

Resource Summary Report

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AtGenExpress - Weigel World

RRID:SCR_000777

Type: Tool

Proper Citation

AtGenExpress - Weigel World (RRID:SCR_000777)

Resource Information

URL: <http://jsp.weigelworld.org/expviz/expviz.jsp>

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Description: A visualization tool with microarray data and sample descriptions from the AtGenExpress project, which contains Affymetrix microarray data for Arabidopsis, a small flowering plant related to mustard and cabbage. This plant is used as a model organism in plant biology.

Synonyms: AtGenExpress, AtGenExpress Weigel World, AtGenExpress Visualization Tool

Resource Type: data or information resource, portal

Defining Citation: [PMID:17376166](#)

Keywords: visualization, microarray, arabidopsis, plant, biology, model, thale cress, arabidopsis thaliana

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: AtGenExpress - Weigel World

Resource ID: SCR_000777

Alternate IDs: nif-0000-30128

Old URLs:

<http://www.weigelworld.org/research/projects/resources/microarray/AtGenExpress/>

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260829T182838+0000

Ratings and Alerts

No rating or validation information has been found for AtGenExpress - Weigel World.

No alerts have been found for AtGenExpress - Weigel World.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Bouain N, et al. (2018) Natural allelic variation of the AZI1 gene controls root growth under zinc-limiting condition. PLoS genetics, 14(4), e1007304.

Robles P, et al. (2018) The Characterization of Arabidopsis mterf6 Mutants Reveals a New Role for mTERF6 in Tolerance to Abiotic Stress. International journal of molecular sciences, 19(8).

Rahmati Ishka M, et al. (2018) A comparison of heat-stress transcriptome changes between wild-type Arabidopsis pollen and a heat-sensitive mutant harboring a knockout of cyclic nucleotide-gated cation channel 16 (cngc16). BMC genomics, 19(1), 549.

Tian F, et al. (2017) Expression and integrated network analyses revealed functional divergence of NHX-type Na⁺/H⁺ exchanger genes in poplar. Scientific reports, 7(1), 2607.

Wu P, et al. (2017) Divergent evolutionary patterns of the MAPK cascade genes in Brassica rapa and plant phylogenetics. Horticulture research, 4, 17079.

Fernández-Bautista N, et al. (2017) HOP3 a new regulator of the ER stress response in Arabidopsis with possible implications in plant development and response to biotic and abiotic stresses. Plant signaling & behavior, 12(5), e1317421.

Wang W, et al. (2017) Genome-wide Analysis and Expression Divergence of the Trihelix family in Brassica Rapa: Insight into the Evolutionary Patterns in Plants. Scientific reports, 7(1), 6463.

Fahy D, et al. (2017) Impact of salt stress, cell death, and autophagy on peroxisomes: quantitative and morphological analyses using small fluorescent probe N-BODIPY. Scientific reports, 7, 39069.

Batth R, et al. (2017) Transcript Profiling Reveals the Presence of Abiotic Stress and Developmental Stage Specific Ascorbate Oxidase Genes in Plants. Frontiers in plant science, 8, 198.

Bi C, et al. (2017) Overexpression of the transcription factor NF-YC9 confers abscisic acid hypersensitivity in Arabidopsis. Plant molecular biology, 95(4-5), 425.

Wu P, et al. (2017) Comprehensive Analysis of the CDPK-SnRK Superfamily Genes in Chinese Cabbage and Its Evolutionary Implications in Plants. *Frontiers in plant science*, 8, 162.

Mainali HR, et al. (2017) Soybean cyclophilin GmCYP1 interacts with an isoflavonoid regulator GmMYB176. *Scientific reports*, 7, 39550.

Zang X, et al. (2017) Overexpression of wheat ferritin gene TaFER-5B enhances tolerance to heat stress and other abiotic stresses associated with the ROS scavenging. *BMC plant biology*, 17(1), 14.

Labusch C, et al. (2016) Transcription of TIR1-Controlled Genes Can be Regulated within 10 Min by an Auxin-Induced Process. Can TIR1 be the Receptor? *Frontiers in plant science*, 7, 995.

Kobayashi K, et al. (2016) Transcriptional Regulation of Tetrapyrrole Biosynthesis in *Arabidopsis thaliana*. *Frontiers in plant science*, 7, 1811.

Zhang J, et al. (2016) Molecular evolution and expression divergence of the *Populus euphratica* Hsf genes provide insight into the stress acclimation of desert poplar. *Scientific reports*, 6, 30050.

Shen EP, et al. (2014) Correlation of *Pseudomonas aeruginosa* genotype with antibiotic susceptibility and clinical features of induced central keratitis. *Investigative ophthalmology & visual science*, 56(1), 365.

Mounet F, et al. (2012) Down-regulation of a single auxin efflux transport protein in tomato induces precocious fruit development. *Journal of experimental botany*, 63(13), 4901.

Ma HS, et al. (2010) The salt- and drought-inducible poplar GRAS protein SCL7 confers salt and drought tolerance in *Arabidopsis thaliana*. *Journal of experimental botany*, 61(14), 4011.

Verelst W, et al. (2007) MADS-complexes regulate transcriptome dynamics during pollen maturation. *Genome biology*, 8(11), R249.