GENE ONTOLOGY (GO)

- Wilver Martínez Martínez
- Giovanny Silva Rincón

What is GO?

- The Gene Ontology (GO) project is a collaborative effort to address the need for consistent descriptions of gene products in different databases. The project began as a collaboration between three model organism databases, FlyBase (*Drosophila*), the *Saccharomyces Genome Database* (SGD) and the Mouse Genome Database (MGD), in 1998.

What is GO?

- The GO project has developed three structured controlled vocabularies (ontologies) that describe gene products in terms of their associated biological processes, cellular components and molecular functions in a species-independent manner. There are three separate aspects to this effort: first, the development and maintenance of the ontologies themselves; second, the annotation of gene products, which entails making associations between the ontologies and the genes and gene products in the collaborating databases; and third, development of tools that facilitate the creation, maintenance and use of ontologies.

What is an ontology?

Ontologies are 'specifications of a relational vocabulary'. In other words they are sets of defined terms like the sort that you would find in a dictionary, but the terms are networked. The terms in a given vocabulary are likely to be restricted to those used in a particular field, and in the case of GO, the terms are all biological.

The Ontologies

- The three organizing principles of GO are **cellular component**, **biological process** and **molecular function**. A gene product might be associated with or located in one or more cellular components; it is active in one or more biological processes, during which it performs one or more molecular functions. For example, the gene product cytochrome c can be described by the molecular function term **oxidoreductase activity**, the biological process terms **oxidative phosphorylation** and **induction of cell death**, and the cellular component terms **mitochondrial matrix** and **mitochondrial inner membrane**.

The Ontologies are used to categorize gene products.

- **Biological process ontology:**

  Which process is a gene product involved in?

- **Molecular function ontology:**

  Which molecular function does a gene product have?

- **Cellular component ontology:**

  Where does a gene product act?

Terms in the Gene Ontology

- Each entry in GO has a unique numerical identifier of the form **GO:nnnnnnn**, and a term name, e.g. **cell**, **fibroblast growth factor receptor binding** or **signal transduction**. Each term is also assigned to one of the three ontologies, molecular function, cellular component or biological process.
- Many GO terms have synonyms; GO uses 'synonym' in a loose sense, as the names within the synonyms field may not mean exactly the same as the term they are attached to.

The Gene Ontology is like a dictionary

Each concept has:

- **a name**
- **a definition**
- **an ID number**

term: transcription initiation

ID: GO:0006352

definition: Processes involved in the assembly of the RNA polymerase complex at the promoter region of a DNA template resulting in the subsequent synthesis of RNA from that promoter.

Species-specific terms

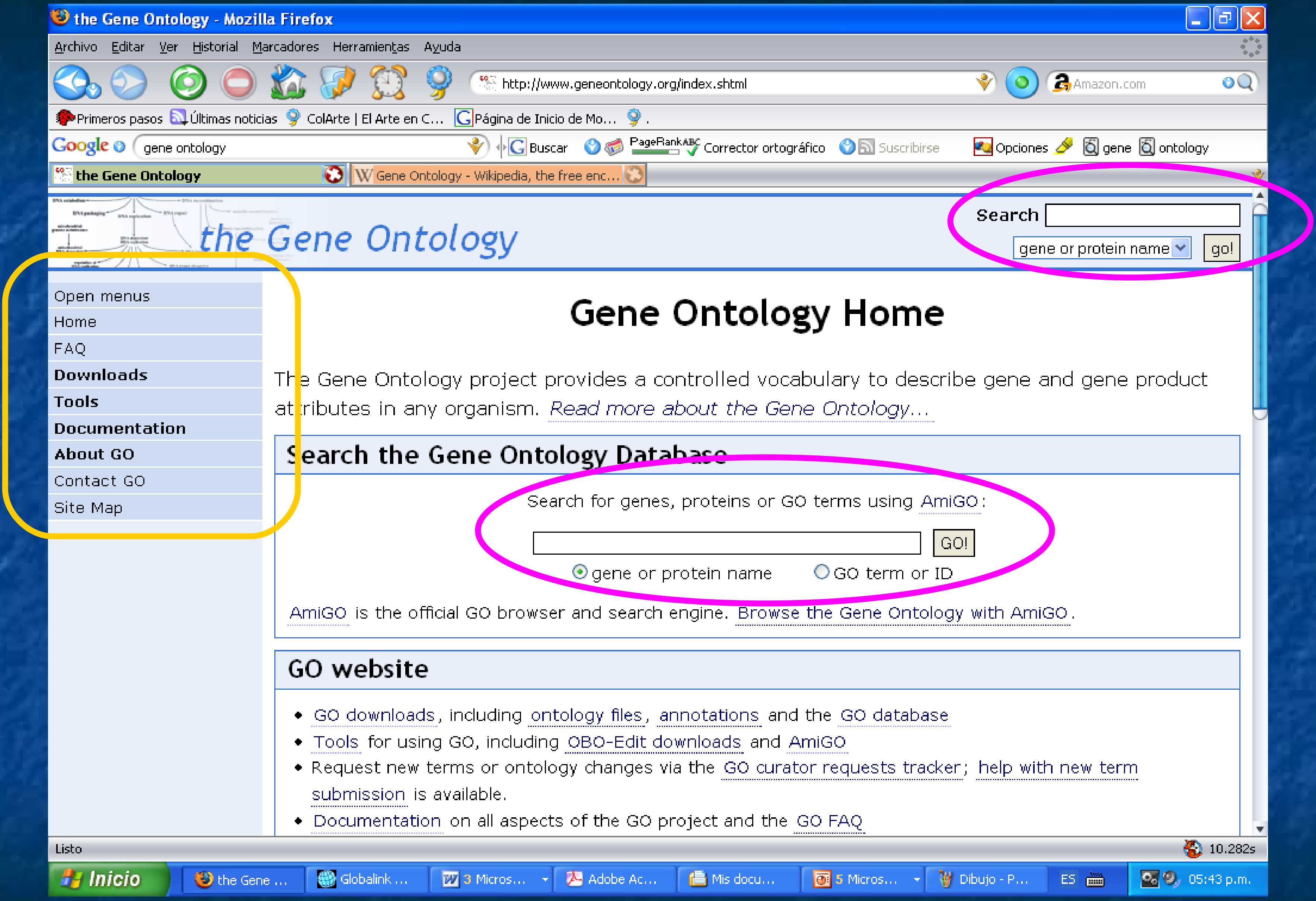
- The convention is to include any term that can apply to more than one taxonomic class of organism. To specify the class of organisms to which a term is applicable, GO uses the designator *sensu*, 'in the sense of'; for example, **trichome differentiation(sensu Magnoliophyta)** represents the differentiation of plant hair cells

Obsolete terms

- The term and ID still exist in the GO database, but the term is marked as obsolete, and a comment added, giving a reason for the obsoletion and recommending alternative terms where appropriate.

What GO is NOT

- Gene products: e.g. cytochrome c is not in the ontologies, but attributes of cytochrome c, such as **oxidoreductase activity**, are.
- Processes, functions or components that are unique to mutants or diseases: e.g. **oncogenesis** is not a valid GO term because causing cancer is not the normal function of any gene.
- Attributes of sequence such as intron/exon parameters: these are not attributes of gene products and will be described in a separate sequence ontology (see the OBO website for more information).
- Protein domains or structural features.
- Protein-protein interactions.
- Environment, evolution and expression.
- Anatomical or histological features above the level of cellular components, including cell types.
- GO is not a database of gene sequences, nor a catalog of gene products. Rather, GO describes how gene products



the Gene Ontology

Search

gene or protein name go!

- Open menus
- Home
- FAQ
- **Downloads**
- **Tools**
- **Documentation**
- **About GO**
- Contact GO
- Site Map

Gene Ontology Home

The Gene Ontology project provides a controlled vocabulary to describe gene and gene product attributes in any organism. *Read more about the Gene Ontology...*

Search the Gene Ontology Database

Search for genes, proteins or GO terms using AmiGO:

GO!

