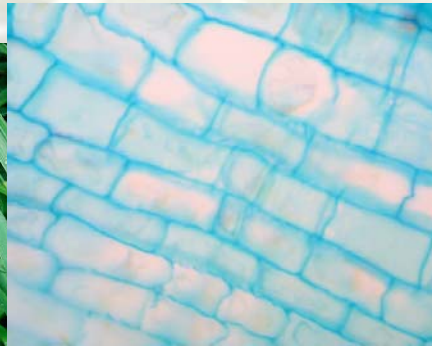


Welcome to the Quantitative Trait Loci (QTL) Tutorial

This tutorial will describe how to navigate the section of Gramene that provides information on Quantitative Trait Loci (QTL). QTL are a statistical creation that identifies a particular region of the genome as containing one or more genes that are associated with the trait being assayed or measured.



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.

Trait Categories in Trait Ontology

Traits at Gramene are identified by Trait Ontology (TO), and are categorized according to:

Abiotic stress: Traits related to stresses from abiotic environment, e.g., water, light, temperature, or chemical.

Anatomy: Traits directly measuring plant parts such as root, stem or leaf.

Biochemical: Biochemical and physiological traits, e.g., enzyme activity.

Biotic stress: Traits related to stresses from pests and pathogens.

Development: Traits related to plant and plant part development. Also includes maturity related traits.

Quality: Traits of economic importance that may affect product quality.

Sterility or fertility: Traits related to male and female flower sterility or fertility, including incompatibility.

Vigor: Traits related to growth and dormancy.

Yield: Traits contributing directly to yield based on economic value.

Gramene Home Page

The image shows the Gramene Home Page, a resource for comparative grass genomics. The page has a green header with the Gramene logo and the tagline "A Resource for Comparative Grass Genomics". Below the header is a navigation bar with links: Search, Genomes, Download, Resources, About, and Help. The main content area is divided into several sections. On the left, there is a "Quick Search" section with a dropdown menu set to "All Available", a search box, and a "Search" button. Below this is a "Have Questions...?" section with a list of links: tutorials, Feedback, Email, FAQ, and Gramene tips. In the center, there is a vertical sidebar with links: Genomes-Ensembl, Maps-CMap, Markers, QTL, Diversity, Genes, Proteins, Pathways, Ontologies, Literature, Sequences-BLAST, and All-GrameneMart. On the right, there is a "Quick Start" section with text about searching for genomes, synteny, and sequence alignment. Below this is a "Genetic Diversity" section with a link to search for SNP and SSR allelic variation. At the bottom, there is a "Biochemical Pathways" section with a link to search for rice pathways and a "Literature" section with a link to search for literature. A callout box with a pointer to the "QTL" link in the sidebar contains the text "Click here to open QTL Home Page".

GRAMENE *A Resource for Comparative Grass Genomics*

Search | Genomes | Download | Resources | About | Help

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.
- Ask questions through [Feedback](#) or [Email](#).
- See [FAQ](#) for questions and answers.
- Browse all Gramene tips (below) for help on searches.

Gramene Tips:

QTL

Quick Start

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

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

[eat](#), [Barley](#), [Oats](#), [Sorghum](#), and other grasses, of different types and species.

Identification Tool ([SSRIT](#)); or search by [marker](#) [Rice](#) (*[Oryza sativa](#)*), [Maize](#), [Sorghum](#) and [Others](#).

s or [QTL](#) database for important phenotype-related loci such as [Rice Genes](#), don't forget to explore traits in [Ontologies](#).

GENETIC DIVERSITY **NEW**: Search for SNP and SSR allelic variation on loci of [rice](#), [maize](#), and [wheat](#) germplasms.

BIOCHEMICAL PATHWAYS **NEW**: Search for ALL the rice pathways on [starch metabolism](#) or get an overview of the [metabolic network](#). Compare [rice](#) and [Arabidopsis](#) pathway datasets.

LITERATURE: Search the literature for your friends and topics of interest.

QTL Home Page

Click here to do a **comprehensive search** for multiple traits or terms
(Slide 12)

 [QTL Home](#) | [Simple Search](#) | [Power Search](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Gramene QTL Database

QTL Quick Search:

Quantitative Trait Loci (QTL) are essentially a statistical creation that identifies a particular region of the genome containing a gene (or genes) that is associated with a trait being assayed or measured. They are shown as intervals across a chromosome where the trait of association is plotted for each marker used in the mapping experiment.

