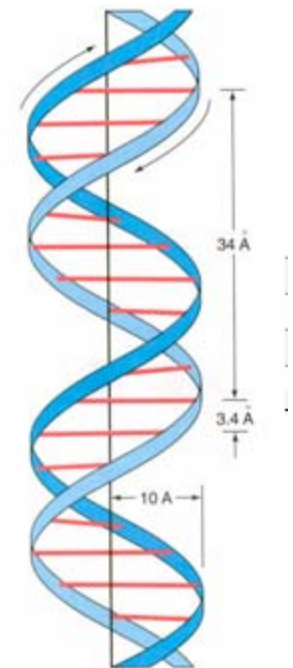
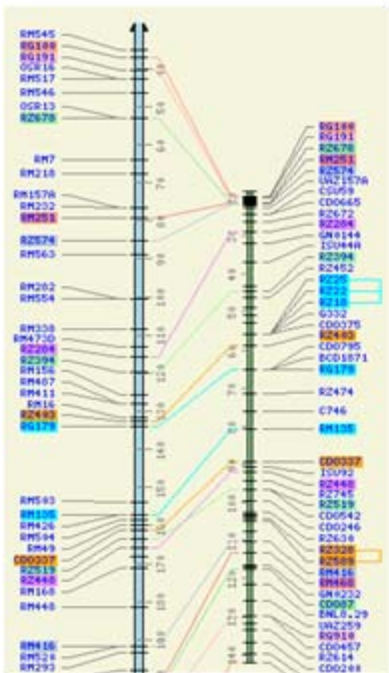




Welcome to the Gene and Allele Database Tutorial

This tutorial will describe how to navigate the section of Gramene that provides descriptions of alleles associated with morphological, developmental, and agronomically important phenotypes and variants of physiological characters, biochemical functions and isozymes.

Many genes in Gramene also have map positions and sequencing data.



Tutorial Tips



If you are viewing this tutorial with Adobe Acrobat Reader, click the "bookmarks" on the left hand side of the Reader for easier navigation.

Note! Although we continually work to make Gramene compatible with all browsers, there are problems with some browser versions. If you're having difficulty viewing Gramene, try using a different browser. Please report any problems with browsers through Gramene Feedback.

Gramene Home Page

The screenshot shows the Gramene website interface. At the top, the header includes the 'GRAMENE' logo, the tagline 'A Resource for Comparative Grass Genomics', the version 'V24 (March 2007)', and a navigation bar with links: Search, Genomes, Species, Download, Resources, About, Help, and Feedback. A left sidebar contains a 'Quick Search' box, a list of modules (Genomes-Ensembl, Maps-CMap, Markers, QTL, Diversity, Genes, Proteins, Pathways, Ontologies, Literature, Sequences-BLAST, All-GrameneMart), and a 'Have Questions...?' section. The main content area features a 'Quick Start' section with links to various genomic resources. A right sidebar lists 'Featured News' and 'Visit with us at' upcoming meetings. A green callout bubble with the text 'Click here to open gene search' points to the 'Genes' link in the left sidebar.

GRAMENE *A Resource for Comparative Grass Genomics* V24 (March 2007)

Search | Genomes | Species | Download | Resources | About | Help | Feedback

Quick Search

Search a single module or all available modules plus online documentation.

Diversity, Pathways, BLAST and Mart not available in this search.

Have Questions...?

- Gramene now has [tutorials](#) for every module, also recommended for experienced users.
- Ask questions through [Feedback](#) or [Email](#).
- See [FAQ](#) for questions and

Genomes-Ensembl
Maps-CMap
Markers
QTL
Diversity
Genes
Proteins
Pathways
Ontologies
Literature
Sequences-BLAST
All-GrameneMart

Quick Start

enced genomes for [Rice](#), [Maize](#) & [Arabidopsis](#); Look for [rice/maize synteny](#); Narrow your Search for sequence alignment with [BLAST](#); search by [Gene Ontology](#).

[Map](#) or [ProSite](#) or Browse by Gene Ontology using [GO Slim](#).

physical maps for [Rice](#), [Wild Rice](#), [Maize](#), [Wheat](#), [Barley](#), [Oats](#), [Sorghum](#), and other [Comparative Map Viewer \(CMap\)](#) to compare maps of different types and species.

markers (RFLPs, SSRs, etc.), DNA Probes (Primers, Overgos, etc.), Genomic Sequences (GSSs, ESTs, etc.); Use the Simple Sequence Repeat

ies, including [Rice \(Oryza sativa\)](#), [Maize](#), [Sorghum](#) and [Others](#).

