

# Gramene's Ontologies Tutorial

This database is a collective resource of structured controlled vocabularies (Ontologies) for knowledge domains and their associations.

## Knowledge Domains:

Plant Ontology (PO)

Plant Structure (morphology, organs, tissue and cell types) and Development\*

Growth stages (plant growth and developmental stages)

Trait Ontology (TO)

Plant traits and phenotypes

Gene Ontology (GO)

Molecular function

Biological process

Cellular component

Environment Ontology (EO)

Gramene's taxonomy ontology (GR tax)

## Associations:

Use this database to quickly find Ensembl rice genes (from TIGR's rice genome assembly), proteins from SWISSPROT-TrEMBL representing Poaceae (grass) family, rice genes, QTL and map sets.

**Note: Remember that different ontologies are for different purposes and do not overlap with each other.  
For more information on each ontology type please visit the current ontologies section at Gramene**

# 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 Home Page with a navigation menu at the top. The menu includes links for Search, Genomes, Species, Download, Resources, About, Help, and Feedback. Below the menu is a search bar with the text "Find anything" and a magnifying glass icon. The main content area is divided into several sections:

- Left Sidebar:**
  - GRAMENE Home** logo and navigation menu.
  - A Resource for Comparative Grass Genomics**
  - Release # 26** (September 2007)
  - News**
    - October 15-17, 2007 - 5th International Symposium of Rice Functional Genomics in Tsukuba, Japan
    - NEW Sept 2007, V 26 release notes.
    - NEW Gramene July/August Newsletter
  - Have Questions...?**
    - NEW Quick Search Help
    - Tutorials - See what you can do and how to do it.
    - Ask questions through Feedback or Email.
    - See FAQ.
  - Outreach Calendar
  - Presentation Materials
- Navigation Menu:**
  - Search
  - Genomes-Ensembl
  - Maps-CMap
  - Markers
  - QTL
  - Diversity
  - Genes
  - Proteins
  - Pathways
  - Ontologies** (highlighted by an orange callout box with the text "Click here to open ontology search")
  - Literature
  - Sequences-BI
  - All-Gramene
  - Simpl
- Quick Start:**
  - ed genomes for *Oryza Sativa*, *Oryza rufipogon*, Maize & Arabidopsis; Look
  - your search with GrameneMart; Search for sequence alignment with
  - logy.
  - or PopSite or Browse by Gene Ontology using GO Slim.
  - se genetic or physical maps for Wild Rice (*Oryza* sp. from OMAP), Rice,
  - Sorghum, and other grasses, or use the Comparative Map Viewer (CMap)
  - types and species. View map detail information
  - ic marks (RFLPs, SSRs, etc.), DNA Probes (Primers, Overgos, etc.),
  - ences (GSSs, ESTs, etc.). Search by species
  - by species and type such as Rice SSR. Use the
- Visit with us at:**
  - Sept 21-22 Agricultural Ontology Service (AOS) Workshop
  - Jan 12-16, 2008 PAG XVI
- Gramene Tip:**
  - Users can submit ontology (controlled vocabulary) information to Gramene.
  - Browse All Tips
- GRAMENE Tip:**
  - GRAMENE is a curated, open-source, 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.

## Module Home-Page layout

Module home pages provide the following information:

- **Searching/Browsing** – links to different types of searches.
- **Other Tools** – if applicable, links to different tools used in this module.
- **Help** – links to help pages, tutorials, release notes, FAQ and other helpful documentation.
- **Download** – information on where to download the database.
- **Feedback** – How to contact Gramene
- **Acknowledgements** – Other programs that contribute to this data.
- **Quicklinks and external links** – when appropriate these links are provided.

# Ontology Home Page

Click here if you need more help on Ontology

Ontologies Search | [Browse](#) | [Ontology Submission](#) | [Tutorial](#) | [FAQ](#) | [Help](#)

Gramene Ontologies

[Browse Current Ontologies](#)

Find:



Ontology (opt.):  Gene Ontology (GO)  Plant Structure (PO)  Growth Stage (G)

2. Click to browse terms or to learn more about their use and key concepts.

E.g., [flower](#) or [TO:0000303](#).