The Gramene QTL Database includes QTL identified for numerous agronomic traits in rice, maize, barley, oat, and sorghum. This is on presenting the QTLs with information on associated trait and the marker used for mapping. The database also provides a browser for the integration of rice QTL to the rice genome. Following the protocol developed in our database, out of total rice QTL, 1000 markers on the genome have been anchored to the rice genome. This will allow users to access a specific QTL or browser QTL by searching traits on the rice genome browser. The data can be downloaded in bulk from the database.

Enter term for **quick search**

Click here for a **simple search** by trait or term
(slides 6-11).

For more information about the current release, see the [QTL Release Notes](#).

Help

See the [Tutorial](#) for an overview on how to use the QTL database. For more information, see the [help page](#).

QTL Search or Browse Option:

The user can search the QTL database by typing a query and restricting the search by any one or all of the following. Use the symbol * for wild card

Click for view most recent **release notes**.

1. Simple Search: by Trait

The screenshot shows the 'QTL Search' web interface. At the top, there's a navigation bar with links: 'QTL Home', 'Simple Search', 'Power Search', 'Help', 'Tutorial', 'FAQ', and 'Feedback'. Below this is a section titled 'QTL Search' with a subtitle 'Search by Trait Category:'. Underneath, there are links for various trait categories: 'Abiotic stress', 'Anatomy', 'Biochemical', 'Biotic stress', 'Development', 'Quality', 'Sterility or fertility', 'Vigor', and 'Yield'. A horizontal line separates this from the search form. The search form has three main sections: 'Search for *:', 'Search in:', and 'Species:'. The 'Search for *:' section has a text input field containing 'BAVEGPH' and a small example '* eg, develop'. The 'Search in:' section has a dropdown menu currently showing '-All Fields-' with a list of options: 'Trait Name', 'Trait Symbol', 'Trait Synonyms', 'Trait Category', 'Linkage Group', 'Published QTL Symbol', 'TO Accession', and 'QTL Accession ID'. The 'Species:' section has a dropdown menu currently showing '-All Species-' with a list of species: 'Barley', 'Foxtail millet', 'Maize', 'Oat', 'Pearl millet', 'Rice', 'Tetraploid wheat', 'Wheat', and 'Wild rice'. To the right of the dropdowns are 'Submit' and 'Reset' buttons. At the bottom of the page, there are logos for various institutions and links for 'Site Map', 'About', and 'Cite Gramene'. Annotations are provided in callout boxes: 'a. Search by trait name, symbol or category, chromosome #, QTL symbol or accession ID. Wildcard searches include the * (i.e. seed*)' points to the search input field; 'b. Limit search by term field. Default searches all fields.' points to the 'Search in:' dropdown; 'c. Limit search by species if desired.' points to the 'Species:' dropdown; and 'd. Click submit. (Slides 8-11)' points to the 'Submit' button. An orange arrow points from the title '1. Simple Search: by Trait' to the 'Simple Search' link in the navigation bar. A starburst graphic is placed over the 'Simple Search' link.

Click a trait to **browse QTL** in that trait category (Slide 7)

a. **Search** by trait name, symbol or category, chromosome #, QTL symbol or accession ID. Wildcard searches include the * (i.e. seed*)

b. Limit search by term **field**. Default searches all fields.

c. Limit search by **species** if desired.

d. Click **submit**. (Slides 8-11)

Simple Search: Browse by Trait Ontology

[QTL Home](#) | [Simple Search](#) | [Power Search](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

QTL Search

Search by Trait Category:

[Abiotic stress](#) | [Anatomy](#) | [Biochemical](#) | [Biotic stress](#) | **[Development](#)** | [Quality](#) | [Sterility or fertility](#) | [Vigor](#) | [Yield](#)

OR

Search for *:

Search in:

Species:

* eg, [development](#), [vegetative*](#), [VGTM](#), [QTL*](#), [AQEZ](#)

Click on the column titles to view a sorted display list.

There were 17 traits found under the category "Development."

