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

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

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

or

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

Browsing the Ontology Database

ntologies 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)
Trait Ontology™ (TO) 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.	BROWSE	Ontology + Definitions
Gene Ontology™ (GO) Developed by the Gene Ontology Consortium 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.		All ontologies + Definitions
Molecular Function: The tasks performed by individual gene products; example is Rubisco	BROWSE	-"-
Biological Process: Broad biological goals, such as photosynthesis or ripening, that are accomplished by ordered assemblies of molecular functions.	BROWSE	-"-
Cellular Component: Subcellular structures, locations, and macromolecular complexes; examples include chloroplast, telomere, vacuole, nucleus, etc. .	BROWSE	-"-
Plant Ontology™ (PO) Gramene is collaborating with The Plant Ontology Consortium (POC) to ... ure (anatomy) and growth stages.		
Plant Structure (PO): The controlled vocabulary of plant structu... es. Examples are stamen, gynoecium, petal, parenchyma, guard ce...	BROWSE	Ontology + Definitions
Cereal Plant Growth Stages (GRO): The controlled vocabulary... arious cereal plants. Examples are germination, seedling, booting, flowering, e..., wheat, wheat, oat and barley.	BROWSE	Ontology + Definitions
Environment Ontology (EO) 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.	BROWSE	Ontology + Definitions

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

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

Find: alpha-amylase

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

Options: ☐ Exact Match ☐ Include Obsolete Terms

E.g., **flower** or **TO:0000303**.

Gene Ontology (GO) search results

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Ontology Term Accession Detail

"alpha-amylase activity" (GO:0004556)

Term Name	alpha-amylase activity
Term Accession	GO:0004556
Aspect	Molecular Function
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	The GO browser of Gene Ontology Database

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.

Definition of the term

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

⊟ **Derivation**

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:0004...)
      ▪ [i] amylase activity (GO:0016160) #181 ⊞
        ▪ [i] alpha-amylase activity (GO:0004556) #107

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

External references used for defining terms or making associations.

Database Cro...

⊞ **Parents (1)**

Children (0)

⊟ **Associations (107)**

⊞ Ensembl arabidopsis gene (8)
⊞ Ensembl rice gene (10)
⊞ Gene (10)
⊞ Protein (79)

Click to expand.

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

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⊟ **Associations (107)**

⊟ Ensembl arabidopsis gene (8)
Arabidopsis thaliana (8)
⊟ Ensembl rice gene (10)
Oryza sativa (10)
⊟ Gene (10)
Oryza sativa (10)
⊟ Protein (79)

...ops tauschii (3)	Avena fatua (2)
Eleusine coracana (1)	Hordeum vulgare (25)
Hordeum vulgare subsp. spontaneum (2)	Oryza sativa (3)
Oryza sativa (japonica cultivar-group) (13)	Sorghum bicolor (2)
Triticum aestivum (18)	Zea mays (10)

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
alpha-amylase activity	Gene	GR:0060043	Amy1	Amylase-1	RAmy1A/C|Amy1A|Alpha-amylase-1A|Amy1A/C*	Oryza sativa	IMP (Causse-M-A et al., 1994, PMID 7896104)
alpha-amylase activity	Gene	GR:0060076	Amy10	Amylase(Beta)-10	Bet...		IMP
alpha-amylase activity	Gene	GR:0060044	Amy2	Amylase-2	Am...		IMP (Causse-M-A et al., 1994, PMID 7896104)
alpha-amylase activity	Gene	GR:0061333	Amy3	Amylase-3	RAmy1A/C|Amy1C|Alpha-amylase-1A|Amy1A/C*	Oryza sativa	IMP (Causse-M-A et al., 1994, PMID 7896104)
alpha-amylase activity	Gene	GR:0060045	Amy4	Amylase-4	Amy2A*|Alpha-amylase-2A|RAmy2A	Oryza sativa	IMP (Causse-M-A et al., 1994, PMID 7896104)
alpha-amylase activity	Gene	GR:0060046	Amy5	Amylase-5	Amy3A|RAmy3A/B/C|Alpha-amylase-3A|Amy3A/B/C*	Oryza sativa	IMP (Causse-M-A et al., 1994, PMID 7896104)
alpha-amylase activity	Gene	GR:0061...			|RAmy3A/B/C|Alpha-amylase-3A|Amy3A/B/C*	Oryza sativa	IMP (Shiraishi-M et al., 1986)
alpha-amylase activity	Gene	GR:00...			|RAmy3A/B/C|Alpha-amylase-3A|Amy3A/B/C*	Oryza sativa	IMP
alpha-amylase activity	Gene	GR:0060...					
alpha-amylase activity	Gene	GR:0061...					