The Ontologies database provides a collective information for structured controlled vocabularies (ontologies) for the following knowledge domains and their associations to various objects such as QTL, phenotype gene, proteins and rice genes.

or

- Plant Ontology (PO)
    - Plant Structure (morphology and all types)\*
    - Growth stages (plant)
  - Trait Ontology (TO)
    - Plant traits and
  - Gene Ontology (GO)\*\*
    - Molecular function
    - Biological process
    - Cellular component
  - Environment Ontology (E)
  - Gramene's taxonomy of plants
- [\* Developed by the Plant Ontology Consortium]

1. Type term name and click search. (option- to limit a search, click box of desired ontology type)

The vocabularies are derived from the Gene Ontology Consortium, accompanied by appropriate definitions. Through this effort, the database as member of Gene Ontology Consortium, aims to foster consistency and encourages international usage of these ontologies in the annotation of data objects.

## Search or Browse Options

- [Home Page](#) Search the Ontologies database by keyword, and optionally filter by ontology. Get an introduction to ontologies.
- [Browse](#) Browse by a specific ontology, get a general introduction to the ontologies in Gramene, or download the ontologies and definitions.

## Help

- [Help](#) Presents an overview on how to use the Ontologies database and lists explanations of field names.
- [Tutorial](#) More in-depth than the help pages, use the tutorial for an example of using the database, see how it integrates other datasets, and get tips to increase your data search efficiency.
- [FAQ](#) Frequently Asked Questions - see what questions users have asked, and get the developers answers.
- [Release Notes](#) For more information about the most recent release.
- [Evidence codes](#) Defines the evidence codes and explains how they are used for PO annotation of genes/gene products/phenotypes

## Ontology Submission

9/24/07



# Browsing the Ontology Database

[Ontologies Search](#) | [Browse](#) | [Ontology Submission](#) | [Tutorial](#) | [FAQ](#) | [Help](#)

Links to the most up to date versions of ontology flat files are provided below. Definitions of the terms in all ontologies are contained in respective definition files. You may wish to download the flat files and view them by using a stand alone ontology browser [DAG-EDIT](#)

Current Ontologies	Browse	Download (in OBO format)
<b>Trait Ontology™ (TO)</b> It is a controlled vocabulary to describe each trait as a distinguishable feature, characteristic, quality or phenotypic feature of a developing or mature individual. Examples are glutinous endosperm, disease resistance, plant height, photosensitivity, male sterility, etc.	<a href="#">BROWSE</a>	<a href="#">Ontology + Definitions</a>
<b>Gene Ontology™ (GO)</b> Developed by the <a href="#">Gene Ontology Consortium</a> to help annotate information on gene products (not the genes) using the following three organizing principles of molecular function, biological process and cellular component. Copyright © Gene Ontology Consortium.		<a href="#">All ontologies + Definitions</a>
<b>Molecular Function:</b> The tasks performed by individual gene products; example is Rubisco	<a href="#">BROWSE</a>	..
<b>Biological Process:</b> Broad biological goals, such as photosynthesis or ripening, that are accomplished by ordered assemblies of molecular functions.	<a href="#">BROWSE</a>	..
<b>Cellular Component:</b> Subcellular structures, locations, and macromolecular complexes; examples include chloroplast, telomere, vacuole, nucleus, etc. .	<a href="#">BROWSE</a>	..
<b>Plant Ontology™ (PO)</b> Gramene is collaborating with The Plant Ontology Consortium ( <a href="#">POC</a> ) to develop a controlled vocabulary for plant structure and growth stages.		
<b>Plant Structure (PO):</b> The controlled vocabulary of plant structure and growth stages. Examples are stamen, gynoecium, petal, parenchyma, guard cell, etc.	<a href="#">BROWSE</a>	<a href="#">Ontology + Definitions</a>
<b>Cereal Plant Growth Stages (GRO):</b> The controlled vocabulary of growth stages for various cereal plants. Examples are germination, seedling, booting, flowering, etc. wheat, oat and barley.	<a href="#">BROWSE</a>	<a href="#">Ontology + Definitions</a>
<b>Environment Ontology (EO)</b> It represents a controlled vocabulary to describe different types of supplemental environments that have been reported in the experimental profiles of gene expression and phenotype (mutant and QTL) studies on cereal plants.	<a href="#">BROWSE</a>	<a href="#">Ontology + Definitions</a>

