

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: data or information resource, database

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

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: 20260905T133140+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 40 mentions in open access literature.

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

Oliver C, et al. (2022) Accumulation dynamics of ARGONAUTE proteins during meiosis in Arabidopsis. Plant reproduction, 35(2), 153.

Kalachova T, et al. (2022) DIACYLGLYCEROL KINASE 5 participates in flagellin-induced signaling in Arabidopsis. Plant physiology, 190(3), 1978.

Deveaux Y, et al. (2021) Transcriptome Analysis Reveals Putative Target Genes of APETALA3-3 During Early Floral Development in Nigella damascena L. Frontiers in plant science, 12, 660803.

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

Chardon F, et al. (2020) The Consequences of a Disruption in Cyto-Nuclear Coadaptation on the Molecular Response to a Nitrate Starvation in Arabidopsis. Plants (Basel, Switzerland), 9(5).

Soulie MC, et al. (2020) Plant nitrogen supply affects the Botrytis cinerea infection process and modulates known and novel virulence factors. Molecular plant pathology, 21(11), 1436.

Kamal KY, et al. (2019) Differential transcriptional profile through cell cycle progression in Arabidopsis cultures under simulated microgravity. Genomics, 111(6), 1956.

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).

Cuello C, et al. (2019) A systems biology approach uncovers a gene co-expression network associated with cell wall degradability in maize. PloS one, 14(12), e0227011.

Del Prete S, et al. (2019) Extensive nuclear reprogramming and endoreduplication in mature leaf during floral induction. BMC plant biology, 19(1), 135.

- 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.
- 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.
- Martins S, et al. (2017) Brassinosteroid signaling-dependent root responses to prolonged elevated ambient temperature. Nature communications, 8(1), 309.
- 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.
- 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.
- Dumas AS, et al. (2016) Unraveling the early molecular and physiological mechanisms involved in response to phenanthrene exposure. BMC genomics, 17(1), 818.
- 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.
- Liu Z, et al. (2015) A Conserved Cytochrome P450 Evolved in Seed Plants Regulates Flower Maturation. Molecular plant, 8(12), 1751.
- 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.
- Ruelland E, et al. (2014) Salicylic acid modulates levels of phosphoinositide dependent-phospholipase C substrates and products to remodel the Arabidopsis suspension cell transcriptome. Frontiers in plant science, 5, 608.