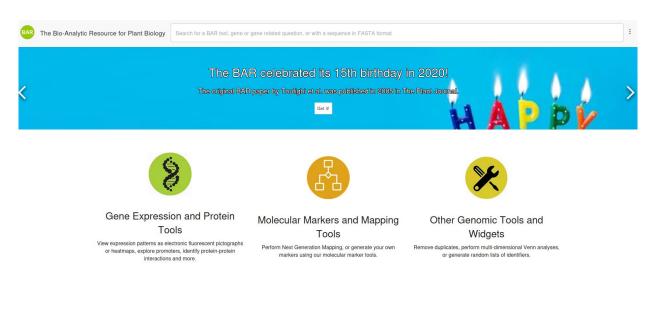


### **BIO-ANALYTIC RESOURCE FOR PLANT BIOLOGY**

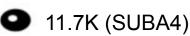
Asher Pasha Nicholas Provart

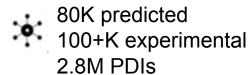
Bio-Analytic Resource, CAGEF University of Toronto, Canada Plant Biology 2024

June 22, 2024



175M (100M A. th.)







29K Phyre2 26k AlphaFold2 885 from PDB

10+M nsSNPs (1135 ..... ecotypes)

## **Global Core Biodata Resource**



The BAR was designated as a Global Core Biodata Resource in 2023 by the Global Biodata Coalition.

# **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. The data can be reused in any external apps.

### New BAR Homepage (with GAIA search input)

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.

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.

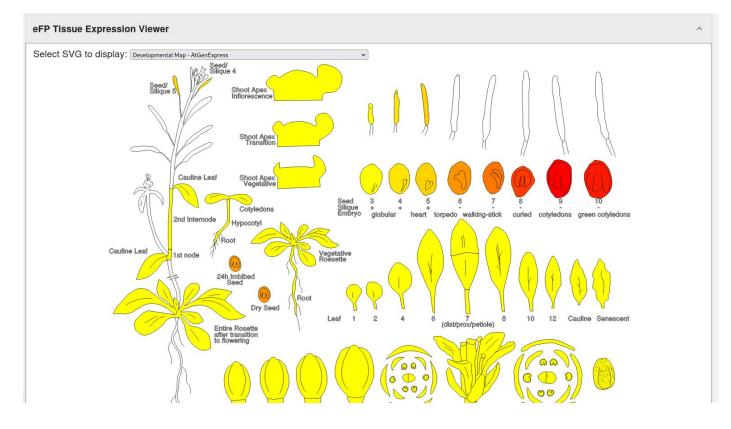
AP2/B3-like transcriptional factor family protein. The highest subcellular localization of ABI3 is the nucleus. ABI3 has 1 splice variant. ABI3 has been shown experimentally to interact with 94 proteins, including At2g25890 and At4g17730.

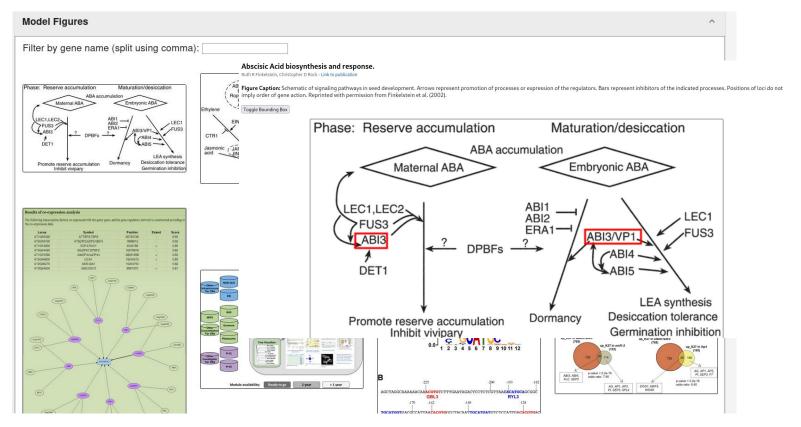
In peer reviewed gene model maps, ABI3 has found to also co-occur with ABI5, FUS3, LEC1 and more. ABI3 has been found in the following modules: Signaling Pathways in Seed Development, Interactions between Sugar and Hormone Signaling in Arabidopsis, Module for ABA signaling pathway in osmotic stress responses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