3. Click on "BROWSE" to navigate through the desired ontology type.

# Searching the Ontology Database

Type your query  
*e.g. Example is a search for  
function alpha-amylase*

Select “Gene Ontology” to search the  
GO database (or select one or more  
others appropriate to your term.)  
*(Molecular Function is part of Gene  
Ontology)*

Click search icon

The screenshot shows the search interface for the Ontology Database. At the top, there are navigation links: [Ontologies Search](#), [Browse](#), [Ontology Submission](#), [Tutorial](#), [FAQ](#), and [Help](#). Below these is a search bar with the text "Find: alpha-amylase" and a magnifying glass icon. Underneath the search bar, the "Ontology:" section is highlighted with a red oval and contains several radio button options:  Gene (GO),  Plant Structure (PO),  Growth Stage (GRO),  Trait (TO),  Environment (EO), and  Taxonomy (GR\_tax). Below the ontology options, there is an "Options:" section with  Exact Match and  Include Obsolete Terms. In the bottom right corner, there is a small text link: "E.g., [flower](#) or [TO:0000303](#)".

# Gene Ontology (GO) search results

*Exact ontology term*

*Definition of the ontology term*

Ontologies Search | Browse | Ontology Submission | Tutorial | FAQ | Help

alpha-amylase

Ontology:  Gene (GO)  Plant Structure (PO)  Growth Stage (GRO)  Trait (TO)  Environment (EO)  Taxonomy (Tax)

Options:  Exact Match  Include Obsolete Terms

E.g., flower or TO:0000303

Ontology Terms 1 to 5 of 5

Term Accession	Aspect	Term Name	Synonyms	Definition
<a href="#">GO:0004556</a>	Molecular Function	alpha-amylase activity	1,4-alpha-D-glucan glucohydrolase activity, glycogenase activity	Catalysis of the endohydrolysis of 1,4-alpha-D-glucosidic linkages in polysaccharides containing three or more 1,4-al...
<a href="#">GO:000574</a>	Molecular Function	oligo-1,6-glucosidase activity	isomaltase activity, oligosaccharide alpha-1,6-glucosidase activity, sucrose-isomaltase activity	Catalysis of the hydrolysis of 1,6-alpha-D-glucosidic linkages in some oligosaccharides produced from starch and glyc...
<a href="#">GO:000576</a>	Molecular Function	alpha-amylase inhibitor activity		Stops, prevents or reduces the activity of alpha-amylase.
<a href="#">GO:000577</a>	Biological Process	pancreatic juice secretion		The regulated release of pancreatic juice by the exocrine pancreas into the upper part of the intestine. Pancreatic j...
<a href="#">GO:000578</a>	Molecular Function	glucan 1,4-alpha-maltohydrolase activity	1,4-alpha-D-glucan alpha-maltohydrolase activity, glucan-1,4-alpha-maltohydrolase activity, maltogenic alpha-amylase	Catalysis of the hydrolysis of (1->4)-alpha-D-glucosidic linkages in polysaccharides so as to remove successive alpha...

*Synonyms (if any)*

*Ontology Accession for the ontology term. Select to view detailed information. (see next slide)*



# Ontology Term Accession Detail

<b>"alpha-amylase activity" (GO:0004556)</b>	
Term Name	alpha-amylase acti
Term Accession	GO:0004556
Aspect	Molecular Functi
Synonyms (2)	1,4-alpha-D-gluc activity
Definition	Catalysis of the endoh of 1,4-alpha-D-glucosidic linkages in linked D-glucose uni
Comment	None
Source Ontology Database	<a href="#">The GO browser of Gene Ontology Database</a>
<b>Derivation</b> function (GO:0003674) #150800 ⊕ lytic activity (GO:0003824) #56888 ⊕ [i] hydrolase activity (GO:0016787) #16444 ⊕ ▪ [i] hydrolase activity, acting on glycosyl bonds (GO:0016798) #1885 ⊕ ▪ [i] hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004556) #107 ▪ [i] amylase activity (GO:0016160) #181 ⊕ ▪ [i] <b>alpha-amylase activity (GO:0004556) #107</b>	
Database Cro	
<b>Parents (1)</b> Children (0)	
<b>Associations (107)</b> ⊕ Ensembl arabidopsis gene (8) ⊕ Ensembl rice gene (10) ⊕ Gene (10) ⊕ Protein (79)	
<b>Associations (107)</b> Ensembl arabidopsis gene (8) Arabidopsis thaliana (8) Ensembl rice gene (10) Oryza sativa (10) Gene (10) Oryza sativa (10) Protein (79) Oryzopsis tauschii (3) Eleusine coracana (1) Hordeum vulgare (25) Hordeum vulgare subsp. spontaneum (2) Oryza sativa (japonica cultivar-group) (13) Sorghum bicolor (2) Triticum aestivum (18) Avena fatua (2) Zea mays (10)	

