

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 13, 2026

[miRNAKey](#)

RRID:SCR_004813

Type: Tool

Proper Citation

miRNAKey (RRID:SCR_004813)

Resource Information

URL: <http://ibis.tau.ac.il/miRNAkey/>

Proper Citation: miRNAKey (RRID:SCR_004813)

Description: A software pipeline for the analysis of microRNA Deep Sequencing data.

Abbreviations: miRNAKey

Resource Type: software resource

Defining Citation: [PMID:20801911](#)

Keywords: bio.tools

Resource Name: miRNAKey

Resource ID: SCR_004813

Alternate IDs: OMICS_00364, biotools:mirnakey

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

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260912T195617+0000

Ratings and Alerts

No rating or validation information has been found for miRNAKey.

No alerts have been found for miRNAKey.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Grillone K, et al. (2020) Non-coding RNAs in cancer: platforms and strategies for investigating the genomic "dark matter". Journal of experimental & clinical cancer research : CR, 39(1), 117.

Modai S, et al. (2019) HIV-1 infection increases microRNAs that inhibit Dicer1, HRB and HIV-EP2, thereby reducing viral replication. PloS one, 14(1), e0211111.

Ba??os-Lara MDR, et al. (2018) Comparative analysis of miRNA profile in human dendritic cells infected with respiratory syncytial virus and human metapneumovirus. BMC research notes, 11(1), 432.

Bisgin H, et al. (2018) Evaluation of Bioinformatics Approaches for Next-Generation Sequencing Analysis of microRNAs with a Toxicogenomics Study Design. Frontiers in genetics, 9, 22.

Bai J, et al. (2015) NGSmirPlant: comprehensive characterization of the small RNA transcriptomes of plants. Protein & cell, 6(6), 397.

Jorge NA, et al. (2012) Bioinformatics of Cancer ncRNA in High Throughput Sequencing: Present State and Challenges. Frontiers in genetics, 3, 287.