Resource Summary Report

Generated by <u>NIF</u> on May 5, 2025

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.

Abbreviations: psRNATarget

Synonyms: psRNATarget: A Plant Small RNA Target Analysis Server

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

Defining Citation: PMID:21622958

Keywords: bio.tools

Funding:

Availability: Acknowledgement requested

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: 20250505T054240+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 988 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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.

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.

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).

Medina-Calzada Z, et al. (2025) An intron-split microRNA mediates cleavage of the mRNA encoded by low phosphate root in Solanaceae. Planta, 261(2), 27.

Spycha?a J, et al. (2025) Unraveling Effects of miRNAs Associated with APR Leaf Rust Resistance Genes in Hybrid Forms of Common Wheat (Triticum aestivum L.). International journal of molecular sciences, 26(2).

Sarwar S, et al. (2025) Genome-Wide Identification and In Silico Expression Analysis of CCO Gene Family in Citrus clementina (Citrus) in Response to Abiotic Stress. Plants (Basel, Switzerland), 14(2).

Guo A, et al. (2025) The miR3367-IncRNA67-GhCYP724B module regulates male sterility by modulating brassinosteroid biosynthesis and interacting with Aorf27 in Gossypium hirsutum. Journal of integrative plant biology, 67(1), 169.

Maghraby A, et al. (2025) Genome-wide identification, characterization, and functional analysis of the CHX, SOS, and RLK genes in Solanum lycopersicum under salt stress. Scientific reports, 15(1), 1142.

Maghraby A, et al. (2024) Genome-wide identification and evolutionary analysis of the AP2/EREBP, COX and LTP genes in Zea mays L. under drought stress. Scientific reports, 14(1), 7610.

Mahalle RM, et al. (2024) Identification of differentially expressed miRNAs associated with diamide detoxification pathways in Spodoptera frugiperda. Scientific reports, 14(1), 4308.

Tabatabaeipour SN, et al. (2024) Comprehensive transcriptomic meta-analysis unveils new responsive genes to methyl jasmonate and ethylene in Catharanthusroseus. Heliyon, 10(5), e27132.

Divya D, et al. (2024) Genome-wide characterization and expression profiling of E2F/DP gene family members in response to abiotic stress in tomato (Solanum lycopersicum L.). BMC plant biology, 24(1), 436.

Sun MS, et al. (2024) Regulatory microRNAs and phasiRNAs of paclitaxel biosynthesis in Taxus chinensis. Frontiers in plant science, 15, 1403060.

Rudy E, et al. (2024) Unveiling the role of epigenetics in leaf senescence: a comparative study to identify different epigenetic regulations of senescence types in barley leaves. BMC plant biology, 24(1), 863.

Spycha?a J, et al. (2024) Expression patterns of candidate genes for the Lr46/Yr29 "slow rust" locus in common wheat (Triticum aestivum L.) and associated miRNAs inform of the gene conferring the Puccinia triticina resistance trait. PloS one, 19(9), e0309944.

Fu C, et al. (2024) Genome-wide identification and molecular evolution of Dof transcription factors in Cyperus esculentus. BMC genomics, 25(1), 667.

Ji Z, et al. (2024) Genome-Wide Identification and Expression Analysis of BrBASS Genes in Brassica rapa Reveals Their Potential Roles in Abiotic Stress Tolerance. Current issues in molecular biology, 46(7), 6646.

Shen M, et al. (2024) Genome mining of WOX-ARF gene linkage in Machilus pauhoi underpinned cambial activity associated with IAA induction. Frontiers in plant science, 15, 1364086.

Okay A, et al. (2024) Omics approaches to understand the MADS-box gene family in common bean (Phaseolus vulgaris L.) against drought stress. Protoplasma, 261(4), 709.

Liu S, et al. (2024) Alternative polyadenylation profiles of susceptible and resistant rice (Oryza sativa L.) in response to bacterial leaf blight using RNA-seq. BMC plant biology, 24(1), 145.