

BIO-ANALYTIC RESOURCE FOR PLANT BIOLOGY

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Plant Biology 2023

August 6, 2023

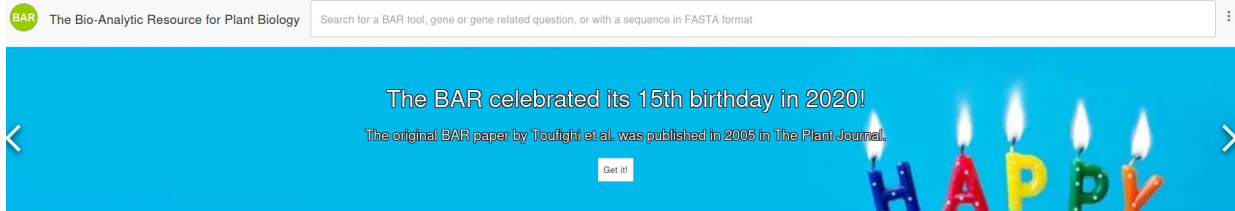


@vegan_asher@genomic.social



@BAR_PlantBio@genomic.social

Bio-Analytic Resource



Gene Expression and Protein Tools

View expression patterns as electronic fluorescent pictographs or heatmaps, explore promoters, identify protein-protein interactions and more.



Molecular Markers and Mapping Tools

Perform Next Generation Mapping, or generate your own markers using our molecular marker tools.



Other Genomic Tools and Widgets

Remove duplicates, perform multi-dimensional Venn analyses, or generate random lists of identifiers.

<https://bar.utoronto.ca/>



175M (100M *A. th.*)



11.7K (SUBA4)



80K predicted
100+K experimental
2.8M PDIs



29K Phyre2
26k AlphaFold2
885 from PDB



10+M nsSNPs (1135 ecotypes)

BAR and FAIR Principles

- **Findable:** BAR datasets can be easily searched on the BAR homepage and GAIA app.
- **Accessible:** BAR datasets do not require authentication or authorization and are publicly available.
- **Interoperable:** BAR and ThaleMine webservices provide data in JSON and XML formats that can be easily integrated into workflows.
- **Reusable:** BAR includes datasets that are publicly available and do not require a subscription. So the data can be reused in any external apps.

New BAR Homepage (with GAIA search input)

BAR

The Bio-Analytic Resource for Plant Biology

Search for a BAR tool, gene or gene related question, or with a sequence in FASTA format



Welcome to the BAR!

Web-based tools for visualizing functional genomics and other data.



Gene Expression and Protein Tools

View expression patterns as electronic fluorescent pictographs or heatmaps, explore promoters, identify protein-protein interactions and more.



Molecular Markers and Mapping Tools

Perform Next Generation Mapping, or generate your own markers using our molecular marker tools.



Other Genomic Tools and Widgets

Remove duplicates, perform multi-dimensional Venn analyses, or generate random lists of identifiers.

<https://bar.utoronto.ca/>

GAI: Gene Search

BAR

ABI3

[BAR Tools](#) | [Summary](#) | [Gene Reference into Function](#) | [External Database IDs](#) | [GO Functions](#) | [Homologs](#) | [Expression](#) | [Interactions](#) | [Gene Information](#) | [Model Figures](#) | [Publications](#) | [Patents](#)

"ABI3" - GENERAL

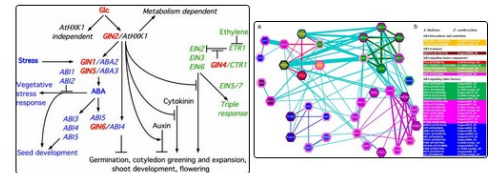
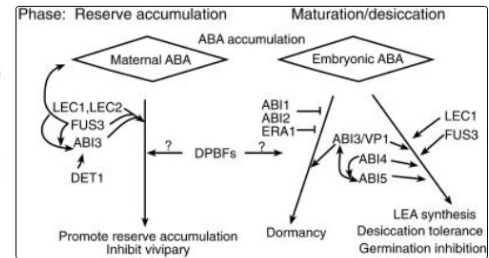
TL;DR: AP2/B3-like transcriptional factor family protein. In addition, both FUS3 and LEC1 regulate positively the abundance of the ABI3 protein in the seed. In peer reviewed gene model maps, ABI3 has found to also co-occur with ABI5, FUS3, LEC1 and more.

AP2/B3-like transcriptional factor family protein. The highest subcellular localization of ABI3 is the nucleus. ABI3 has 1 splice variant. ABI3 has been shown experimentally to interact with 94 proteins, including At2g25890 and At4g17730.

In peer reviewed gene model maps, ABI3 has found to also co-occur with ABI5, FUS3, LEC1 and more. ABI3 has been found in the following modules: Signaling Pathways in Seed Development, Interactions between Sugar and Hormone Signaling in Arabidopsis, Module for ABA signaling pathway in osmotic stress responses of *Z. xanthoxylum* roots and more pathways.

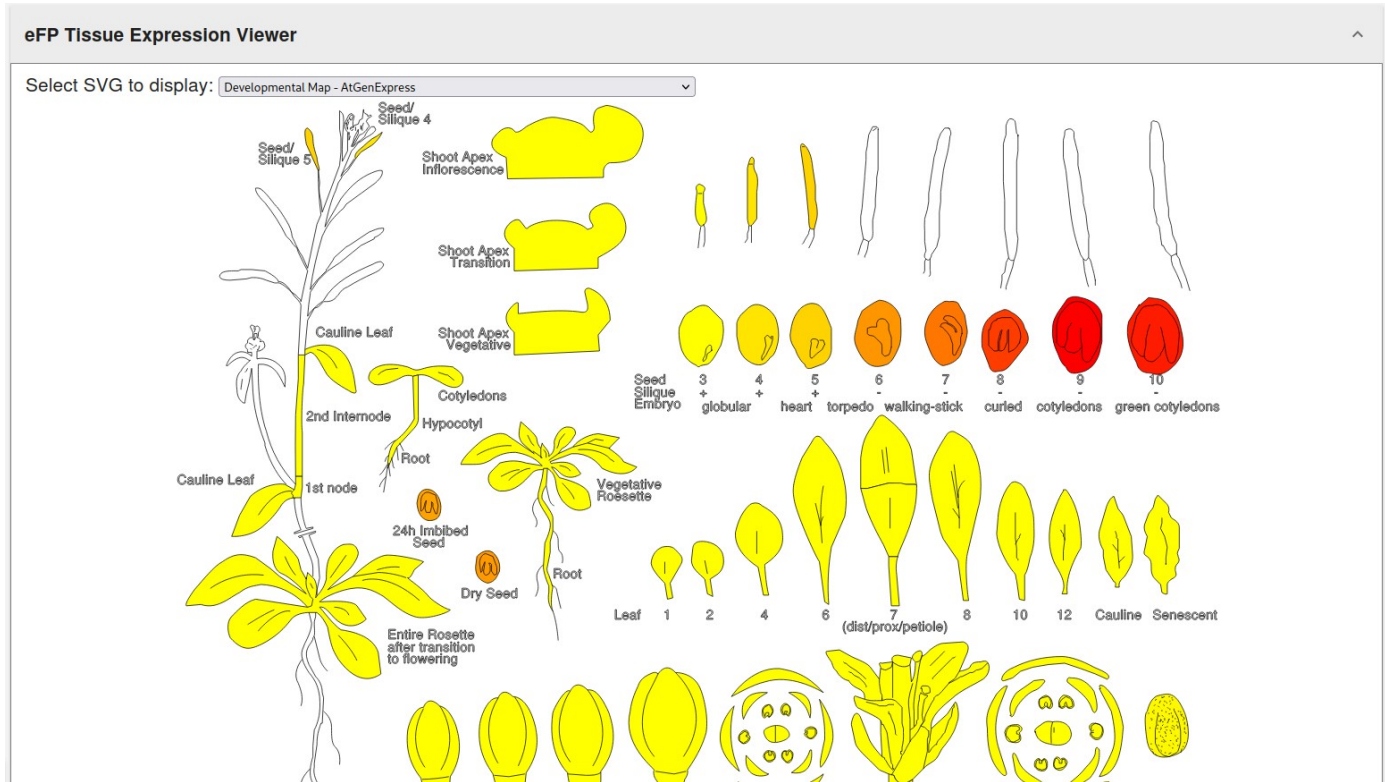
A curated summary of ABI3 is: Homologous to the maize transcription factor Viviparous-1. Full length ABI3 protein binds to the highly conserved RY motif [DNA motif CATGCA(TG)], present in many seed-specific promoters, and the B3 domains of this transcription factor is necessary for the specific interaction with the RY element. Transcriptional activity of ABI3 requires the B3 DNA-binding domain and an activation domain. In addition to the known N-terminal-located activation domain, a second transcription activation domain was found in the B1 region of ABI3. ABI3 is essential for seed maturation. Regulator of the transition between embryo maturation and early seedling development. Putative seed-specific transcriptional activator. ABI3 is a central regulator in ABA signaling and is unstable in vivo. It interacts with and can be polyubiquitinated by AIP2 in vivo. Based on double mutant analyses, ABI3 interacts genetically with both FUS3 and LEC1 and is involved in controlling accumulation of chlorophyll and anthocyanins, sensitivity to abscisic acid, and expression of the members of the 12S storage protein gene family. In addition, both FUS3 and LEC1 regulate positively the abundance of the ABI3 protein in the seed. Alternative splicing of ABI3 is developmentally regulated by SUA (AT3G54230).