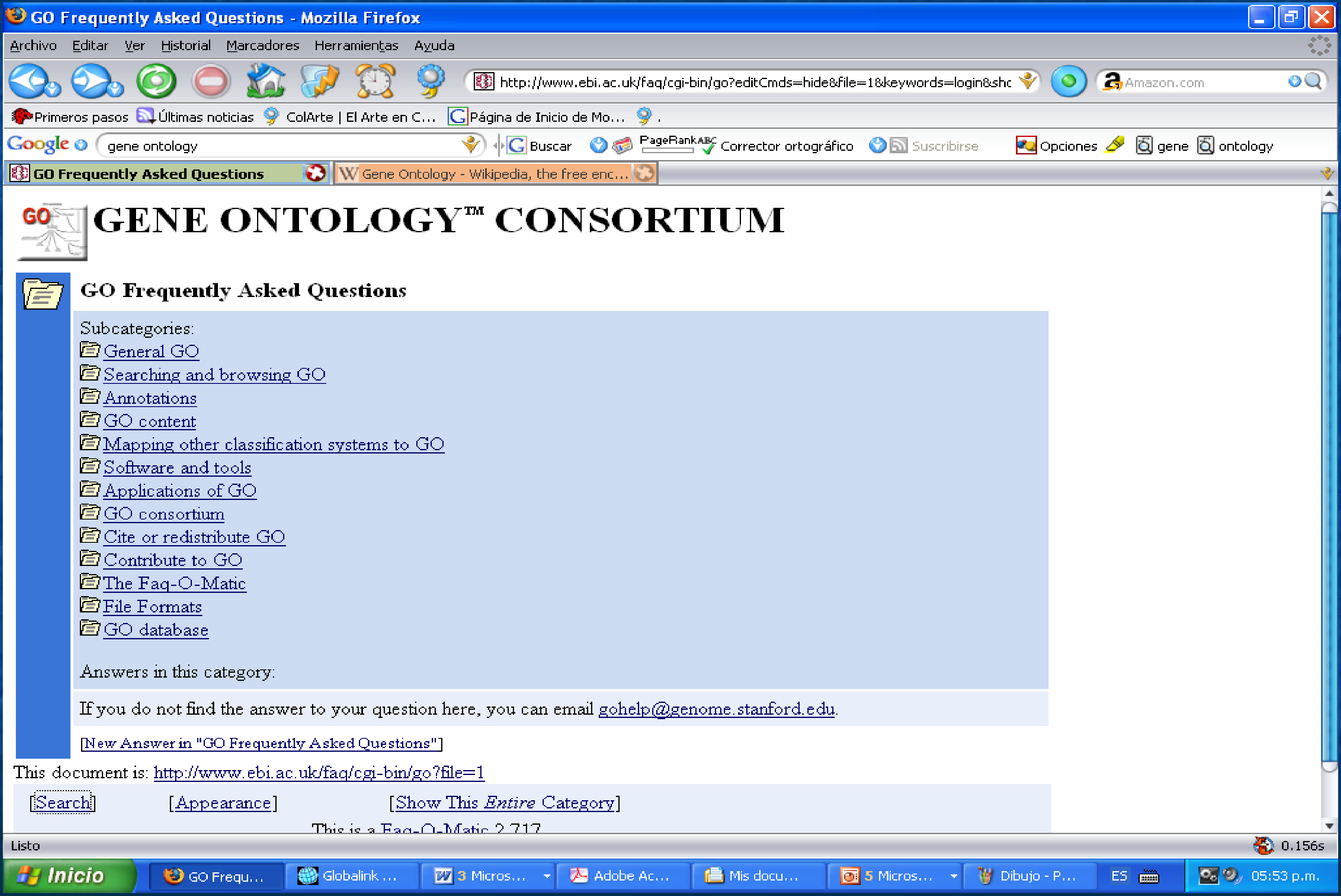
● gene or protein name ○ GO term or ID

AmiGO is the official GO browser and search engine. Browse the Gene Ontology with AmiGO.

GO website

- GO downloads, including ontology files, annotations and the GO database
- Tools for using GO, including OBO-Edit downloads and AmiGO
- Request new terms or ontology changes via the GO curator requests tracker; help with new term submission is available.
- Documentation on all aspects of the GO project and the GO FAQ

FAQ



GENE ONTOLOGY™ CONSORTIUM

GO Frequently Asked Questions

Subcategories:

- General GO
- Searching and browsing GO
- Annotations
- GO content
- Mapping other classification systems to GO
- Software and tools
- Applications of GO
- GO consortium
- Cite or redistribute GO
- Contribute to GO
- The Faq-O-Matic
- File Formats
- GO database

Answers in this category:

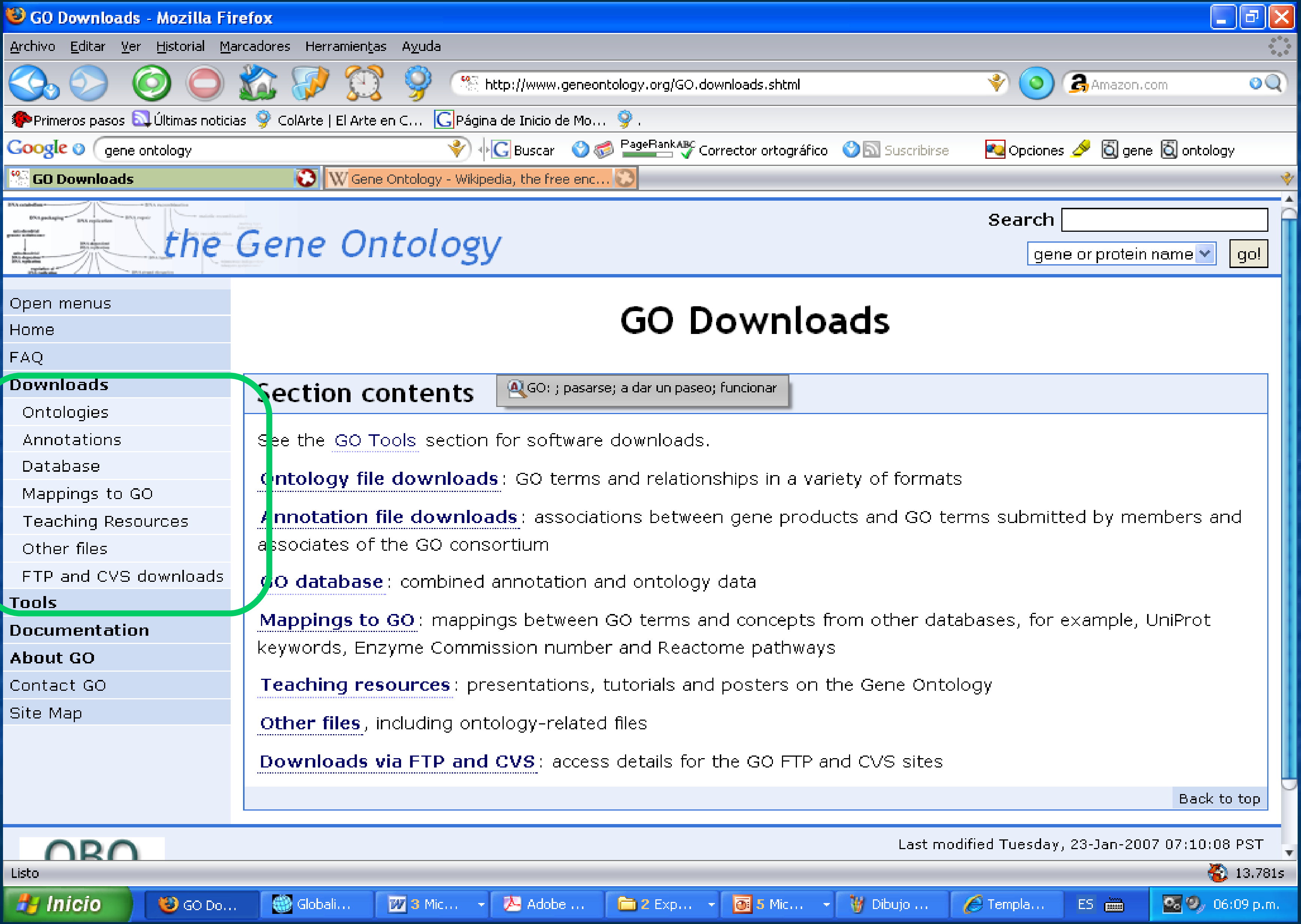
If you do not find the answer to your question here, you can email gohelp@genome.stanford.edu.

