

The guide of integrated plant phenome databases

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Contents

1. Introduction.....	1
2. Outline of database contents.....	1
2.1 Phenome Integration of <i>Arabidopsis</i> mutants.....	2
2.2 The Database of Curated Plant Phenome.....	3
3. Quick Start: How to search for bio items in plant phenome databases	5
3.1 Search genes involved in the focused phenotypes	5
3.2 Search bioresources (mutants) from the focused phenotype	6
4. Advanced search for improved bioinformatic studies	8
4.1 Gene-phenotype search started from TAIR locus DB: Reasoning of unknown roles or functions of focused gene.....	8

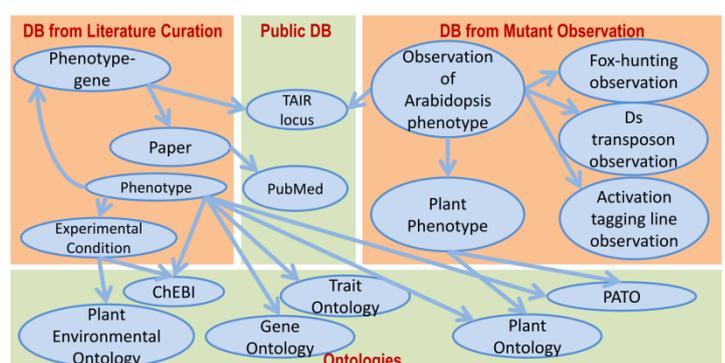
1. Introduction

A phenome represents the combination of various kinds of characteristics of organisms, expressed in response to genomic and environmental factors and observed by certain experimental methods. It is an important resource for future progress in functional genomics. To study relationships between phenotypes and other omic information collected from multiple databases, it is desirable to standardize phenotype terminology with common ontologies, and to standardize expression of relationships between phenomic data and other omics information.

We integrated phenome data of the *Arabidopsis* into our original database platform named RIKENBASE (<http://database.riken.jp>). It is based on Semantic Web technology, and supports some unique functions, including the PosMed high-speed semantic searching system, which facilitates bioinformatics analyses of integrated omics datasets.

2. Outline of database contents

RIKENBASE includes two major databases of *Arabidopsis* phenome. Items on these databases have links to various kind of omics and literature data in public databases, and users can easily collect related information of the focused topic (see figure).



Here the abstracts of these databases related to *Arabidopsis* phenome are shown. Some simple examples of searching bio-items using these contents are presented in the next section.

2.1 Phenome Integration of *Arabidopsis* mutants

Arabidopsis Phenome Database

Contents List		About this database
RIKEN Phenome Integration of Arabidopsis Mutants	Curated Plant Phenome	
Observation of Arabidopsis phenotype Plant phenotype	Phenotype abnormality Experimental condition Phenotype-gene Outcome paper	Manual Data list Contact us

RIKEN Phenome Integration of Arabidopsis Mutants

observation of *Arabidopsis* phenotype

"Observation" data presented here derived from observation by contributors of each mutant.

Observation data are distinguished by phenotype, method of mutation, mutant ID etc., and standardized with appropriate ontology terms.

The listed observation data are correspond to original observation data one-to-one, which are presented in databases including [Ds tagging line](#), [activation tagging line](#), and [Fox-hunting line](#).

Original phenome observation data
Hyperlinks to phenome information of [Ds/Ac/Fox line](#)

observed phenotype
Phenotypes in standardized format using ontology terms

modified gene
[AGI codes](#) of genes overexpressed or knocked-out genes for each mutant

Search by PO and PATO terms
Check the categories and Click "Search" button.

