Resource Summary Report

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CATdb: a Complete Arabidopsis Transcriptome database

RRID:SCR_007582

Type: Tool

Proper Citation

CATdb: a Complete Arabidopsis Transcriptome database (RRID:SCR_007582)

Resource Information

URL: http://urgv.evry.inra.fr/CATdb

Proper Citation: CATdb: a Complete Arabidopsis Transcriptome database

(RRID:SCR_007582)

Description: CATdb collects together all the information on transcriptome experiments done at URGV with CATMA micro arrays. All data in CATdb come from the URGV micro array platforms. Common procedures are used including any steps from the experiment design to the statistical analyses. Directed through a WEB interface, biologists enter the standard description of each experimental step (extraction, labelling, hybridization and scanning). Then, normalization and statistical analyses are done following a set of selected methods depending on the experimental design and array types.

Synonyms: CATdb

Resource Type: database, data or information resource

Keywords: catma, microarray, transcriptome, bio.tools, FASEB list

Funding:

Resource Name: CATdb: a Complete Arabidopsis Transcriptome database

Resource ID: SCR_007582

Alternate IDs: nif-0000-02639, biotools:catdb

Alternate URLs: https://bio.tools/catdb

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250430T055516+0000

Ratings and Alerts

No rating or validation information has been found for CATdb: a Complete Arabidopsis Transcriptome database.

No alerts have been found for CATdb: a Complete Arabidopsis Transcriptome database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Lopez D, et al. (2021) Early transcriptional response to gravistimulation in poplar without phototropic confounding factors. AoB PLANTS, 13(1), plaa071.

Sawicki M, et al. (2019) On a Cold Night: Transcriptomics of Grapevine Flower Unveils Signal Transduction and Impacted Metabolism. International journal of molecular sciences, 20(5).

Voxeur A, et al. (2017) Altered lignification in mur1-1 a mutant deficient in GDP-L-fucose synthesis with reduced RG-II cross linking. PloS one, 12(9), e0184820.

Martins S, et al. (2017) Brassinosteroid signaling-dependent root responses to prolonged elevated ambient temperature. Nature communications, 8(1), 309.

Audonnet L, et al. (2017) JMJ24 antagonizes histone H3K9 demethylase IBM1/JMJ25 function and interacts with RNAi pathways for gene silencing. Gene expression patterns: GEP, 25-26, 1.

Mai HJ, et al. (2016) Iron homeostasis in Arabidopsis thaliana: transcriptomic analyses reveal novel FIT-regulated genes, iron deficiency marker genes and functional gene networks. BMC plant biology, 16(1), 211.

Damiani I, et al. (2016) Nod Factor Effects on Root Hair-Specific Transcriptome of Medicago truncatula: Focus on Plasma Membrane Transport Systems and Reactive Oxygen Species

Networks. Frontiers in plant science, 7, 794.

Pedroza-Garcia JA, et al. (2016) Role of the Polymerase ? sub-unit DPB2 in DNA replication, cell cycle regulation and DNA damage response in Arabidopsis. Nucleic acids research, 44(15), 7251.

Dumas AS, et al. (2016) Unraveling the early molecular and physiological mechanisms involved in response to phenanthrene exposure. BMC genomics, 17(1), 818.

Zaag R, et al. (2015) GEM2Net: from gene expression modeling to -omics networks, a new CATdb module to investigate Arabidopsis thaliana genes involved in stress response. Nucleic acids research, 43(Database issue), D1010.

Liu Z, et al. (2015) A Conserved Cytochrome P450 Evolved in Seed Plants Regulates Flower Maturation. Molecular plant, 8(12), 1751.

Ruelland E, et al. (2014) Salicylic acid modulates levels of phosphoinositide dependentphospholipase C substrates and products to remodel the Arabidopsis suspension cell transcriptome. Frontiers in plant science, 5, 608.

Garcia AV, et al. (2014) Salmonella enterica flagellin is recognized via FLS2 and activates PAMP-triggered immunity in Arabidopsis thaliana. Molecular plant, 7(4), 657.

Planchais S, et al. (2014) BASIC AMINO ACID CARRIER 2 gene expression modulates arginine and urea content and stress recovery in Arabidopsis leaves. Frontiers in plant science, 5, 330.

Arias MC, et al. (2014) From dusk till dawn: the Arabidopsis thaliana sugar starving responsive network. Frontiers in plant science, 5, 482.

Lange H, et al. (2014) The RNA helicases AtMTR4 and HEN2 target specific subsets of nuclear transcripts for degradation by the nuclear exosome in Arabidopsis thaliana. PLoS genetics, 10(8), e1004564.

Djafi N, et al. (2013) The Arabidopsis DREB2 genetic pathway is constitutively repressed by basal phosphoinositide-dependent phospholipase C coupled to diacylglycerol kinase. Frontiers in plant science, 4, 307.

Ranocha P, et al. (2013) Arabidopsis WAT1 is a vacuolar auxin transport facilitator required for auxin homoeostasis. Nature communications, 4, 2625.

Jubault M, et al. (2013) Partial resistance to clubroot in Arabidopsis is based on changes in the host primary metabolism and targeted cell division and expansion capacity. Functional & integrative genomics, 13(2), 191.

Bourbousse C, et al. (2012) Histone H2B monoubiquitination facilitates the rapid modulation of gene expression during Arabidopsis photomorphogenesis. PLoS genetics, 8(7), e1002825.