

Welcome to the Protein Database Tutorial

This tutorial will describe how to navigate the section of Gramene that provides collective information on proteins from grasses (family *Poaceae/Gramineae*). The protein entries are annotated by associating the following ontology concepts if known:

- Gene Ontology (GO)
 - Molecular function of the gene product.
 - Biological process in which the gene product is involved.
 - Cellular component where the gene product is localized.
- Plant Ontology
 - Plant structure where the gene is expressed (PO)
 - Plant growth stage at which the gene is expressed (GRO)

*** Only rice (*Oryza*) protein entries are manually curated.**

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

www.gramene.org

GRAMENE *A Resource for Comparative Grass Genomics*

Search Genomes Species Download Resources About Help Feedback

Quick Search

All Available

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 answers.

Gramene Tip:

You can contact Gramene either by e-mailing us at gramene@gramene.org or by sending a question to the curators and developers at Gramene on any page by selecting the Feedback button in the top right hand corner.

- [Browse All Tips](#)

Quick Start

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

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

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

Genetic markers (RFLPs, SSRs, etc.), DNA Probes (Primers, Overgos, etc.), Genomic Regions (GSSs, ESTs, etc.); Use the Simple Sequence Repeat Identification Tool for species, including [Rice \(Oryza sativa\)](#), [Maize](#), [Sorghum](#) and [Others](#).

Genomic database for important phenotype-related loci such as [Rice Genes](#), [Rice QTL](#), [Maize QTL](#). Don't forget to explore [Rice Genes](#) and [Rice QTL](#).

GENETIC DIVERSITY: Search for [rice](#), [maize](#), and [wheat](#) germplasms.

BIOCHEMICAL PATHWAY: Search for [rice](#) and [maize](#) metabolism or get an overview of the [metabolic network](#). Compare [rice](#) and [maize](#) network.

LITERATURE: Search the [Rice](#) and [Maize](#) literature.

SUBMISSION: Submit a [Rice Gene](#) or [Ontology Term](#) to Gramene.

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](#)

Gramene is a curated, open-source, web-accessible data resource for comparative genome analysis in the grasses. Our goal is to facilitate the study of cross-species homology relationships using information derived from public projects involved in genomic and EST sequencing, protein structure and function analysis, genetic and physical mapping, interpretation of biochemical pathways, gene and QTL localization and descriptions of phenotypic characters and mutations.

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

SPECIES

USDA

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Search Proteins

2. Click to limit search by species or object type. (slide 5)

4. Click to browse by **Gene Ontology** (slides 17-18.) (See *Ontology tutorial*)

The screenshot shows the GRAMENE Protein Database search interface. At the top is a green header with the GRAMENE logo and navigation links: Search, Genomes, Download, Resources, About, Help. Below this is a secondary navigation bar with links: Protein Home, Advanced Search, Search by Pfam or PROSITE, Browse by GO Slim, Documents, Tutorial, FAQ, Help. The main search area has a 'Protein Database' title, a search input field containing 'heading date', and a 'Search' button. Below the search bar, there is a list of search criteria: 'Search by name, SPTreMBL ID, Protein_ID(PID), GI number, cultivar' followed by examples 'e.g. P93436, alcohol, indica' and a 'HELP' link. The page content below the search bar includes a section titled 'Protein Database at Gramene' and a paragraph explaining that users can search by protein name, SPTreMBL ID, or Protein Sequence. It also mentions that users can browse by species or object type. A callout points to the 'Search by Pfam or PROSITE' link in the secondary navigation bar. Another callout points to the 'Search' button. A third callout points to the search input field. A fourth callout points to the 'Browse by GO Slim' link. A fifth callout points to the 'Possible searches' section at the bottom of the page.

Protein Database

heading date Search

Search by name, SPTreMBL ID, Protein_ID(PID), GI number, cultivar [e.g. P93436 , alcohol , indica] HELP

Protein Database at Gramene

You can search the protein database using either of the following methods:

1. Search by entering a term and clicking search (slides 6-13.)

2. Click to Search by Pfam or PROSITE (slides 14-16).

3. Click to limit search by species or object type. (slide 5)

4. Click to browse by Gene Ontology (slides 17-18.) (See Ontology tutorial)

Possible searches. Click some examples to get you started.