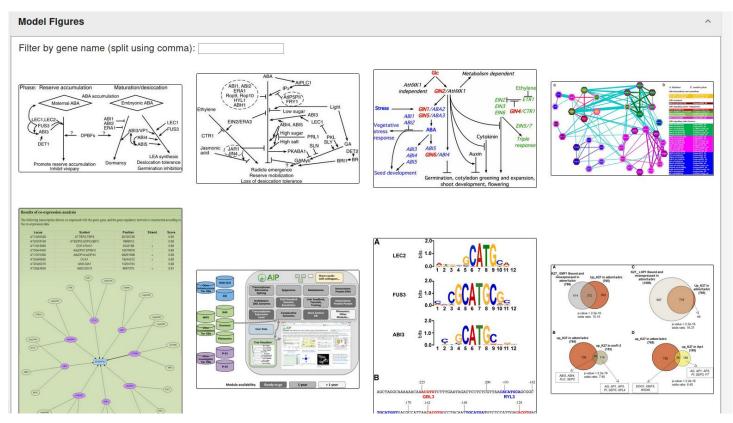
A curated summary of ABI3 is: Homologous to the maize transcription factor Viviparous-1. Full length ABI3 protein binds to the highly conserved RY motif [DNA motif CATGCA(TG)], present in many seed-specific promoters, and the B3 domains of this transcription factor is necessary for the specific interaction 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 by polyubiquitinated by AIP2 in vivo. Based on double mutant analyses, ABI3 interacts genetically with both FUS3 and LEC1 and is involved in controlling accumulation, 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).

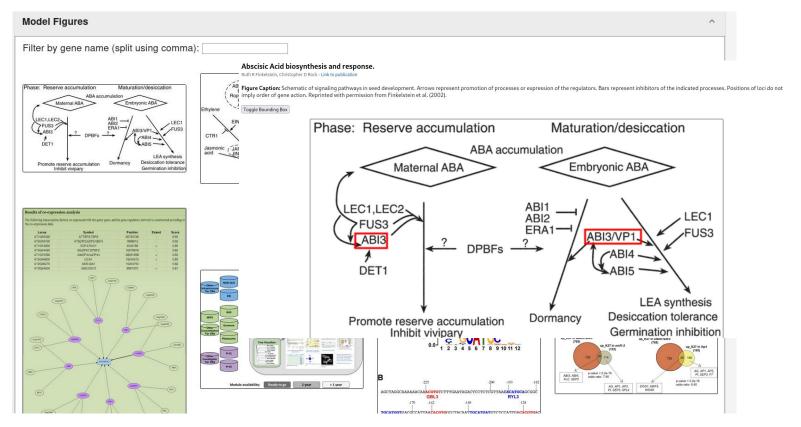
Recent publications suggest the following: 1) For example, WUSCHEL-related homeobox, LEC2/FUS3/ABI3, and HEME ACTIVATOR PROTEIN3 families can control plant seed embryonic initiation and development. 2) Furthermore, VvKEG interacted with the ABA-responsive transcription factor ABSCISIC ACID-INSENSITIVE3 (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*.

#### Phase: Reserve accumulation Maturation/desiccation ABA accumulation Maternal ABA Embryonic AB LEC1.LEC2 LEC1 ABI2 >FUS3 FRA1 FUS3 ABI3/VP1 ABI3 DPBEs -ARIA DET1 LEA synthesis Desiccation tolerance Dormancy Promote reserve accumulation Inhibit vivipary Germination inhibition AtHOX1 . on, cotyledon greening and exp shoot development, flowering





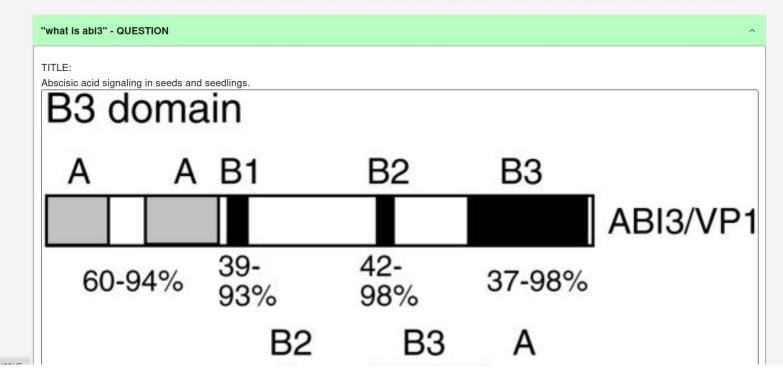




### **GAIA:** Question Search

what is abi3

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



## Homepage: BLAST Search



MKSLHVAANAGDLAEDCGILGGDADDTVLMDGIDEVGREIWLDDHGGDNNHVHGHQDDDLIVHHDPSIFYGDLPTLPDFPCMSSSSSSTSPAPVNAIVSSASSSSAASSSTSAASWAILRSDGEDPTPNQNQYASGNCDDSSGALQSTAS IPLDSSQGFGCGEGGGDCIDMMETFGYMDLLDSNEFFDTSAIFSQDDDTQNPNLMDQTLERQEDQVVVPMMENNSGGDMQMMNSSLEQDDDLAAVFLEWLKNNKETVSAEDLRKVKIKKATIESAARRLGGGKEAMKQLLKLILEWVQTNHL RRTTTTTTNLSYQQSFQQDPFQNPNPNNNNLIPPSDQTCFSPSTWVPPPPQQQAFVSDPGFGYMPAPNYPPQPEFLPLLESPPSWPPPQSGPMPHQQFPMPPTSQYNQFGDPTGFNGYNMNPYQYPYVPAGQMRDQRLLRLCSSATKEARKKR MARQRRFLSHHHRHNNNNNNNQQQTQIGETCAAVAPQLNPVATTATGGTWMYWPNVPAVPPQLPPVMETQLPTMDRAGSASAMPRQQVVPDRRQGWKPEKNLRFLLQKVLKQSDVGNLGRIVLPKKEAETHLPELEARDGISLAMEDIGT SRVWNMRYRFWPNNKSRMYLLENTGDFVKTNGLQEGDFIVIYSDVKCGKYLIRGVKVRQPSGQKPEAPPSSAATKRQNKSQRNINNNSPSANVVVASPTSQTVK

Nucleotide databases	[Select all]	Protein databases [Select all]	
☐ Arabidopsis thaliana ☐ Nucl ☐ Spruce		Arabidopsis thaliana	
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.