Recent publications suggest the following: 1) For example, WUSCHEL-related homeobox, LEC2/FUS3/ABI3, and HEME ACTIVATOR PROTEIN3 families can control plant seed embryonic initiation and development. 2) Furthermore, VvKEG interacted with the ABA-responsive transcription factor ABSCISIC ACID-INSENSITIVE3 (ABI3). 3) In addition, qPCR analysis found that under ABA treatment, *LSH8* positively mediated the expression of downstream ABA-related genes of *ABI3*, *ABI5*, *RD29B* and *RAB18*.



<https://bar.utoronto.ca/gaia/> (Sullivan, *et al.*, in prep)

GAlA: Gene Search

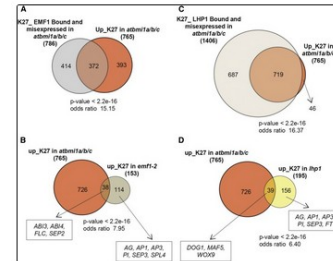
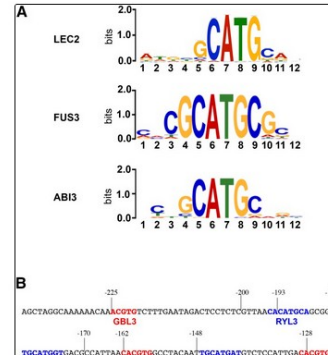
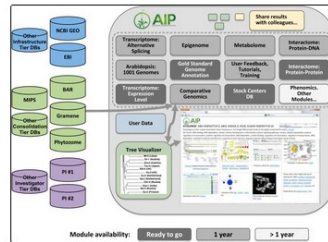
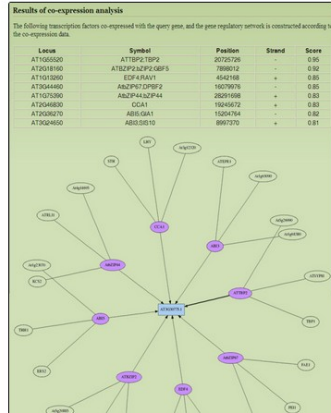
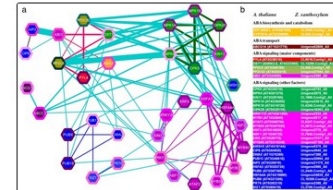
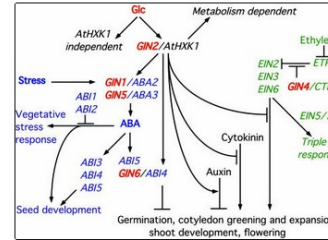
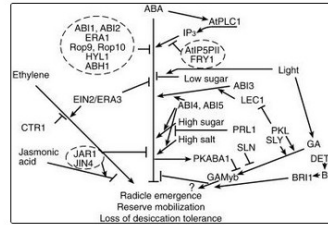
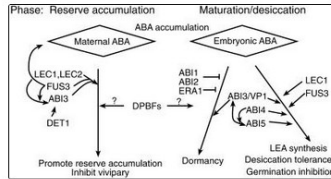


<https://bar.utoronto.ca/gaia/> (Sullivan, *et al.*, in prep)

GAEA: Gene Search

Model Figures

Filter by gene name (split using comma):



<https://bar.utoronto.ca/gaia/> (Sullivan, et al., in prep)

GAIA: Gene Search

Model Figures

Filter by gene name (split using comma):

Abscisic Acid biosynthesis and response.

Ruth R Finkelstein, Christopher D Rock - [Link to publication](#)

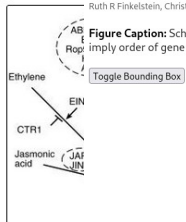
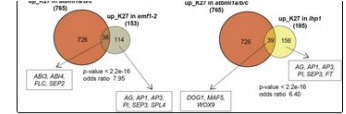
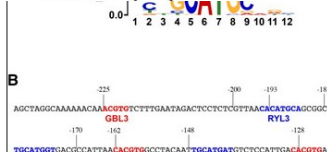
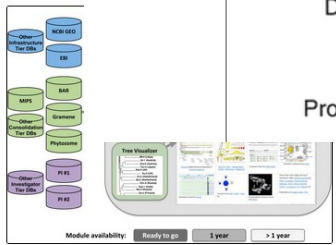
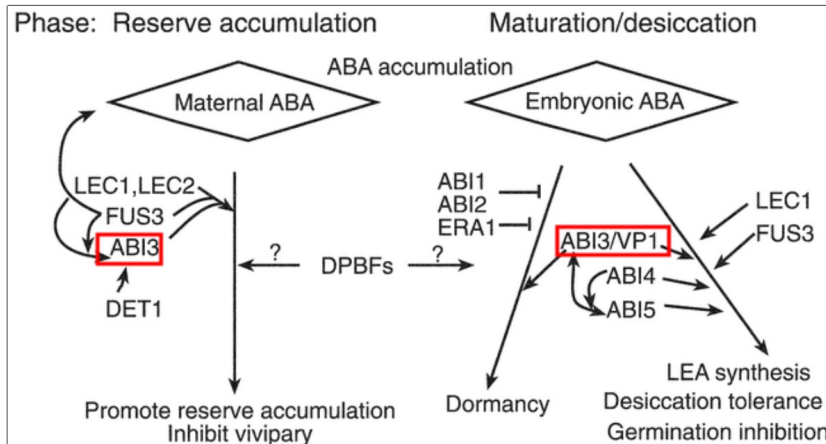
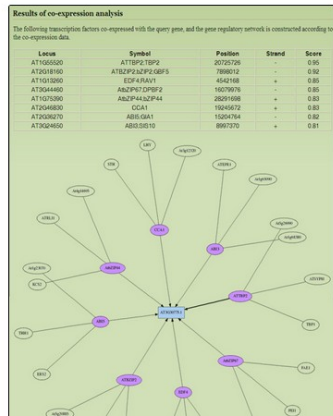
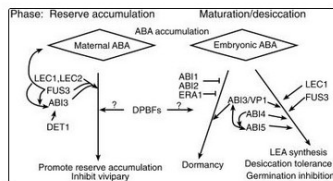


Figure Caption: Schematic of signaling pathways in seed development. Arrows represent promotion of processes or expression of the regulators. Bars represent inhibitors of the indicated processes. Positions of loci do not imply order of gene action. Reprinted with permission from Finkelstein et al. (2002).