[New Answer in "GO Frequently Asked Questions"]

This document is: http://www.ebi.ac.uk/faq/cgi-bin/go?file=1

[Search] [Appearance] [Show This *Entire* Category]

This is a Faq-O-Matic 2.717



GO Downloads

Section contents

GO: ; pasarse; a dar un paseo; funcionar

See the GO Tools section for software downloads.

Ontology file downloads: GO terms and relationships in a variety of formats

Annotation file downloads: associations between gene products and GO terms submitted by members and associates of the GO consortium

GO database: combined annotation and ontology data

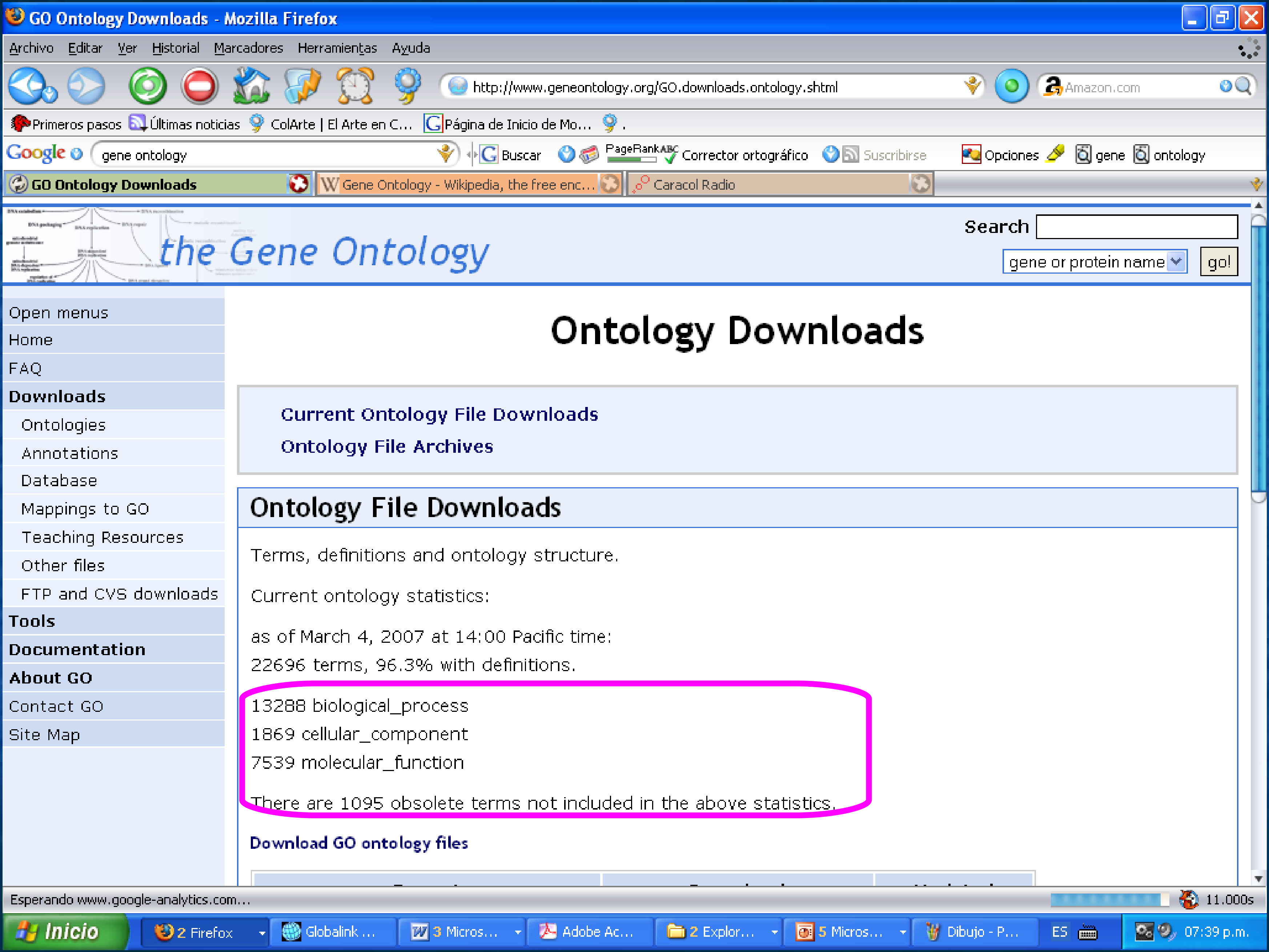
Mappings to GO: mappings between GO terms and concepts from other databases, for example, UniProt keywords, Enzyme Commission number and Reactome pathways

Teaching resources: presentations, tutorials and posters on the Gene Ontology

Other files, including ontology-related files

Downloads via FTP and CVS: access details for the GO FTP and CVS sites

Last modified Tuesday, 23-Jan-2007 07:10:08 PST



Ontology Downloads

Current Ontology File Downloads

Ontology File Archives

Ontology File Downloads

Terms, definitions and ontology structure.

Current ontology statistics:

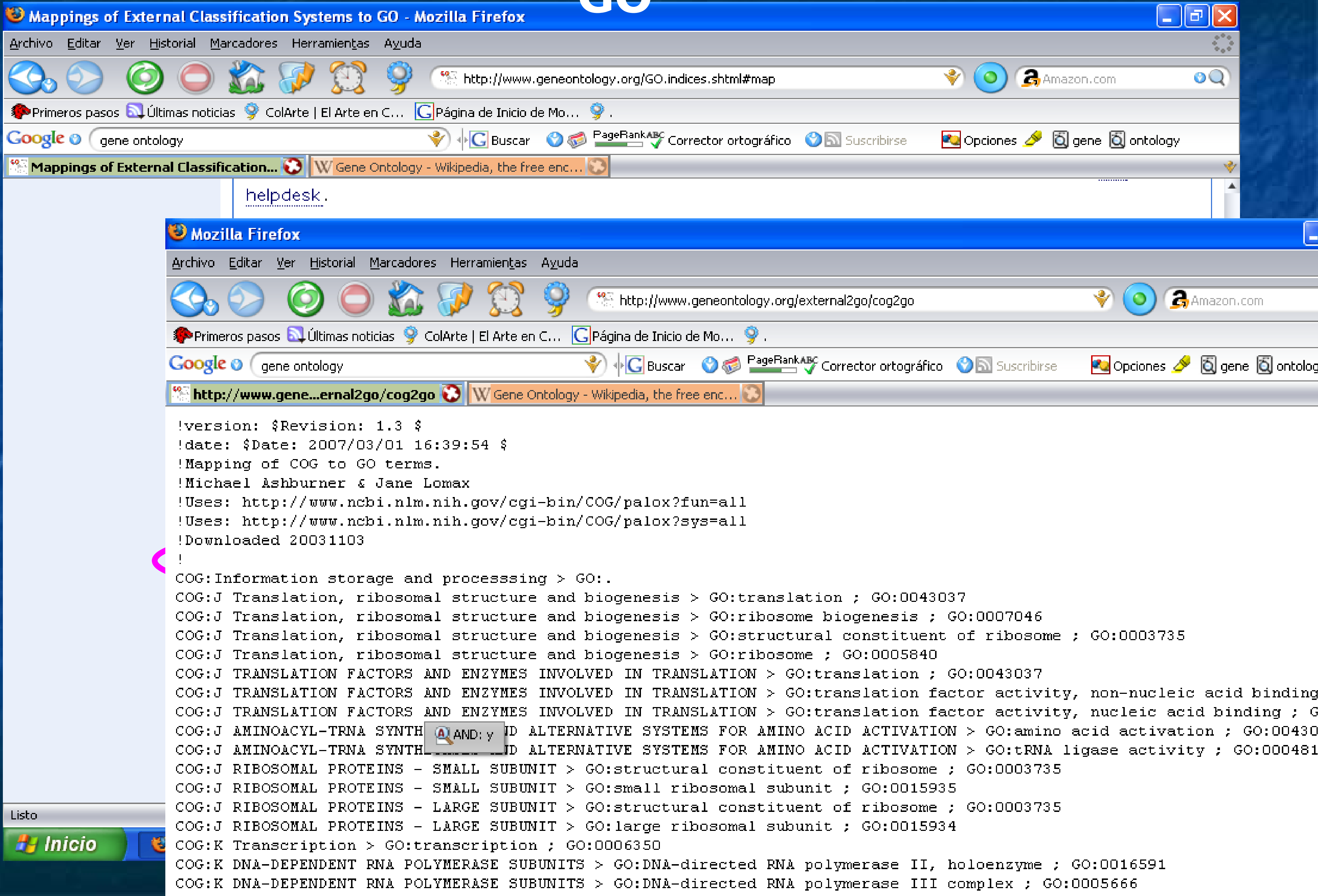
as of March 4, 2007 at 14:00 Pacific time:
22696 terms, 96.3% with definitions.