## Homepage: BLAST Search



♀ Help & Support

BLASTP: 1 query, 2 databases Second Edit 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

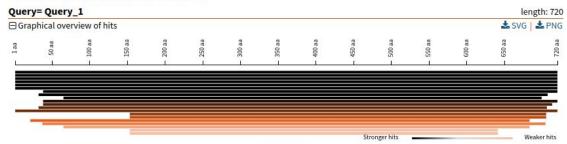
Full XML report

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

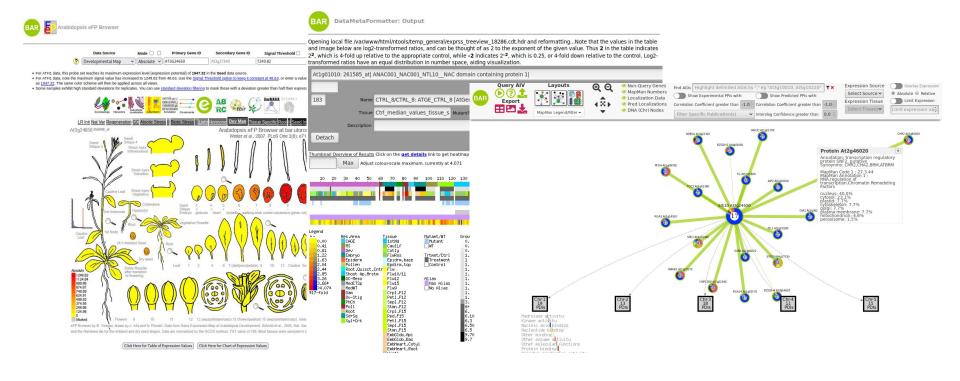


View More ¥

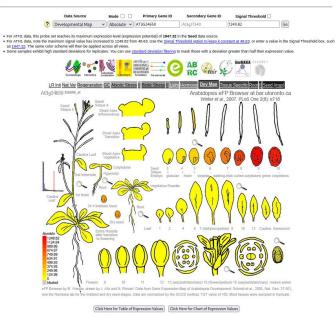
➡ Length distribution of matching sequences
 ➡ Sequences producing significant alignments

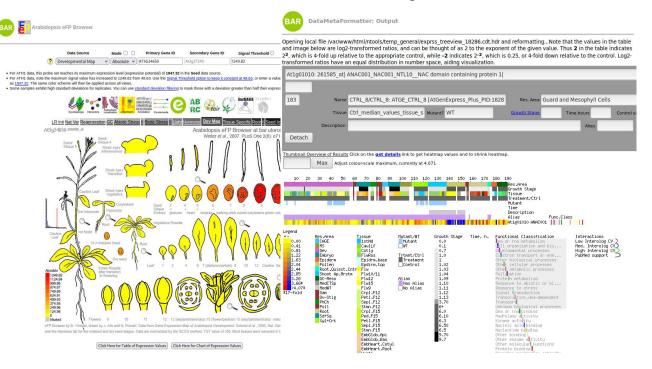
# 1. 2. 3. 4. 5.

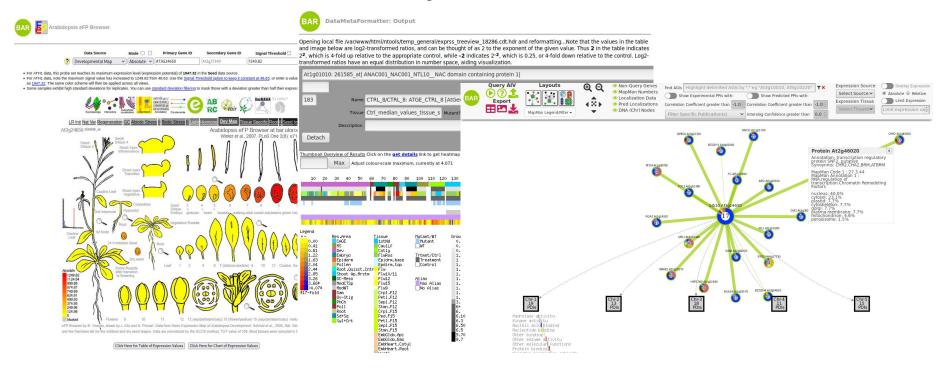
		Query coverage				
ŧ	Similar sequences	(%)	Total score	E value	Identity (%)	BAR Tools
ι.	AT3G24650.1   Symbols: ABI3, AtABI3, SIS10   SUGAR INSENSITIVE	100	3881	0	100%	ePlant eFP
2.	Csa15g050420.1	100	2897	0	90.2%	ePlant
3.	Csa01g030760.1	100	2832	0	89.4%	ePlant
1.	Csa01g030760.2	100	2832	0	89.4%	ePlant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