<https://bar.utoronto.ca/gaia/> (Sullivan, et al., in prep)

GAIA: Question Search

BAR

what is abi3

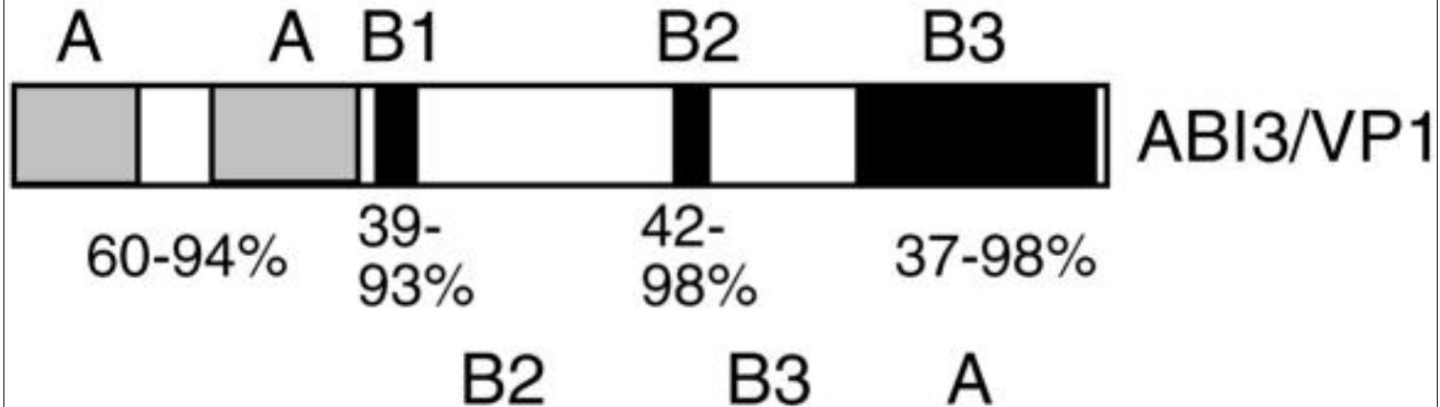
BAR Tools | Summary | Gene Reference into Function | External Database IDs | GO Functions | Homologs | Expression | Interactions | Gene Information | Model Figures | Publications | Patents

"what is abi3" - QUESTION

TITLE:

Abscisic acid signaling in seeds and seedlings.

B3 domain



<https://bar.utoronto.ca/gaia/> (Sullivan, *et al.*, in prep)

Homepage: BLAST Search

```
MKSLHVAANAGDLAEDCGILGGDADDTVLMGIDEVGREIWLDDHGGDNNHVHGHQDDDLIVHHDPSIFYGDLPTLPDFPCSSSSSSSTSPAPVNAIVSSASSSSAASSTSSAASWAILRSDGEDPTPNQNYASGNCDDSSGALQSTAS  
IPLDSSQGFQCGEGGGDCIDMMETFGYMDLLDSNEFFDTS AIFSQDDDTQNPMLMDQTLERQEDQVVVPMENNSGGDMQMMNSLEQDDDLAAVFLWLNKNETVSAEDLRKVKIKKATIESAARRLGGGKEAMKQLLKLILEWVQTNHL  
RRTTTTTTNLSYQQSFQDDPFQNPNNNNLIPSPDQTCFSPSTWVPPPPQQQAFVSDPGFGYMPAPNYPPQPEFLPLESPPSWPPPPQSGMPHQQFMPPTSQYNQFGDPTGFNGYNMNPYQYYPVYVAGQMRDQRLRLCSSATKEARKKR  
MARQRRFLSHHHRHNNNNNNNNNNQNTQIGETCAAVAPQLNPVATTATGGTWYWPVNPVAVPPQLPPVMETQLPTMDRAGSASAMPRQVVPDRRQGWKPEKNLRFLLQKVLKQSDVGNLGRIVLPKKEAETHLEPEARDGISLAMEDI  
SRVWMMRYRFWPNKSRMYLLENTGDFVKTNGLQEGDFIVIYSDVKCGKYLIRGVKVRQPSGQKPEAPPSSAATKRQNKSRQINNNNSPSANVVVASPTSQTVK
```

Nucleotide databases [\[Select all\]](#)

- Arabidopsis thaliana
- Nucl
- Spruce

Protein databases [\[Select all\]](#)

- Arabidopsis thaliana
- Prot

Advanced parameters:

eg: -evalue 1.0e-5 -num_alignments 100

Open results in new tab

BLAST

Please cite data sources and the paper describing our SequenceServer BLAST interface. *Perform BLAST analyses.*

<https://bar.utoronto.ca/blast/> (Sullivan, *et al.*, in prep)

Homepage: BLAST Search

BLASTP: 1 query, 2 databases

[Edit search](#) | [New search](#)

Download FASTA, XML, TSV

[FASTA of all hits](#)

[FASTA of selected hit\(s\)](#)

[Alignment of all hits](#)

[Alignment of selected hit\(s\)](#)

[Standard tabular report](#)

[Full tabular report](#)

[Full XML report](#)

Share results

[Share to cloud](#)

SequenceServer 2.1.0 using BLASTP 2.14.0+, query submitted on 2023-08-03 21:39:45 UTC

Databases: Arabidopsis thaliana, Prot (985386 sequences, 364523406 characters)

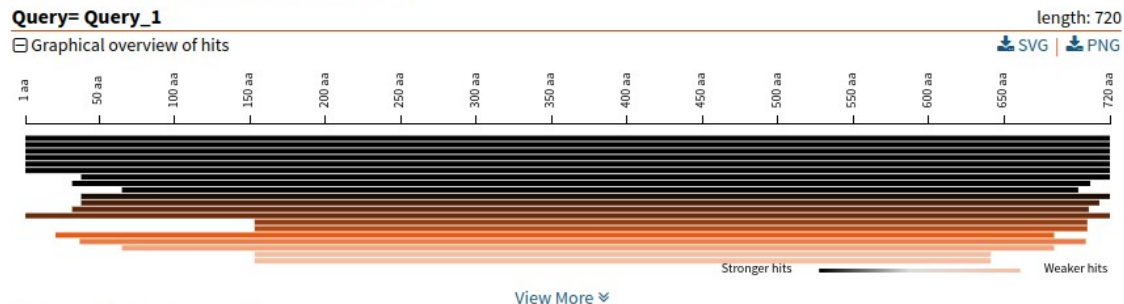
Parameters: evalue 1e-05, matrix BLOSUM62, gap-open 11, gap-extend 1, filter F

Please cite: <https://doi.org/10.1093/molbev/msz185>

Queries and their top hits: chord diagram

Query= Query_1

Graphical overview of hits



Length distribution of matching sequences

Sequences producing significant alignments

#	Similar sequences	Query coverage (%)	Total score	E value	Identity (%)	BAR Tools
1.	AT3G24650.1 Symbols: ABI3, AtABI3, SIS10 SUGAR INSENSITIVE ...	100	3881	0	100%	ePlant eFP
2.	Csa15g050420.1	100	2897	0	90.2%	ePlant
3.	Csa01g030760.1	100	2832	0	89.4%	ePlant
4.	Csa01g030760.2	100	2832	0	89.4%	ePlant
5.	Csa19g036630.1	100	2806	0	89.2%	ePlant

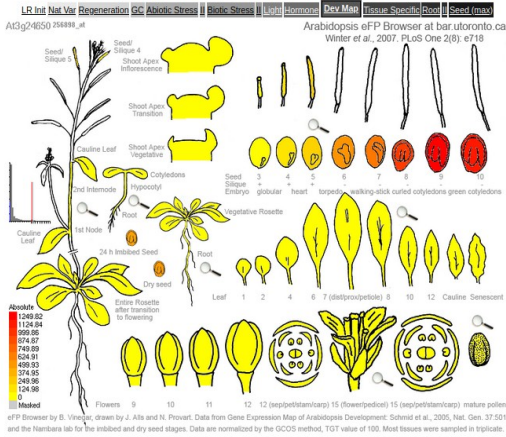
<https://bar.utoronto.ca/blast/> (Sullivan, *et al.*, in prep)

Bio-Analytic Resource

Data Source: Mode: Primary Gene ID: AT3G24650 Secondary Gene ID: AT3g27340 Signal Threshold: 1249.82

Developmental Map: Absolute

- For ATH1 data, this probe set reaches its maximum expression level (expression potential) of 1947.32 in the Seed data source.
- For ATH1 data, note the maximum signal value has increased to 1249.82 from 49.63. Use the [Signal Threshold option to keep it constant at 49.63](#) or enter a value in the Signal Threshold box, such as [1947.32](#). The same color scheme will then be applied across all views.
- Some samples exhibit high standard deviations for replicates. You can use [standard deviation filtering](#) to mask those with a deviation greater than half their expression value.