Items 1 to 17 of 17

Trait Name	Trait Symbol	TO Accession	Number of QTL	
albino plantlet differentiation frequency	ALBPTLDFQ	TO:0000467		
anthesis silking interval	ANTSKIT	TO:0000467		
basic vegetative phase	BAVEGPH	TO:0000467		
days to flower	DTFL	TO:0000344		View
days to heading	DTHD	TO:0000137	712	View
days to maturity	DTMT	TO:0000469	28	View
days to silk	DTSLK	TO:0000658	50	View
days to tassel	DTTS	TO:0000629	8	View
female flowering	FEMFLW	TO:0000359	0	View
leaf elongation rate	LFELRATE	TO:0000360		View
leaf senescence	LFSNS	TO:0000249		View
male flowering	MALEFLW	TO:0000365		View
phyllon	PHYLLCHRON	TO:0000659		View
growth time	RGTM	TO:0000365		
elongation rate	SHELRATE	TO:0000365		
	TIBUDDOR	TO:0000365		
	VGTM	TO:0000365		

Click for a list of these QTL

Number of QTL that are detected for this trait and listed in the QTL database

B. Click to view trait summary from the Ontology Database (Slide 10) **See Ontology Tutorial**

Results for simple search

There were 4 QTL for “BAVEGPH” (Basic Vegetative Phase.)

QTL Search
 Search by Trait Category:
[Abiotic stress](#) | [Anatomical](#) | [Biotic stress](#) | [Development](#) | [Quality](#) | [Sterility or fertility](#) | [Vigor](#) | [Yield](#)
 OR
 Search for *: in: Species:
* eg, development, vegetative*, VGTm, QTL

Click on the hyperlinked column titles to **sort list** by that column

Click to download **tab delimited results data**

QTLs 1 to 4 of 4

QTL Accession ID	Species Name	Trait Symbol	Trait Name	Published Symbol	Trait Synonyms	Trait Category	Linkage Group	Map	Position
AQF087	Rice	BAVEGPH	basic vegetative phase			Development	1	Rice-JNIG W1944/Peik QTL 2002-1	0.00-28.20 cM
AQF088	Rice	BAVEGPH	basic vegetative phase			Development	1	Rice-JNIG W1944/Peik QTL 2002-1	247.40-267.70 cM
AQF089	Rice	BAVEGPH	basic vegetative phase			Development	4	Rice-JNIG W1944/Peik QTL 2002-1	57.9-110.0 cM
AQF090	Rice	BAVEGPH	basic vegetative phase			Development	6	Rice-JNIG W1944/Peik QTL 2002-1	110.0-110.0 cM

Click to go to **QTL Detail Page** (slide 9)

Click to view **position location on map** (slide 11)

Click to go to **Map Set Info** (see Maps tutorial)

Note: Results from all search options display this table format

QTL Detail

QTL Home | Simple Search | Power Search | Help | Tutorial | FAQ

Details for QTL "AQF088" (b

Gramene-assigned QTL accession ID

Gramene-assigned standardized trait symbol; Click to view all QTL with this symbol

QTL symbol as assigned in the publication cited.

Linkage group (chromosome) QTL has been mapped to; Click to view all QTL on this chromosome

Click to view QTL detail in markers db, or to view position on Map or genome browser (*Slide 11*)

Click to view source literature (rice) or database (maize, wheat)





QTL Accession ID	AQF088									
Species	Oryza sativa (Rice)									
Trait Symbol	BAVEGPH									
Trait Name	basic vegetative phase									
Published Symbol										
Trait Synonym(s)										
Trait Category	Development									
Chromosome	1									
Mappings	Species	Map Type	Map Set	Name						
	Oryza sativa (Rice)	QTL	JNIG W1944/Peik QTL 2002	BAVEGPH	1	247,4	26,57	View in Mappings DB	View Comparative Map	Experimental
				VEGPH	Chr. 1	31,373,895	31,375,850	View in Mappings DB	View in Genome Browser	Inferred
Related Ontologies	Plant Structure	whole plant (PO:0000003)				Evidence	IAGP			
	Plant Growth and Development Stage	A vegetative growth (PO:0007134)				Evidence	SM			
	Species Ontology	Oryza sativa (GR_tax:013681)				Evidence	SM			
						Evidence	Gramene Lit. 7750			
Comments	Related with heading behavior.									
DBXRefs	Gramene Literature	Cai-W Morishima-H, QTL clusters reflect character associations in wild and cultivated rice. Theoretical and applied genetics. 104. 2002. pp. 1217-1228								

3/22/07

Trait Ontology (TO) Accession

 [Term](#) | [Annotations](#)

Summary for TO Term: *basic vegetative phase* (TO:0000461)