This is the Protein Home Page

Advanced Search

The screenshot shows the 'Protein Search' interface. At the top, there is a navigation bar with links: [Protein Home](#), [Advanced Search](#), [Search by Pfam or PROSITE](#), [Browse by GO Slim](#), [Documents](#), [Tutorial](#), [FAQ](#), and [Help](#). The 'Advanced Search' link is highlighted with a red starburst. Below the navigation bar, the 'Protein Search' section contains three main input fields: 'Search for *:', 'Search in:', and 'Species:'. The 'Search for *:' field contains the text 'heading date'. The 'Search in:' field has a dropdown menu with 'All Fields' selected, and a list of other options: Name, Accession, Protein_ID(PID), SPTreMBL ID, GenBank ID(GI), Cultivar, and All Fields. The 'Species:' field has a dropdown menu with 'Oryza (rice)' selected, and a list of other options: Zea (corn), Triticum (wheat), Hordeum (barley), Avena (oats), Secale (rye), Aegilops, Sorghum, Pennisetum (millet), Saccharum, and All Poaceae. To the right of the 'Species:' field, there is a 'Search' button and a 'Clear' button. Below the 'Search' button, there is a link to 'view help'. Three callouts are present: 1. A red starburst callout pointing to the 'Advanced Search' link. 2. A callout pointing to the 'Search for *:' field with the text: 'Enter a term. Use star (*) before/after/both in your query text to extend your searches. e.g. alcohol*, *alcohol, *alcohol*. Don't put star if you want an exact search'. 3. A callout pointing to the 'Search in:' dropdown menu with the text: 'Select the field your term is in. Select "All fields" if you are uncertain.'. 4. A callout pointing to the 'Species:' dropdown menu with the text: 'Optionally, select a species to search.'. 5. A callout pointing to the 'Search' button with the text: 'Click "search"'. The date '3/22/07' is in the bottom left corner, and the number '5' is in the bottom right corner.

[Protein Home](#) | [Advanced Search](#) | [Search by Pfam or PROSITE](#) | [Browse by GO Slim](#) | [Documents](#) | [Tutorial](#) | [FAQ](#) | [Help](#)

Protein Search

Search for *: Search in: Species:

9436, *alcohol*, *indica*, Or [view help](#)

Zea (corn)
Triticum (wheat)
Hordeum (barley)
Avena (oats)
Secale (rye)
Aegilops
Sorghum
Pennisetum (millet)
Saccharum
All Poaceae

Enter a term. Use star (*) before/after/both in your query text to extend your searches. e.g. alcohol*, *alcohol, *alcohol*. Don't put star if you want an exact search

Select the field your term is in. Select "All fields" if you are uncertain.

Optionally, select a species to search.

Click "search"

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5

1. Term Search: Results using “heading date”

To order results by column, click on the hyperlinked column titles.

Protein Home | Advanced Search | Search by Pfam or PROSITE | Search by GO Slim | Documents | Tutorial | FAQ | Help

Protein Search

Search for *: heading date Species: Oryza (rice) Search Clear

*eg, P93436, *alcohol*, *indica*, Or view help

Items 1 to 9 of 9.

Accession No.	Names/Symbols/Synonyms	Organism (cultivar)	Evidence codes
Q9FE92	Flowering date-1 Hd1 Heading date-1 K Lf Lm Photoperiod-sensitivity-1 Rs Se1	<i>Oryza sativa</i> (GINBOZU)	ISS RCA IGI IMP IEP IC
Q9FD09	Hd1 P0038C05.23 Hd1 Heading date-1 K Lf Lm P0038C05.14 Photoperiod-sensitivity-1 Rs Se1	<i>Oryza sativa</i> (japonica cultivar-group) (Nipponbare)	ISS IEP RCA IGI IMP IC
Q9AR27	Casein kinase II alpha subunit OSCKA2 Casein kinase II alpha subunit Hd6 Heading date-6 OsCkA2	<i>Oryza sativa</i> (indica cultivar-group) (Kasalath)	RCA ISS IGI IMP IC
Q9AQU1	Casein kinase II alpha subunit OSCKA2 Casein kinase II alpha subunit Hd6 Heading date-6 OsCkA2	<i>Oryza sativa</i> (japonica cultivar-group) (Nipponbare)	RCA ISS IGI IMP IC
Q9FRZ7	Flowering date-1 Hd1 Heading date-1 K Lf Lm Photoperiod-sensitivity-1 Rs Se1	<i>Oryza sativa</i> (Not available)	ISS IGI IMP IEP IC
Q9FRZ6	Flowering date-1 Hd1 Heading date-1 K Lf Lm Photoperiod-sensitivity-1 Rs Se1	<i>Oryza sativa</i> (Not available)	ISS IGI IMP IEP IC
Q93WM7	Hd3a protein Heading date-3a Putative phosphatidylethanolamine-binding protein	<i>Oryza sativa</i> (indica cultivar-group) (Kasalath)	ISS IGI IMP IEP IC
Q93WI9	Hd3a protein Heading date-3a Putative phosphatidylethanolamine-binding protein	<i>Oryza sativa</i> (japonica cultivar-group) (Nipponbare)	ISS IGI IMP IEP IC
Q05KQ3	Heading date-1 Hd1 Heading date-1 K Lf Lm Photoperiod-sensitivity-1 Rs Se1	<i>Oryza sativa</i> (indica cultivar-group) (Kasalath)	ISS IGI IMP IEP IC

Click the accession number to view the detail information page for a protein (*next slide*)

Lists the type of experiments carried out to ascertain the protein's function. Click to obtain more information.