13288 biological_process
1869 cellular_component
7539 molecular_function

There are 1095 obsolete terms not included in the above statistics.

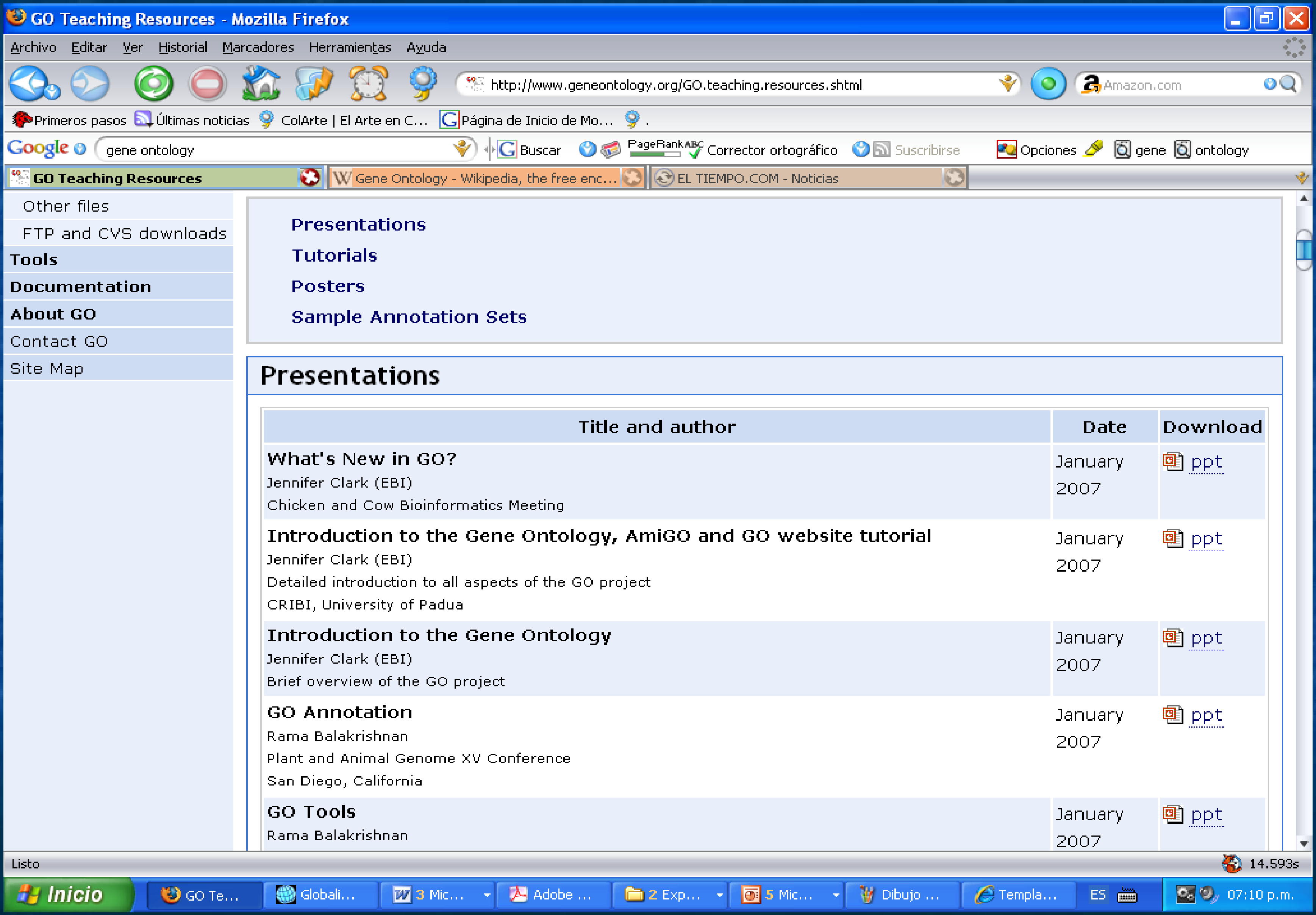
Download GO ontology files

Mappings of External Classification Systems to GO



```
!version: $Revision: 1.3 $
!date: $Date: 2007/03/01 16:39:54 $
!Mapping of COG to GO terms.
!Michael Ashburner & Jane Lomax
!Uses: http://www.ncbi.nlm.nih.gov/cgi-bin/COG/palox?fun=all
!Uses: http://www.ncbi.nlm.nih.gov/cgi-bin/COG/palox?sys=all
!Downloaded 20031103
!
COG:Information storage and processing > GO:.
COG:J Translation, ribosomal structure and biogenesis > GO:translation ; GO:0043037
COG:J Translation, ribosomal structure and biogenesis > GO:ribosome biogenesis ; GO:0007046
COG:J Translation, ribosomal structure and biogenesis > GO:structural constituent of ribosome ; GO:0003735
COG:J Translation, ribosomal structure and biogenesis > GO:ribosome ; GO:0005840
COG:J TRANSLATION FACTORS AND ENZYMES INVOLVED IN TRANSLATION > GO:translation ; GO:0043037
COG:J TRANSLATION FACTORS AND ENZYMES INVOLVED IN TRANSLATION > GO:translation factor activity, non-nucleic acid binding
COG:J TRANSLATION FACTORS AND ENZYMES INVOLVED IN TRANSLATION > GO:translation factor activity, nucleic acid binding ; G
COG:J AMINOACYL-TRNA SYNTH        ID ALTERNATIVE SYSTEMS FOR AMINO ACID ACTIVATION > GO:amino acid activation ; GO:00430
COG:J AMINOACYL-TRNA SYNTH        ND ALTERNATIVE SYSTEMS FOR AMINO ACID ACTIVATION > GO:tRNA ligase activity ; GO:000481
COG:J RIBOSOMAL PROTEINS - SMALL SUBUNIT > GO:structural constituent of ribosome ; GO:0003735
COG:J RIBOSOMAL PROTEINS - SMALL SUBUNIT > GO:small ribosomal subunit ; GO:0015935
COG:J RIBOSOMAL PROTEINS - LARGE SUBUNIT > GO:structural constituent of ribosome ; GO:0003735
COG:J RIBOSOMAL PROTEINS - LARGE SUBUNIT > GO:large ribosomal subunit ; GO:0015934
COG:K Transcription > GO:transcription ; GO:0006350
COG:K DNA-DEPENDENT RNA POLYMERASE SUBUNITS > GO:DNA-directed RNA polymerase II, holoenzyme ; GO:0016591
COG:K DNA-DEPENDENT RNA POLYMERASE SUBUNITS > GO:DNA-directed RNA polymerase III complex ; GO:0005666
```