TRAITS: Search the [Genes](#) of [Maize QTL](#). Don't forget to e

GENETIC DIVERSITY: Search and [wheat](#) germplasms.

BIOCHEMICAL PATHWAYS: Search for ALL the rice pathways on [starch biosynthesis](#) or get an overview of the

Featured News

- [NEW](#) March 2007, V 24 [release notes](#).
- [NEW](#) Gramene Jan/Feb Newsletter
- [Rice News Worldwide](#) from IRRI

Visit with us at

- March 15-18, 2007. [CSHL Plant Genome meeting](#)
- March 22-25, 2007. [Maize Genetics Meeting](#)
- April 16-20, 2007. [ITMI](#)
- May 8-12, 2007. [Biology of Genomes](#)
- July 7-11, 2007. [ASPB](#)

[View Previous Gramene Presentations](#)
[Calendar](#)

Click here to open gene search

3/22/07

See [Navigation_Tutorial](#) for info on navigating Gramene

Gene & Allele Database Home Page

1. Use the general search option, or

The screenshot shows the top navigation bar with links: Gene Home | Search | Submit | Help Documents | Tutorial | FAQ. Below this is a 'Gene Search' section with a text input field, a 'Search' button, and a 'Clear' button. Below the input field is a label: 'Search by Gene Symbol or Name, Chromosome No., Gene Accession, Protein Accession, GeneBank Accession [e.g. dwarf*]'. A green callout bubble points to the 'Search' button with the text 'Use * to search for wildcards'.

Use * to search for wildcards

2. Use the “search” link from the gene menu to select a more limited (specific) search. (see slide 5)

Gene and allele information at Gramene, briefly, Gramene Genes Database, is a curated resource providing collective information about publicly available genes and alleles identified in rice (*Oryza sp.*). It includes descriptions of genes and alleles associated with morphological, physiological, and agronomically important phenotypes, variants of physiological characters, biochemical functions

Users can use keyword to search the Genes database. The search can be restricted to any one of the following: gene symbol, chromosome number, ontology terms (trait ontology, plant structure, growth stage, gene ontology), GeneBank accession and Gramene protein accession. If necessary, the users also can do a search in

For more information on the latest release, see the [Genes Release Notes](#)

Click to view most recent release notes

For searching for a gene, click [here](#).

[Submit](#)

For submitting a gene, click [here](#).

[Help Documents](#)

For help documents, click [here](#).

[Tutorial](#)

* For tutorial, click [here](#).

3/22/07

Search Options

1. Search by **term** (*next slide*)

GRAMENE Genes

Find anything Search

Search Genomes Download [Genes](#) [About](#) [Help](#) [Feedback](#)

[Gene Home](#) [Search](#) [Submit](#) [Help](#) [Tutorial](#) [FAQ](#)

Gene Search

Search for *:	Search in:	Gene Type:	Species:	Has Phenotype:	
<input type="text"/>	Gene Symbol & Name	All Gene Types	All Species	<input type="checkbox"/>	<input type="button" value="Search"/>
					<input type="button" value="Clear"/>

* eg, [d1](#), [dwarf-1](#), [GR:0060184](#), [flower*](#), [*tillering stage*](#) Or [view help](#)

OR

Browse by [Ontology Database](#) [Trait](#), [Plant Structure](#), [Growth Stage](#)

2. Click an **ontology** to retrieve a list of genes in that ontology.

You may also browse for a gene via **Literature Database**.
Go to the Literature Database in Gramene. Literature detail will display genes in the "Associated Data" field.

Search_Genes

GRAMENE Genes

Search Genomes Download Resources

Gene Home | Search | Submit | Help | Tutorial | FAQ

Search Feedback

Gene Search

Search for: * Search in: Gene Symbol & Name Gene Type: All Gene Types Species: All Species Has Phenotype: ☒ Search Clear

Gene Symbol & Name Gene Accession Chromosome No. TO: Trait Q: Plant Structure Growth Stage Molecular Component Molecular Function Biological Process

Not sequenced CDS (Protein coding) rRNA (Ribosomal RNA) tRNA (Transfer RNA) Pseudogene (non-functional) Not classified All Gene Types

Rice Mouse All Species

1a/b. Enter a **term** and select what **field** to search. When you don't know the exact term, add the wildcard (*) to your search. For example, to browse genes by alphabetical order, enter the letter and wildcard (example "A*")

Select Gene type

1d. Select species to search

1e. Click "Search" to view results

1c. Genes that have been associated with an observable trait are classified as "has phenotype."