Headings on Detail Page

GRAMENE *Proteins*

[Search](#) | [Genomes](#) | [Download](#) | [Resources](#) | [About](#) | [Help](#)

[Protein Home](#) | [Advanced Search](#) | [Search by Pfam or PROSITE](#) | [Browse by GO Slim](#) | [Documents](#) | [Tutorial](#) | [FAQ](#) | [Help](#)

Protein Search

Search for *: Search in: Species:

* eg, P93436, *alcohol*, *indica*, Or [view help](#)

[General Information](#) | [Associations](#) | [Similarity to Other Proteins](#) | [Features](#) | [References Used for Curation](#) | [FASTA Sequence](#)

General Information about Q9FE92

Accession	Q9FE92
Name	Flowering date-1
Symbol	Not available
Synonym(s)	Hd1, Heading date-1, K, Lf, Lm, Photoperiod-sensitivity
E.C. Number(s)	Not available
Gene Name(s)	Fl1 (Flowering date-1)

*The **protein navigation menu** is still listed along the top of the page.*

*But When accessing protein information, the **protein detail menu** is also shown. It is located below the search box, but at the top of the detail page. Select detail items to see detail information.*

Protein Detail: General Information

Shows the names of the protein molecule based on its function or phenotype. Often it is same as the gene name.

all the alternate names (aliases) by which the molecule is called in various databases and in scientific literature

Click for **BLASTP** query to find best match(es) to peptide sequences deduced from the TIGR rice gene models.

Cross references to GenBank and SWISSPROT protein entries.

Click for **gene detail** (See Genes tutorial)

A textual description of the protein

Shows the designated Enzyme Commission (E.C.) number. The EC numbers link to GenomeNet, Japan

Species and cultivar (stock) from which the gene was sequenced. Species links to Gramene's Taxonomy ontology for further information.

General Information Associated Genes Similarity to Other Proteins References Used for Curation FASTA Sequence		
General Information about Q9FE92		
Accession	Q9FE92	
Name	Flowering date-1	
Symbol	Not available	
Synonym(s)	Hd1, Heading date-1, K, Lf, Lm, Photoperiod-sensitivity-1, Rs, Se1	
E.C. Number(s)	Not available	
Gene Name(s)	Fl1 (Flowering date-1)	
Organelle	Not available	
Best hits to TIGR rice gene models	LOC_Os06g16340 Click here to generate a BLASTP query	
Accession Numbers	GenBank	TREMBL
	BAB17632	Q9FE92
Organism(s)	Species	Cultivar
	Oryza sativa	GINBOZU (GRIN , IRIS)
Comment	<p>Fl1 (Hd1) is a homeobox gene. The CONSTANS gene (At5g15840) from Arabidopsis and encodes a protein with a zinc finger domain. The major gene controlling photoperiodic sensitivity in rice, Hd1, is allelic to Hd1. The same allele of Hd1 mRNA detected under both SD and LD conditions suggests that the gene is bifunctional under both SD and LD conditions, promoting heading under SD conditions and inhibiting it under LD conditions. As compared to Arabidopsis, rice is a short-day plant and its heading is promoted by short photoperiods. Photoperiod sensitivity is dominant to heading date and maturity in rice. Strong photoperiodic sensitivity is dominant over insensitivity. (Imported from Gene ID: 40060860)</p>	

Protein Detail: Associations

[General Information](#) |
 [Associations](#) |
 [Similarity to Other Proteins](#) |
 [Features](#) |
 [References Used for Curation](#) |
 [FASTA Sequence](#)

Associations			
Term Type	Term	Reference	Evidence
Molecular Function	DNA binding(GO:0003677)	gramene.literature 8030	RCA With InterPro IPR002926
		gramene.literature 5127	ISS
	zinc ion binding(GO:0008270)	gramene.literature 8030	RCA With InterPro IPR000315
Biological Process		gramene.literature 5127	ISS
	transcription factor activity(GO:0003700)	gramene.literature 5127	ISS
	photoperiodism(GO:0009648)	gramene.literature 11089	IC
	inflorescence development(GO:0010229)	gramene.literature 5127	IGI
	long-day photoperiodism(GO:0048571)	gramene.literature 5127	IGI
			IEP
	GO:0000004(GO:0000004)	gramene.literature 11089	IC
Cellular Component	short-day photoperiodism(GO:0048572)	gramene.literature 5127	IGI
			IEP
	nucleus(GO:0005618)	gramene.literature 5127	ISS
Plant Structure	floret (sensu Poaceae)(GO:0006318)	gramene.literature 11089	IC
	inflorescence(Poaceae)	gramene.literature 5127	IC
			IEP
Plant Growth and Development Stage	meristem(PO:0009010)	gramene.literature 11089	IC
	seed(PO:0009010)	gramene.literature 11089	IC
	leaf(PO:0009025)	gramene.literature 5127	IC
	inflorescence emergence	gramene.literature 5127	IC
Cereal Plant Growth Stage	FR.04 fruit ripening	gramene.literature 11089	IC
	stem elongation(Poaceae)	gramene.literature 11089	IC
	04-stem elongation	gramene.literature 11089	IC
Trait	06-heading stage(Poaceae)	gramene.literature 11089	IC
	09-mature grain stage	gramene.literature 11089	IC
Keyword	days to heading(TO)	gramene.literature 11089	IC

Click to view the **Reference(s)** used to assign the ontology term.

