

Resource Summary Report

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

MIReNA

RRID:SCR_013024

Type: Tool

Proper Citation

MIReNA (RRID:SCR_013024)

Resource Information

URL: <http://www.lgm.upmc.fr/mirena/index.html>

Proper Citation: MIReNA (RRID:SCR_013024)

Description: A software tool to find microRNAs with high accuracy and no learning at genome scale and from deep sequencing data.

Abbreviations: MIReNA

Resource Type: software resource

Defining Citation: [PMID:20591903](#)

Availability: Acknowledgement requested, CeCILL license

Resource Name: MIReNA

Resource ID: SCR_013024

Alternate IDs: OMICS_00377

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260912T195757+0000

Ratings and Alerts

No rating or validation information has been found for MIReNA.

No alerts have been found for MIReNA.

Data and Source Information

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Acquadro A, et al. (2020) Whole genome resequencing of four Italian sweet pepper landraces provides insights on sequence variation in genes of agronomic value. Scientific reports, 10(1), 9189.

Acquadro A, et al. (2020) "Mind the Gap": Hi-C Technology Boosts Contiguity of the Globe Artichoke Genome in Low-Recombination Regions. G3 (Bethesda, Md.), 10(10), 3557.

Acquadro A, et al. (2017) Genome reconstruction in *Cynara cardunculus* taxa gains access to chromosome-scale DNA variation. Scientific reports, 7(1), 5617.

Xue B, et al. (2016) Integrated Strategy Improves the Prediction Accuracy of miRNA in Large Dataset. PloS one, 11(12), e0168392.

Scaglione D, et al. (2016) The genome sequence of the outbreeding globe artichoke constructed de novo incorporating a phase-aware low-pass sequencing strategy of F1 progeny. Scientific reports, 6, 19427.

Paytuv?? Gallart A, et al. (2016) GREENC: a Wiki-based database of plant lncRNAs. Nucleic acids research, 44(D1), D1161.

Hattori H, et al. (2014) p53 shapes genome-wide and cell type-specific changes in microRNA expression during the human DNA damage response. Cell cycle (Georgetown, Tex.), 13(16), 2572.

Shi Z, et al. (2013) High-throughput sequencing reveals extraordinary fluidity of miRNA, piRNA, and siRNA pathways in nematodes. Genome research, 23(3), 497.