For Help, click Help, Tutorial or FAQ

Be aware of wildcards. For example, searches for *dwarf, dwarf*, and *dwarf* will all give different results.

Results for Gene Search by Term / Key word

[Gene Home](#) | [Search](#) | [Submit](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Gene Search

Gene Type:
CDS (Protein)

[Advanced Search](#) Or [view help](#)

Browse by Ontology Database [Transcription](#), [Morphology](#), [Growth Stage](#)

There are 87 entries for rice genes with CDS and phenotype

Click to view next 25 results as needed.

Items 1 to 25 of 87. Page 1 of 4 | [Next](#)

Species	Gene Symbol	Gene Name	Synonyms	TO	PO	GRO	GO	EO	Chr. No.	Gene Type	Accession
Rice	AID1	Anther Indehiscence1	OsAID1	spikelet sterility, tiller number, male sterility, pollen sterility, pollen free, days to heading	stomium (sensu Poaceae), endothecium (sensu Poaceae), G anther dehiscence, leaf, septum	stamen stage ST6-5	regulation of programmed cell death, pollen maturation, transcription factor activity, anther dehiscence, nucleus, regulation of transcription, DNA-dependent, DNA binding	green house study	6	protein (g)	GR:0800010
							mitochondrion, proton-transporting two-sector ATPase				

Click on a gene symbol to view the detail page for that particular gene (for tutorial select "d1" and see slide 9)

Click on linked column headings to sort table by that column

Gene Detail

Information on gene detail pages will differ depending upon the amount of gene annotation available:

1. Fully annotated genes (slides 9-17)
2. Maize genes integrated from MaizeGDB (slide 18)
3. Sorghum Genes (slide 19)
4. Rice genes under curation (slide 20)

Gene Detail Page - Fully Annotated Genes

General Info

Summary for Gene: *d1* (GR:0060184)

[General Info](#) | [Allele and Germplasm](#) | [Sequence Association](#) | [Map Position](#) | [Ontology Association](#) | [References](#)

General Information

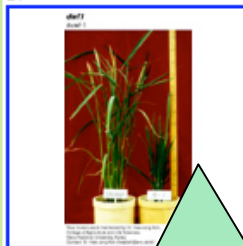
Accession	GR:0060184
Gene Symbol	<i>d1</i>
Gene Name	<i>dwarf-1</i>
Gene Synonym(s)	<i>dwarf1</i> , <i>daikoku dwarf</i> , <i>de-binding protein alpha-1 subunit, RGA1</i>
Species	<i>Rice</i>
Chromosome No.	5
Gene Type	CDS (Protein coding)
Has Phenotype	yes
Description	A typical small grain dwarf type with short and compact panicles and small, round floral organs.

Select desired detailed info from menu and click.

Phenotypic Image



1. Dwarf type in the 'Shiokar'



3. Dwarf plant and small grain

- *Gramene internal unique accession.*
- *Gene symbols according to the Gene Nomenclature System.*
- *Gene name: Traditional gene names*
- *List of synonyms that have been used for the gene.*
- *Species which the gene belongs to.*
- *Chromosome or linkage group on which the gene is located.*
- *Gene Type: "Not sequenced", CDS (Protein coding), rRNA (Ribosomal RNA), tRNA (Transfer RNA), Pseudogene (non-functional), and "Not classified".*
- *Has Phenotype: Show whether a gene has phenotype or not.*
- *Description*
- *Images, if available*
- *Curator comments of interest from the literature.*

Click a thumbnail to enlarge image.