Click terms to view **Ontology Information**
(See *Ontology Tutorial*)

Lists the type of experiments carried out to ascertain the protein's function. Click on a code for it's explanation.

Protein Detail: Similarities

 [General Information](#) | [Associations](#) | [Similarity to Other Proteins](#) | [Features](#) | [References Used for Curation](#) | [FASTA Sequence](#)

Click these options to link to NCBI's **BLink** to display the graphical output of pre-computed BLASTP results against the non-redundant (nr) protein database from NCBI.

Similarity to Other Proteins

Viridiplantae Green plants
-Embryophytes (plants)
-Magnoliophytes (flowering plants)
-Monocots | Grasses | Rice | Maize | Sorghum | Wheat | Barley | Rye | Oat | Sugarcane
-Dicots | Brassicaceae | Arabidopsis | Fabaceae (Legumes) | Solanaceae | Cucurbitaceae
Others : [Fungi](#) | [Metazoa](#)
3D protein structures : [BLink from NCBI](#) | [Sequence Annotated by Structure \(SAS\)](#)

Click these options to find if there are any known proteins that share the **structural homology** with the given protein

Protein Detail : Features

 [General Information](#) | [Associations](#) | [Similarity to Other Proteins](#) | [Features](#) | [References Used for Curation](#) | [FASTA Sequence](#)



Click to learn more about the **Protein Family** to which the protein belongs (if applicable).

Click to view a list of other protein entries that belong to this **Protein family** or share the Pfam/PROSITE domain.

Protein Features		
Pfam (Infor)	PF00643 ; zf-B_box PF06203 ; CCT	All Members of this Family All Members of this Family
Prosite (Infor)	PS51017 ; CCT	Sequence info. not available All Members of this Family
Physio-chemical features	Q9FE92	
ProtoMap (Info)	Q9FE92_ORYSA	

Click to link to **PROSITE** database for info describing the various PROSITE signatures the respective protein entry carries (if applicable).

Click to link to protein entry in **ProtoMap** database at Cornell University.

Click to link the **ExPASy** server for analyses of physiochemical features analyzed by **ProtParam** tool.

Protein Detail: References

[General Information](#) | [Associations](#) | [Similarity to Other Proteins](#) | [Features](#) | [References Used for Curation](#) | [FASTA Sequence](#)

Lists of all the references used for annotation of the selected protein.

References Used for Curation

1. [Yano-M Katayose-Y Ashikari-M Yamanouchi-U Monna-L Fuse-T Baba-T Yamamoto-K Umehara-Y Nagamura-Y Sasaki-T](#)
Hd1, a major photoperiod sensitivity quantitative trait locus in rice, is closely related to the Arabidopsis flowering time gene CONSTANS
The Plant cell, 2000, vol.12, pp.2473-2484
2. [Jaiswal-P Ren-L Zhao-W Schmidt-S-C Ratnapu-K-K Lincoln-S McCouch-S](#)
Gene Ontology Annotation By The Gramene Database
Gramene database, 2003, vol.1, pp.1-1
3. [Jaiswal-P Ren-L Ravenscroft-D Lincoln-S McCouch-S](#)
Mapping ontology associations between gene and protein entries in the Gramene database.
Gramene database, 2006, vol.1, pp.1-1

Search the Literature Database for Additional References

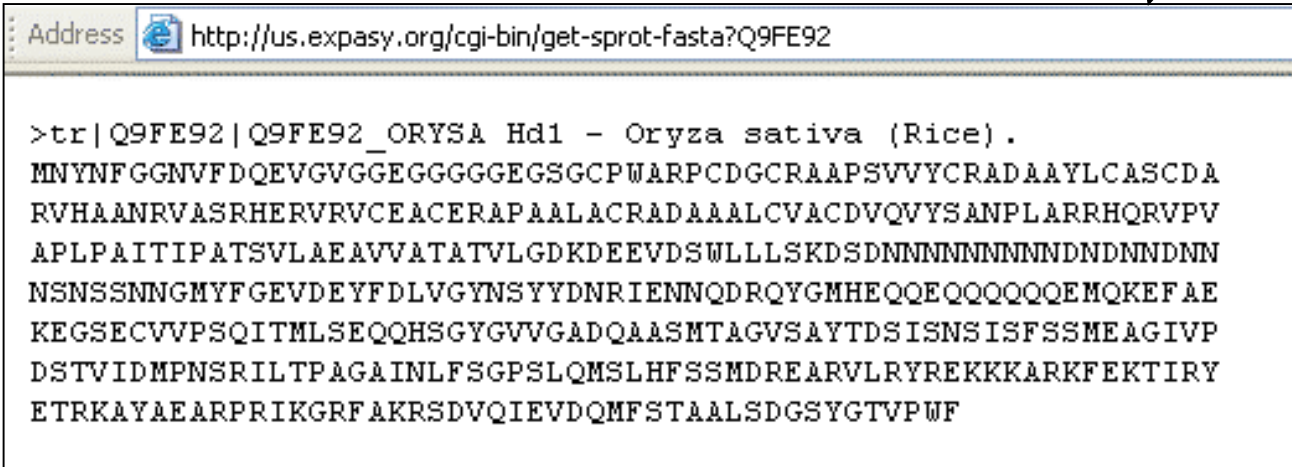
Click to see **Literature Detail Page** for that reference (*See Literature tutorial*).