<input type="checkbox"/> Seed Germination Stage	<input type="checkbox"/> Axillary Shoot System	<input type="checkbox"/> Seedling
<input type="checkbox"/> Whole Plant Development Stage	<input type="checkbox"/> Flower	<input type="checkbox"/> Stem
<input type="checkbox"/> Whole Plant Flowering Stage	<input type="checkbox"/> Flower Bud	<input type="checkbox"/> Trichome
<input type="checkbox"/> Whole Plant Growth Stage	<input type="checkbox"/> Fruit	<input type="checkbox"/> Vascular Leaf
	<input type="checkbox"/> Root	
	<input type="checkbox"/> Seed	

- URL: http://database.riken.jp/db/arabidopsis_mutant_phenome
- Contents:
 - Updated phenome data of *Arabidopsis* mutants developed in RIKEN
 - ✧ Phenotypes of each mutant are shown in the standardized form with terms of Plant Ontology and PATO, such as “rosette leaf:round”.
 - ✧ Genetic variation of each mutant

Remarks: RIKEN has contributed greatly to progress in the study of plant omics. Remarkable work includes the development of bioresources covering genomic and phenomic data for large-scale collections of *Arabidopsis thaliana* mutant lines, namely Ds transposon lines, activation tagging lines, and FOX-hunting lines. The original databases of these mutant lines were developed and opened separately by developers of each mutant line. RIKEN Phenome Integration of Arabidopsis Mutants at http://database.riken.jp/db/arabidopsis_mutant_phenome covers updated phenome data of these mutants. To cancel inconsistency of existing descriptions of phenotypes, data instances are expressed in principle with a simple format called Entity-Quality (EQ) formalism. Data standardization and construction of RDF data were achieved by the RIKENBASE development team.

2.2 The Database of Curated Plant Phenome

RIKENBASE

Arabidopsis Phenome Database

Contents List		
RIKEN Phenome Integration of Arabidopsis Mutants Observation of Arabidopsis phenotype Plant phenotype	Curated Plant Phenome Phenotype abnormality Experimental condition Phenotype-gene Outcome paper	About this database Manual Data list Contact us

[Reference](#)
[Add Reference](#)

Database of Curated Plant Phenome

Literature Curation

Phenotype-gene: combination of phenotype observation and gene modification found by literature curation

Here the combinations of [phenotypic variation](#) and the possibly corresponding [genes](#) are defined as instances. Each of them has links to phenotype, gene and [reference papers](#).

Useful Links

- [TAIR 10 locus](#)
- [PubMed](#)

Search by GO and PO terms
Check the categories and Click "Search" button.

<input type="checkbox"/> Flower	<input type="checkbox"/> Seedling	<input type="checkbox"/> Shoot System
<input type="checkbox"/> Seed	<input type="checkbox"/> Apical Meristem	<input type="checkbox"/> Portion of Meristem Tissue
<input type="checkbox"/> Fruit	<input type="checkbox"/> Stem	<input type="checkbox"/> Vascular Leaf
<input type="checkbox"/> Root Initial Cell	<input type="checkbox"/> Cellular Compartment	<input type="checkbox"/> Leaf Lamina
<input type="checkbox"/> Epidermis	<input type="checkbox"/> Whole Plant	

phenotype-gene

External ID Individual description
Date last modified 2013-11-18

Page(s) [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [Next](#) | 1 - 20 of 823 Show

phenotype-gene	annotation	has_mutation	outcome_paper	Attrib
<input type="text" value="Filter"/> <input type="button" value="Clear"/>	<input type="text" value=""/>	<input type="text" value=""/>	<input type="text" value=""/>	
dark red seed for AT3G27670	dark red seed	AT3G27670	Chen Xinbo et al. 2005 Oct. Plant Physiol. 139(2):909-19.	http/
decreased density of nitrate for AT5G50200	decreased density of nitrate	AT5G50200	Kawachi Tahei et al. 2006 Oct. Plant Cell Physiol. 47(10):1437-41.	http/
delayed growth for AT4G12720	delayed growth	AT4G12720	Bartsch Michael et al. 2006 Apr. Plant Cell 18(4):1039-51.	http/
delayed growth for AT4G31120	delayed growth	AT4G31120	Pei Yanxi et al. 2007 Aug. Plant Physiol. 144(4):1913-23.	http/
delayed leaf senescence for AT1G69490	delayed leaf senescence	AT1G69490	Guo Yongfeng et al. 2006 May. Plant J. 46(4):601-12.	http/

