

Resource Summary Report

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AREX

RRID:SCR_002170

Type: Tool

Proper Citation

AREX (RRID:SCR_002170)

Resource Information

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

Proper Citation: AREX (RRID:SCR_002170)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. The Arabidopsis gene Expression Database collects Arabidopsis gene expression data from genome-wide and gene-specific sources and integrative search tools are provided. Currently the database contains only root gene expression data, but has the capability to contain data from any part of the plant. The aim of Arabidopsis gene Expression Database is to: (1) Integrate genome-wide and gene-specific ("traditional") types of expression pattern data, using ontologies to describe data whenever possible, in particular to describe expression patterns. (2) Provide user-friendly search tools, for example to search for genes expressed with a certain pattern, or to search for the expression pattern of specific genes (from gene-specific experiments and from microarray data). Expression pattern predicted from the microarray data is called digital in situ.

Abbreviations: AREX

Synonyms: The Arabidopsis Gene Expression Database, Arabidopsis Gene Expression Database

Resource Type: database, data or information resource

Keywords: expression, gene, arabidopsis, genome, microarray, pattern

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: AREX

Resource ID: SCR_002170

Alternate IDs: nif-0000-20955

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260805T044034+0000

Ratings and Alerts

No rating or validation information has been found for ARES.

No alerts have been found for ARES.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Viswanathan M, et al. (2025) Enhancing amide proton transfer imaging in ischemic stroke using a machine learning approach with partially synthetic data. NMR in biomedicine, 38(1), e5277.

Kleimaier D, et al. (2020) The cellular heat shock response monitored by chemical exchange saturation transfer MRI. Scientific reports, 10(1), 11118.

Lu B, et al. (2020) Overexpression of Melon Tonoplast Sugar Transporter CmTST1 Improved Root Growth under High Sugar Content. International journal of molecular sciences, 21(10).

Khlebnikov V, et al. (2017) On the transmit field inhomogeneity correction of relaxation-compensated amide and NOE CEST effects at 7T. NMR in biomedicine, 30(5).

Roycewicz PS, et al. (2014) Cell wall properties play an important role in the emergence of lateral root primordia from the parent root. Journal of experimental botany, 65(8), 2057.

Stenzel I, et al. (2012) ALLENE OXIDE CYCLASE (AOC) gene family members of Arabidopsis thaliana: tissue- and organ-specific promoter activities and in vivo heteromerization. Journal of experimental botany, 63(17), 6125.

Alejandro S, et al. (2012) AtABCG29 is a monolignol transporter involved in lignin biosynthesis. Current biology : CB, 22(13), 1207.

Liu SL, et al. (2011) Organ and cell type-specific complementary expression patterns and regulatory neofunctionalization between duplicated genes in Arabidopsis thaliana. Genome biology and evolution, 3, 1419.

Sapienza PJ, et al. (2010) Using NMR to study fast dynamics in proteins: methods and applications. Current opinion in pharmacology, 10(6), 723.

ten Hove CA, et al. (2010) SCHIZORIZA encodes a nuclear factor regulating asymmetry of stem cell divisions in the Arabidopsis root. Current biology : CB, 20(5), 452.

Ma S, et al. (2007) Integration of Arabidopsis thaliana stress-related transcript profiles, promoter structures, and cell-specific expression. Genome biology, 8(4), R49.

Kwak SH, et al. (2007) The role of the SCRAMBLED receptor-like kinase in patterning the Arabidopsis root epidermis. Developmental biology, 302(1), 118.

Tetko IV, et al. (2006) Spatiotemporal expression control correlates with intragenic scaffold matrix attachment regions (S/MARs) in Arabidopsis thaliana. PLoS computational biology, 2(3), e21.

Wang H, et al. (2006) Prediction of trans-antisense transcripts in Arabidopsis thaliana. Genome biology, 7(10), R92.