Click to search for **more references** on this protein that are in the literature database but were not cited in the curation (*See Literature tutorial*).

Protein Detail Page: FASTA Sequence

 [General Information](#) | [Associations](#) | [Similarity to Other Proteins](#) | [Features](#) | [References Used for Curation](#) | [FASTA Sequence](#)

Click here to download the sequence in FASTA format



```
>tr|Q9FE92|Q9FE92_ORYSA Hd1 - Oryza sativa (Rice).  
MNYNFGGNVFDQEVGVGGEGGGGEGSGCPWARPCDGCRAAPSVVYCRADAAYLCASDA  
RVHAANRVASRHERVRVCEACERAPAALACRADAAALCVACDVQVYSANPLARRHQRPV  
APLPAITIPATSVLAEAVVATATVLGDKDEEVDSWLLLSKSDSDNNNNNNNNNDNDNDNN  
NSNSSNNGMYFGEVDEYFDLVGYNSYYDNRIENNQDRQYGMHEQQEQQQQQEQEMQKEFAE  
KEGSECVVPSQITMLSEQQHSYGTVGADQAASMTAGVSAYTDSISNSISFSSMEAGIVP  
DSTVIDMPNSRILTPAGAINLFSGPSLQMSLHFSSMDREARVLRREKKKARKFEKTIRY  
ETRKAYAEARPRIKGRFAKRSVDVQIEVDQMFSTAALSDGSYGTVPWF
```

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*For bulk download of all the sequences please visit our ftp site
ftp://gramene.org/pub/gramene/CURRENT_RELEASE/data/protein*

Search by Pfam or PROSITE

The screenshot shows the 'Protein Database' search page. At the top, a navigation bar contains links: [Protein Home](#), [Advanced Search](#), [Search by Pfam or PROSITE](#), [Browse by GO Slim](#), [Documents](#), [Tutorial](#), [FAQ](#), and [Help](#). The 'Search by Pfam or PROSITE' link is highlighted with a red jagged line. Below the navigation bar, the 'Protein Database' section has a search form. The label 'Search by Pfam or PROSITE:' is in red. The search input field contains the text 'Cytochrome'. To the right of the input field is a 'Search' button. Below the input field, there is a list of examples: [e.g. [PF00281](#) , [Ribosomal_L5](#) , [PS50255](#) , [CYTOCHROME_B5_2](#)].

From the protein search section, click on the “**Search by Pfam or PROSITE**” for this search option.

Search Pfam / PROSITE by either a name or an id as given in examples.

**Note: Some proteins do not have associations to Pfam and PROSITE features. This will restrict your search.*

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Results of Pfam or PROSITE Search

The off-site database that shares protein information with the Gramene database

Search by Pfam or PROSITE | [Browse by GO](#)

Protein Database

Search by Pfam or PROSITE:

[e.g. [PF00281](#) , [Ribosomal_L5](#) , [PS50255](#) , [CYTOCHROME_B5_2](#)]

Pfam Accession IDs. Click to find proteins in that protein family (*see next slide*)

15 matching results have been found.

#	Type	ID	Name
1	Pfam	PF00033	cytochrome_b_N
2	Pfam	PF00032	cytochrome_b_C
3	Pfam	PF00034	cytochrome_c
4	Pfam	PF01333	Apocytochrome_F
5	Pfam	PF02167	Cytochrome_C1
6	Pfam	PF03188	Cytochrome_B561
7	PROSITE	PS00191	CYTOCHROME_B5_1
8	PROSITE	PS00190	CYTOCHROME_C
9	PROSITE	PS00086	CYTOCHROME_P450
10	PROSITE	PS00192	CYTOCHROME_B_HEME
11	PROSITE	PS50939	CYTOCHROME_B561
12	PROSITE	PS00537	CYTOCHROME_B561
13	PROSITE	PS50255	
14	PROSITE	PS00193	
15	PROSITE	PS00191	

Actual name of the Pfam/PROSITE Class.

PROSITE Accession IDs. Click to find proteins that belong to that ID.

List of Proteins belonging to Pfam or PROSITE Entry

[Protein Home](#) | [Advanced Search](#) | [Search by Pfam or PROSITE](#) | [Browse by GO Slim](#) | [Documents](#) | [Tutorial](#) | [FAQ](#) | [Help](#)

Click to link with the **Pfam** or **PROSITE** database for more information.

or PROSITE:

00281 , Ribosomal_L5 , PS50255

Download the
ids/accessions in
various formats

Matrix displays
summary of all the
Pfam/PROSITE
domains the given
list of proteins share
in addition to these
(e.g PF00033).

