

Resource Summary Report

Generated by [NIF](#) on Aug 11, 2026

[miR-PREFeR](#)

RRID:SCR_003353

Type: Tool

Proper Citation

miR-PREFeR (RRID:SCR_003353)

Resource Information

URL: <https://github.com/hangelwen/miR-PREFeR>

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Description: An accurate, fast, and easy-to-use plant miRNA prediction software tool using small RNA-Seq data. It utilizes expression patterns of miRNA and follows the criteria for plant microRNA annotation to accurately predict plant miRNAs from one or more small RNA-Seq data samples of the same species.

Synonyms: miRNA PREdiction From small RNA-Seq data, miR-PREFeR: microRNA PREdiction From small RNAseq data

Resource Type: software resource

Defining Citation: [PMID:24930140](#)

Keywords: standalone software, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: miR-PREFeR

Resource ID: SCR_003353

Alternate IDs: biotools:mir-prefer, OMICS_04637

Alternate URLs: <https://bio.tools/mir-prefer>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260808T185803+0000

Ratings and Alerts

No rating or validation information has been found for miR-PREFeR.

No alerts have been found for miR-PREFeR.

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 [NIF](#) .

Zhan J, et al. (2024) Premeiotic 24-nt phasiRNAs are present in the Zea genus and unique in biogenesis mechanism and molecular function. bioRxiv : the preprint server for biology.

Gao C, et al. (2024) Adaptive regulation of miRNAs/milRNAs in tissue-specific interaction between apple and Valsa mali. Horticulture research, 11(5), uhae094.

Zhan J, et al. (2024) Premeiotic 24-nt phasiRNAs are present in the Zea genus and unique in biogenesis mechanism and molecular function. Proceedings of the National Academy of Sciences of the United States of America, 121(21), e2402285121.

Ruan Q, et al. (2024) Regulation of endogenous hormone and miRNA in leaves of alfalfa (Medicago sativa L.) seedlings under drought stress by endogenous nitric oxide. BMC genomics, 25(1), 229.

Moraga C, et al. (2022) BrumiR: A toolkit for de novo discovery of microRNAs from sRNA-seq data. GigaScience, 11.

Kunej U, et al. (2021) Identification and Characterization of Verticillium nonalfalfae-Responsive MicroRNAs in the Roots of Resistant and Susceptible Hop Cultivars. Plants (Basel, Switzerland), 10(9).

Zhao Y, et al. (2019) Identification of Exogenous Nitric Oxide-Responsive miRNAs from Alfalfa (Medicago sativa L.) under Drought Stress by High-Throughput Sequencing. Genes, 11(1).

Liu M, et al. (2017) Profiling of drought-responsive microRNA and mRNA in tomato using high-throughput sequencing. BMC genomics, 18(1), 481.