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

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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)

Click to submit your ontology suggestions

Help

Help	overview on how to use the Ontologies database and lists explanations of field
Tutorial	in-depth than the help pages, use the tutorial for an exaple of using the database, see increase your data search efficiency.
FAQ	Frequently Asked Questions - see what questions users have asked, and get the developers
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 produc

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/. 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 Genom 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]

Learn more about ontologies from these publications

Acknowledgements

- Plant Ontology has been developed and contributed by th[e]ant llaborating 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 G 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]

Evidence Codes

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

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) 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.

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 searchs, 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
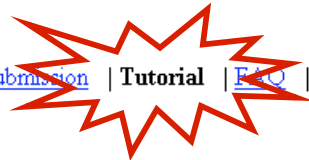
Ontologies Tutorial

Select your preferred format:

- PowerPoint
- Adobe PDF

About Ontologies (Powerpoint)

Release Notes

Different options available for all browsers

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FAQs

Search FAQ

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 an[...] 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 [...]tion available from the current ontologies section to discover an appropriate term and the datas[...]

Browsing ontology requires an understanding the concept of a h[...] its parent term. related to each other and are described as parent terms and child [...]st. types of parent-child relationships in ontologies, see the term to term relationships [...]
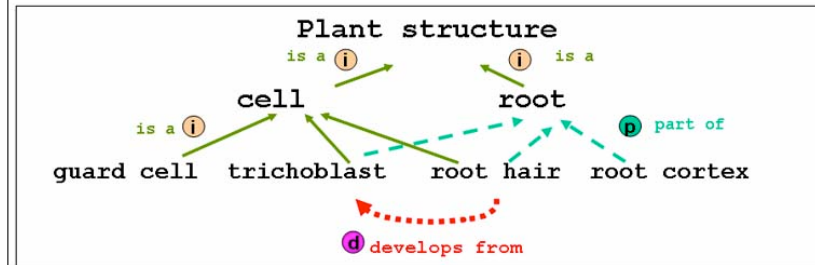
1. Click on the "Browse" link to the right of the ontology of interest.
2. The resulting page will be layed out in the manner of "Ontology Search Results", i[...] terms.
3. Drill down through the ontology to locate terms of interest. But, keeping in mind tha[...] through the ontology. Each term will display a number after it, which reflects the nu[...] 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. Onto[...]
- **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.

Plant structure

is a (i)   is a (i)

cell   **root**

is a (i)   (p) part of

guard cell   trichoblast   root hair   root cortex

(d) develops from

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).
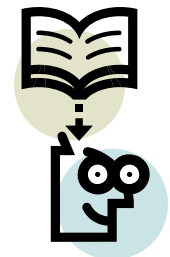
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Action Steps: Things you can do

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

GRAMENE *A Resource for Comparative Grass Genomics*

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

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

or
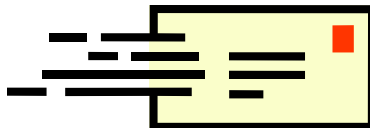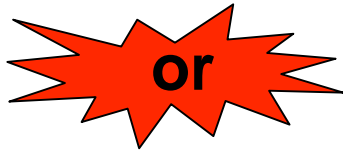
Email Gramene at gramene@gramene.org