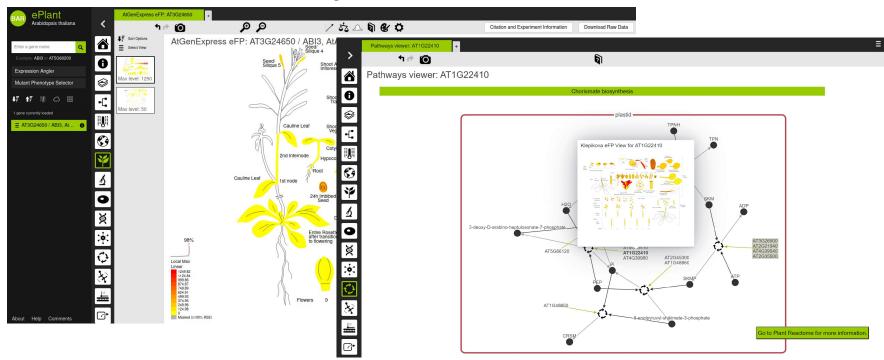




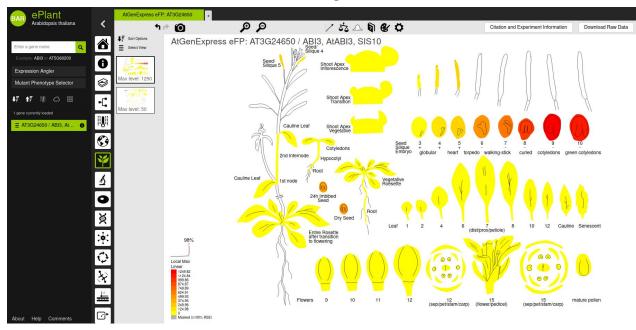




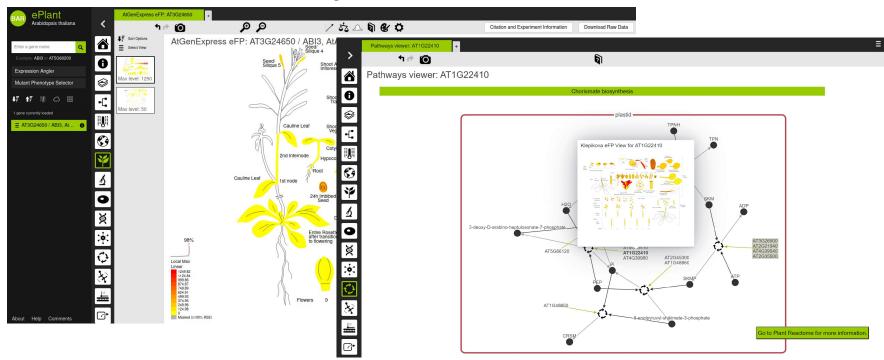
### ePlant: Improved User Interface



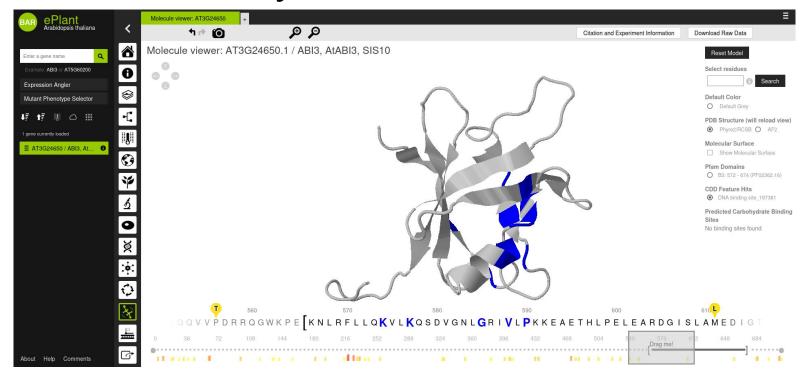
### ePlant: Improved User Interface



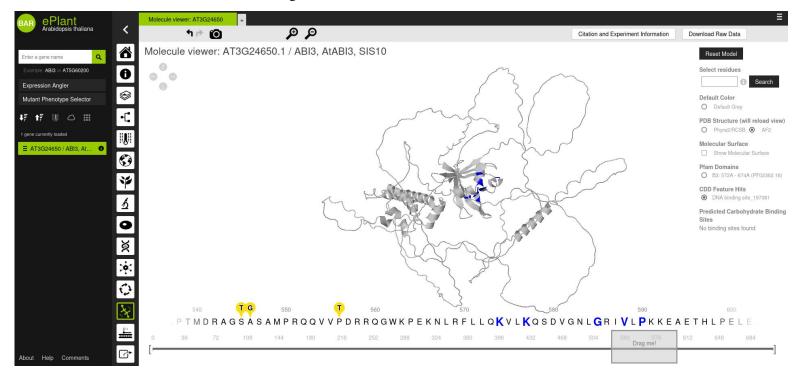
### ePlant: Improved User Interface



### ePlant: Phyre2 and AF2 Structures



### ePlant: Phyre2 and AF2 Structures



### ePlants



### AGENT





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



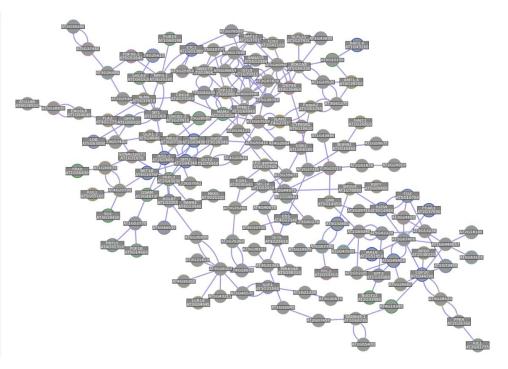
Enter AGI (AT5G23020), AGI-pair (AT3G24520-AT3G12580), tissue/experiments (auto-suggestions), or 'all' to see all networks



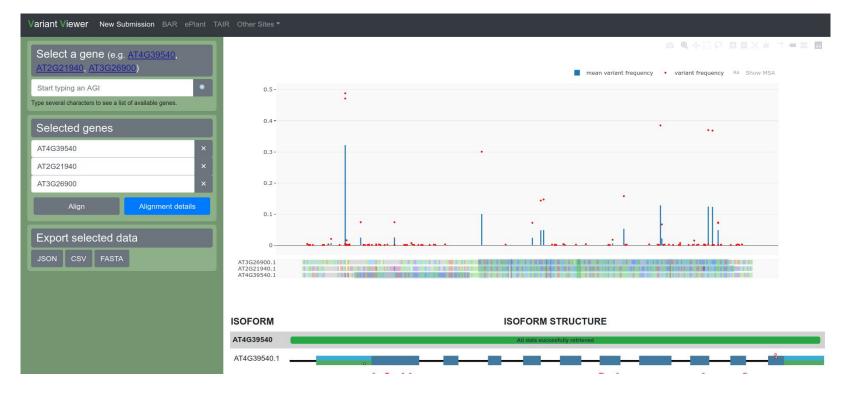
https://bar.utoronto.ca/AGENT (Lau et al., 2021) https://doi.org/10.1101/2021.04.28.441830

### AGENT





## New Tool: Variant Viewer for SNPs



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

### eFP-Seq Browser

	Î Title ∳	RNA-Seq Coverage	n r <sub>pb</sub> •	eFP (RPKM)	RPKM (	Details \$
≡ BAR eFP-Seq Browser	Filter		Filter	0 N	Filter	Filter
1) Enter a gene name or AGI ID AT2G24270	Aerial part of long-day-grown 4-leaf-stage seedling with mock (NaCI) treatment		0.57	*	370.51	E-MTAB-1668:24hCS-RNA Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details 👻
2) Select a dataset Araport 11 RNA-seq data	Transcription profiling of Arabidopsis plants overexpressing SIHsfA3 (thale cress)		0.58	*	379.32	GSM798296: mRNASeq_WT_rep2 Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details ←
3) Select options Absolute Relative Y-axis Scale Absolute Max	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 ▼
Auto 1196	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 👻
LOAD DATA	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 👻