GO Teaching Resources



Other files
FTP and CVS downloads
Tools
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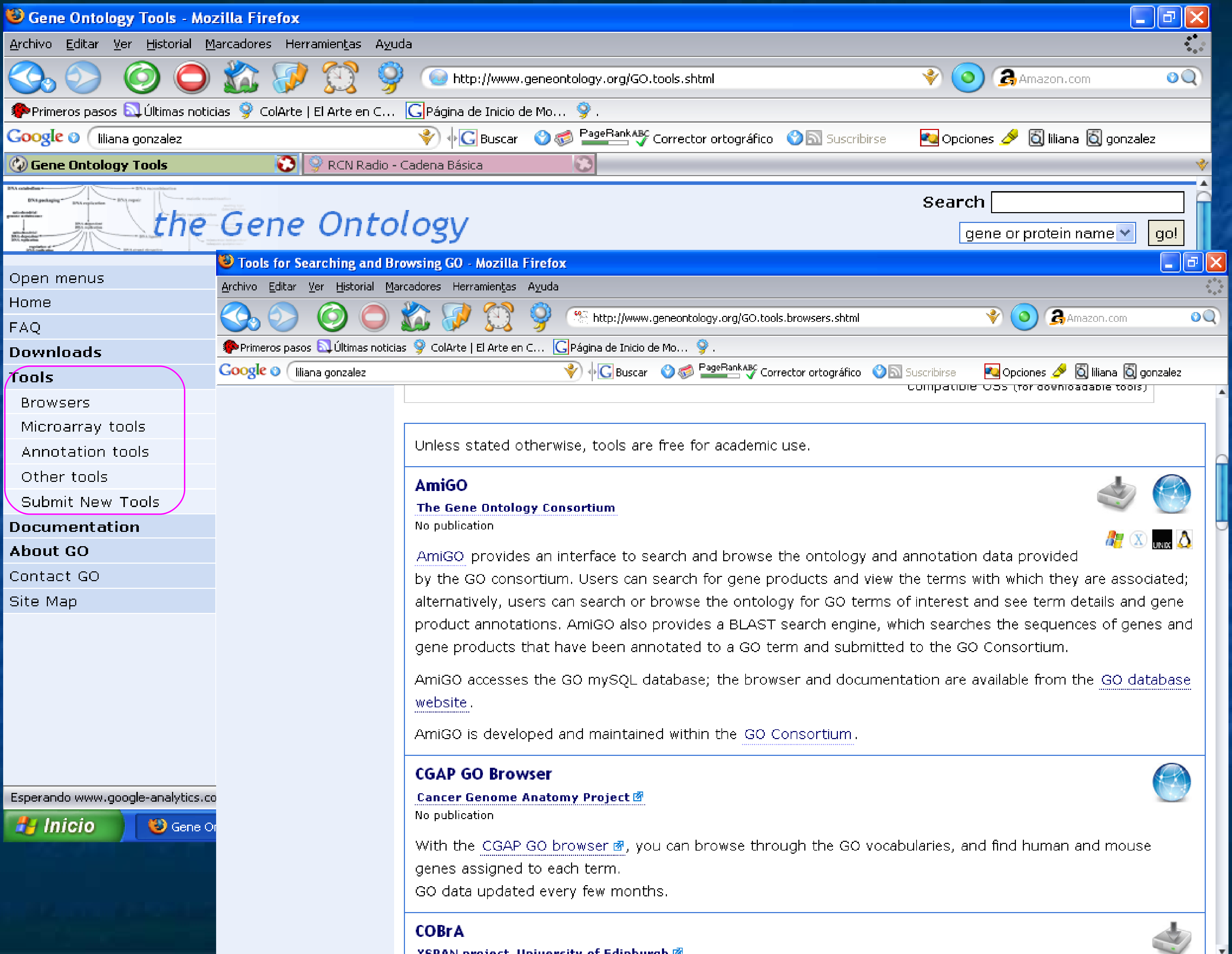
Presentations
Tutorials
Posters
Sample Annotation Sets

Presentations

Title and author	Date	Download
What's New in GO? Jennifer Clark (EBI) Chicken and Cow Bioinformatics Meeting	January 2007	ppt
Introduction to the Gene Ontology, AmiGO and GO website tutorial Jennifer Clark (EBI) Detailed introduction to all aspects of the GO project CRIBI, University of Padua	January 2007	ppt
Introduction to the Gene Ontology Jennifer Clark (EBI) Brief overview of the GO project	January 2007	ppt
GO Annotation Rama Balakrishnan Plant and Animal Genome XV Conference San Diego, California	January 2007	ppt
GO Tools Rama Balakrishnan	January 2007	ppt



Unless stated otherwise, tools are free for academic use.

AmiGO

The Gene Ontology Consortium

No publication

AmiGO provides an interface to search and browse the ontology and annotation data provided by the GO consortium. Users can search for gene products and view the terms with which they are associated; alternatively, users can search or browse the ontology for GO terms of interest and see term details and gene product annotations. AmiGO also provides a BLAST search engine, which searches the sequences of genes and gene products that have been annotated to a GO term and submitted to the GO Consortium.

AmiGO accesses the GO mySQL database; the browser and documentation are available from the GO database website.

AmiGO is developed and maintained within the GO Consortium.

CGAP GO Browser

Cancer Genome Anatomy Project

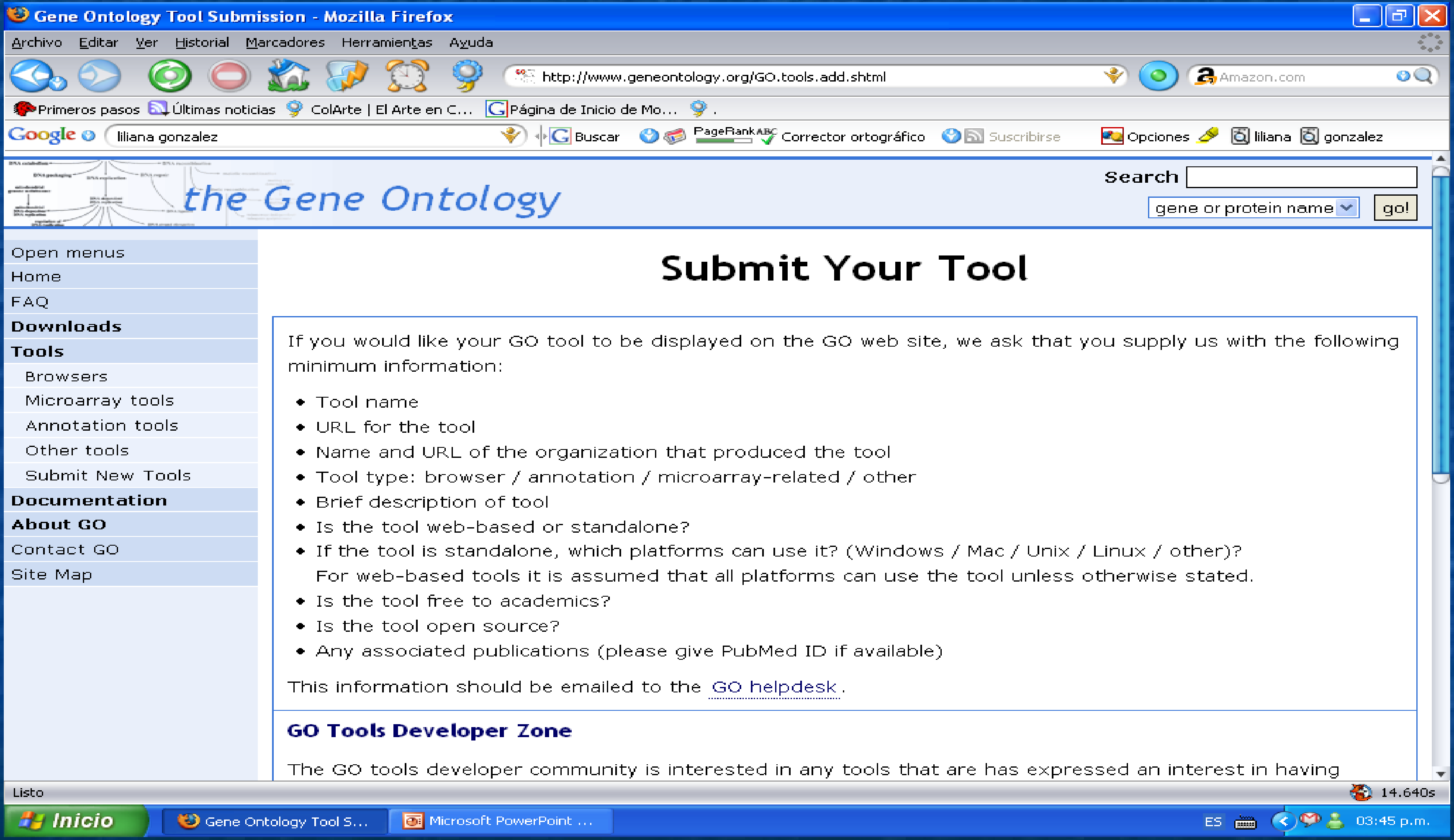
No publication

With the CGAP GO browser, you can browse through the GO vocabularies, and find human and mouse genes assigned to each term.
GO data updated every few months.