- URL: http://database.riken.jp/db/curated_plant_phenome
- Contents:
 - Standardized phenotypes of *Arabidopsis thaliana* collected via literature curation of published scientific papers.
 - Relationships between phenotypic and genetic variation (i.e. standardized phenotypes and AGI code).
 - Environmental factors in observing phenotypes.
 - Reference data of evidence papers for data mentioned above.
- Remarks:
 - We picked up over 820 relationships of phenotypic variation and genes by careful reading of published papers. Various types of phenotypes, such as morphological variation, stress response, seed productivity etc., are covered.
 - Each phenotype listed in the former step was carefully interpreted and standardized with ontology terms. We also took a serious view of environmental factors with which phenotypes were observed. They were also standardized and stored in the presented database. Ontologies used for standardization are listed in the following table.

Ontology	Covered field	Example	Reference
Plant Ontology (PO)	organ	flower	Cooper et al. 2013
	developmental stage	flowering	
Plant Trait Ontology (TO)	developmental stage	flowering time	Youens-Clark et al. 2011
The ontology of phenotypic qualities (PATO)	physical quality	increased length	Mungall et al. 2010
Gene Ontology (GO)	biological process	nitrogen fixation	Ashburner et al. 2000
	cellular component	chloroplast	
	molecular function	glycerate kinase activity	
Plant Environment Ontology (EO)	environmental condition	long day length regimen	Jaiswal et al. 2002
Chemical Entities of Biological Interest (ChEBI)	chemical compound	sugar	Hastings et al. 2013

3. Quick Start: How to search for bio items in plant phenome databases

Here shows some simple example to find notable bioitems such as genes and mutants using the presented databases.

3.1 Search genes involved in focused phenotypes

The screenshot shows the RIKENBASE Arabidopsis Phenome Database search interface. At the top, there is a search bar with the keyword "delayed flowering" and buttons for "Search" and "Clear". Below the search bar, the "Arabisidopsis Phenome Database" header is displayed, followed by a "Contents List" menu with options like "RIKEN Phenome Integration of Arabidopsis Mutants", "Curated Plant Phenome", and "About this database".

The main content area is titled "Database of Curated Plant Phenome" and features a "Phenotype abnormality" section. This section includes a description of standardized phenotypes and a list of search results. The search results are displayed in a table with columns for "Hit Content" and "Phenotype abnormality". The results include terms like "delayed whole plant flowering stage in environment of long day length regimen" and "delayed whole plant flowering stage".

On the left side, there is a "Search: Related Categories" sidebar showing a list of categories filtered by "delayed flowering". The categories include Athaliana locus (TAIR10 Locus (2)), Plant Phosphoproteome Database (At-OsOrthologCluster (8), AtPeptide-Locus (2)), RIKEN Phenome Integration of Arabidopsis (observation of Arabidopsis phenotype (1), plant phenotype (1)), Plant Phenome (phenotype-gene (37), outcomePaper (7), Phenotype abnormality (5)), PosMed ABRC References (References (23)), Athaliana gene (AT_TAIR_exon (91), AT_TAIR_gene (13)), PosMed dataset for ABRC (ABRC Germplasm (43)), and ARTADE2 predicted gene model database (Tiling_Array_Analysis_Result (41), TAIR gene model for ARTADE2 (1)).

1. Access to the “Database of Curated Plant Phenome” (http://database.riken.jp/db/curated_plant_phenome). Click “Phenotype abnormality” under top menu bar.
2. Enter keyword (ex: “delayed flowering”) in search box.

- Click a search button, and a list of hit phenotypes will appear at the lower part of the page (See upper figure).