eFP Overview Download table as CSV	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
Download table as image Compare gene variants	Aerial part of 3-week-old soil-grown plant	A A A A A A A A A A A A A A A A A	0.52	*	739.79	Seeding2, SRA: SRS419145 Show: Alignments in IGB Go to: NCBI SRA or PubMed Show More Details
Generate Data Upload Data	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 +
Help Sign In	Carpels collected manually from stage 8-13 flowers		0.61		367.53	carpel, GSM1359146, SRA: SRS58 Show: Alignments in IGB

https://bar.utoronto.ca/eFP-Seq\_Browser/ (Sullivan et al., 2019)

### ThaleMine

ne Templates Lists QueryBuilder	Regions	Data Sources	API 🔔 MyMine		Contact Us
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mes, identifiers or keywords for genes,		Gene	er a list of identifiers.	~	ThaleMine enables you to analyze
oteins, ontology terms, authors, etc. (e.g. , APL_ARATH, lateral root development,					Arabidopsis thaliana genes, proteins, gene
omerville).			50, AT1G05240, T1G05260, AT1G1454	0.	expression, protein-protein interactions, orthologs, and more.
.g. AT3G24650, FT, APL ARATH			T1G15950, AT1G2411		Use plain text or structured queries for
.g. A13024030, FT, APL_ARATH					interactive gene and protein reports.
			advanced		
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GENES AND PROTEINS		HOI	MOLOGY	FUNCTION	INTERACTIONS
The gene models and other genome annota	ations in The	aleMine are provid	ded by a variety of sour	ces including: NC	BI, TAIR Read more
Query for genes and proteins:					
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Gene      Transposable Elements					populatemphes
					10

(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.