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Exact ontology term

Links to source that originally developed this ontology.

The lineage of alpha-amylase activity as a molecular function

+ Indicates expandable tree. Click on term to expand.

Number of database objects associated in the database with this term.

External references used for defining terms or making associations.

Definition of the term

Term-term relationship [i]: IS A (type of) – see help file for more information

Click to expand.

Click to get a complete list of associations with the given ontology term (see next slide.)

Click to view the term and its children (indirectly associated to parent term if any) for which the object type was annotated (see previous slide)

# Ontology Associations

## Gene Associations for Molecular Function Term "alpha-amylase activity" from species "Oryza sativa"

Back to Term [GO:0004556](#)

Associations 1 to 10 of 10

Term Name	Object Type	Object Accession ID	Object Symbol	Object Name	Object Synonyms	Object Species	Evidence
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0060043</a>	Amy1	Amylase-1	RAmy1A/CIAmy1AIAmy1A/C*	Oryza sativa	IMP (Causse-M-A et al., 1994, PMID 7896104)
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0060076</a>	Amy10	Amylase(Beta)-10	Beta		IMP
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0060044</a>	Amy2	Amylase-2	Am		IMP (Causse-M-A et al., 1994, PMID 7896104)
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0061333</a>	Amy3	Amylase-3	RAmy1A/CIAmy1CIAmy1A/C*	Oryza sativa	IMP (Causse-M-A et al., 1994, PMID 7896104)
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0060045</a>	Amy4	Amylase-4	Amy2A*IAmy2A	Oryza sativa	IMP (Causse-M-A et al., 1994, PMID 7896104)
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0060046</a>	Amy5	Amylase-5	Amy3AIRAmy3A/B/CIAmy3A/B/C*	Oryza sativa	IMP (Causse-M-A et al., 1994, PMID 7896104)
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0061333</a>			IRAmy3A/B/CIAmy3A/B/C*	Oryza sativa	IMP (Shiraishi-M et al., 1986)
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0061333</a>			IRAmy3A/B/CIAmy3A/B/C*	Oryza sativa	IMP
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0061333</a>					
<a href="#">alpha-amylase activity</a>	Gene	<a href="#">GR:0061333</a>					

Method used to ascertain this association. Click on code for description.

Links to the original entry in Gramene database. Click for TIGR gene report in Gramene. (See Genomes Tutorial)

- IMP inferred from mutant phenotype**
- Any gene mutation / knockout (or deletion) / disruption
  - Over expression / ectopic expression of wild-type or mutant genes
  - Anti-sense experiments
  - RNAi experiments
  - Specific protein inhibitors
- IGI inferred from genetic interaction**
- Traditional genetic interactions such as suppressors, synthetic lethals, etc.
  - Functional and/or genetic complementation
  - Rescue experiments
  - Inference about one gene drawn from the phenotype of a mutation in a different gene
  - Also where a mutation in one gene (gene A) provides information about the function, process, or component of another gene (gene B; i.e. annotate
- IPI inferred from physical interaction**
- 2-hybrid interactions or 3-hybrid interactions
  - Co-purification

## Searching other ontologies

Previous slides presented the gene ontology (GO) example. The same procedure must be followed if you would like to search other ontologies.

