

Resource Summary Report

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CATMA - Complete Arabidopsis Transcriptome MicroArray

RRID:SCR_007578

Type: Tool

Proper Citation

CATMA - Complete Arabidopsis Transcriptome MicroArray (RRID:SCR_007578)

Resource Information

URL: <http://www.catma.org>

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Description: A database of Arabidopsis Gene-specific Sequence Tags (GSTs) designed and produced by the CATMA consortium. The aim of CATMA is the design and production of high quality GSTs covering most Arabidopsis genes. The GST repertoire is used by numerous groups for the production of DNA arrays for transcript profiling experiments. The database contains information about the GST probes, the PCR primers used for their amplification and the genes to which they hybridize, together with other information such as details of the groups involved and quality control results. CATMA microarrays constitute the foundation of the CAGE project aiming at the construction of a gene expression reference database for Arabidopsis. The CATMA GSTs are also the basic materials in the AGRIKOLA project focusing on the large-scale systematic RNAi silencing of Arabidopsis genes. CATMA is a consortium of research groups from eight European countries. All CATMA members are public laboratories, some with ties to private research institutions.

Abbreviations: CATMA

Synonyms: Complete Arabidopsis Transcriptome MicroArray

Resource Type: data or information resource, database

Keywords: gene-specific sequence tag, arabidopsis, dna array, transcript profiling, software

Resource Name: CATMA - Complete Arabidopsis Transcriptome MicroArray

Resource ID: SCR_007578

Alternate IDs: nif-0000-02641

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260905T133140+0000

Ratings and Alerts

No rating or validation information has been found for CATMA - Complete Arabidopsis Transcriptome MicroArray.

No alerts have been found for CATMA - Complete Arabidopsis Transcriptome MicroArray.

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 [PRECISE-TBI](#) .

Belda-Palaz??n B, et al. (2016) Relevance of the Axis Spermidine/eIF5A for Plant Growth and Development. *Frontiers in plant science*, 7, 245.

Jenkins DJ, et al. (2013) A temporal switch model for estimating transcriptional activity in gene expression. *Bioinformatics (Oxford, England)*, 29(9), 1158.

Spadafora ND, et al. (2012) Perturbation of cytokinin and ethylene-signalling pathways explain the strong rooting phenotype exhibited by Arabidopsis expressing the *Schizosaccharomyces pombe* mitotic inducer, *cdc25*. *BMC plant biology*, 12, 45.

Ravet K, et al. (2012) Iron and ROS control of the DownSTream mRNA decay pathway is essential for plant fitness. *The EMBO journal*, 31(1), 175.

Brenner WG, et al. (2012) Transcript profiling of cytokinin action in Arabidopsis roots and shoots discovers largely similar but also organ-specific responses. *BMC plant biology*, 12, 112.

ten Hove CA, et al. (2011) Trans-repression of gene activity upstream of T-DNA tagged RLK902 links Arabidopsis root growth inhibition and downy mildew resistance. *PloS one*, 6(4), e19028.

Mochida K, et al. (2010) Genomics and bioinformatics resources for crop improvement. *Plant & cell physiology*, 51(4), 497.

De Rybel B, et al. (2010) A novel aux/IAA28 signaling cascade activates GATA23-dependent specification of lateral root founder cell identity. *Current biology : CB*, 20(19), 1697.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.