COBrA

XSPAN project, University of Edinburgh

Submit Your Tool



Submit Your Tool

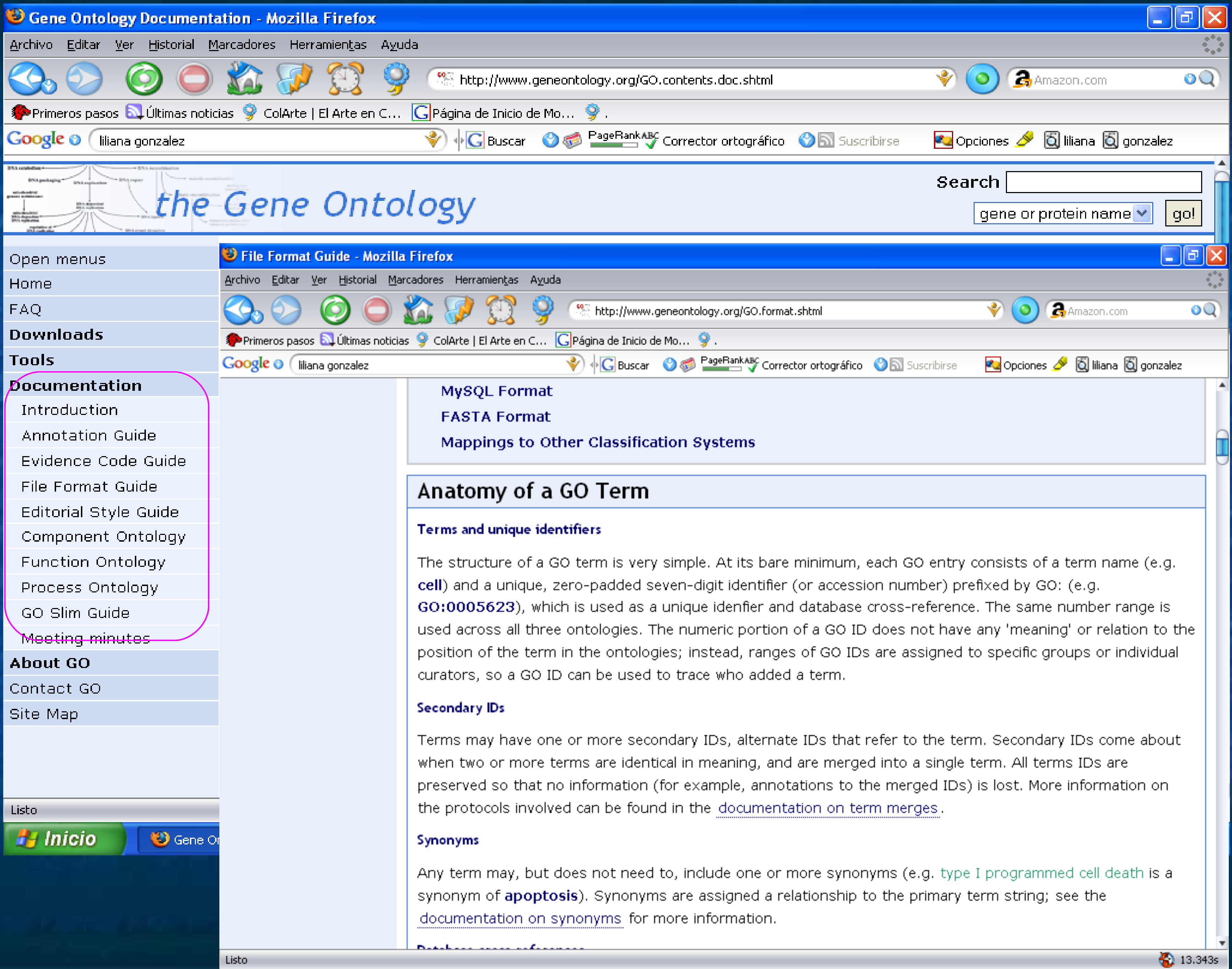
If you would like your GO tool to be displayed on the GO web site, we ask that you supply us with the following minimum information:

- Tool name
- URL for the tool
- Name and URL of the organization that produced the tool
- Tool type: browser / annotation / microarray-related / other
- Brief description of tool
- Is the tool web-based or standalone?
- If the tool is standalone, which platforms can use it? (Windows / Mac / Unix / Linux / other)?
  For web-based tools it is assumed that all platforms can use the tool unless otherwise stated.
- Is the tool free to academics?
- Is the tool open source?
- Any associated publications (please give PubMed ID if available)

This information should be emailed to the GO helpdesk.

GO Tools Developer Zone

The GO tools developer community is interested in any tools that are has expressed an interest in having



Anatomy of a GO Term

Terms and unique identifiers

The structure of a GO term is very simple. At its bare minimum, each GO entry consists of a term name (e.g. **cell**) and a unique, zero-padded seven-digit identifier (or accession number) prefixed by GO: (e.g. **GO:0005623**), which is used as a unique idenfier and database cross-reference. The same number range is used across all three ontologies. The numeric portion of a GO ID does not have any 'meaning' or relation to the position of the term in the ontologies; instead, ranges of GO IDs are assigned to specific groups or individual curators, so a GO ID can be used to trace who added a term.