The following table suggests the type of objects that are associated with different types of ontologies:

Ontology	Associated object types
Gene Ontology	Ensembl rice genes (from rice genome assembly) Proteins from SWISSPROT-TrEMBL
Plant Ontology Plant structure or anatomy (PO) Cereal plant growth stages (GRO)	phenotype genes phenotype genes
Trait Ontology	Phenotype genes QTL
Environment Ontology	Coming soon
Gramene Taxonomy Ontology	Proteins from SWISSPROT-TrEMBL QTL Map sets

# Other Options From Ontologies

The lower half of the ontologies home page offers other helpful resources.

*Link to Evidence Code definitions. (see next slide)*

## Help

<a href="#">Help</a>	Overview on how to use the Ontologies database and lists explanations of field codes.
<a href="#">Tutorial</a>	For more in-depth than the help pages, use the tutorial for an example of using the database, see <a href="#">here</a> to increase your data search efficiency.
<a href="#">FAQ</a>	Frequently Asked Questions - see what questions users have asked, and get the developers' answers.
<a href="#">Release Notes</a>	For more information about the most recent release.
<a href="#">Evidence codes</a>	Defines the evidence codes and explains how they are used for PO annotation of genes/gene products.

Click to submit your ontology suggestions

## Ontology Submission

Any suggestions for the addition, replacement or modification of the controlled vocabulary can be made via the Plant Ontology Consortium [here](#)

## Download

The data can be downloaded in bulk from our FTP Plant Ontology archive at [ftp://ftp.gramene.org/pub/gramene/CURRENT\\_RELEASE/data/ontology/](ftp://ftp.gramene.org/pub/gramene/CURRENT_RELEASE/data/ontology/). The ontology files are organized by ontology type(s).

Click to download ontologies

## Publications

- Gramene: development and integration of trait and gene ontologies for rice. *Comparative and Functional Genomics*, 2002, Vol 3(2), April, 2002. [see [Abstract](#)] or [[search for full text \(search for "91016047"\)](#)].
- The Plant Ontology™ Consortium and Plant Ontologies. *Comparative and Functional Genomics*, 2002, Vol 3(2), April, 2002. [see [Abstract](#)] or [[search for full text \(search for "91016119"\)](#)].
- Creating the gene ontology resource: design and implementation. *Genome Research*, 2001, Vol 11(8), 1425-1433. [[Abstract](#)] [[Full Text](#)]
- Gene Ontology: tool for the unification of biology. *Nature Genetics*, 2000, 25: 25-29. [[Abstract](#)] [[Full Text](#)]

## Acknowledgements

- Plant Ontology has been developed and contributed by the Plant Ontology Consortium (POC) collaborating with The Plant Ontology Consortium (POC) to develop the controlled vocabulary for plant structure (anatomy) and growth stages.
- Gene Ontology has been developed and contributed by the Gene Ontology Consortium (GOC). GOC associations are based on Gramene curation and [Interpro](#) assignments. Results are available at:
  - Gramene [[view](#)]
  - Gene Ontology Consortium [[view](#)] - [[download](#)]
  - Help on Gene Ontology associations [[view](#)]

*Learn more about ontologies from these publications*



This is a list of evidence codes used in curation at Gramene. These are the basis for ascertaining associations.

# Evidence Codes

## Controlled Vocabulary and Ontology for Plants

### Evidence codes:

In order to help standardize the way evidence codes are used for curation of the various databases in Gramene ([www.gramene.org](http://www.gramene.org)) eg. Protein, Mutant, QTL, etc. by using the necessary Ontology viz.

**GO** (Gene Ontology) for describing genes and their products.

**TO** (Trait Ontology) for description of phenotypic traits related to mutants and QTLs.

**PO** (Plant Ontology) for describing plant specific morphology, anatomy and development related terms.

The codes are listed along with examples (not exhaustive lists) of the kinds of experiments that would fall into each category. For every evidence category, there is a flexibility for the curators to exercise judgement about the quality of the evidence, and how well it supports annotation to a node within each ontology. The distinction between "TAS" and "NAS" is particularly sensitive to interpretation. We will appreciate your feedback, if you think that we should include other types of methodologies under the sub-categories and expand the framework of evaluation. Please feel free to communicate your thoughts at [gramene@gramene.org](mailto:gramene@gramene.org).