The screenshot shows the RIKENBASE Arabidopsis Phenome Database interface. At the top, there is a search bar with the text 'delayed flowering' and buttons for 'Search' and 'Clear'. Below the search bar is a navigation menu with 'Contents List' and 'About this database'. The 'Contents List' is divided into two columns: 'RIKEN Phenome Integration of Arabidopsis Mutants' and 'Curated Plant Phenome'. The 'Curated Plant Phenome' column lists 'Phenotype abnormality', 'Experimental condition', 'Phenotype-gene', and 'Outcome paper'. The 'About this database' column lists 'Manual', 'Data list', and 'Contact us'. Below the navigation menu, there is a search results section. On the left, a sidebar shows 'Search: Related Categories' with a list of categories: 'RIKEN Phenome Integration of Arabidopsis Mutants' (1), 'Athaliana locus' (2), and 'Plant Phenome' (37). The main content area shows the search results for 'delayed flowering', with a table of results. The first result is 'delayed whole plant flowering stage in environment of long day length regimen'. The table has columns for 'quality_in_pato', 'during_process_named', 'in_experimental_condition', and 'phenotype-gene ("annotation" is delayed whole plant...)'. The 'phenotype-gene' column contains a list of gene IDs and their corresponding phenotypes.

- Click a link (Ex: "delayed whole plant flowering stage in environment of long day length regimen"), and a new table will appear which includes information about phenotype-gene interaction, derived from literature curation (See upper figure).
- Click a "phenotype-gene" item (Ex: "delayed whole plant flowering stage in environment of long day length regimen for AT1G26830"), and detailed reference data will appear. It includes links to PubMed, with which users can access original description to check validity of search results.

phenotype-gene (Plant Phenome)

delayed whole plant flowering stage in environment of long day length regimen for AT1G26830

annotation	delayed whole plant flowering stage in environment of long day length regimen	Show Detail	Search Related Information
has_mutation	AT1G26830	Show Detail	Search Related Information
outcome_paper	Dieterle Monika et al. 2005 Feb. Plant J. 41(3):386-99.	Show Detail	Search Related Information

3.2 Search bioresources (mutants) from focused phenotype

It is possible to search *Arabidopsis* mutants from keywords related to focused phenotype, by the following steps.

1. Access to “RIKEN Phenome Integration of *Arabidopsis* mutants” (http://database.riken.jp/db/arabidopsis_mutant_phenome).

The screenshot displays the RIKEN Phenome Database interface. At the top, a search bar contains the query "flower:abnormal,shape" with "Search" and "Clear" buttons. Below the search bar is the "Arabidopsis Phenome Database" header. A "Contents List" table is visible, with columns for "RIKEN Phenome Integration of Arabidopsis Mutants" and "Curated Plant Phenome". The "RIKEN Phenome Integration of Arabidopsis Mutants" column lists "Observation of Arabidopsis phenotype" and "Plant phenotype". The "Curated Plant Phenome" column lists "Phenotype abnormality", "Experimental condition", "Phenotype-gene", and "Outcome paper". To the right, an "About this database" section includes links for "Manual", "Data list", and "Contact us".

The main content area is titled "RIKEN Phenome Integration of Arabidopsis Mutants" and features a search box with the query "flower:abnormal,shape". Below the search box, a "Search by PO and PATO terms" section is active, showing a list of categories and subcategories. The "Flower" category is selected, and the "flower:abnormal,shape" subcategory is checked. Other categories include "Seed Germination Stage", "Axillary Shoot System", "Seedling", and "Whole Plant Development Stage".

On the left side, a "Reference" section lists two papers:

1. Nakazawa M, Ichikawa T, Ishikawa A, Kobayashi H, Tsuchida Y, Kawashima M, Suzuki K, Muto S, Matsui M Activation tagging, a novel tool to dissect the functions of a gene family. *Plant J* 2003; 741-750
2. Sakurai T, Satou M, Akiyama K, Iida K, Seki M, Kuromori T, Ito T, Konagaya A, Toyoda T, Shinozaki K. RARGE: a large-scale database of RIKEN Arabidopsis resources ranging from transcriptome to phenotype. *Nucleic Acids Research* 2005;

Below the search results, a "Search: Related Categories" box shows the following results:

- RIKEN Phenome Integration of Arabidopsis mutants
 - observation of Arabidopsis phenotype (1)
 - plant phenotype (1)
- PosMed dataset for Fox line
 - FOX line (41)
- PosMed dataset for DS tagging line
 - DS tagging line (3)

2. Specify keywords using the menu at the center of the page. This menu allows to specify organ names or growth stage. Users can see detailed categories by clicking “Show subcategories” button. For example, “flower:abnormal,shape” is selected in this text. Alternatively, users can enter the keywords directly in the search box at the top of this page.

