

Resource Summary Report

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psRNATarget

RRID:SCR_013321

Type: Tool

Proper Citation

psRNATarget (RRID:SCR_013321)

Resource Information

URL: <http://plantgrn.noble.org/psRNATarget/>

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Description: A plant small RNA target analysis server which features two important analysis functions: 1) reverse complementary matching between miRNA and target transcript using a proven scoring schema, and 2) target site accessibility evaluation by calculating unpaired energy (UPE) required to "open" secondary structure around miRNA's target site on mRNA. PsRNATarget incorporates recent discoveries in plant miRNA target recognition, e.g. it distinguishes translational and post-transcriptional inhibition, and it reports the number of miRNA/target site pairs that may affect miRNA binding activity to target transcript. PsRNATarget is designed for high-throughput analysis of next-generation data with an efficient distributed computing back-end pipeline that runs on a Linux cluster. The server front-end integrates three simplified user-friendly interfaces to accept user-submitted or preloaded miRNAs and transcript sequences; and outputs a comprehensive list of miRNA / target pairs along with the online tools for batch downloading, key word searching and results sorting., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: psRNATarget

Synonyms: psRNATarget: A Plant Small RNA Target Analysis Server

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:21622958](#)

Keywords: bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: psRNATarget

Resource ID: SCR_013321

Alternate IDs: OMICS_00414, biotools:psrnatarget

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

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260821T042902+0000

Ratings and Alerts

No rating or validation information has been found for psRNATarget.

No alerts have been found for psRNATarget.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1117 mentions in open access literature.

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

Pei L, et al. (2026) ZmmiR1432-ZmCML21-ZmPMA2 Module Affects Maize Low Phosphate Tolerance via Regulating Organic Acid Secretion. Plant biotechnology journal, 24(2), 921.

Zhang Q, et al. (2026) Enhancing apple disease resistance via magnetic nanoparticle-mediated delivery of artificial miRNAs that suppress a tRNA-derived small RNA targeting a disease-resistant gene. Plant communications, 7(3), 101681.

Wang J, et al. (2026) Identification and Expression Analysis of the Potato (*Solanum tuberosum* L.) stu-miR482 Family Under Exogenous 24-Epibrassinolide Treatments and Alkaline Salt Stress. Plants (Basel, Switzerland), 15(12).

Yin Y, et al. (2026) Nanomaterial-mediated delivery of tomato miR393 intrinsically targeting a cell wall-related gene of *Botrytis cinerea* confers efficient control of gray mold disease. Plant communications, 7(3), 101615.

Ke Q, et al. (2026) Population and pangenome analyses uncover the evolutionary dynamics of the peroxidase gene family in barley. BMC genomics, 27(1).

Gai W, et al. (2026) PsGA2ox2 is a novel target of miR159 involved in endodormancy regulation in tree peony (*Paeonia suffruticosa*). Molecular horticulture, 6(1).

Nie H, et al. (2026) Transcriptome analysis reveals long noncoding RNAs involved in the tuber anthocyanin synthesis of potato (*Solanum tuberosum* L.). BMC plant biology, 26(1).

- Ma Y, et al. (2025) Genome-wide identification of the WRKY gene family in poplar and the positive role of PsnWRKY95 in response to cadmium stress. *PloS one*, 20(9), e0332076.
- Zhao H, et al. (2025) New insights into the salt-responsive regulation in eelgrass at transcriptional and post-transcriptional levels. *Frontiers in plant science*, 16, 1497064.
- Liao H, et al. (2025) Rice transcription factor bHLH25 confers resistance to multiple diseases by sensing H₂O₂. *Cell research*, 35(3), 205.
- Islam MSU, et al. (2025) Genome-wide identification and characterization of cation-proton antiporter (CPA) gene family in rice (*Oryza sativa* L.) and their expression profiles in response to phytohormones. *PloS one*, 20(1), e0317008.
- Jeon G, et al. (2025) Impact of Culture Duration on the Properties and Functionality of Yeast-Derived Extracellular Vesicles. *Biomaterials research*, 29, 0201.
- Xue LJ, et al. (2025) Overexpression of plasma membrane SUT1 in poplar alters lateral sucrose partitioning in stem and promotes leaf necrosis. *Plant direct*, 9(3), e70023.
- Soltani Z, et al. (2025) Comparative meta-analysis of barely transcriptome: Pathogen type determines host preference. *PloS one*, 20(6), e0320708.
- Ruf A, et al. (2025) Extracellular Vesicles From *Xylella fastidiosa* Carry sRNAs and Genomic Islands, Suggesting Roles in Recipient Cells. *Journal of extracellular vesicles*, 14(6), e70102.
- Gao Z, et al. (2025) Cell-Type Specific miRNA Regulatory Network Responses to ABA Stress Revealed by Time Series Transcriptional Atlases in Arabidopsis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(9), e2415083.
- Hansel-Fr??se AFF, et al. (2025) Petri net modeling and simulation of post-transcriptional regulatory networks of human embryonic stem cell (hESC) differentiation to cardiomyocytes. *Journal of integrative bioinformatics*, 22(1).
- Guimaraes PM, et al. (2025) miRNA-Mediated Regulation of *Meloidogyne arenaria* Responses in Wild *Arachis*. *International journal of molecular sciences*, 26(22).
- Liu X, et al. (2025) Integrated metabolome-transcriptome analyses reveal key pathways regulating staminate catkin development and pollen maturation in *Betula platyphylla*. *Frontiers in plant science*, 16, 1581560.
- Zhao W, et al. (2025) A double-agent microRNA regulates viral cross-kingdom infection in animals and plants. *The EMBO journal*, 44(9), 2446.