[Click Here for Table of Expression Values](#) [Click Here for Chart of Expression Values](#)

<https://bar.utoronto.ca/>

Bio-Analytic Resource

Data Source: Developmental Map Mode: Absolute Primary Gene ID: AT3G24650 Secondary Gene ID: At3g27340 Signal Threshold: 1249.82

Opening local file /var/www/html/ntools/temp_general/exprss_treeview_18286.cdt.hdr and reformatting... Note that the values in the table and image below are log2-transformed ratios, and can be thought of as 2 to the exponent of the given value. Thus 2 in the table indicates 2², which is 4-fold up relative to the appropriate control, while -2 indicates 2⁻², which is 0.25, or 4-fold down relative to the control. Log2-transformed ratios have an equal distribution in number space, aiding visualization.

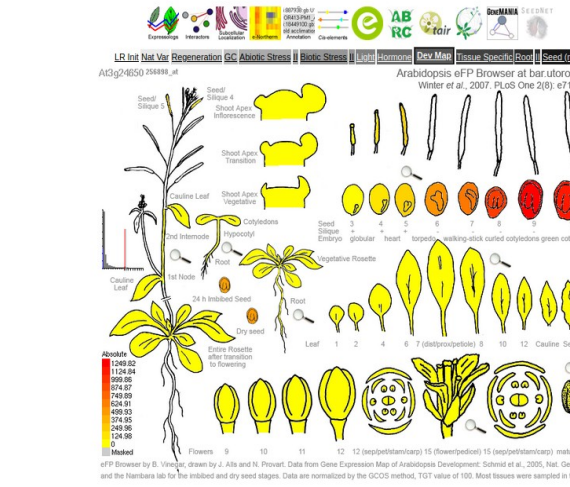
- For ATH1 data, this probe set reaches its maximum expression level (expression potential) of 1947.32 in the Seed data source.
- For ATH1 data, note the maximum signal value has increased to 1249.82 from 49.63. Use the [Signal Threshold option to keep a constant at an ex](#) or enter a value in [Field 26](#). The same color scheme will then be applied across all views.
- Some samples exhibit high standard deviations for replicates. You can use [standard deviation filtering](#) to mask those with a deviation greater than half their express

At1g01010: 261585_at| ANAC001_NAC001_NTL10_NAC domain containing protein 1

183 Name: CTRL_8/CTRL_8: ATGE_CTRL_8 [AtGenExpress_Plus_PID:1828] Res. Area: Guard and Mesophyll Cells

Tissue: Ctrl_median_values_tissue_s Mutant: WT Growth Stage: Time hours: Control s:

Description: Alias: Detach:



Bio-Analytic Resource

Data Source: Developmental Map Mode: Primary Gene ID: AT3G24650 Secondary Gene ID: AT3g27340 Signal Threshold: 1249.82

Opening local file /var/www/html/ntools/temp_general/exprs_treeview_18286.cdt.hdr and reformatting... Note that the values in the table and image below are log2-transformed ratios, and can be thought of as 2 to the exponent of the given value. Thus 2 in the table indicates 2², which is 4-fold up relative to the appropriate control, while -2 indicates 2⁻², which is 0.25, or 4-fold down relative to the control. Log2-transformed ratios have an equal distribution in number space, aiding visualization.

- For ATH1 data, this probe set reaches its maximum expression level (expression potential) of 1947.32 in the Seed data source.
- For ATH1 data, note the maximum signal value has increased to 1249.82 from 49.63. Use the [Signal Threshold option to keep a constant at an ex](#) or enter a value as [Expr2](#). The same color scheme will then be applied across all views.
- Some samples exhibit high standard deviations for replicates. You can use [standard deviation filtering](#) to mask those with a deviation greater than half their express

At1g01010: 261585_at| ANAC001_NAC001_NTL10_NAC domain containing protein 1]

183 Name: CTRL_8/CTRL_8: ATGE_CTRL_8 [ATGen] Tissue: Ctrl_median_values_tissue_s Mutant: []

Detach

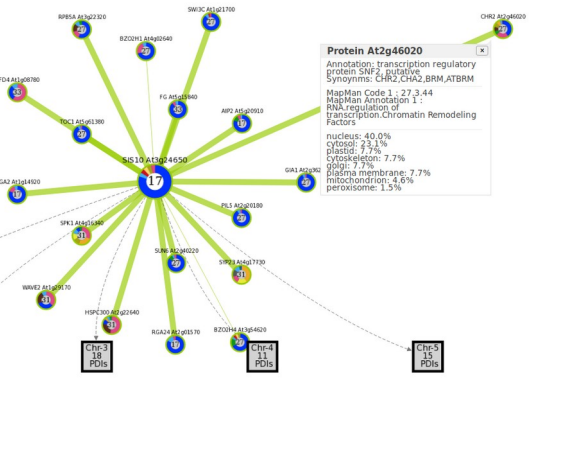
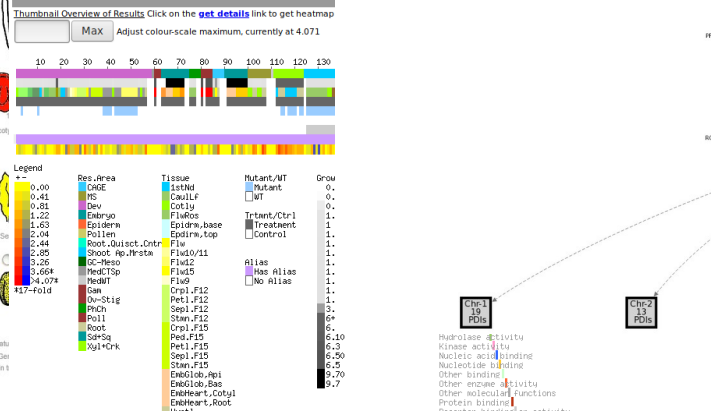
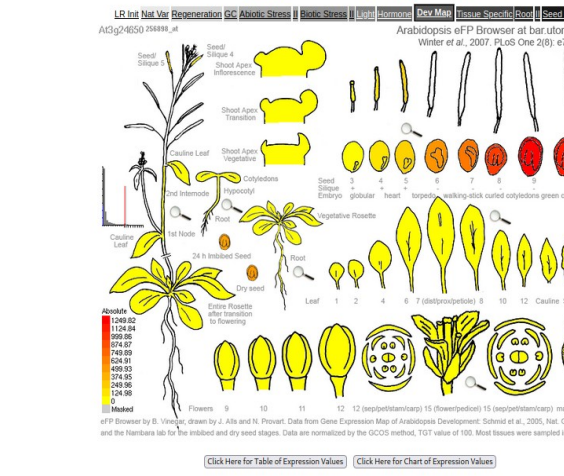
Query AIV: Export, MapMan Legend/Filter

Layouts: Non-Query Genes, MapMan Numbers, Localization Data, Pred Localizations, DNA (Chr) Nodes