	Quick Links: Summary Genomics Proteins Function Interactions Expression Homology Other	
ThaleMine v5.1.0-20230710 Data mining on Arabidopsis thaliana	Expression	Genomics Proteins Function Interactions Expression Homology Other
~	eFP Visualization	
Home Templates Lists QueryBuilder Regions Data Sources AP	Data Source: BAR	
	Data Source: Klepikova Atlas	▲ Save as List • 🗟 Generate Python code 🕞 🗈 Export
Gene : ABI3 A. thaliana		
DB identifier <sup>0</sup> AT3G24650 Secondary Identifier <sup>0</sup> locus:209	Kiepikova Arabidopsis Acias err browser at bar.utoronto.ca	
Name <sup>0</sup> ABA INSENSITIVE 3 Brief Description AP2/B3-Iii protein	Klepikova <i>et al.</i> 2016. Plant J. 88:1058-1070 Young leaf	x
TAIR Computational Description AP2/B3-like transcriptional factor family protein;(source:Araport1 TAIR Curator Summary Homologous to the maize transcription factor Viviparous-1. Full k	(petiole/lamina)	Proteins Proteins Organism . Name Length
many seed-specific promoters, and the B3 domains of this transc of ABI3 requires the B3 DNA-binding domain and an activation do	Nypocity Root Without	Arabidopsis thaliana 720
activation domain was found in the B1 region of ABI3. ABI3 is ess seedling development. Putative seed-specific transcriptional activ		Arabidopsis tranana 720 Arabidopsis tranana 429
by polyubiquitinated by AIP2 in vivo. Based on double mutant and	Days (dry) 1 2 3 Cotyledons apex Days	Prioriuopas crimana 442
accumulation of chlorophyll and anthocyanins, sensitivity to abso FUS3 and LEC1 regulate positively the abundance of the ABI3 pro	after 1-day-old seedling Intermediate leaf 1 Intermediate leaf 2 (petiole/vein/jamina) (petiole/vein/jamina)	
TAIR Short Description AP2/B3-like transcriptional factor family protein TAIR Aliases ABI3, AtABI3, SIS10	Flower 1 2 3 4 5 6-8 9-11 12-14 15-18 19+	
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Manage Columns  T Manage Filters	Young flower Carpel of 6th/7th flower	
< Manage Relationships	Mature flower (sep/stam/carp) (sti/ovu/carp) Senescent leaf (sep/pet/stam(fil/anth(closed/open))/carp) (petiole/vein)	
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	At 8th flower Silique 2 Senescent	
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¢x····⊤ lai Gene Rifs	Absolute 50.22 Without 1st internode	WAVES PILS
Annotation		WAVE2 PIL5
ABA-INSENSITIVE 3 with or without FUSCA3 highly up-regulates lipid droplet proteins and activates	4018 seeds 3515 3013 2511 Silique	SYP23
accumulation.	20.09	GA1 BZIP25
ABI3 and PIL5 collaboratively activate the expression of SOM mRNA by directly binding to and inte with each other at the SOM promoter.	1004 With 1004 seeds	ABIS ABIS TOCI
	0 Masked	SPK1
ABI3 controls embryo degreening through Mendel's Llocus.	Silique 1 2 3 4 5 6 7 8	BZO2HA C GAI
ABI3 expression ceases following the completion of germination in both tomato and Arabidopsis s suggesting that expression of this gene does not regulate germination.	Data from A high resolution map of the Arabidopsis thaliana developmental transcriptome based on RNA-seq profiling: Klepikova et al., 2016, Plant J. 88:1058-1070. Tota RNA was extracted with RNeasy Plant Kit and Illumina cDNA libraries were generated using the respective manufacturer's protocols. cDNA was then sequenced using	NRPB5
ABI3 mediates dehydration stress signaling in Arabidopsis through regulation of a group of genes	Illumina HiSeq2000 with a 50bp read length. The read data are publicly available in NCGT's Sequence Read Archive under the BioProject ID 314076 (accession: PRIMA314076). Reads were aligned to the reference TAIR10 genome (Lamesch et al., 2012) using TopHat (Transmell et al., 2009). Default TopHat settings and job resource	
Abis mediates denyoration stress signaling in Arabidopsis through regulation of a group of genes a role primarily during stress recovery phase.	parameters were used, with read groups unspecified. Reads per gene were counted with an in-house Python script using functions from the HTSeq package (Anders et al 2015). Reads were filtered so that only uninterrupted reads corresponding to a region within exactly one gene were used for RPKM calculation. If a gene's expression lev	el
ABSCISIC ACID-INSENSITIVE3 (ABI3) regulates the developmental expression of HsfA9.	is not displayed, this indicates the reads for this gene did not pass the filtering criteria. RPKM values were compiled using an in-house R script.	Show the following interaction types: Genetic All Physical

