Resource Summary Report

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Database of Arabidopsis Transcription Factors

RRID:SCR_007101
Type: Tool

Proper Citation

Database of Arabidopsis Transcription Factors (RRID:SCR_007101)

Resource Information

URL: http://datf.cbi.pku.edu.cn/

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Description: Database that collects all arabidopsis transcription factors (totally 1922 Loci; 2290 Gene Models) and classifies them into 64 families. It uses not only locus (gene), but also gene model (transcript, protein) and the detail information is for each gene model not for locus. It adds multiple alignment of the DNA-binding domain of each family, Neighbor-Joining phylogenetic tree of each family, the GO annotation, homolog with the Database of Rice Transcription Factors (DRTF). It also keeps old information items such as the unique cloned and sequenced information of about 1200 transcription factors, protein domains, 3D structure information with BLAST hits against PDB, predicted Nuclear Location Signals, UniGene information, as well as links to literature reference.

Abbreviations: DATF

Resource Type: data or information resource, database

Defining Citation: PMID:15731212

Keywords: gene, alignment, arabidopsis, binding, clone, dna, domain, locus, phylogenetic tree, transcription, chromosome, transcription factor, blast, family, bio.tools, FASEB list

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China 863 Programs 2006AA02Z334;
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Availability: Free

Resource Name: Database of Arabidopsis Transcription Factors

Resource ID: SCR_007101

Alternate IDs: nif-0000-21112, OMICS_00551, biotools:datf

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

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250507T060449+0000

Ratings and Alerts

No rating or validation information has been found for Database of Arabidopsis Transcription Factors.

No alerts have been found for Database of Arabidopsis Transcription Factors.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 36 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Kababji AM, et al. (2024) Synthetic directed evolution for targeted engineering of plant traits. Frontiers in plant science, 15, 1449579.

Garcia-Molina A, et al. (2020) Translational Components Contribute to Acclimation Responses to High Light, Heat, and Cold in Arabidopsis. iScience, 23(7), 101331.

Karanja BK, et al. (2019) Genome-wide characterization of the AP2/ERF gene family in radish (Raphanus sativus L.): Unveiling evolution and patterns in response to abiotic stresses. Gene, 718, 144048.

Huang J, et al. (2018) Transcriptome analysis of nitric oxide-responsive genes in upland cotton (Gossypium hirsutum). PloS one, 13(3), e0192367.

Graf A, et al. (2017) Parallel analysis of Arabidopsis circadian clock mutants reveals different scales of transcriptome and proteome regulation. Open biology, 7(3).

Muhammad D, et al. (2017) More than meets the eye: Emergent properties of transcription factors networks in Arabidopsis. Biochimica et biophysica acta. Gene regulatory mechanisms, 1860(1), 64.

Song S, et al. (2017) Genome-Wide Organization and Expression Profiling of the SBP-Box Gene Family in Chinese Jujube (Ziziphus jujuba Mill.). International journal of molecular sciences, 18(8).

Mazur MJ, et al. (2017) Arabidopsis TCP Transcription Factors Interact with the SUMO Conjugating Machinery in Nuclear Foci. Frontiers in plant science, 8, 2043.

Becker MG, et al. (2017) SeqEnrich: A tool to predict transcription factor networks from co-expressed Arabidopsis and Brassica napus gene sets. PloS one, 12(6), e0178256.

Yang T, et al. (2016) Genome-Wide Identification, Evolutionary Analysis and Expression Profiles of LATERAL ORGAN BOUNDARIES DOMAIN Gene Family in Lotus japonicus and Medicago truncatula. PloS one, 11(8), e0161901.

Hung CY, et al. (2016) Gibberellin deficiency is responsible for shy-flowering nature of Epipremnum aureum. Scientific reports, 6, 28598.

Cao PB, et al. (2015) Genome-wide analysis of the AP2/ERF family in Eucalyptus grandis: an intriguing over-representation of stress-responsive DREB1/CBF genes. PloS one, 10(4), e0121041.

Costa MC, et al. (2015) A gene co-expression network predicts functional genes controlling the re-establishment of desiccation tolerance in germinated Arabidopsis thaliana seeds. Planta, 242(2), 435.

Chen R, et al. (2015) Gene-to-metabolite network for biosynthesis of lignans in MeJA-elicited Isatis indigotica hairy root cultures. Frontiers in plant science, 6, 952.

Shu Y, et al. (2015) Genome-Wide Analysis of the AP2/ERF Superfamily Genes and their Responses to Abiotic Stress in Medicago truncatula. Frontiers in plant science, 6, 1247.

García-Cano E, et al. (2015) Interaction of Arabidopsis Trihelix-Domain Transcription Factors VFP3 and VFP5 with Agrobacterium Virulence Protein VirF. PloS one, 10(11), e0142128.

Lai B, et al. (2015) Transcriptomic analysis of Litchi chinensis pericarp during maturation with a focus on chlorophyll degradation and flavonoid biosynthesis. BMC genomics, 16(1), 225.

Pruneda-Paz JL, et al. (2014) A genome-scale resource for the functional characterization of Arabidopsis transcription factors. Cell reports, 8(2), 622.

Leister D, et al. (2014) Identification of target genes and transcription factors implicated in translation-dependent retrograde signaling in Arabidopsis. Molecular plant, 7(7), 1228.

Wang M, et al. (2014) Genome and transcriptome analysis of the grapevine (Vitis vinifera L.) WRKY gene family. Horticulture research, 1, 14016.