3. The new page includes observation data of *Arabidopsis* mutant of which “observed phenotype” is “flower:abnormal,shape”.

observation of *Arabidopsis* phenotype (RIKEN Phenome Integration of *Arabidopsis* mutants)

F06248_obs_5 (FOX hunting)

[\[Browse list of all records\]](#)

Original phenome observation data	F06248_obs_5 Hide Detail Search Related Information	
		
	hasPhenotypicData	flower:others Show Detail Search Related Information
	isObservationForGeneration	T1 Show Detail Search Related Information
	hasLineData	F06248 Show Detail Search Related Information
observation of <i>Arabidopsis</i> phenotype (“Original phenome observation data” is F06248_obs_5)	F06248_obs_5 (FOX hunting) Search Related Information	
observed phenotype	flower:abnormal,shape Hide Detail Search Related Information	
	quality in PATO	abnormal, shape
	entity in PO	flower Search Related Information
	observation of <i>Arabidopsis</i> phenotype (“observed phenotype” is flower:abnormal,sha...)	106 subjects Search Related Information
	FOX line (“observed phenotype” is flower:abnormal,sha...)	41 subjects Search Related Information
	Ds tagging line (“observed phenotype” is flower:abnormal,sha...)	16-0443-1, 15-3580-1, 15-2793-1 Show Detail Search Related Information

4. Click “Show Detail” button of “Original phenome observation data”, and original information opened by developers of mutants. Furthermore, “Show Detail” of “observed phenotype” is linked to information of other mutant lines showing same phenotypes. In the presented example, users can find that 41 Fox line and 3 Ds tagging line mutants share a phenotype, “morphology of flower is abnormal”.

The presented example shows that users effectively can find useful mutants for their research for the focused phenotype, by cross-database search of “Ds tagging”, “Activation tagging” and “FOX-hunting” mutants.

4. Advanced search for improved bioinformatic studies

RIKENBASE integrates databases not only of phenome but of various kinds of omics.

4.1 Gene-phenotype search started from TAIR locus DB: Reasoning of unknown roles or functions of focused gene

Here we show an example of search using The Database of Plant Phenome and the Database of *A. thaliana* locus, by which users can deepen knowledge about biological roles or functions of focused *Arabidopsis* genes.

The first example is about genes related to “abscisic acid beta-glucosidase” as a keyword. Abscisic acid is a well-known plant hormone involved in drought stress, and abscisic acid beta-glucosidase has an important role for biosynthesis of abscisic acid. Information of related genes are covered by TAIR locus database, which is integrated in RIKENBASE as well as the Database of Curated Plant Phenome.

1. Access to the TAIR locus database (https://database.riken.jp/sw/en/TAIR10_Locus/crib102u0i/).
2. Enter “abscisic acid beta-glucosidase” as keyword into search box at the top of the page (See Figure below).

RIKENBASE abscisic acid beta-glucosidase [Search] [PosMed Search] [researcher]

Search: Related Categories

The followings are filtered by 'abscisic acid beta-glucosidase' [Clear Keyword]

- Swiss-Prot
 - Swiss-Prot Plants (3)
- A.thaliana locus
 - TAIR10 Locus (1)
- ARTADE2 predicted gene model database
 - Tiling Array Analysis Result (46)
 - ARTADE2_Gene (Ver.20100511) (36)
 - TAIR_gene_model (on ARTADE2DB) (ver. TAIR9) (1)
 - Genes with tiling-array support (Annotated) (19)
 - Novel gene models (Predicted) (9)
- TAIR GO Annotation
 - TAIR GO Annotation (1)
- Gene Ontology
 - abscisic acid glucose ester beta-glucosidase a

Download RDF/OWL [Browse on Genome]

TAIR10 Locus
Date last modified 2012-06-29

Page(s) 1 1 - 1 of 1 Show 20 [Download this table]