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tware IBAR

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						Sea	rch: e.g. AT1G01	1640 GO
ene : ABI3	A thaliana							
	AT3G24650	Secondary Identifier	locus:2093166					
amo D		Brief Description	AP2/B3-like transcr	iptional factor fa	amily			
	ABA INSENSITIVE 3		protein					
IR Computational Desc IR Curator Summary		criptional factor family protein;(se le maize transcription factor Vivip			ana			
IR Short Description IR Aliases	activation domain seedling developm by polyubiquitinat accumulation of c FUS3 and LEC1 re	he B3 DNA-binding domain and a was found in the B1 region of At ment. Putative seed-specific trans ted by AIP2 in vivo. Based on do hhorophyll and anthocyanins, ser gulate positively the abundance criptional factor family protein 10	BI3. ABI3 is essential for scriptional activator. ABI3 uble mutant analyses, AB nsitivity to abscisic acid,	seed maturation is a central reg 13 interacts gen and expression	n. Regulator of t julator in ABA s etically with bot of the members	he transition ignaling an th FUS3 and s of the 125	n between emb d is unstable in d LEC1 and is ir storage protein	ryo maturation and early vivo. It interacts with and ca volved in controlling n gene family. In addition, bot
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ABA INSENSITIVE 3	Brief Description	AP2/B3-like transcri	ptional factor fa	mily			
	I ranscriptional factor family protein;(source:	protein					
many seed-s of ABI3 requi activation do seedling dev by polyubiqu accumulatior	to the maize transcription factor Viviparous pecific promoters, and the B3 domains of th rest the B3 DA-binding domain and an acti- main was found in the B1 region of ABI3. At lognment, Putative seed-specific transcription itinated by AIP2 in vivo. Based on double m of chlorophyll and anthocyanins, sensitivit C1 regulate positively the abundance of the	his transcription fact ivation domain. In au BI3 is essential for s ional activator. ABI3 nutant analyses, ABI ity to abscisic acid, a	dition to the kn seed maturation is a central reg is interacts gen and expression	for the specific nown N-terminal Regulator of t ulator in ABA s etically with bot of the members	c interactio I-located an he transitio ignaling an th FUS3 an s of the 125	n with the RY electivation domain on between emb of is unstable in d LEC1 and is in storage protein	ement. Transcriptional activit n, a second transcription ryo maturation and early vivo. It interacts with and ca volved in controlling n gene family. In addition, bo
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AIR Aliases ABI3, AtABI3							
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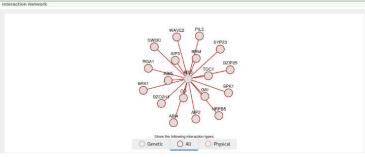
#### Function

ABI3\_ARATH-2

Gene Ontology	
cellular component	
cytosol a	ECO
nucleus 0	ECO
molecular function	
DNA-binding transcription factor activity	ECO
sequence-specific DNA binding	ECO
DNA binding B	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 <sup>a</sup>	ECO
embryo development ending in seed dormancy	ECO