Proteins that belong to PF00033 ; cytochrome_b_N ([protein ids\(1\)](#)) ([protein ids\(2\)](#)) ([matrix](#))

#	Name	Organism (Cultivar)	SPTrembl Ac	GenBank id	Extended Pfam Info.
1	Cytochrome b6	<i>Hordeum vulgare</i> (Sabarlis)	P60161	1617031 , 11596	P60161
2	Cytochrome b6	<i>Oryza nivara</i> (Not available)	Q6ENE4	49615025	Q6ENE4
	Cytochrome b	<i>Oryza sativa (indica cultivar-group)</i> (IR36)	P14833	117874	P14833
	Cytochrome b	<i>Oryza sativa (japonica cultivar-group)</i> (Nipponbare)	Q8HNC3	23495409	Q8HNC3
	Cytochrome b	<i>Oryza sativa (japonica cultivar-group)</i> (Nipponbare)	P12123	117874	P12123
	Cytochrome b	<i>Saccharum spontaneum</i>	Q6L372	18701	Q6L372
	Cytochrome b		Q6ENT4	49659541	Q6ENT4
8	Cytochrome b			578659 , 12363 , 13928234	P60162
9	Apocytochrome b	(Not available)	G0	13649946	Q9B3G0
10	Cytochrome b			13700	P07747
11	Ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b			Not available	Q7M2D4
12	Apocytochrome b			40795008	Q6R9D5
13	Cytochrome b	<i>Zea mays</i> (Not available)	P04165	13905	P04165
14	CYTOCHROME B6	<i>Zea mays</i> (Not available)	P05642	Not available	P05642

Protein Name as
recorded in
Gramene. Click to
view the detail
information.

Click to view the
Swiss-Prot
protein entry
page.

Click to view the
GenBank (NCBI)
protein entry page.

Click to view the **Pfam**
annotation (column not
available for PROSITE).

Browse by GO Slim

 [Protein Home](#) | [Search by Pfam or PROSITE](#) | [Browse by GO Slim](#) | [Documents](#) | [Tutorial](#) | [FAQ](#)

Protein Database

☐ Wildcards On

Click to search category in GO
(See *Ontology tutorial*).

Browse by Molecular Function

- catalytic activity (enzyme)
- **enzyme regulator**
- signal transducer
- antioxidant activity
- structural molecule activity
- transporter
- transcription regulator
- translation regulator
- DNA binding
- RNA binding
- nucleotide binding

Browse by Biological Process

- amino acid metabolism
- carbohydrate metabolism
- lipid metabolism
- nucleic acid metabolism
- protein metabolism
- cell cycle
- cell organization
- cell communication
- stress response
- transport
- electron transport
- photosynthesis
- energy pathway

Browse by Cellular Component

- nucleus
- mitochondria
- plastid
- endoplasmic reticulum
- cytosol
- ribosome
- chromosome
- cytoskeleton

Click a term to quickly **browse the Ontology database** to find a list of proteins associated with these particular keywords
(See *Ontology tutorial*).

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Note: Many proteins do not have associations to Gene Ontology (GO) terms. This will restrict your search.

Results for GO Slim

Summary for GO Term: *enzyme regulator activity* (GO:0030234)

Term Name	enzyme regulator activity
Synonym	enzyme modulator.
Aspect	Molecular Function
Definition	Modulates the activity of an enzyme.
External References	GOC:mah
Source Ontology Database Link	The GO browser of Gene Ontology Database.
Derivation	

The **GO term details** include name, synonyms, definition and comments (if any).

- [all \(all\)](#) #512041
 - [\[i\] molecular function \(GO:0003674\)](#) #133742
 - [\[i\] enzyme regulator activity \(GO:0030234\)](#) #928
 - [\[i\] enzyme inhibitor activity \(GO:0004857\)](#) #779
 - [\[i\] enzyme activator activity \(GO:0008047\)](#) #21
 - [\[i\] acetylglutamate kinase regulator activity \(GO:0010307\)](#) #0
 - [\[i\] cyclin-dependent protein kinase 5 activator regulator activity \(GO:0016536\)](#) #0
 - [\[i\] kinase regulator activity \(GO:0019207\)](#) #63
 - [\[i\] phosphatase regulator activity \(GO:0019208\)](#) #50
 - [\[i\] nitric-oxide synthase regulator activity \(GO:0030235\)](#) #0
 - [\[i\] guanylate cyclase regulator activity \(GO:0030249\)](#) #0
 - [\[i\] GTPase regulator activity \(GO:0030695\)](#) #44
 - [\[i\] histone deacetylase regulator activity \(GO:0035033\)](#) #0
 - [\[i\] histone acetyltransferase regulator activity \(GO:0035034\)](#) #0
 - [\[i\] guiding stereospecific synthesis activity \(GO:0042349\)](#) #0
 - [\[i\] ornithine decarboxylase regulator activity \(GO:0042979\)](#) #0
 - [\[i\] caspase regulator activity \(GO:0043028\)](#) #0
 - [\[i\] methionine adenosyltransferase regulator activity \(GO:0048270\)](#) #0

Number of proteins associated with this term.