Term Name	basic vegetative phase
Synonym	BAVEGPH.
Aspect	Trait
Derivation	<ul style="list-style-type: none">• all (all) #512041 <ul style="list-style-type: none">◦ [i] trait ontology (TO:0000387) #13161 <ul style="list-style-type: none">▪ [i] growth and development trait (TO:0000357) #3184 <ul style="list-style-type: none">▪ [i] vegetative growth time (TO:0000369) #27 <ul style="list-style-type: none">▪ [i] basic vegetative phase (TO:0000461) #4
Parent Term (1)	<ul style="list-style-type: none">• [i] vegetative growth time (TO:0000369)

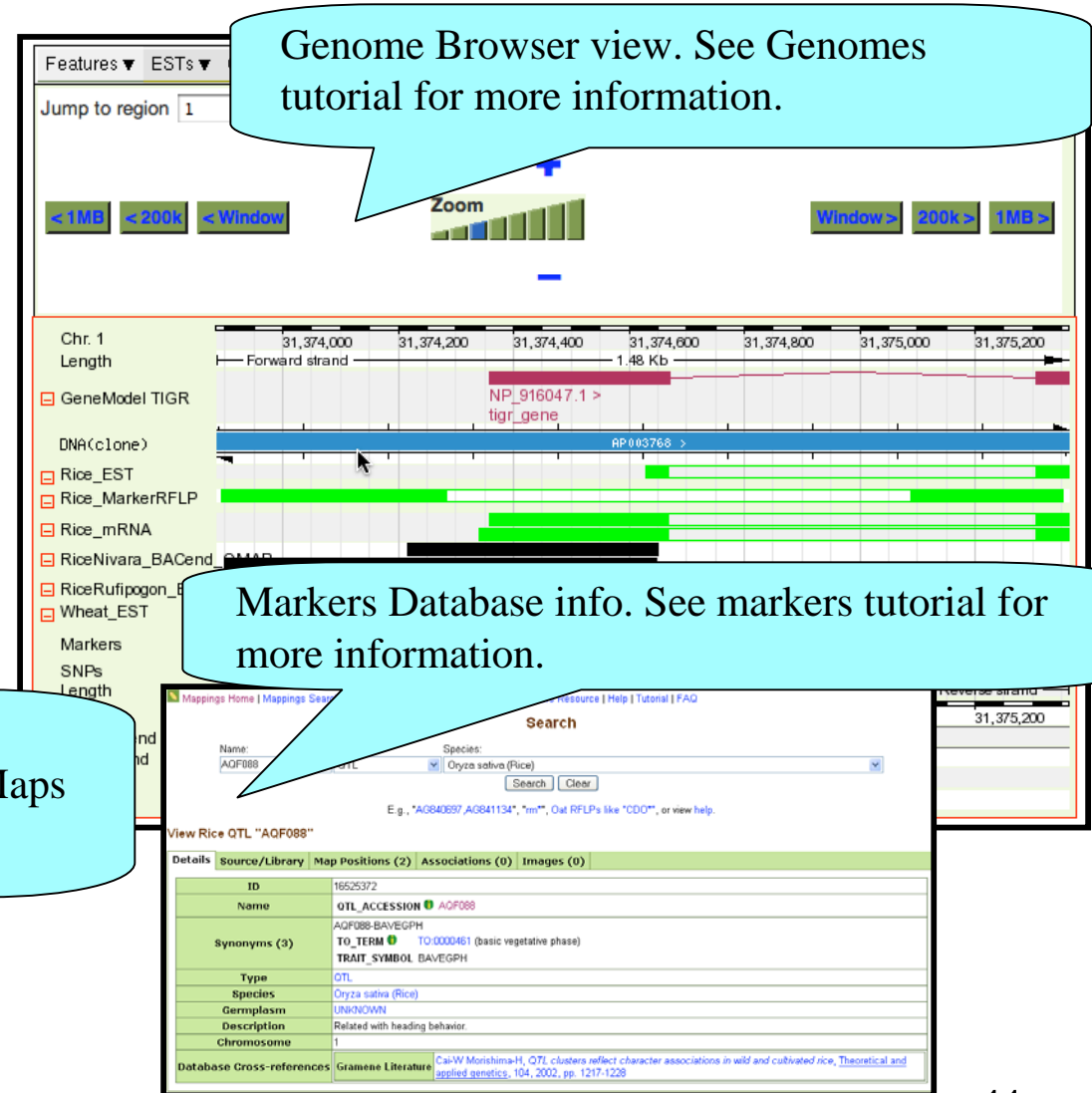
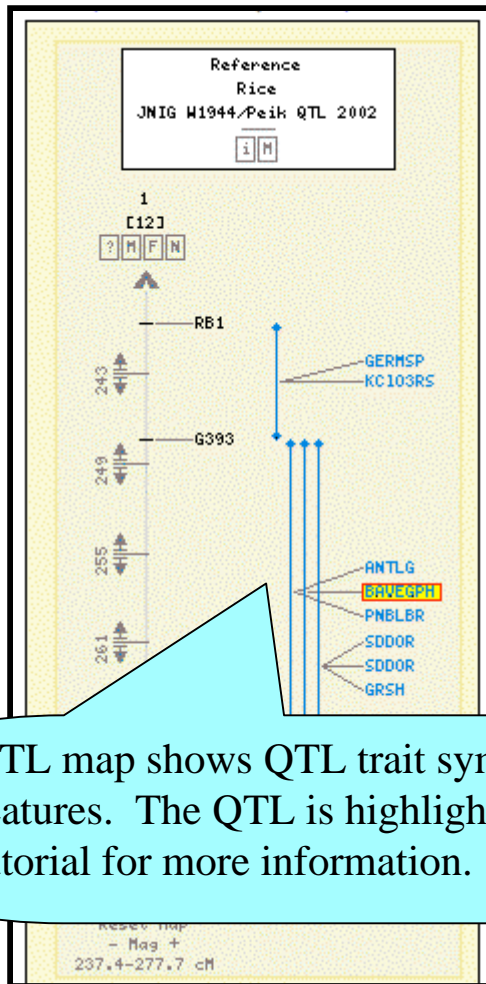
Total Number of Annotations:	4 objects, 4 associations QTL(4)
QTL:	Oryza sativa(4)