Curator Comments

The protein is a single copy. A1 re-early h-ense t-ice b-elicitors active OsRac1, a small GTPase Rac of rice, blast. The gene expression was induced by an av

Gene Detail Page - Fully Annotated Genes

Allele and Germplasm

[General Info](#) | [Allele and Germplasm](#) | [Sequence Association](#) | [Map Position](#) | [Ontology Association](#) | [References](#)

Shows one or multiple allele names for a particular gene. Detailed information for the specific allele can be displayed when you click the allele name. (slide 11)

Allele	d1.wt1, d1.1, d1.2, d1.3, d1.4, d1.5, d1.6, d1.7, d1.8, d1.9, d1.10, d1.11
Germplasm	A59, C19, Nipponbare, D25, E017, Akage-1, CM392, Kinmaze, A23, Shiohari, Taichung65, CM1361-1, DK22, ID-1, DKT-1, DKT-2, Daikoku, HO532, FL2, HO533, HO537, HO538, HO541, HO552, CM382, CM1792, T65d1 (Taichung 65-Daikoku dwarf)

Shows one or multiple germplasm names for the particular gene. Click to view summary of the germplasm (Slide 13)

Allele Summary Page

Summary for Allele: *d1.wt1* (GR:0060184_1)

Accession	GR:0060184_1
Allele Symbol	<i>d1.wt1</i>
Allele Name	dwarf-1
Allele Description	Wild type.
Description of Allelic Interaction	Dominant.
Study	Nagao-1951a , Fujisawa-1999a
Germplasm	Nipponbare , Kinmaze , Shiokari , Taichung65
Gene	dwarf-1

Select for more detailed information on the referenced study(ies) (*see next slide*).

Select to return to gene detail page.

Ontology Association

Trait	plant height(TO:0000207) , seed size(TO:0000391)
Plant Structure	seed(PO:0009010) , whole plant(PO:0000003)
Cereal Plant Growth Stage	06-heading stage(GRO:0007044) , 09-mature grain stage(GRO:0007045)
Molecular Function	GTP binding(GO:0005525)

Allele designation: Different alleles of the same gene are distinguished by a decimal between the name of the gene and the number that follows, e.g., *gle1.1*. The synonyms for that allele are also listed following the allele designation.

Allele description: Provided if alleles give phenotypic differences.

Description of allelic interaction: Provided if the information about the interaction with other alleles or loci is available.

Allele Study Page

Study: Nagao-1951a

Study Name	Nagao-1951a
Year	1951
Season	NA
Location	Hokkaido University, Japan
Study Type	Field Study
Environmental Factors	NA
Allele	Ap.1 (A-S, A.1, Sp.1), d1.wt1, dwf3.1 (d3.1), dwf4.1 (d4.1), dwf5.1 (d5.1), Pn.1, Pr.1, Rc.0 (Rc+), Rd.1, st2.1, cps.1, n1.2, clw.1, d2.wt1, dwf6.1

Select for detailed information on other genes in the study.

Reference

1. [Nagao-S.](#)
Genic analysis and linkage relationship of characters in rice.
Advances in genetics.1951;4:181-212.

Provides a list of one or several studies or assays for that particular allele. Select to view literature entry for this publication.

Study name: Constructed of [author name] + [year of publication] + [a, b, c . . .] to differentiate among multiple studies for the same investigator and year.

Year: If the year of the study is not available the year of the publication will be used.

Season: The seasons in which the study was done.

Location: If not available, first author or principal investigator's address will be used

Study type: Choices include field, greenhouse, growth chamber, and laboratory.

Environmental factors: Text description of environmental conditions for a particular study,

Germplasm Summary Page

Summary for Germplasm: A59

Accession	A59
Location	Nagao's lab
Wild Type	A59
Mutagen	spontaneous
Mutagenesis Method	NA
Gene	dwarf-1

Select to return to gene detail page.

Accession: *Germplasm accession or cultivar name associated with gene.*

Location *The laboratory where the related germplasm was used*

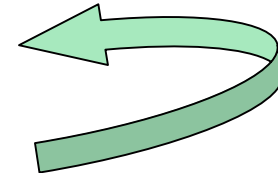
Wild Type: *accession or cultivar name of the wild type used to generate the mutant line.*

Mutagen: *Mutagen used to generate the mutant allele.*

Mutagenesis Method: *Detailed mutagenesis method used to generate the mutant allele.*

Gene Detail Page - Fully Annotated Genes

Sequence Association



[General Info.](#) | [Allele and Germplasm](#) | [Sequence Association](#) | [Map Position](#) | [Ontology Association](#) | [References](#)

Click to view the nucleotide sequence link for each protein from the National Center for Biotechnology Information.

Select to view more information from Gramene's Protein database (*See Protein tutorial*).