Icon informs you that child terms exist. Click the term to expand the tree.

The term's lineage in a molecular function category tree, and its children.

Annotations:	863 objects, 928 associations
Gene(2)	Ensembl rice gene(185) Ensembl maize gene(5) Arabidopsis gene(214) Protein(454)
Oryza sativa(2)	
Oryza sativa(185)	
Zea mays(8)	
Ensembl arabidopsis gene:	Arabidopsis thaliana(214)
Protein:	
Aegilops bicornis(1)	Aegilops longissima(2) Aegilops markgrafii(3) Aegilops searsii(1)
Aegilops speltoides(7)	Aegilops tauschii(8) Avena fatua(2) Avena sativa(1)
Coix lacryma-jobi(2)	Eleusine indica(1) Festuca pratensis(1) Hordeum vulgare(1)
Lolium perenne(1)	Oryza sativa(31) Oryza rufipogon(7) Oryza sativa(31)
Oryza sativa (japonica cultivar-group)(129)	Saccharum(1) Secale cereale(6) Setaria italica(2)
Tripsacum dactyloides(2)	Triticum baeticum(1) Triticum monococcum(5) Triticum turgidum subsp. durum(4)
Triticum urartu(3)	Triticum aestivum(5) Zea mays(32)
Zea perennis(8)	

A summary of the total number of **Annotations** to the given Gene Ontology (GO) term.

Links to Gramene proteins associated with term.

Documents

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Resources offering information and Help regarding the protein database.

Documents:

- ◆ [Help document](#)
- ◆ [Evidence codes](#)
- ◆ [Database release notes](#)

Gene ontology (GO) associations:

Associations are based on [Gramene curation](#). Download in bulk from:

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- ◆ GO Consortium [[download](#)]
- ◆ For help on association file please consult the [README file](#)

Download Sequences:

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- ◆ SP_TrEMBL:
[Oryza](#), [Zea](#), [Avena](#), [Hordeum](#),
[Triticum](#), [Aegilops](#), [Secale](#), [Sorghum](#),
[Pennisetum](#), [Lolium](#), [Saccharum](#),
◆ [O.sativa indica](#) (Yu et. al. 2002)

Cellular localization predictions:

[Predotar](#) and [TargetP](#) were used to predict localization to plastid, mitochondria and secretory vesicular localization. The method used is described in [Gramene reference 7047](#).

- ◆ Download [Predotar predictions](#)
- ◆ Download [TargetP predictions](#)

[TMHMM](#) (v. 2.0) was used to predict Transmembrane localization. The method used is described in [Gramene reference 7047](#).

- ◆ Download [TMHMM predictions](#)

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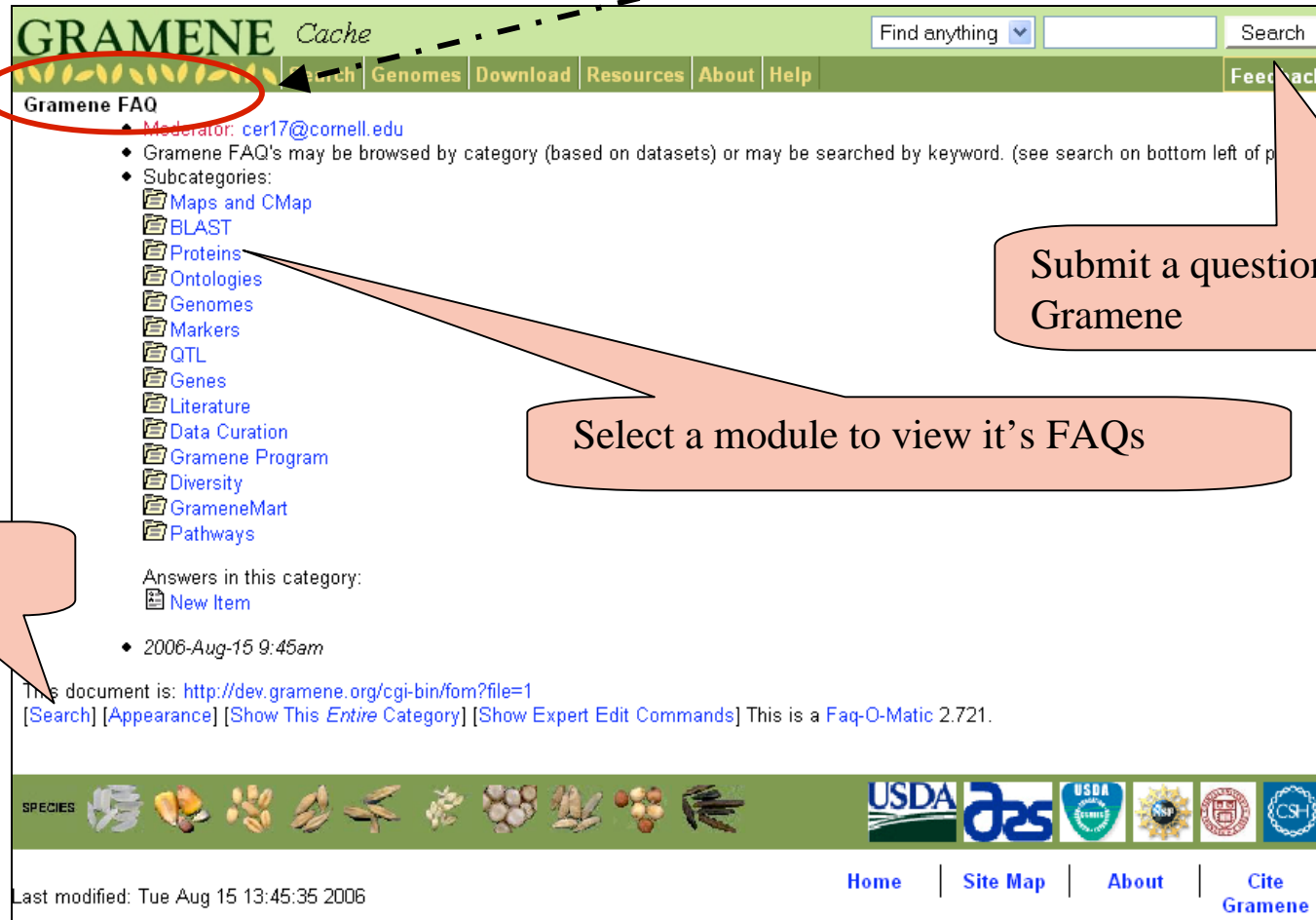