“Basic Vegetative phase” is an example of “vegetative growth time”, which is a growth and development trait.

Number of associations this term has to the database. In this case, they are all QTL

See Ontology Tutorial for more information on ontology

Mappings



To construct a comprehensive query, select **criteria to include** in your search

3. Power Search

To construct a comprehensive query, select **criteria to exclude** in your search

QTL Home | Simple Search | Power Search | Help | Tutorial | FAQ

QTL Power Search

Include		Exclude	
Trait Names:	<ul style="list-style-type: none"> seed dormancy (SDDOR) seed fertility (SDFRT) seed length (SDLG) seed length to width ratio (SDLGWDR) seed longevity (SDLNG) 		<ul style="list-style-type: none"> 100-grain weight (HGRWT) 100-seed weight (HSDWT) 1000-grain weight (TGRWT) 1000-seed weight (TSDWT) abaxial stomata (ABSTOM)
Species:	<ul style="list-style-type: none"> Rice Sorghum Tetraploid wheat Wheat Wild rice 		<ul style="list-style-type: none"> Barley Foxtail millet Maize Oat Pearl millet
Linkage Groups:	1*		10*, 11*, 12*

*You may indicate multiple traits, species, and linkage groups to include or exclude.
Hold the "Control" or "Command" key to select traits and species,
and separate linkage groups with spaces or commas, e.g., "1, 11 7H."*

Submit Reset Clear Form

To select multiple trait names or species, hold "Control" (or "Command" on Mac) key while selecting multiple traits.

To search rice chromosome 1, type "1*" in the "Include" field of "Linkage Groups". With the wild card the linkage groups with the names of "1a", "1b", and so forth, will be included. However, it will also include other chromosomes that begin with 1, so I will type "10*", "11*" and "12*" in the "Exclude" field of "Linkage Groups".

Click to submit (results will appear in the format as on slide 8.)

QTL Help

 [QTL Home](#) | [Simple Search](#) | [Power Search](#) | [Help](#) | [Tutorial](#) | [FAQ](#)



Gramene QTL Database

Help Document:

The database provides the following types of information on a QTL:

- **QTL:** A quantitative trait locus.
- **QTL accession ID:** The Gramene QTL accession ID is unique for each QTL.
- **Trait name:** The name of the trait for which the QTL was detected.
- **Trait symbol:** A standardized abbreviation for the trait assigned by Gramene curators. The symbol is displayed as a QTL feature name in maps.
- **Trait synonym(s):** Other names for the trait.
- **Trait category:** Each trait belongs to a parent trait category. These are assigned by agronomic importance.
 - **Abiotic stress:** Traits related to stresses from abiotic environment, e.g., water, light, temperature, or chemical.
 - **Anatomy:** Traits directly measuring plant parts such as root, stem or leaf.
 - **Biochemical:** Biochemical and physiological traits, e.g., enzyme activity.
 - **Biotic stress:** Traits related to stresses from pests and pathogens.
 - **Development:** Traits related to plant and plant part development. Also includes maturity related traits.
 - **Quality:** Traits of economic importance that may affect product quality.
 - **Sterility or fertility:** Traits related to male and female flower sterility or fertility, including incompatibility.
 - **Vigor:** Traits related to growth and dormancy.
 - **Yield:** Traits contributing directly to yield based on economic value.
- **Species:** The species in which the QTL was detected.
- **Linkage group:** The linkage group or the chromosome number on which the QTL was mapped.
- **Published QTL symbol:** QTL symbol assigned by the author in the source paper.
- **Map position:** Links to the QTL map and displays the QTL feature position in Maps.
- **Comments:** Any comments by the Gramene curators.
- **DBXRefs:** Links to the Gramene citation record where the information on the QTL was published.

QTL help file shows database summary, description of terms, and search help.

QTL search/browse options:

A. Simple Search

Using the "Simple Search", the user can browse through the QTL database by trait categories and traits or search for a term in one or all the fields.

Option 1: Browse by Traits

The user can browse the QTL by trait categories and the trait names.

QTL Tutorial

 [QTL Home](#) | [Simple Search](#) | [Power Search](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

QTL Tutorial

Select your preferred format:

- ♦ [PowerPoint](#)
- ♦ [Adobe PDF](#)

Tutorial link offers
PowerPoint or PDF formats.

Release Notes

Links to other tutorials

Gramene Tutorials: [Navigation](#) | [Overview](#) | [Genomes](#) | [GrameneMart](#) | [BLAST](#) | [Maps](#) | [Mappings](#) | [Proteins](#) | [Ontologies](#) | [Genes](#) | [QTL](#) | [Diversity](#) | [Pathways](#) | [Literature](#)

Free associated software:



[PowerPoint viewer](#)

Download free software
for viewing tutorial

FAQ



The screenshot shows the Gramene FAQ page. At the top is the 'GRAMENE Cache' header with a search bar and navigation links: Search, Genomes, Download, Resources, About, Help, Feedback. Below the header is the 'Gramene FAQ' section, which includes a moderator email (cer17@cornell.edu) and instructions on how to browse or search FAQs. A list of subcategories is provided, each with a folder icon: Maps and CMap, BLAST, Proteins, Ontologies, Genomes, Markers, QTL, Genes, Literature, Data Curation, Gramene Program, Diversity, GrameneMart, and Pathways. The 'QTL' category is highlighted with a callout box. Below the list, there is a section for 'Answers in' and a 'New Item' link. At the bottom, there is a date '2006-Aug-15 9:25' and a footer with the document URL and a list of links: [Search], [Appearance], [Show This Entire Category], [Show Expert Edit Commands], and a note about the Faq-O-Matic version (2.721).

GRAMENE Cache

Find anything Search

Search Genomes Download Resources About Help Feedback

Gramene FAQ

Moderator: cer17@cornell.edu

- Gramene FAQ's may be browsed by category (based on datasets) or may be searched by keyword. (see search on bottom left of page)
- Subcategories:
 - Maps and CMap
 - BLAST
 - Proteins
 - Ontologies
 - Genomes
 - Markers
 - QTL
 - Genes
 - Literature
 - Data Curation
 - Gramene Program
 - Diversity
 - GrameneMart
 - Pathways

Answers in

New Item

2006-Aug-15 9:25

This document is: <http://dev.gramene.org/cgi-bin/fom?file=1>
[Search] [Appearance] [Show This Entire Category] [Show Expert Edit Commands] This is a Faq-O-Matic 2.721.

Submit a question to Gramene

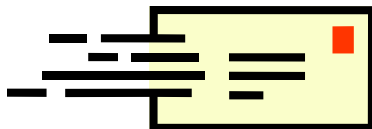
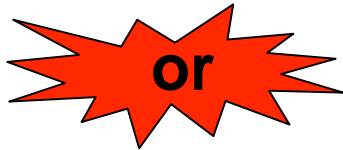
Select module for FAQ

Search FAQ by keyword

Contact Gramene



Use the feedback button, located at the top of every page, to provide feedback or to ask questions about Gramene.



Email Gramene at gramene@gramene.org