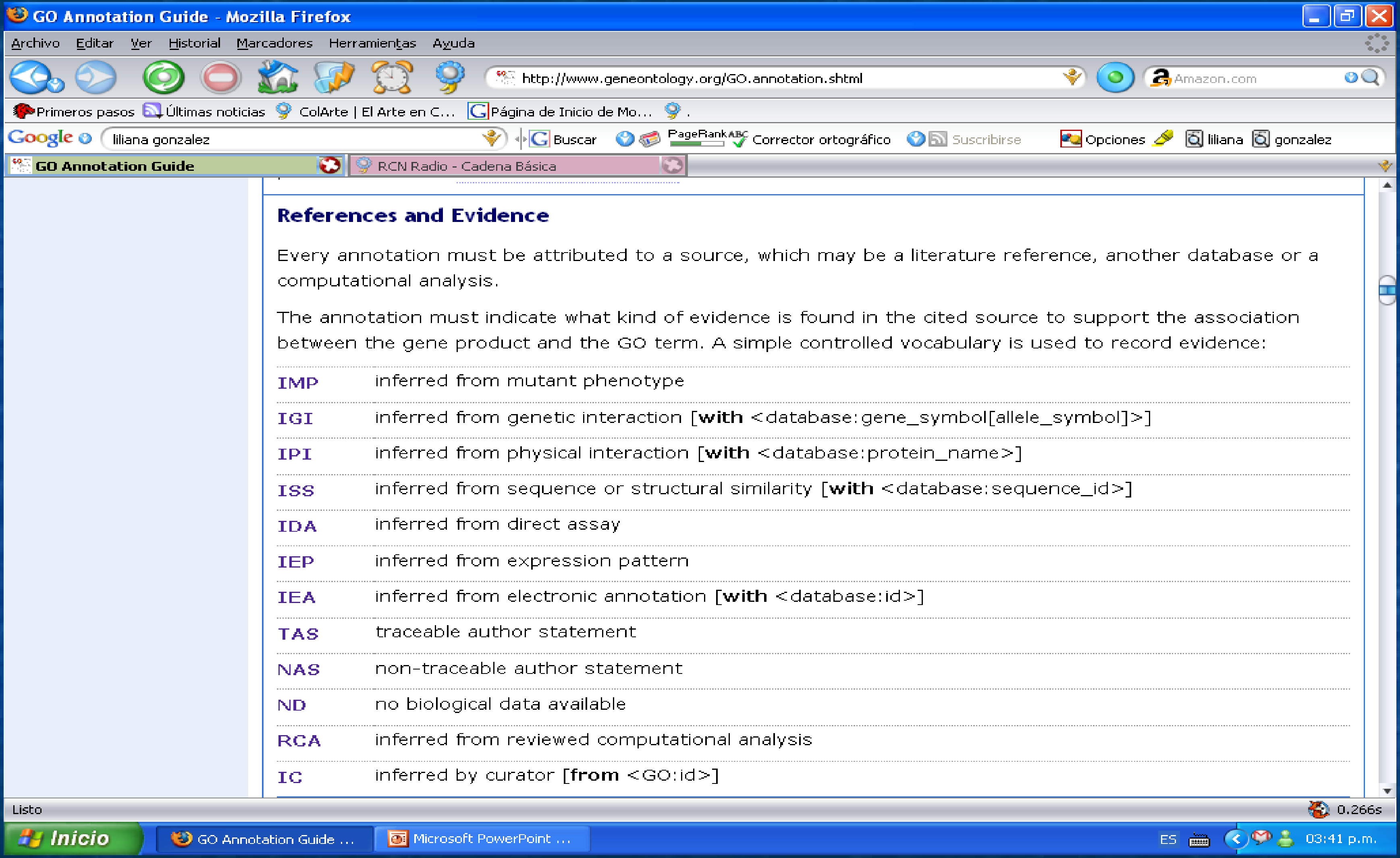
Secondary IDs

Terms may have one or more secondary IDs, alternate IDs that refer to the term. Secondary IDs come about when two or more terms are identical in meaning, and are merged into a single term. All terms IDs are preserved so that no information (for example, annotations to the merged IDs) is lost. More information on the protocols involved can be found in the documentation on term merges.

Synonyms

Any term may, but does not need to, include one or more synonyms (e.g. type I programmed cell death is a synonym of **apoptosis**). Synonyms are assigned a relationship to the primary term string; see the documentation on synonyms for more information.

GO Annotation Guide



References and Evidence

Every annotation must be attributed to a source, which may be a literature reference, another database or a computational analysis.

The annotation must indicate what kind of evidence is found in the cited source to support the association between the gene product and the GO term. A simple controlled vocabulary is used to record evidence:

IMP	inferred from mutant phenotype
IGI	inferred from genetic interaction [**with** <database:gene_symbol[allele_symbol]>]
IPI	inferred from physical interaction [**with** <database:protein_name>]
ISS	inferred from sequence or structural similarity [**with** <database:sequence_id>]
IDA	inferred from direct assay
IEP	inferred from expression pattern
IEA	inferred from electronic annotation [**with** <database:id>]
TAS	traceable author statement
NAS	non-traceable author statement
ND	no biological data available
RCA	inferred from reviewed computational analysis
IC	inferred by curator [**from** <GO:id>]

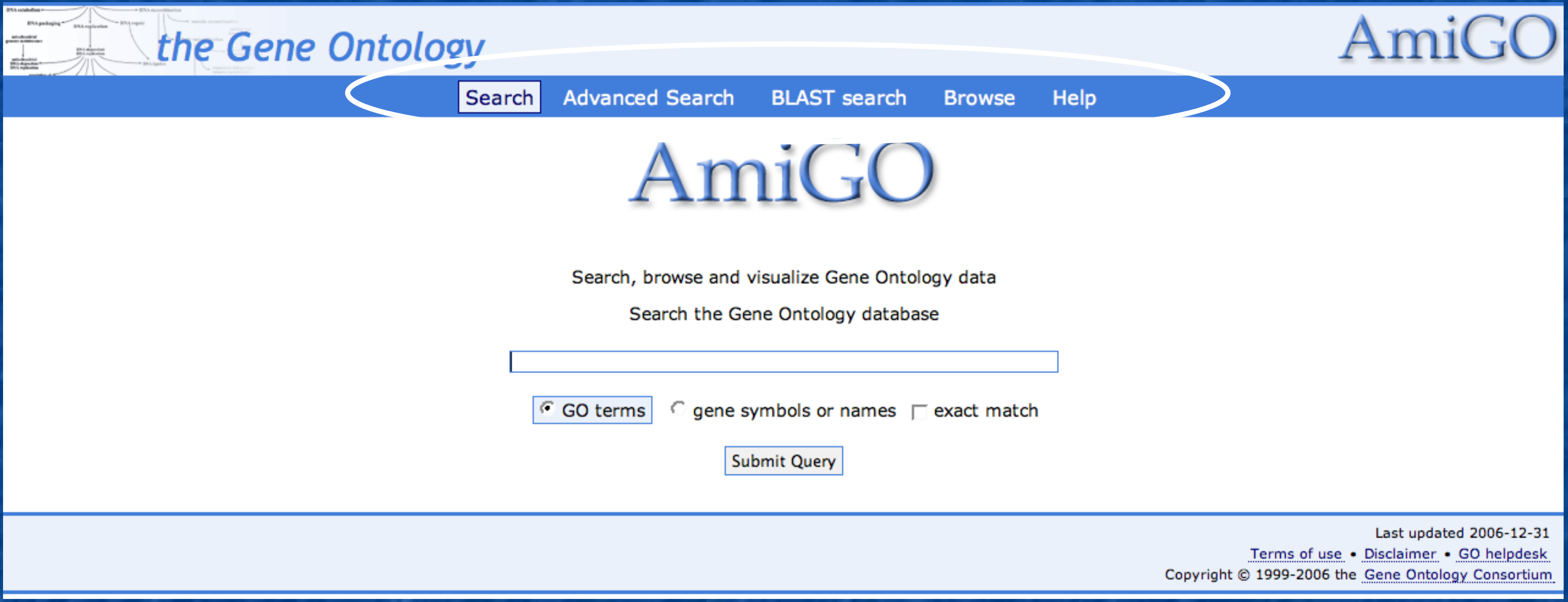
AmiGO

What is AmiGO?

- Web application that reads from the GO Database (mySQL)
- Allows to
  - browse the ontologies
  - view annotations from various species
  - compare sequences using BLAST (GOst)

AmiGO

http://www.godatabase.org



Search, browse and visualize Gene Ontology data

Search the Gene Ontology database

● GO terms ○ gene symbols or names ☐ exact match

Last updated 2006-12-31

Terms of use • Disclaimer • GO helpdesk

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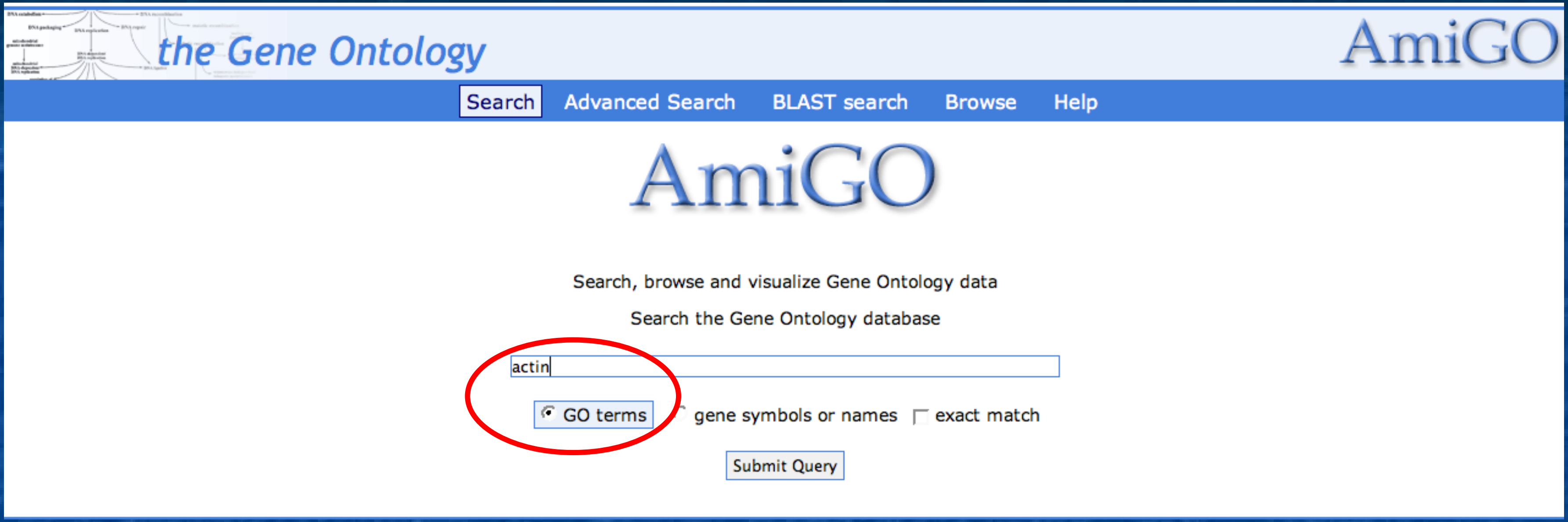
Basic Search