### **IC** *inferred by curator*

- To be used for those cases where an annotation is not supported by any evidence, but can be reasonably inferred by a curator from other GO annotations, for which evidence is available

### **IDA** *inferred from direct assay*

- Enzyme assays
- In vitro reconstitution (e.g. transcription)
- Immunofluorescence (for specific localization either / both in a tissue type or in a cellular component)
- Cell fractionation (for cellular component)
- Physical interaction / binding assay (sometimes appropriate for cellular component)

### **IEA** *inferred from electronic annotation*

- Annotations based on "hits" in sequence similarity searches, if they have not been reviewed by curators (curator-reviewed hits would get ISS)
- Annotations transferred from database records, if not reviewed by curators (curator-reviewed items may use RCA, or the reviewing process may lead to print references for the annotation)

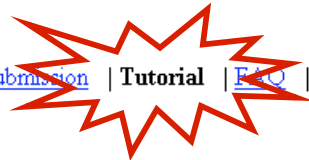
### **RCA** *inferred from Reviewed Computational Analysis*

- Predictions based on large-scale experiments (e.g. genome-wide two-hybrid, genome-wide synthetic interactions)
- Predictions based on integration of large-scale datasets of several types
- Text-based computation (e.g. text mining)
- This code is used for annotations based on a non-sequence-based computational method, where the results have been reviewed by an author or a curator. As noted above, IEA should be used for any computational annotations that are not checked for accuracy by a curator (or by the authors of a paper describing such analysis), and sequence comparisons that have been reviewed use ISS. For microarray results alone, IEP is preferred, but RCA is used when microarray results are combined with results of other types of large-scale experiments.



# Tutorial

[Ontologies Search](#) | [Browse](#) | [Ontology Submission](#) | **Tutorial** | [FAQ](#) | [Help](#)



## Ontologies Tutorial

Select your preferred format:

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[About Ontologies \(Powerpoint\)](#)

[Release Notes](#)

*Different options available for all browsers*

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Search FAQ

## FAQs

### **Ontologies**

#### **What is an ontology and why do we need it?**

An ontology is a standardized (controlled) glossary of keywords arranged in a structured order or a network based on biological concepts. Each vocabulary term has a fixed identification and a definition. It allows the users to query the different databases or subsections of a database using the same keywords and different databases have implemented the commonly adopted ontologies).

#### **Is there a tutorial or help section on how to use the Ontologies database?**

#### **What types of ontologies does the Gramene database use?**

#### **Who develops these ontologies and can I participate in their development?**

#### **Can I suggest a new term to be included in an ontology?**

#### **Can I use Gramene's ontologies for use in the curation of my own data sets?**

#### **How can I get a list of all the proteins or genes associated to a given ontology term in Gramene?**

#### **What is the GO/GRO/TO number after a given ontology term?**

#### **What is the number after the # sign found in an ontology term's derivation or tree?**

#### **What do [i] and [p] stand for in a term's derivation or tree?**

These represent the relationship type of a given term to its parent term (view an example of a term's derivation. [i] stands for "INSTANCE OF / IS A / TYPE OF" and [p] stands for "PART OF". Example 1. Seed is an instance of whole plant: whole plant --[i] seed Example 2. Embryo is an instance of whole plant and is also part of seed: whole plant --[i] embryo ---[i] seed ----[p] embryo

#### **What does a "+" symbol next to a given ontology term imply?**

#### **Can I download any of the ontology data?**

#### **Is there any data including locus name and GO allowed to download?**

#### **Where in the current trait ontology I could find wheat quality trait / rheological trait?**

#### **I have a genelist from barley and would like to compare it to the H. vulgare gene ontology lists. Is there a way to do that?**