Sequence Association	
Protein	Gramene Protein: P49083 , Q43604
Nucleotide (DNA)	GenBank Nucleotide: AB026176 , AB026177 , AB026178 , AB026179 , AB026180 , AB028602 , AB028603 , D38232
	Rice Ensembl Gene: LOC_Os05g25890

Select to view Tigr gene report in Genome browser (*See Genomes tutorial*).

Gene Detail Page - Fully Annotated Genes

Map Position

[General Info.](#) | [Allele and Germplasm](#) | [Sequence Association](#) | [Map Position](#) | [Linkage Association](#) | [References](#)

Select to view d1 in marker DB.

Map Position [View in Marker DB]				
#	Map Set Name	Linkage Group	Start Position	Stop Position
1	JRGP Nipponbare/Kasalath RFLP	5	58.40 cM	60.70 cM
2	Hokkaido Morphological 2000	5	30.00 cM	30.00 cM
3	Gramene Annotated Nipponbare Sequence 2006	CH15	15531427.00 bp	15537142.00 bp

Chromosome the feature is located on.

Select to view the gene feature detail in Maps (*See Maps tutorial*).

Gene Detail Page - Fully Annotated Genes

Ontology Associations

[General Info.](#) | [Allele and Germplasm](#) | [Sequence Association](#) | [Map Position](#) | [Ontology Association](#) | [References](#)

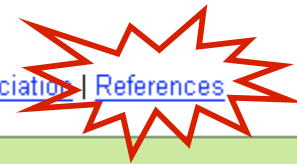
Ontology Association	
Trait	internode length (TO:0000145), leaf color (TO:0000326), leaf lamina color (TO:0000299), leaf length (TO:0000135), leaf shape (TO:0000492), leaf width (TO:0000370), panicle length (TO:0000040), panicle type (TO:0000089), plant height (TO:0000207), red light sensitivity (TO:0000158), seed shape (TO:0000484), seed size (TO:0000391), stem length (TO:0000576)
Plant Structure	inflorescence (PO:0009049), leaf (PO:0009025), leaf lamina (PO:0020039), seed (PO:0009010), stem (PO:0009047), stem internode (PO:0020142), whole plant (PO:0000003)
Plant Growth and Development Stage	2 formation of axillary shoot (PO:0007073), 5 fruit formation (PO:0007042), 6 ripening (PO:0007010), FR.04 fruit ripening complete (PO:0007038), LP.05 five leaves visible (PO:0007065), LP.06 six leaves visible (PO:0007123), booting (PO:0007014), inflorescence emergence from flag leaf sheath (PO:0007041), leaf production (PO:0007133), stem elongation (PO:0007089)
Cereal Plant Growth Stage	02-seedling (GRO:0007047), 03-tillering stage (GRO:0007049), 04-stem elongation stage (GRO:0007048), 05-booting stage (GRO:0007148), 06-heading stage (GRO:0007044), 07-milk stage (GRO:0007046), 08-dough stage (GRO:0007042), 09-mature grain stage (GRO:0007045)
Cellular Component	heterotrimeric G-protein complex (GO:0005834)
Molecular Function	GTP binding (GO:0005525), GTPase activity (GO:0003924), signal transducer activity (GO:0004871)
Biological Process	G-protein coupled receptor protein signaling pathway (GO:0007186), defense response to pathogen (GO:0042829), development (GO:0007275), gibberellic acid mediated signaling pathway (GO:0009738), alpha-dependent (GO:0042388)

Click links to go to the Ontology Database within Gramene. (See *Ontology tutorial*).

Gene Detail Page - Fully Annotated Genes

References

[General Info.](#) | [Allele and Germplasm](#) | [Sequence Association](#) | [Map Position](#) | [Ontology Association](#) | [References](#)



Reference	
DBxref	Oryzabase: 673
1. Parnell-F-R, Rangaswamy-Ayyangar-G-N, Ramiah-K.	
The inheritance of characters in rice. Il. Mem. Dept. Agr. Indian Bot.1922,"Ser., 11":185-208.	
2. Sugimoto-S.	
Some examples of the production of anomalous races in rice. Japan. J. Genet.1923, 1:71-75.	
3. Akemine-M.	
Inheritance of dwarfism in rice plants. Rept. Japan Sci. Assoc. 1923, 1:108-114.	
4. Akemine-M.	
Inheritance of dwarfism in rice plants. Rept. Japan Sci. Assoc. 1923, 1:108-114.	
5. Nagaike-T.	
Studies on the inheritance of characters in rice. Rept. Japan Sci. Assoc. 1923, 1:108-114.	

