

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, service resource, data analysis service, production 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: 20260728T043423+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 1040 mentions in open access literature.

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

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.

Liao H, et al. (2025) Rice transcription factor bHLH25 confers resistance to multiple diseases by sensing H₂O₂. *Cell research*, 35(3), 205.

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.

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.

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.

Ruf A, et al. (2025) Extracellular Vesicles From *Xylella fastidiosa* Carry sRNAs and Genomic Islands, Suggesting Roles in Recipient Cells. *Journal of extracellular vesicles*,

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).

Joshi P, et al. (2025) Identification of miRNAs associated with *Aspergillus flavus* infection and their targets in groundnut (*Arachis hypogaea* L.). *BMC plant biology*, 25(1), 345.

Zhao W, et al. (2025) A double-agent microRNA regulates viral cross-kingdom infection in animals and plants. *The EMBO journal*, 44(9), 2446.

Qian X, et al. (2025) The Potassium Utilization Gene Network in *Brassica napus* and Functional Validation of BnaZSHAK5.2 Gene in Response to Potassium Deficiency. *International journal of molecular sciences*, 26(2).

Zhang J, et al. (2025) Genome-wide identification of the Sec14 gene family and the response to salt and drought stress in soybean (*Glycine max*). *BMC genomics*, 26(1), 73.

Khaskhali S, et al. (2025) Expression profile and characterization of respiratory burst oxidase homolog genes in rice under MeJA, SA and Xoo treatments. *Scientific reports*, 15(1), 5936.

Nasfi S, et al. (2025) A pipeline for validation of *Serendipita indica* effector-like sRNA suggests cross-kingdom communication in the symbiosis with *Arabidopsis*. *Journal of experimental botany*, 76(6), 1811.

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.

Wang F, et al. (2025) Function of floral fragrance-related microRNAs and their targets in *Hedychium coronarium*. *BMC genomics*, 26(1), 430.

Kan W, et al. (2025) Genome-Wide Identification and Expression Analysis of TaDES1 Gene Family Responded to Biotic and Abiotic Stress in Wheat (*Triticum aestivum* L.). *Food science & nutrition*, 13(7), e70504.

Paudel DB, et al. (2025) Transcriptomic changes associated with infection of *Nicotiana benthamiana* plants with tomato ringspot virus (genus *Nepovirus*) during the acute symptomatic stage and after symptom recovery. *PloS one*, 20(9), e0328517.

Silvestri A, et al. (2025) A fungal sRNA silences a host plant transcription factor to promote arbuscular mycorrhizal symbiosis. *The New phytologist*, 246(3), 924.