

Resource Summary Report

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C-mii

RRID:SCR_010839

Type: Tool

Proper Citation

C-mii (RRID:SCR_010839)

Resource Information

URL: <http://www3a.biotec.or.th/c-mii/>

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Description: A software tool for plant miRNA and target identification. C-mii pipelines are based on combined steps and criteria from previous studies and also incorporated with several tools such as standalone BLAST and UNAFold and pre-installed databases including miRBase, UniProt, and Rfam. C-mii provides following distinguished features. First, it comes with graphical user interfaces of well-defined pipelines for both miRNA and target identifications with reliable results. Second, it provides a set of filters allowing users to reduce the number of results corresponding to the recently proposed constraints in plant miRNA and target biogenesis. Third, it extends the standard computational steps of miRNA target identification with miRNA-target folding module and GO annotation. Fourth, it supplies the bird eye views of the identification results with info-graphics and grouping information. Fifth, it provides helper functions for database update and auto-recovery to ease system usage and maintenance. Finally, it supports the multi-project and multi-thread management to improve the computational speed.

Abbreviations: C-mii

Synonyms: C-mii: A software for Computational miRNA identifcaion, C-mii (A software for Computational miRNA identifcaion)

Resource Type: software resource

Defining Citation: [PMID:23281648](#)

Keywords: ubuntu linux, windows

Availability: GNU General Public License

Resource Name: C-mii

Resource ID: SCR_010839

Alternate IDs: OMICS_00394

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260815T182410+0000

Ratings and Alerts

No rating or validation information has been found for C-mii.

No alerts have been found for C-mii.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Srivastava A, et al. (2024) In silico identification of papaya genome-encoded microRNAs to target begomovirus genes in papaya leaf curl disease. *Frontiers in microbiology*, 15, 1340275.

Zinati Z, et al. (2016) In silico identification of miRNAs and their target genes and analysis of gene co-expression network in saffron (*Crocus sativus* L.) stigma. *Molecular biology research communications*, 5(4), 233.

Singh N, et al. (2016) Identification and analysis of miRNAs and their targets in ginger using bioinformatics approach. *Gene*, 575(2 Pt 2), 570.

Prakash P, et al. (2015) Identification of conserved and novel microRNAs in *Catharanthus roseus* by deep sequencing and computational prediction of their potential targets. *Gene*, 554(2), 181.