Click to view Oryzabase's information on the selected gene.

Click to go to the reference in Gramene Literature database (*See Literature tutorial*).

Gene Detail Page – Maize Genes

Summary for Gene: *a1* (GR:0200001)

[General Info.](#) | [Map Position](#) | [References](#)

General Information

Accession	GR:0200001
Gene Symbol	<i>a1</i>
Gene Name	<i>anthocyanin</i>
Gene Synonym(s)	bnl(a1), npi51(a1), npi467(a1)
Species	Maize
Chromosome No.	3
Gene Type	Not classified
Has Phenotype	not curated

Gene menu for Maize genes is incomplete, similar to this.

Description

Colorless aleurone, green or brown plant; brown pericarp with P1-rr. With appropriate complementary factors, dominant allele (A1) causes anthocyanin pigments to form in the aleurone, plant and pericarp tissues; recessive or intermediate alleles cause absence or reduction of pigment or substitution of brown pigment in these tissues. Some alleles are compound (alpha and beta, Laughnan 1955) and some alleles (a1-b, alpha) confer dominant brown pericarp. Reference allele (a1) is a Dt1 transposon receptor (Rhoades 1938; Nuffer 1961) as a consequence of the presence of the rDt (Sorrentino et al. 1987 MNL 61:103). Deficiency a1-x1 etc. (Stadler and Roman 1948). Molecular clone (O'Reilly et al. 1985). A1 encodes dihydroquercetin reductase (Reddy et al. 1987). bnl(a1) (pAmu2), npi51(a1)0, npi467(a1)0. P1 activates transcription directly; cold increases transcript accumulation 7-fold (Christie 1994). Promoter P1-binding site, CCTACCAACC, may be two overlapping hexameric binding sites, CCTACC and CCAACC (Grotewold et al 1994 Cell 76:543-553). This gene was originally curated in MaizeGDB Database and the map position was displayed on the maize bins map if feasible.

Map Position

#	Map Set Name	Linkage Group	Start Position	Stop Position
1	Maize Bins	3	139.90 cM	164.80 cM

Reference

DBxref: MaizeGDB: [12000](#)

Gene Detail Page – Sorghum Genes

Summary for Gene: *COMT* (GR:0810002)

[General Info](#) | [Sequence Association](#) | [Ontology Association](#) | [References](#)

General Information	
Accession	GR:0810002
Gene Symbol	<i>COMT</i>
Gene Name	<i>caffeic acid O-methyltransferase</i>
Gene Synonym(s)	bmr, bmr12, bmr18, bmr26, brown midrib, 5-hydroxyconiferaldehyde O-methyltransferase, CA1d-OMT, caffeate O-methyltransferase activity, COMT
Species	<i>Sorghum</i>
Gene Type	CDS (Protein coding)
Has Phenotype	yes
Description	COMT encodes the sorghum brown midrib gene encoding caffeic acid O-methyltransferase

Sequence Association	
Protein	Gramene Protein: Q84X55
Nucleotide (DNA)	GenBank Nucleotide: AY217766

Ontology Association	
Trait	leaf midrib color (TO:0000720)
Plant Structure	midvein (PO:0020139)
Molecular Function	S-adenosylmethionine-dependent methyltransferase activity (GO:0008757), caffeate O-methyltransferase activity (GO:0047763)
Biological Process	lignin biosynthesis (GO:0009809)

Reference	
DBxref	E.C. Number(s): 2.1.1.68

1. Bout-S, Vermerris-W.

A candidate-gene approach to clone the sorghum Brown midrib gene encoding caffeic acid O-methyltransferase.
Mol Genet Genomics.2003;269:205-214.

Gene Detail Page - Rice Genes Under Curation

Summary for Gene: *Acp1* (GR:0060006)

[General Info](#) | [Map Position](#) | [Ontology Association](#) | [References](#)

General Information

Accession	GR:0060006
Gene Symbol	<i>Acp1</i>
Gene Name	<i>Acid phosphatase-1</i>
Species	Rice
Chromosome No.	12
Gene Type	Not sequenced
Has Phenotype	yes
Description	under curation

Gene menu for rice genes that are still under curation will be incomplete until they are fully curated.