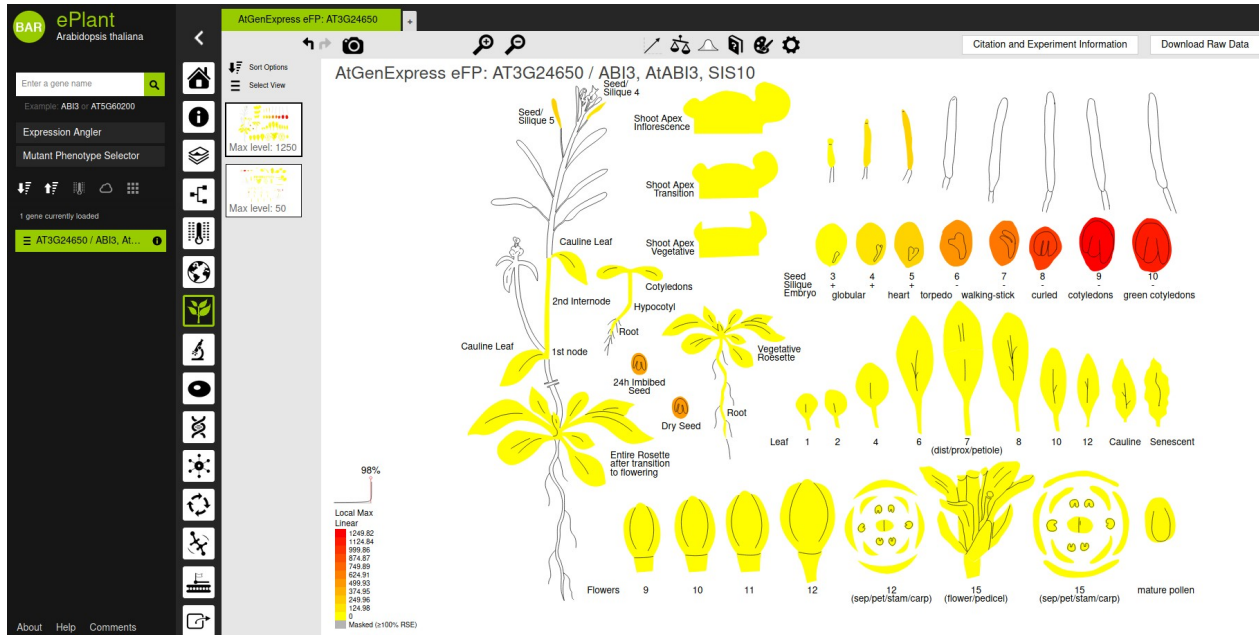
Filter Specific Publication(s): Interlog Confidence greater than: 0.0

Find AGs: Highlight delimited AGIs by: eg "AT3g10010,AT5g10220" Show Experimental PPIs with: Show Predicted PPIs with: Correlation Coefficient greater than: -1.03 Correlation Coefficient greater than: -1.00

Expression Source: Overlay Expression, Absolute, Relative, Expression Tissue, Limit Expression, Select Tissues, Limit expression val

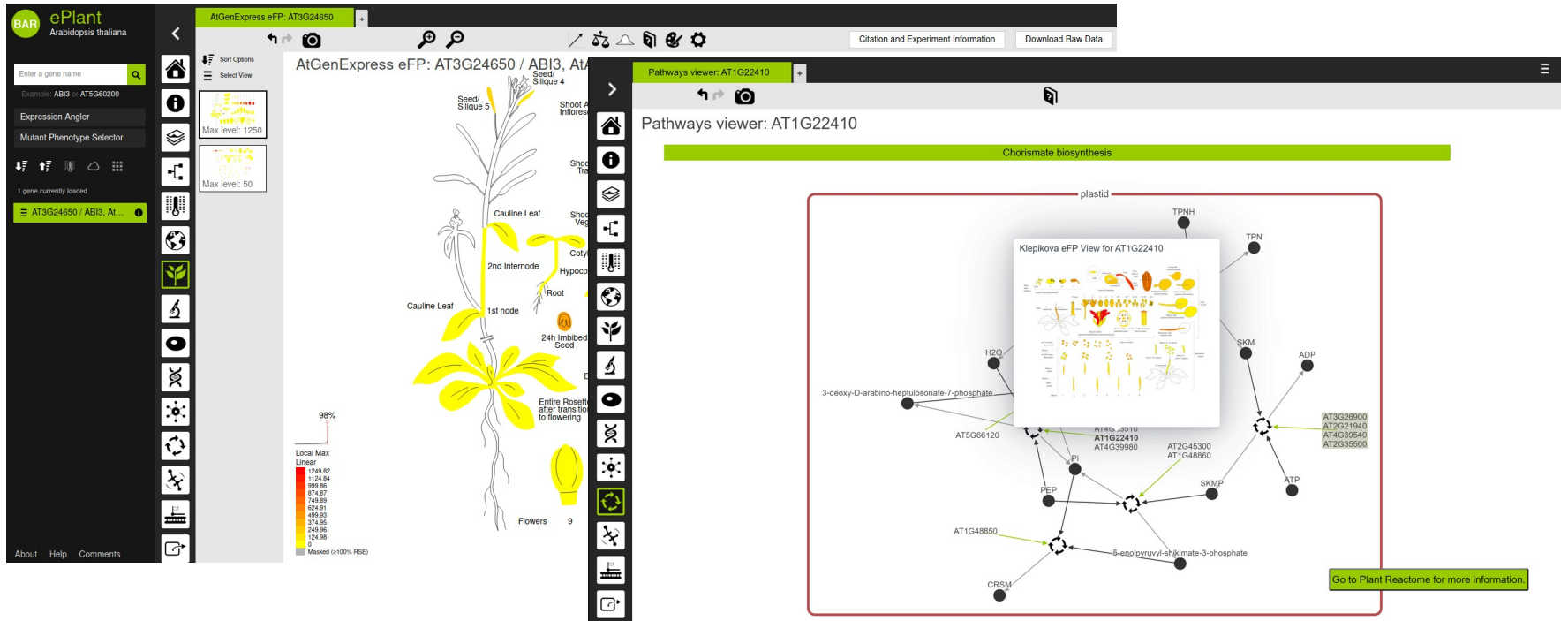


ePlant: Improved User Interface



<https://bar.utoronto.ca/eplant/> (Waese et al., 2017, Waese-Perlman et al. In prep.)
<https://doi.org/10.1101/2021.04.28.441805>

ePlant: Improved User Interface



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<https://doi.org/10.1101/2021.04.28.441805>

ePlant: Phyre2 and AF2 Structures

Molecule viewer: AT3G24650.1 / ABI3, AtABI3, SIS10

Reset Model

Select residues

Default Color

PDB Structure (will reload view)

Molecular Surface

Pfam Domains

CDD Feature Hits

Predicted Carbohydrate Binding Sites

Q Q V V P D R R Q G W K P E [K N L R F L L Q K V L K Q S D V G N L G R I V L P K K E A E T H L P E L E A R D G I S L A M E D I G T

<https://bar.utoronto.ca/eplant/> (Waese et al., 2017, Waese-Perlman et al. In prep.)
<https://doi.org/10.1101/2021.04.28.441805>

ePlant: Phyre2 and AF2 Structures

The screenshot displays the ePlant Molecule viewer interface for the protein AT3G24650.1 / ABI3, AtABI3, SIS10. The central 3D model shows the protein structure in a ribbon representation, with a grey molecular surface overlaid on a portion of it. The interface includes a search bar on the left, a navigation toolbar, and a sequence viewer at the bottom. The sequence viewer shows the amino acid sequence: P T M D R A G S A S A M P R Q Q V V P D R R Q G W K P E K N L R F L L O K V L K Q S D V G N L G R I V L P K K E A E T H L P E L E. Residues 108 (T) and 109 (G) are highlighted in yellow, and residue 216 (T) is highlighted in orange. A 'Drag me!' box is present over residues 540-576. The right sidebar contains controls for 'Reset Model', 'Select residues', 'Default Color', 'PDB Structure (will reload view)', 'Molecular Surface', 'Pfam Domains', 'CDD Feature Hits', and 'Predicted Carbohydrate Binding Sites'.

<https://bar.utoronto.ca/eplant/> (Waese *et al.*, 2017, Waese-Perlman *et al.* In prep.)
<https://doi.org/10.1101/2021.04.28.441805>

ePlants

ePlant



Info **Go** Pub

ePlant Maize



Info **Go**

ePlant Poplar



Info **Go**

ePlant Tomato



Info **Go**

ePlant Camelina



Info **Go**

ePlant Soybean



Info **Go**

ePlant Potato



Info **Go**

ePlant Barley V3



Info **Go**

ePlant Barley V1




Info **Go**

ePlant Medicago



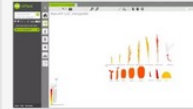
Info **Go**

ePlant Eucalyptus



Info **Go**

ePlant Rice



Info **Go**

ePlant Willow



Info **Go**

ePlant Sunflower




Info **Go**

ePlant Cannabis



Info **Go**

ePlant Wheat



Info **Go**

ePlant Sugarcane



Info **Go**

**Legacy ePlant
(PLOS ONE
version)**



Info **Go** Pub

AGENT

BAR



Enter AGI (AT5G23020), AGI-pair (AT3G24520-AT3G12580), tissue/experiments (auto-suggestions), or 'all' to see all networks

<https://bar.utoronto.ca/AGENT> (Lau *et al.*, 2021)
<https://doi.org/10.1101/2021.04.28.441830>

AGENT

BAR

α GENT

Enter AGI (AT5G23020), AGI-pair (AT3G24520-AT3G12580), tissue/experiments (auto-suggestions), or 'all' to see all networks

α GENT

APETALA2 x

BAR

Zhang et al. (BMC Plant Biology, 2019) Flowering Development Network

Existing time-course gene expression data for flower development was used to find dynamical network biomarker to create a gene regulatory network.