#### **Can I use the ontology term files provided on your website? How do I obtain a license agreement?**

Feedback: Submit a question to Gramene

Click to expand or collapse a question or answer

# Help

## Gramene Ontology (Controlled Vocabulary) Database Help Document

### Ontology search/browse options:

#### A. Quick Search

1. From the Ontologies home page, enter a keyword into the "Quick Search" Box. Keywords may include: Term name (e.g. [days to heading](#), [defense response](#), [Zea mays](#)); Term\_id or an accession (e.g. [303](#) or [TO:0000303](#)); Synonyms (e.g. [culm length](#) or [panicle](#)); Or any word that you think can fetch an appropriate query result (EXCEPT THE GENE NAMES AND SYMBOLS). The default search uses wildcards, so a search for "flower" will include "flowering" and "smallflower".
2. Optionally limited your search by one or more ontologies by checking the desired ontology types (GO/PO/GRO/TO/EO/GR\_tax) below the text search box.
3. To turn off the wildcard feature, check the "Exact Match" option.
4. Obsolete terms will not be returned by default. If you wish to include obsolete terms in your search, check the "Include Obsolete Terms" option.
5. Click on the search icon.

Remember that different ontologies are for different purposes and for selection of terms please visit the [current ontologies](#) section.

#### B. Browse Ontologies

If you are not familiar with the ontology types, their usage, term [ontologies](#) section to discover an appropriate term and the data

Browsing ontology requires an understanding the concept of a hierarchy related to each other and are described as parent terms and child types of parent-child relationships in ontologies, see the [term to term relationships](#)

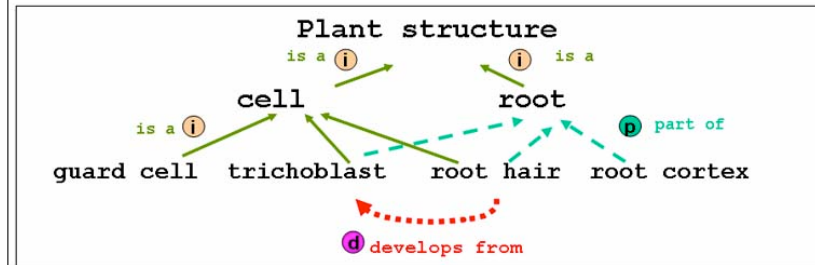
1. Click on the "Browse" link to the right of the ontology of interest.
2. The resulting page will be laid out in the manner of "Ontology Search Results", in terms.
3. Drill down through the ontology to locate terms of interest. But, keeping in mind that through the ontology. Each term will display a number after it, which reflects the number please consult the [association](#) section of this help document.

### Ontology Search Results:

The query results table will give you a list of terms that matched your search. Select the one TO/PO/GRO/GO term at a time, along with additional information on term name. Ont

- **Term name:** Name of the ontology term, by which it is called.
- **Term accession:** A stable ontology term id
- **Aspect:** suggesting a given term belongs to which type of ontology

Use Help file for assistance on developing a search, understanding the results, or in understanding ontologies.



#### Statement looks like

- Trichome, root hair, root cortex are part of root
- Trichoblast, root hair and guard cell are instances of cell
- **Root hair develops from** trichoblast
- Cell and root are instances of plant structure

#### Plant Structure

```
i-- cell
 | i-- guard cell
 | i-- root hair
 | i-- trichoblast
 | d-- root hair
 i-- root
  p-- root cortex
  p-- trichoblast
  d-- root hair
```

Please note that terms in the ontology may have more than one parent (e.g. trichoblast, has two parents, cell and root. Same as root hair).



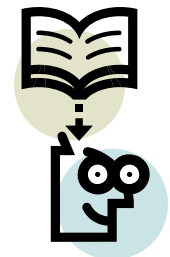
## Action Steps: Things you can do

### 1) Make Suggestions

- Send us your review of the terms, definitions and relationships to ensure accuracy.
- Suggest new terms, definitions, or improvements to current structures.
- If you find incorrect associations, let us know.

### 2) Use Ontologies

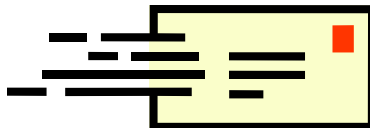
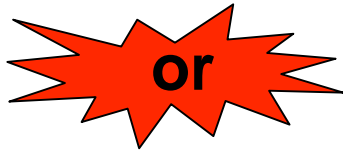
- Use current ontology terms in describing your data in publications and databases.
- If your project on cereal plants (especially rice [Oryza]) is generating data sets that may require these kinds of annotations and associations, we will be happy to help guide you through the annotation process and in setting up an Ontology database.



# 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](mailto:gramene@gramene.org)