Map Position [\[View in Marker DB \]](#)

#	Map Set Name	Start Position	Stop Position
1	IGCN ZhaiYeQing 8/JingXi 17 19	12	2.90 cM
2	Hokkaido Morphological 2000	12	67.00 cM
3	JRGP Nipponbare/Kasalath RFLP	12	95.40 cM

Ontology Association

Molecular Function	acid phosphatase activity (GO:0003993)
--------------------	--

Reference

DBxref	Oryzabase: 966
--------	--------------------------------

1. [Pai-C, Endo-T, Oka-H-I.](#)

Genic analysis for acid phosphatase isozymes in *Oryza perennis* and *O. sativa*.
Canadian journal of genetics and cytology. Journal canadien de genetique et de cytologie.1975;17(4):637-650.

2. [Endo-T.](#)

How to Submit Newly Identified Genes

GRAMENE Genes Find anything Search

Gene Home | Search | **Submit** | Help Documents | Tutorial | FAQ

Search by Gene Symbol or Name, Chromosome, or Bank Accession [e.g. dwarf* or

Gramene Gene and Allele Database

Gene and allele database at Gramene, briefly, Gramene Genes Database, is a curated resource providing collective information about publicly available genetically identified genes and alleles that are of agronomically important.

In addition to the gene symbol, gene name, gene accession and Gene ID, the database also provides information on gene structure, gene expression, gene function, and gene interaction.

As a collaboration between the Gramene Genes Database and the Gramene Gene Expression Database, the database provides information on gene expression data.

[Search or Browse](#)
For searching for a gene or allele

[Submit](#)
For submitting a gene or allele

[Help Documents](#)
For help documents

[Tutorial](#)
* For tutorial, click here for: [PDF](#).

Gramene Curation Group
G15, Bradfield Hall
Plant Breeding, Cornell University
Ithaca, NY 14853, USA

Users are encouraged to send us your comments and suggestions. Please help us correct any errors or omissions.

Rice Gene Online Submission Form
Please use this form to submit information about a rice gene to Gramene. A confirmation email will be sent to you by our curators within two days.

Note: Fields with asterisks (*) are mandatory.

Basic Rice Gene Information

* Gene Name

* Phenotypic Description

Other Description

Reference for the Rice Gene

Ref. Category

Curator (internal use only)

Ref. Source

* Reference Detail (please provide the complete citation for the reference(s))

Help Documents

[Gene Home](#) | [Search](#) | [Submit](#) | **[Help Documents](#)** | [Tutorial](#) | [FAQ](#)

[How to Search/Browse/Access the Gramene Genes Database](#)

Option-1: Search for a gene

The user can search the Gramene Genes Database by typing a keyword in the "Search for" field, selecting the species field and any one of the following selection fields:

- Gene Symbol & Name
- Gene Accession
- Chromosome No.
- TO: Trait
- PO: Plant Structure
- GRO: Growth Stage
- GO: Cellular Component
- GO: Molecular Function
- GO: Biological Process
- EO: Environment
- GenBank Accession
- Gramene Protein Accession

Help documentation includes notes from the most recent database update, detailed notes about the information found in the database, and help on using the search tools.

For example, in order to find the gene [dwarf-15](#), the user can type gene symbol, dwf15 or gene name, dwarf-15 in "Search for" field, select "Gene Symbol & Name" in "Search in", and select "Rice" in "Species", and then submit his search to find the related information. Also, the user can include wild cards in "Search for" field, so, with a searching of "**tillering stage*" for "GRO: Growth Stage", the user can find all genes associated with the tillering stage.

The user can also select "has phenotype" or use the following gene types to filter his research results:

- Not sequenced
- CDS (Protein coding)
- rRNA (Ribosomal RNA)
- tRNA (Transfer RNA)
- Pseudogene (non-functional)
- Not classified

For instance, the user can select "CDS (Protein coding)" in the "Gene Type" field and further choose "has phenotype" to find all genes with both coding

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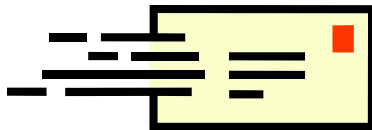
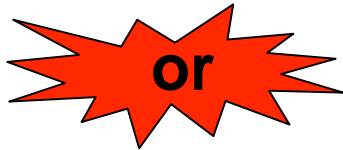
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