DNB

Flower

CBP20

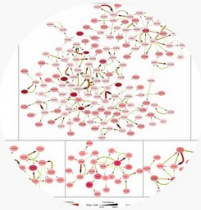
LEA

NAP12

RIE1

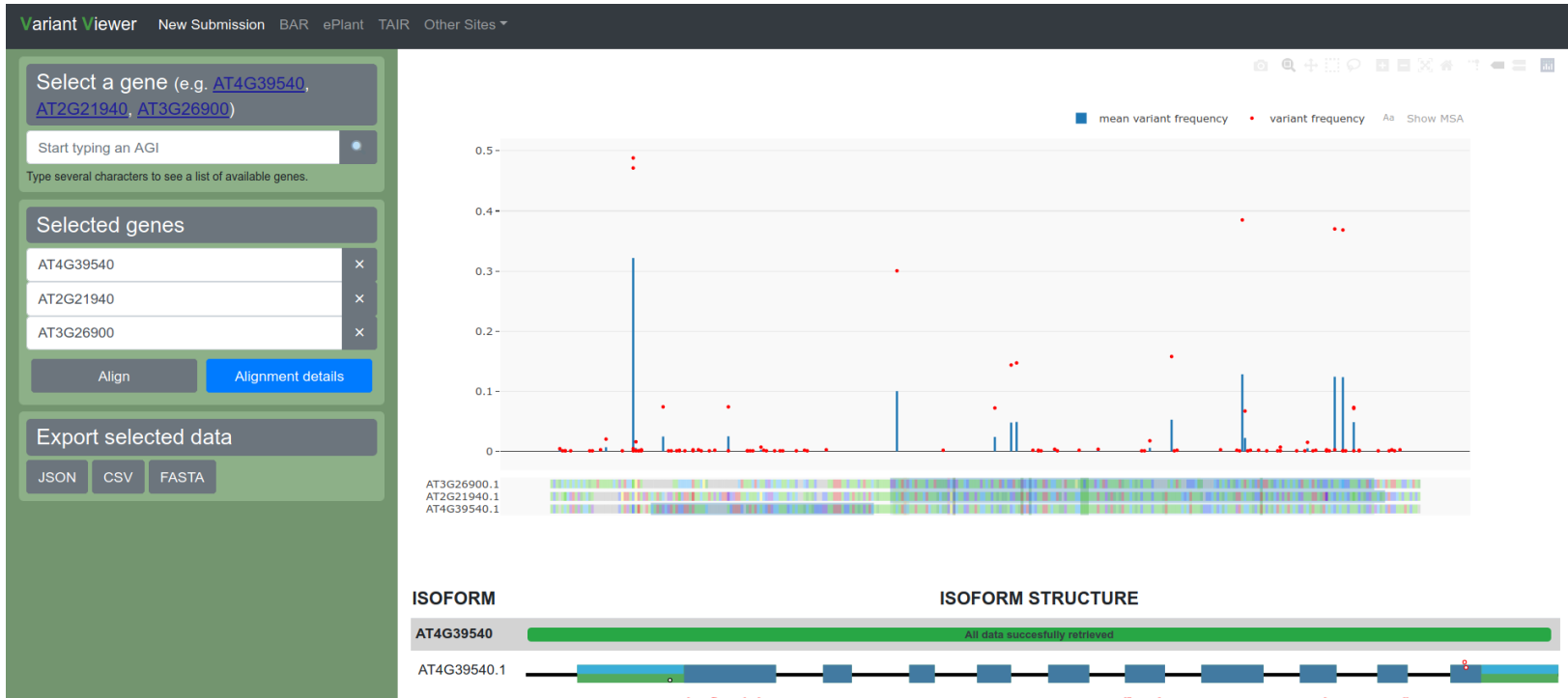
APETALA2

CBC



<https://bar.utoronto.ca/AGENT> (Lau *et al.*, 2021)
<https://doi.org/10.1101/2021.04.28.441830>

New Tool: Variant Viewer for SNPs



<https://bar.utoronto.ca/VariantViewer/> (Cumming *et al.*, 2021)
<https://doi.org/10.1101/2021.04.21.440793>

eFP-Seq Browser

The screenshot displays the eFP-Seq Browser interface. On the left is a sidebar with search and navigation options. The main area shows a table of RNA-Seq coverage tracks for various Arabidopsis samples. Each row includes a title, a coverage plot, an eFP (RPKM) value, an RPKM value, and a details link.

Title	RNA-Seq Coverage	eFP (RPKM)	RPKM	Details
Aerial part of long-day-grown 4-leaf-stage seedling with mock (NaCl) treatment		0.57	370.51	E-MTAB-1668:24NC5-RNA Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Transcription profiling of Arabidopsis plants overexpressing SlHsfA3 (thale cress)		0.58	379.32	GSM798296: mRNASeq_WT_rep2 Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Aerial part of 4-week-old plant		0.57	500.29	GSM994838: SRA: SRS360059 Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Aerial part of 3-week-old soil-grown plant		0.52	243.41	Seeding1.SRA: SRS419144 Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Aerial part of 3-week-old soil-grown plant		0.50	235.16	Seeding1.SRA: SRS419144 Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Aerial part of 3-week-old soil-grown plant		0.52	614.72	Seeding2_SRA: SRS419145 Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Aerial part of 3-week-old soil-grown plant		0.52	739.79	Seeding2_SRA: SRS419145 Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Carpels collected manually from stage 8-13 flowers		0.61	316.71	carpel: GSM1359146, SRA: SRS58... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Carpels collected manually from stage 8-13 flowers		0.61	367.53	carpel: GSM1359146, SRA: SRS58... Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details

https://bar.utoronto.ca/eFP-Seq_Browser/ (Sullivan *et al.*, 2019)

ThaleMine



ThaleMine v5.1.0-20230710 Data mining on *Arabidopsis thaliana*

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Search: e.g. AT1G01640 GO

Search

Search ThaleMine. Enter **names, identifiers** or **keywords** for genes, proteins, ontology terms, authors, etc. (e.g. *FT*, *APL_ARATH*, lateral root development, Somerville).

e.g. AT3G24650, FT, APL_ARATH

SEARCH

Analyse

Enter a **list of identifiers**.

Gene

e.g. AT1G02850, AT1G05240, AT1G05250, AT1G05260, AT1G14540, AT1G14550, AT1G15950, AT1G24110,

[advanced](#)

ANALYSE

First Time Here?

ThaleMine enables you to analyze *Arabidopsis thaliana* **genes, proteins, gene expression, protein-protein interactions, orthologs**, and more.

Use plain text or structured queries for interactive gene and protein reports.

TAKE A TOUR (VIA FLYMINE)

GENES AND PROTEINS | HOMOLOGY | FUNCTION | INTERACTIONS

The gene models and other genome annotations in ThaleMine are provided by a variety of sources including: NCBI, TAIR [Read more](#)

Query for genes and proteins:

- Gene → Protein sequence
- Gene → CDS sequence
- Gene → Transposable Elements

» [More queries](#)

popular templates

(Pasha *et al.*, 2020)

ThaleMine

- ThaleMine v5.1.0-20230710 was release with InterMine 5.1.0 and data as of July 10, 2023.
- TAIR datasets upgraded to public release 20220630
- Panther dataset is upgraded to 17.0
- BioGrid data are upgraded to 4.4.233
- BAR eFP images are now loaded using a new Python 3 based web service with cached images.
- We continue to support InterMine staff.

