal differentiation. Nucleic acids research, 43(15), 7462.

Wang C, et al. (2013) Computational approaches in detecting non- coding RNA. Current genomics, 14(6), 371.