Hit Content	TAIR10 Locus	description	synonym	gene type
<p>beta glucosidase 18 (BGLU18); FUNCTIONS IN: abscisic acid glucose ester beta-glucosidase activity, hydrolase activity, hydrolyzing O-glycosyl compounds, identical protein binding; INVOLVED IN: in 6 processes; LOCATED IN: in 6 components; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Glycoside hydrolase, family 1 (InterPro:IPR001360), Glycoside hydrolase, family 1, active site (InterPro:IPR018120), Glycoside hydrolase, catalytic core (InterPro:IPR017853), Glycoside hydrolase, subgroup, catalytic core (InterPro:IPR013781); BEST Arabidopsis thaliana protein match is: beta glucosidase 19 (TAIR:AT3G21370.1); Has 11362 Blast hits to 11017 proteins in 1473 species: Archae - 142; Bacteria - 7866; Metazoa - 708; Fungi - 200; Plants - 1449; Viruses - 0; Other Eukaryotes - 997 (source: NCBI BLink).</p>	AT1G52400	beta glucosidase 18 (BGLU18); FUNCTIONS IN: abscisic acid glucose ester beta-glucosidase activity, hydrolase activity, hydrolyzing O-glycosyl compounds, identical protein binding; INVOLVED IN: in 6 processes; LOCATED IN: in 6 components; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Glycoside hydrolase, family 1 (InterPro:IPR001360), Glycoside hydrolase, family 1, active site (InterPro:IPR018120), Glycoside hydrolase, catalytic core (InterPro:IPR017853), Glycoside hydrolase, subgroup, catalytic core (InterPro:IPR013781); BEST Arabidopsis thaliana protein match is: beta glucosidase 19 (TAIR:AT3G21370.1); Has 11362 Blast hits to 11017 proteins in 1473 species: Archae - 142; Bacteria - 7866; Metazoa - 708; Fungi - 200; Plants - 1449; Viruses - 0; Other Eukaryotes - 997 (source: NCBI BLink).	ATBG1 A. THALIANA BETA-GLUCOSIDASE 1 BGL1 BETA-GLUCOSIDASE HOMOLOG 1 BGLU18 beta glucosidase 18	protein_coding

Reference

1. Lamesch P, Berardini TZ, Li D, Swarbrick D, Wilks C, Sasidharan R, Muller R, Dreher K, Alexander DL, Garcia-Hernandez M, Karthikeyan AS, Lee CH, Nelson WD, Ploetz L, Singh S, Wensel A, Huala E. The Arabidopsis Information Resource (TAIR): improved gene annotation and new tools. *Nucleic Acids Res.* 2012; 40: D1202-10 [See More]

Instance Ranking

Weekly Access Rank for TAIR10 Locus
Top10
2013/08/07 to 2013/08/14

Instance Name	Trend
AT1G52400	up ↗
AT4G30380	up ↗
AT5G57340	up ↗
AT1G01010	up ↗
AT1G51090	up ↗
AT1G55970	up ↗

3. The result suggests that the gene AT1G52400 is involved in production of this enzyme (See upper figure).
4. Click the AT1G52400 link in the result list.

5. Phenome collected by literature curation is shown in the column labeled “phenotype-gene” (Figure below).

RIKENBASE Enter keyword.. Search PosMed Search researcher search Clear

Reference
 1. Lamesch P, Berardini TZ, Li D, Swarbreck D, Wilks C, Sasidharan R, Muller R, Dreher K, Alexander DL, Garcia-Hernandez M, Karthikeyan AS, Lee CH, Nelson WD, Ploetz L, Singh S, Wensel A, Huala E. The Arabidopsis Information Resource (TAIR): improved gene annotation and new tools. *Nucleic Acids Res.* 2012; **40**: D1202-10
[See More](#)

Directory
 CHEBI Chemical entities of biological interest
 RIKENBASE
 Basic Formal Ontology 1.1.1
 Genetics Ontology Lite
 The integrated database of plant omics data
 Genome Annotation
 A.thaliana locus