ThaleMine Gene Search



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Search:

Gene : **ABI3** *A. thaliana*

DB Identifier **AT3G24650** Secondary Identifier **locus:2093166**
Name **ABA INSENSITIVE 3** Brief Description **AP2/B3-like transcriptional factor family protein**

TAIR Computational Description **AP2/B3-like transcriptional factor family protein.(source:Arabot11)**

TAIR Curator Summary **Homologous to the maize transcription factor Viviparous-1. Full length ABI3 protein binds to the highly conserved RY motif [DNA motif CATGGA(TG)], present in many seed-specific promoters, and the B3 domains of this transcription factor is necessary for the specific interaction with the RY element. Transcriptional activity of ABI3 requires the B3 DNA-binding domain and an activation domain. In addition to the known N-terminal-located activation domain, a second transcription activation domain was found in the B1 region of ABI3. ABI3 is essential for seed maturation. Regulator of the transition between embryo maturation and early seedling development. Putative seed-specific transcriptional activator. ABI3 is a central regulator in ABA signaling and is unstable in vivo. It interacts with and can be polyubiquitinated by AIP2 in vivo. Based on double mutant analyses, ABI3 interacts genetically with both FUS3 and LEC1 and is involved in controlling accumulation of chlorophyll and anthocyanins, sensitivity to abscisic acid, and expression of the members of the 12S storage protein gene family. In addition, both FUS3 and LEC1 regulate positively the abundance of the ABI3 protein in the seed. Alternative splicing of ABI3 is developmentally regulated by SUA (AT3G54230).**

TAIR Short Description **AP2/B3-like transcriptional factor family protein**

TAIR Aliases **ABI3, ATABI3, SIS10**

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27 Gene Rifs

Trail: [Gene](#)

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Rows per page: 10

« « « page 1 » » »

<input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> Gene Rifs Annotation	<input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> Gene Rifs last updated	<input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> Gene Rifs Organism	<input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> Gene Rifs Gene	<input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> Gene Rifs PubMed Id
ABA-INSENSITIVE 3 with or without FUSCA3 highly up-regulates lipid droplet proteins and activates oil accumulation.	2022-04-16	A. thaliana	ABI3	34849730
ABI3 and PIL5 collaboratively activate the expression of SOM mRNA by directly binding to and interacting with each other at the SOM promoter.	2011-09-24	A. thaliana	ABI3	21467583
ABI3 controls embryo degreening through Mendel's locus.	2013-12-07	A. thaliana	ABI3	24043799
ABI3 expression ceases following the completion of germination in both tomato and Arabidopsis seeds, suggesting that expression of this gene does not regulate germination.	2010-01-21	A. thaliana	ABI3	16531465
ABI3 mediates dehydration stress signaling in Arabidopsis through regulation of a group of genes that play a role primarily during stress recovery phase.	2017-04-15	A. thaliana	ABI3	27457990
ABSCISIC ACID-INSENSITIVE3 (ABI3) regulates the developmental expression of HsfA9.	2010-01-21	A. thaliana	ABI3	17220197

Lists

This Gene is in one list:
Genes with a Loss-of-Function Mutant Phenotype: Morphological - Vegetative (640)

Links to other Mines

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[CowpeaMine](#) No results
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Search:

Gene : **ABI3** *A. thaliana*

DB Identifier **AT3G24650** Secondary Identifier **locus:2093166**

Name **ABA INSENSITIVE 3** Brief Description **AP2/B3-like transcriptional factor family protein**

TAIR Computational Description **AP2/B3-like transcriptional factor family protein.(source:Araport11)**

TAIR Curator Summary **Homologous to the maize transcription factor Vsvp1. Full length ABI3 protein binds to the highly conserved RY motif [DNA motif CATGGA(TG)], present in many seed-specific promoters, and the B3 domains of this transcription factor is necessary for the specific interaction with the RY element. Transcriptional activity of ABI3 requires the B3 DNA-binding domain and an activation domain. In addition to the known N-terminal-located activation domain, a second transcription activation domain was found in the B1 region of ABI3. ABI3 is essential for seed maturation. Regulator of the transition between embryo maturation and early seedling development. Putative seed-specific transcriptional activator. ABI3 is a central regulator in ABA signaling and is unstable in vivo. It interacts with and can be polyubiquitinated by AIP2 in vivo. Based on double mutant analyses, ABI3 interacts genetically with both FUS3 and LEC1 and is involved in controlling accumulation of chlorophyll and anthocyanins, sensitivity to abscisic acid, and expression of the members of the 12S storage protein gene family. In addition, both FUS3 and LEC1 regulate positively the abundance of the ABI3 protein in the seed. Alternative splicing of ABI3 is developmentally regulated by SUA (AT3G54230).**

TAIR Short Description **AP2/B3-like transcriptional factor family protein**

TAIR Aliases **ABI3, ATABI3, SIS10**

Quick Links: **Summary** Genomics Proteins Function Interactions Expression Homology Other

27 Gene Rifs

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<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Gene Rifs Annotation	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Gene Rifs last updated	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Gene Rifs Organism	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Gene Rifs Gene	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Gene Rifs PubMed Id
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Lists

This Gene is in one list:
 Genes with a Loss-of-Function Mutant Phenotype: Morphological - Vegetative (640)

Links to other Mines

- LegumeMine No results
- SoyMine No results
- MedicMine No results
- CowpeaMine No results
- PeanutMine No results
- BeanMine No results
- ChickpeaMine No results

External Links

- Aracyc
- AceView
- Plant Proteome Database
- SUBA
- Gramene
- GeneVisible
- ABRC
- TAIR
- EnsemblPlants
- PGDD
- AtcisDB
- Plaza
- pp2pro
- NCBI-Entrez
- Pir
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- ATTED-II

Quick Links: **Summary** Genomics Proteins **Function** Interactions Expression Homology Other

2 Proteins

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Showing 1 to 2 of 2 rows

<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Proteins DB Identifier	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Proteins Primary Accession	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Proteins Organism - Name	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> Proteins Length
ABI3_ARATH	Q01593	Arabidopsis thaliana	720
ABI3_ARATH-2	Q01593-2	Arabidopsis thaliana	429

Function

Gene Ontology

cellular component

- cytosol ECO
- nucleus ECO

molecular function

- DNA-binding transcription factor activity ECO
- sequence-specific DNA binding ECO
- DNA binding ECO

biological process

- plastid organization ECO
- abscisic acid-activated signaling pathway ECO
- positive regulation of DNA-templated transcription ECO
- response to auxin ECO
- mitochondria-nucleus signaling pathway ECO
- response to abscisic acid ECO
- embryo development ending in seed dormancy ECO

Interactions

Interaction Network

Show the following interaction types:

- Genetic
- All
- Physical

ThaleMine Gene Search

ThaleMine v5.1.0-20230710 Data mining on *Arabidopsis thaliana*

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Gene : AB13 *A. thaliana*

DB identifier **AT3G24650** Secondary Identifier **locus:206**
 Name **ABA INSENSITIVE 3** Brief Description **AP2/B3-III protein**

TAIR Computational Description **AP2/B3-like transcription factor family protein.[source:Araport1]**
 TAIR Curator Summary **Homologous to the maize transcription factor Viviparous-1. Full length many seed-specific promoters, and the B3 domains of this trans of AB13 requires the B3 DNA-binding domain and an activation domain activation domain was found in the B1 region of AB13. AB13 is essential for seed development. Putative seed-specific transcriptional act by polyubiquitinated by AIP2 in vivo. Based on double mutant accumulation of chlorophyll and anthocyanins, sensitivity to abscisic acid (ABA) and LEC1 regulate positively the abundance of the AB13 promoter. Putative seed-specific transcriptional act by polyubiquitinated by AIP2 in vivo. Based on double mutant accumulation of chlorophyll and anthocyanins, sensitivity to abscisic acid (ABA) and LEC1 regulate positively the abundance of the AB13 promoter.**

TAIR Short Description **AP2/B3-like transcription factor family protein**
 TAIR Aliases **AB13, ATAB13, SIS10**