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♦ Moderator: cer17@cornell.edu


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Search: You can search the protein database using any of the following: SWISSPROT accession number, SPTreMBL ID, Protein Sequence Identifier (Protein_ID), Genbank's GI number, protein name, gene name, species or cultivar.

Advanced Search: It allows customized search by the protein name, accession number, protein id (PID) from NCBI/Uniprot/DDBJ, SPTreMBL ID, GenBank ID, cultivar (germplasm) as well as a selection of the species. In the species list only the major cereal crops are listed. If your species of interest is not listed, please select "All Poaceae family". [CLICK HERE](#) to visit advanced search.

- Use star (*) before/after/both in your query text to extend your searches. e.g. alcohol*, *alcohol, *alcohol*. Don't put star if you want exact match.
- Search results can be sorted by accession number, names/symbol/synonym or organism (species and cultivar) on the results page. [CLICK HERE](#) to link to the protein detail information page.

Rice Protein page

• General Information:

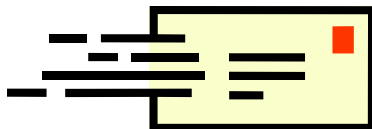
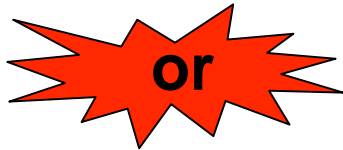
- **Name(s):** Shows the names of the protein molecule based on its function or phenotype. Often it is same as the gene name.
- **Symbol:** Shows the protein symbol.
- **Synonym:** Shows all the alternate names (aliases) by which the molecule is called in various databases and in scientific literature.
- **E.C. Number(s):** Shows the designated [Enzyme Commission](#) (E.C.) number. The EC numbers link to [GenomeNet](#), Japan
- **Gene symbol:** Lists all the gene symbols by which the molecule is called, as designated by the Commission on Plant Gene Nomenclature or by those cited in literature.
- **Best hits to TIGR rice gene models:** The link generates a BLASTP query by using the respective protein sequence against the peptide sequences deduced from the TIGR rice gene models. The query returns a set of best hits on the rice gene models mapped on the TIGR's rice genome assembly of the IRGSP sequence. From the BLAST results page you can use the links to browse the appropriate locus on the rice genome or the TIGR-rice gene model. To learn how to use BLAST search, please visit the [BLAST help document](#)
- **Accession numbers:** Is the [Swissprot](#) accession number, same as the "AC" field from [SWALL](#) (EMBL) record and "ACCESSION" field of [GenBank](#) record of the respective protein entry. Links the protein entry to the other databases namely, [GenBank protein database](#), and [SWISSPROT-TreMBL](#).
- **Database references:** Provides a link to the corresponding entry in the species specific databases such as [GrainGenes](#) (oat, barley, wheat, rye) and [MaizeGDB](#) (maize).
- **Organism:** Represents the taxonomy of the organism from which the protein sequence or the corresponding nucleotide sequence of the gene was derived.
 - **Species:** Shows the Genus and species names and provides link to [Gramene's Taxonomy ontology](#) for further information.
 - **Cultivar:** The name of the variety/stock/germplasm/cultivar (Cv) from which the sequence was derived. The name of the germplasm repositories, like GRIN and IRIS,

Help document provides definitions of terms used, as well as hints for searches.

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