Gene Annotation template
Genome Segment in plant
TAIR10 Locus
TAIR10 Gene Model
TAIR10 Locus position
TAIR10 Gene Model position
TAIR10 Exon position
Mouse MGI Gene
Human HGNC Gene
Mouse Ensembl Gene Annotation Release
Os_RAPDB_Locus
Os_MSU_Locus
Entrez Rat
IGGP_1 (Vitis vinifera)
JGI Selaginella moellendorffii v1.0
RARGE Alternative splicing
JGI Pontr1_1
RIKEN OmicBrowse - Arabidopsis
 TilingArray View-Mathei et al. PCD (2008)

TAIR Locus
TAIR10 Locus (A.thaliana locus)
 AT1G52400 [Original Site](#) [\[Browse list of all records\]](#)

description	beta glucosidase 18 (BGLU18); FUNCTIONS IN: abscisic acid glucose ester beta-glucosidase activity, hydrolase activity, hydrolyzing O-glycosyl compounds, identical protein binding; INVOLVED IN: in 6 processes; LOCATED IN: in 6 components; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Glycoside hydrolase, family 1 (InterPro:IPR001360), Glycoside hydrolase, family 1, active site (InterPro:IPR018120), Glycoside hydrolase, catalytic core (InterPro:IPR017853), Glycoside hydrolase, subgroup, catalytic core (InterPro:IPR013781); BEST Arabidopsis thaliana protein match is: beta glucosidase 19 (TAIR:AT3G21370.1); Has 11362 Blast hits to 11017 proteins in 1473 species: Archae - 142; Bacteria - 7866; Metazoa - 708; Fungi - 200; Plants - 1449; Viruses - 0; Other Eukaryotes - 997 (source: NCBI BLink).
synonym	ATBG1, A. THALIANA BETA-GLUCOSIDASE 1, BGL1, BETA-GLUCOSIDASE HOMOLOG 1, BGLU18, beta glucosidase 18
gene type	protein_coding Search Related Information
locus region	Chr1:19515143-19518411 + Browse on Genome Show Detail Search Related Information
species	Arabidopsis thaliana Show Detail Search Related Information
RARGE Alternative splicing ("A.thaliana(tair locus)" is AT1G52400)	ATU-1-1-13430 Show Detail Search Related Information
RAFL cDNA ("A.thaliana(TAIR Locus)" is AT1G52400)	RAFL05-03-B20, RAFL06-67-J02, RAFL07-10-G07, RAFL09-32-M06 Show Detail Search Related Information
cdna insertion of Riken Arabidopsis Fox-hunting ("containsGeneOfAgi" is AT1G52400)	F01828_1, F10916_1, F17423_1, F19243_1, F20121_1, F21834_1, F22713_1, F29314_1, F30012_1 Show Detail Search Related Information
observation of Arabidopsis phenotype ("modified gene" is AT1G52400)	F01828_obs_2 (FOX hunting), F01828_obs_1 (FOX hunting), F10916_obs_1 (FOX hunting) Show Detail Search Related Information
Swiss-Prot Plants ("TAIR locus" is AT1G52400)	BGL18_ARATH Show Detail Search Related Information
phenotype-gene ("has_mutation" is AT1G52400)	non-functional stomatal movement for AT1G52400, premature during process named seed germination for AT1G52400 Show Detail Search Related Information

6. Click “Show detail” button.

7. A new table appears. Relationships between phenotypes and genes with reference data are listed in this table (Figure below).

phenotype-gene	annotation	has_mutation	outcome_paper
non-functional stomatal movement for AT1G52400	non-functional stomatal movement	AT1G52400	Lee Kwang Hee et al. 2006 Sep. Cell 126(6):1109-2...
premature during process named seed germination f...	premature during process named seed germination	AT1G52400	Lee Kwang Hee et al. 2006 Sep. Cell 126(6):1109-2...

Click texts in “outcome_paper” to view another table showing further detailed reference data including abstract. This table also includes a link to PubMed as “Original site”, where users can easily check validity of shown phenotype-gene relationships based on original descriptions, figures etc.

This example shows that users can search a notable gene closely related to drought tolerance. It is also shown that the focused gene participates in stomatal movement. In the same manner, it is possible to find new research theme by focusing unknown biological role of genes.