

Resource Summary Report

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PlantNATsDB - Plant Natural Antisense Transcripts DataBase

RRID:SCR_013278

Type: Tool

Proper Citation

PlantNATsDB - Plant Natural Antisense Transcripts DataBase (RRID:SCR_013278)

Resource Information

URL: <http://bis.zju.edu.cn/pnatdb/>

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Description: Natural Antisense Transcripts (NATs), a kind of regulatory RNAs, occur prevalently in plant genomes and play significant roles in physiological and/or pathological processes. PlantNATsDB (Plant Natural Antisense Transcripts DataBase) is a platform for annotating and discovering NATs by integrating various data sources involving approximately 2 million NAT pairs in 69 plant species. PlantNATsDB also provides an integrative, interactive and information-rich web graphical interface to display multidimensional data, and facilitate plant research community and the discovery of functional NATs. GO annotation and high-throughput small RNA sequencing data currently available were integrated to investigate the biological function of NATs. A "Gene Set Analysis" module based on GO annotation was designed to dig out the statistical significantly overrepresented GO categories from the specific NAT network. PlantNATsDB is currently the most comprehensive resource of NATs in the plant kingdom, which can serve as a reference database to investigate the regulatory function of NATs.

Abbreviations: PlantNATsDB

Synonyms: Plant Natural Antisense Transcripts DataBase

Resource Type: production service resource, data analysis service, service resource, database, analysis service resource, data or information resource

Defining Citation: [PMID:22058132](#)

Keywords: natural antisense transcript, annotation, high-throughput, small rna sequencing, function, regulatory function, predict, sequence, small rna, blast, bio.tools

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Availability: Free

Resource Name: PlantNATsDB - Plant Natural Antisense Transcripts DataBase

Resource ID: SCR_013278

Alternate IDs: nlx_151492, biotools:plantnatsdb

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

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260804T043512+0000

Ratings and Alerts

No rating or validation information has been found for PlantNATsDB - Plant Natural Antisense Transcripts DataBase.

No alerts have been found for PlantNATsDB - Plant Natural Antisense Transcripts DataBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Zhong J, et al. (2020) A putative AGO protein, OsAGO17, positively regulates grain size and grain weight through OsmiR397b in rice. Plant biotechnology journal, 18(4), 916.

Niu C, et al. (2019) Genome-wide identification of drought-responsive microRNAs in two sets of Malus from interspecific hybrid progenies. Horticulture research, 6, 75.

Lian C, et al. (2018) Exploration of ABA Responsive miRNAs Reveals a New Hormone Signaling Crosstalk Pathway Regulating Root Growth of Populus euphratica. International journal of molecular sciences, 19(5).

Flórez-Zapata NM, et al. (2016) Long non-coding RNAs are major contributors to transcriptome changes in sunflower meiocytes with different recombination rates. *BMC genomics*, 17, 490.

Duan H, et al. (2016) Genome-Wide Analysis of MicroRNA Responses to the Phytohormone Abscissic Acid in *Populus euphratica*. *Frontiers in plant science*, 7, 1184.

Wang L, et al. (2016) Genome-Wide Identification of MicroRNAs and Their Targets in the Leaves and Fruits of *Eucommia ulmoides* Using High-Throughput Sequencing. *Frontiers in plant science*, 7, 1632.

Hu H, et al. (2015) Bioinformatics analysis of small RNAs in pima (*Gossypium barbadense* L.). *PloS one*, 10(2), e0116826.

Liu X, et al. (2015) Long non-coding RNAs and their biological roles in plants. *Genomics, proteomics & bioinformatics*, 13(3), 137.

Britto-Kido Sde A, et al. (2013) Natural antisense transcripts in plants: a review and identification in soybean infected with *Phakopsora pachyrhizi* SuperSAGE library. *TheScientificWorldJournal*, 2013, 219798.