Resource Summary Report

Generated by NIF on Apr 29, 2025

Arabidopsis thaliana Genome Database

RRID:SCR_001901
Type: Tool

Proper Citation

Arabidopsis thaliana Genome Database (RRID:SCR_001901)

Resource Information

URL: http://www.plantgdb.org/AtGDB/

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Description: Database providing a sequence-centered genome view for Arabidopsis thaliana, with a narrow focus on gene structure annotation. The current genome assembly displayed at AtGDB is version TAIR9. Annotated gene models are TAIR10. They have mapped the complete set of 176,915 publicly available Arabidopsis EST sequences onto the Arabidopsis genome using GeneSeqer, a spliced alignment program incorporating sequence similarity and splice site scoring. About 96% of the available ESTs could be properly aligned with a genomic locus, with the remaining ESTs deriving from organelle genomes and non-Arabidopsis sources or displaying insufficient sequence quality for alignment. The mapping provides verified sets of EST clusters for evaluation of EST clustering programs. Analysis of the spliced alignments suggests corrections to current gene structure annotation and provides examples of alternative and non-canonical pre-mRNA splicing.

Abbreviations: AtGDB

Synonyms: Arabidopsis thaliana Genome DB

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

Defining Citation: PMID:16219921, PMID:14681433, PMID:12805580

Keywords: expressed sequence tag, est sequence, contig, gene structure, genome, arabidopsis thaliana, cdna, plant database, blast, annotation

Funding: NSF IOS-0606909;
NSF DBI-0110254;

NSF DBI-0321600

Availability: The community can contribute to this resource

Resource Name: Arabidopsis thaliana Genome Database

Resource ID: SCR_001901

Alternate IDs: nif-0000-02582

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250429T054702+0000

Ratings and Alerts

No rating or validation information has been found for Arabidopsis thaliana Genome Database.

No alerts have been found for Arabidopsis thaliana Genome Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Plackett ARG, et al. (2021) Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. Current biology : CB, 31(20), 4560.

Vieira NG, et al. (2019) Homeologous regulation of Frigida-like genes provides insights on reproductive development and somatic embryogenesis in the allotetraploid Coffea arabica. Scientific reports, 9(1), 8446.

Liu J, et al. (2018) Genome-Wide Characterization of Heat-Shock Protein 70s from Chenopodium quinoa and Expression Analyses of Cqhsp70s in Response to Drought Stress. Genes, 9(2).

Wang P, et al. (2017) Genome-Wide Dissection of the Heat Shock Transcription Factor Family Genes in Arachis. Frontiers in plant science, 8, 106.

Wang P, et al. (2016) Genome-Wide Identification and Comparative Analysis of Cytosine-5 DNA Methyltransferase and Demethylase Families in Wild and Cultivated Peanut. Frontiers

in plant science, 7, 7.

Su LT, et al. (2014) A novel MYB transcription factor, GmMYBJ1, from soybean confers drought and cold tolerance in Arabidopsis thaliana. Gene, 538(1), 46.

Peng Z, et al. (2010) Genome-wide characterization of the biggest grass, bamboo, based on 10,608 putative full-length cDNA sequences. BMC plant biology, 10, 116.

Wilkerson MD, et al. (2006) yrGATE: a web-based gene-structure annotation tool for the identification and dissemination of eukaryotic genes. Genome biology, 7(7), R58.

Schlueter SD, et al. (2006) xGDB: open-source computational infrastructure for the integrated evaluation and analysis of genome features. Genome biology, 7(11), R111.

Wang BB, et al. (2004) The ASRG database: identification and survey of Arabidopsis thaliana genes involved in pre-mRNA splicing. Genome biology, 5(12), R102.