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#### Interactions



	Quick Links: Summary Genomics Proteins Function Interactions Expression Homology Other	
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Gene : ABI3 A. thaliana		
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Name <sup>0</sup> ABA INSENSITIVE 3 Brief Description AP2/B3-Iii protein	Klepikova <i>et al.</i> 2016. Plant J. 88:1058-1070 Young leaf	x
TAIR Computational Description AP2/B3-like transcriptional factor family protein;(source:Araport1 TAIR Curator Summary Homologous to the maize transcription factor Viviparous-1. Full k	(petiole/lamina)	Proteins Proteins Organism . Name Length
many seed-specific promoters, and the B3 domains of this transc of ABI3 requires the B3 DNA-binding domain and an activation do	Nypocity Root Without	Arabidopsis thaliana 720
activation domain was found in the B1 region of ABI3. ABI3 is ess seedling development. Putative seed-specific transcriptional activ		Arabidopsis tranana 720 Arabidopsis thaliana 429
by polyubiquitinated by AIP2 in vivo. Based on double mutant and	Days (dry) 1 2 3 Cotyledons apex Days	Prioriuopas crimana 442
accumulation of chlorophyll and anthocyanins, sensitivity to abso FUS3 and LEC1 regulate positively the abundance of the ABI3 pro	after 1-day-old seedling Intermediate leaf 1 Intermediate leaf 2 (petiole/vein/jamina) (petiole/vein/jamina)	
TAIR Short Description AP2/B3-like transcriptional factor family protein TAIR Aliases ABI3, AtABI3, SIS10	Flower 1 2 3 4 5 6-8 9-11 12-14 15-18 19+	
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Showing rows 1 to 10 of 27 Rows per page: 10	At 1st flower Parts of flower Seeds of 1st silique abscission	
	Seeds	
	At 8th flower Silique 2 Senescent	
	abscission Singue 2 Seriescent Pod of 1st silique (pod + seeds) organs	
¢x····⊤ lai Gene Rifs	Absolute 50.22 Without 1st internode	WAVES PILS
Annotation		WAVE2 PIL5
ABA-INSENSITIVE 3 with or without FUSCA3 highly up-regulates lipid droplet proteins and activates	4018 seeds 3515 3013 2511 Silique	SYP23
accumulation.	20.09	GA1 BZIP25
ABI3 and PIL5 collaboratively activate the expression of SOM mRNA by directly binding to and inte with each other at the SOM promoter.	1004 With 1004 seeds	ABIS ABIS TOCI
	0 Masked	SPK1
ABI3 controls embryo degreening through Mendel's Llocus.	Silique 1 2 3 4 5 6 7 8	BZO2HA C GAI
ABI3 expression ceases following the completion of germination in both tomato and Arabidopsis s suggesting that expression of this gene does not regulate germination.	Data from A high resolution map of the Arabidopsis thaliana developmental transcriptome based on RNA-seq profiling: Klepikova et al., 2016, Plant J. 88:1058-1070. Tota RNA was extracted with RNeasy Plant Kit and Illumina cDNA libraries were generated using the respective manufacturer's protocols. cDNA was then sequenced using	NRPB5
ABI3 mediates dehydration stress signaling in Arabidopsis through regulation of a group of genes	Illumina HiSeq2000 with a 50bp read length. The read data are publicly available in NCGT's Sequence Read Archive under the BioProject ID 314076 (accession: PRIMA314076). Reads were aligned to the reference TAIR10 genome (Lamesch et al., 2012) using TopHat (Transmell et al., 2009). Default TopHat settings and job resource	
Abis mediates denyoration stress signaling in Arabidopsis through regulation of a group of genes a role primarily during stress recovery phase.	parameters were used, with read groups unspecified. Reads per gene were counted with an in-house Python script using functions from the HTSeq package (Anders et al 2015). Reads were filtered so that only uninterrupted reads corresponding to a region within exactly one gene were used for RPKM calculation. If a gene's expression lev	el
ABSCISIC ACID-INSENSITIVE3 (ABI3) regulates the developmental expression of HsfA9.	is not displayed, this indicates the reads for this gene did not pass the filtering criteria. RPKM values were compiled using an in-house R script.	Show the following interaction types: Genetic All Physical

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### ThaleMine Data Sources

Data Category			PubMed
0	TAIR10 Genome assembly (5 chromosomes plus chloroplast and mitochondrial assemblies)	NCBI A - Release TAIR10 (2018/04/06)	Arabidopsis Genome Initiative - PubMed: 11130711
Genome	Araport11 GFF3 data from TAIR	TAIR - Release Araport11 (2016/06/17)	Cheng et al., 2016 - PubMed: 27862469 🕷
	High-quality, manually annotated, non-redundant protein sequence database.	Swiss-Prot 🖲 - Release 2023_03	UniProt Consortium - PubMed: 17142230
Proteins	Computationally analysed records, enriched with automatic annotation	TrEMBL - Release 2023_03	UniProt Consortium - PubMed: 17142230 -
	Protein family and domain assignments to proteins	InterPro 🖹 - Release v95.0	Mitchell et al., 2019 - PubMed: 30398656
	Orthologue relationships based on the interred speciation and gene duplication events in the phylogenetic tree.	Panther A - Release 17.0	Mi et al - PubMed: 23193289 🕷
Homology	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	Phytozome 🏾 - realtime	Goodstein et al - PubMed: 22110026
	Manually curated TAIR functional descriptions	TAIR - Release 20220630	Huala et al - PubMed: 11125061
Curation	Manually curated TAIR gene aliases	TAIR A - Release 20220630	Huala et al - PubMed: 11125061
Gene	GO annotations from Gene Ontology	Gene Ontology - Release 2023-06-11	Berardini et al., 2004 - PubMed: 15173566 Gene Ontology Consortium - PubMed:10802651
Ontology	Several electronic and manual GO annotation methods utilized by UniProt	UniProt a - Release 2023_03	UniProt Consortium - PubMed: 17142230
	Curated set of genetic and physical interactions for Arabidopsis thaliana	BioGRID - Release 4.4.233	Chatr-Aryamontri et al., 2014 - PubMed: 25428363
Interactions	Curated binary and complex protein-protein interactions for Arabidopsis thaliana	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 Arabidopsis thaliana plants.	BAR eFP Webservice * - realtime	Winter et al., 2007 - PubMed: 17684564 Ready 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 (8
	Curated associations between publications and genes from UniProt	UniProt 🖲 - Release 2023_03	UniProt Consortium - PubMed: 17142230
Publications	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

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Ben Vinegar Debbie Winter Richard Song Anjali Silva Rohan Patel Sakshi Shinghal Rachel Woo Ida Liu Wen Kai Cao Bruno Pereira YueXin Yu Hans Yu Jim Fan Fausto de Oliveira Eddi Esteban Guilherme Hosaka Sylva Donaldson Isaiah Hazelwood





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