Resource Summary Report

Generated by NIF on Apr 17, 2025

Cereal Small RNA Database

RRID:SCR_007589
Type: Tool

Proper Citation

Cereal Small RNA Database (RRID:SCR_007589)

Resource Information

URL: http://sundarlab.ucdavis.edu/smrnas/

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Description: CSRDB is a bioinformatics resource for cereal crops consisting of large-scale datasets of maize and rice and small RNA sequences. The sequences were generated by 454 Life Science sequencing. The small RNA sequences have been mapped to the rice genome and available maize genome sequence and are presented in two genome browser datasets using the Generic Genome Browser. Potential target sequences representing mature mRNA sequences have been predicted using the FASTH software from the Zuker lab. and access to the resulting small RNA target pair (SRTP) dataset has been made available through a mysql based relational database. Within the genome browser the small RNAs have links to the SRTP database that will return a list of potential targets. The SRTP database may also be searched independently using both small RNA and target transcript queries. Data linking and integration is the main focus of this interface and to this aim links are present in the SRTP results pages back to the browser and the SRTP database as well as external sites.

Synonyms: CSRDB

Resource Type: database, data or information resource

Keywords: cereal, crop, grain, maize, mrna, rice, small rna, small rna target pair

Funding:

Resource Name: Cereal Small RNA Database

Resource ID: SCR_007589

Alternate IDs: nif-0000-02652

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250412T055202+0000

Ratings and Alerts

No rating or validation information has been found for Cereal Small RNA Database.

No alerts have been found for Cereal Small RNA Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Yang Y, et al. (2021) Applications of Multi-Omics Technologies for Crop Improvement. Frontiers in plant science, 12, 563953.

Iqbal Z, et al. (2021) Toward Integrated Multi-Omics Intervention: Rice Trait Improvement and Stress Management. Frontiers in plant science, 12, 741419.

Li Y, et al. (2020) OsmiR167a-targeted auxin response factors modulate tiller angle via fine-tuning auxin distribution in rice. Plant biotechnology journal, 18(10), 2015.

Hong WJ, et al. (2019) Infrastructures of systems biology that facilitate functional genomic study in rice. Rice (New York, N.Y.), 12(1), 15.

Kyriakidou M, et al. (2018) Current Strategies of Polyploid Plant Genome Sequence Assembly. Frontiers in plant science, 9, 1660.

Kumar A, et al. (2018) ---A web resource for nutrient use efficiency-related genes, quantitative trait loci and microRNAs in important cereals and model plants. F1000Research, 7.

Kang YJ, et al. (2016) Translational genomics for plant breeding with the genome sequence explosion. Plant biotechnology journal, 14(4), 1057.

Dai Z, et al. (2016) OsMADS1 Represses microRNA172 in Elongation of Palea/Lemma Development in Rice. Frontiers in plant science, 7, 1891.

Mao H, et al. (2015) A transposable element in a NAC gene is associated with drought tolerance in maize seedlings. Nature communications, 6, 8326.

Shao C, et al. (2012) Genome-wide identification of reverse complementary microRNA genes in plants. PloS one, 7(10), e46991.

Wang K, et al. (2012) Identification of conserved and novel microRNAs from Liriodendron chinense floral tissues. PloS one, 7(9), e44696.

Ding J, et al. (2012) Finding microRNA targets in plants: current status and perspectives. Genomics, proteomics & bioinformatics, 10(5), 264.

Meng Y, et al. (2012) Large-scale identification of mirtrons in Arabidopsis and rice. PloS one, 7(2), e31163.

Kritsas K, et al. (2012) Computational analysis and characterization of UCE-like elements (ULEs) in plant genomes. Genome research, 22(12), 2455.

Rius SP, et al. (2012) Analysis of the P1 promoter in response to UV-B radiation in allelic variants of high-altitude maize. BMC plant biology, 12, 92.

Zhelyazkova P, et al. (2012) Protein-mediated protection as the predominant mechanism for defining processed mRNA termini in land plant chloroplasts. Nucleic acids research, 40(7), 3092.

Zhang Y, et al. (2011) Evolution of microRNA genes in Oryza sativa and Arabidopsis thaliana: an update of the inverted duplication model. PloS one, 6(12), e28073.

Pfalz J, et al. (2009) Site-specific binding of a PPR protein defines and stabilizes 5' and 3' mRNA termini in chloroplasts. The EMBO journal, 28(14), 2042.