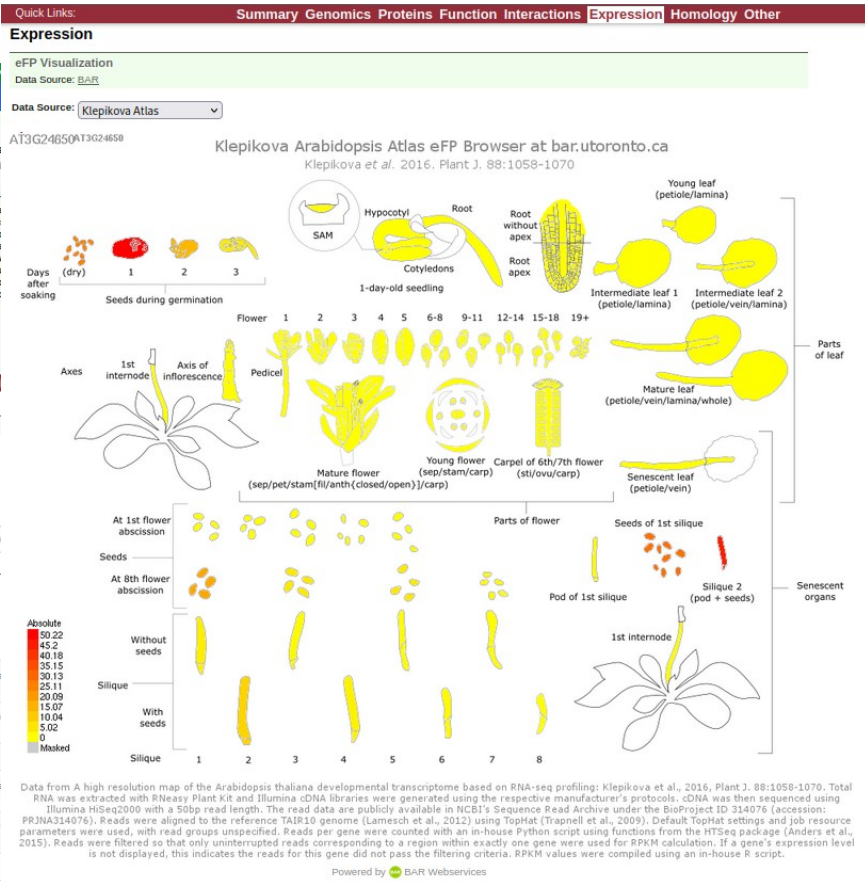
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Quick Links: **Summary** Genomics Proteins Function Interactions Expression Homology Other

27 Gene Rifs
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Gene Rifs Annotation
ABA-INSENSITIVE 3 with or without FUSCA3 highly up-regulates lipid droplet proteins and activates accumulation.
AB13 and PIL5 collaboratively activate the expression of SOM mRNA by directly binding to and interacting with each other at the SOM promoter.
AB13 controls embryo degreening through Mendel's locus.
AB13 expression ceases following the completion of germination in both tomato and <i>Arabidopsis thaliana</i> suggesting that expression of this gene does not regulate germination.
AB13 mediates dehydration stress signaling in <i>Arabidopsis thaliana</i> through regulation of a group of genes a role primarily during stress recovery phase.
ABSCISIC ACID-INSENSITIVE3 (AB13) regulates the developmental expression of HsfA9.



Genomics Proteins Function Interactions Expression Homology Other

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Gene Name	Protein Length
<i>Arabidopsis thaliana</i>	720
<i>Arabidopsis thaliana</i>	429

Gene Rifs Annotation

ABA-INSENSITIVE 3 with or without FUSCA3 highly up-regulates lipid droplet proteins and activates accumulation.

AB13 and PIL5 collaboratively activate the expression of SOM mRNA by directly binding to and interacting with each other at the SOM promoter.

AB13 controls embryo degreening through Mendel's locus.

AB13 expression ceases following the completion of germination in both tomato and *Arabidopsis thaliana* suggesting that expression of this gene does not regulate germination.

AB13 mediates dehydration stress signaling in *Arabidopsis thaliana* through regulation of a group of genes a role primarily during stress recovery phase.

ABSCISIC ACID-INSENSITIVE3 (AB13) regulates the developmental expression of HsfA9.

Show the following interaction types:
 Genetic All Physical

ThaleMine Data Sources

Data Category	Data	Source	PubMed
Genome	TAIR10 Genome assembly (5 chromosomes plus chloroplast and mitochondrial assemblies)	NCBI [ⓧ] - Release TAIR10 (2018/04/06)	Arabidopsis Genome Initiative - PubMed: 11130711 [ⓧ]
	Araport11 GFF3 data from TAIR	TAIR [ⓧ] - Release Araport11 (2016/06/17)	Cheng et al., 2016 - PubMed: 27862469 [ⓧ]
Proteins	High-quality, manually annotated, non-redundant protein sequence database.	Swiss-Prot [ⓧ] - Release 2023_03	UniProt Consortium - PubMed: 17142230 [ⓧ]
	Computationally analysed records, enriched with automatic annotation	TrEMBL [ⓧ] - Release 2023_03	
	Protein family and domain assignments to proteins	InterPro [ⓧ] - Release v95.0	Mitchell et al., 2019 - PubMed: 30398656 [ⓧ]
Homology	Orthologue relationships based on the inferred speciation and gene duplication events in the phylogenetic tree.	Panther [ⓧ] - Release 17.0	Mi et al - PubMed: 23193289 [ⓧ]
	Paralogue relationships based on the inferred speciation and gene duplication events in the phylogenetic tree.	Panther [ⓧ] - Release 17.0	Mi et al - PubMed: 23193289 [ⓧ]
	Phylozome Homologs generated with InParanoid	Phylozome [ⓧ] - realtime	Goodstein et al - PubMed: 22110026 [ⓧ]
Curation	Manually curated TAIR functional descriptions	TAIR [ⓧ] - Release 20220630	Huala et al - PubMed: 11125061 [ⓧ]
	Manually curated TAIR gene aliases	TAIR [ⓧ] - Release 20220630	Huala et al - PubMed: 11125061 [ⓧ]
Gene Ontology	GO annotations from Gene Ontology	Gene Ontology [ⓧ] - Release 2023-06-11	Berardini et al., 2004 - PubMed: 15173566 [ⓧ] Gene Ontology Consortium - PubMed:10802651 [ⓧ]
	Severel electronic and manual GO annotation methods utilized by UniProt	UniProt [ⓧ] - Release 2023_03	UniProt Consortium - PubMed: 17142230 [ⓧ]
Interactions	Curated set of genetic and physical interactions for <i>Arabidopsis thaliana</i>	BioGRID [ⓧ] - Release 4.4.233	Chatr-Aryamontri et al., 2014 - PubMed: 25428363
	Curated binary and complex protein-protein interactions for <i>Arabidopsis thaliana</i>	IntAct [ⓧ] - Downloaded 20230706	Kerrien et al., 2012 - PubMed: 22121220
Expression	Electronic Fluorescent Pictograph (eFP) Visualization paints gene expression information from one of the AtGenExpress data sets or other compendia for a desired gene onto a diagrammatic representation of <i>Arabidopsis thaliana</i> plants.	BAR eFP Webservice [ⓧ] - realtime	Winter et al., 2007 - PubMed: 17684564 [ⓧ] Brady et al., 2009 - PubMed: 19401381 [ⓧ]
Co-Expression	Co-regulated gene relationships deduced from microarray and RNA-seq data via ATTED-II web services	ATTED-II Co-expression [ⓧ] - realtime	Obayashi et al., 2014 - PubMed: 24334350 [ⓧ]
Publications	Curated associations between publications and genes from UniProt	UniProt [ⓧ] - Release 2023_03	UniProt Consortium - PubMed: 17142230 [ⓧ]
	Publications from InterPro	InterPro [ⓧ] - Release v95.0	Mitchell et al., 2019 - PubMed: 30398656 [ⓧ]
	Publications from NCBI	NCBI [ⓧ] - Downloaded 20230706	Maglott et al., 2007 - PubMed: 17148475 [ⓧ]
GeneRIF	Concise phrase describing gene function and publication associated with NCBI Gene records	NCBI [ⓧ] - Downloaded 20230706	Maglott et al., 2007 - PubMed: 17148475 [ⓧ]

Acknowledgments

Kiana Toufighi
Ryan Austin
Siobhan Brady
Nina Wang
Hardeep Nahal
Joe Wu
Matthew Ierullo
Ron Ammar
Vincent Lau
Matt Cumming
Michael Dong
Matthew Ierullo
Anna van Weringh
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