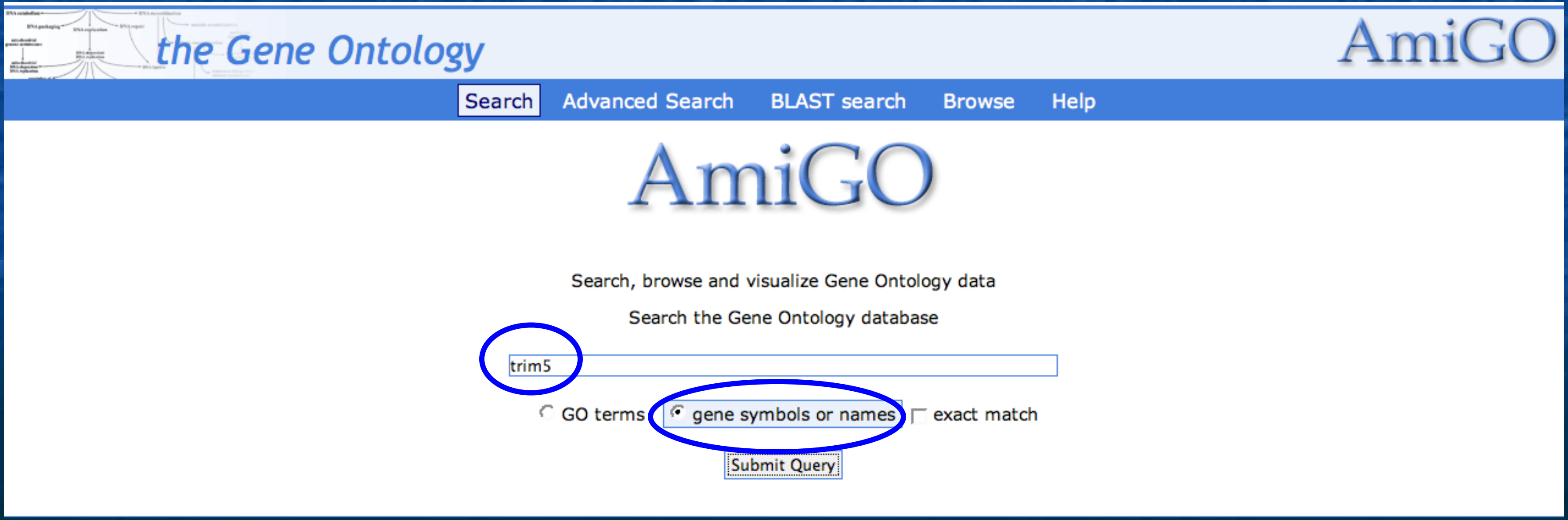


Search, browse and visualize Gene Ontology data

Search the Gene Ontology database

actin

● GO terms ○ gene symbols or names ☐ exact match

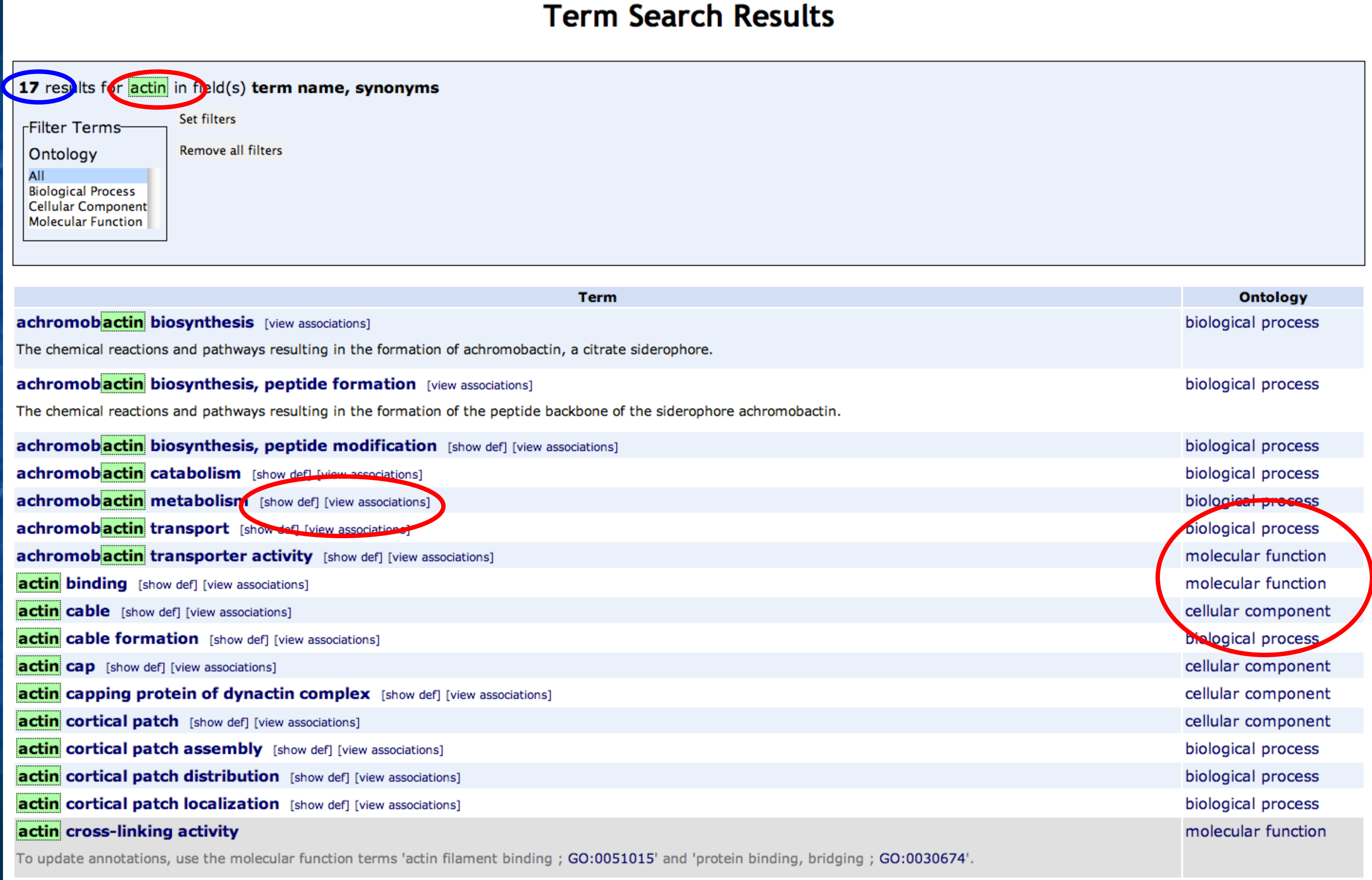


Search, browse and visualize Gene Ontology data

Search the Gene Ontology database

trim5

○ GO terms ● gene symbols or names ☐ exact match

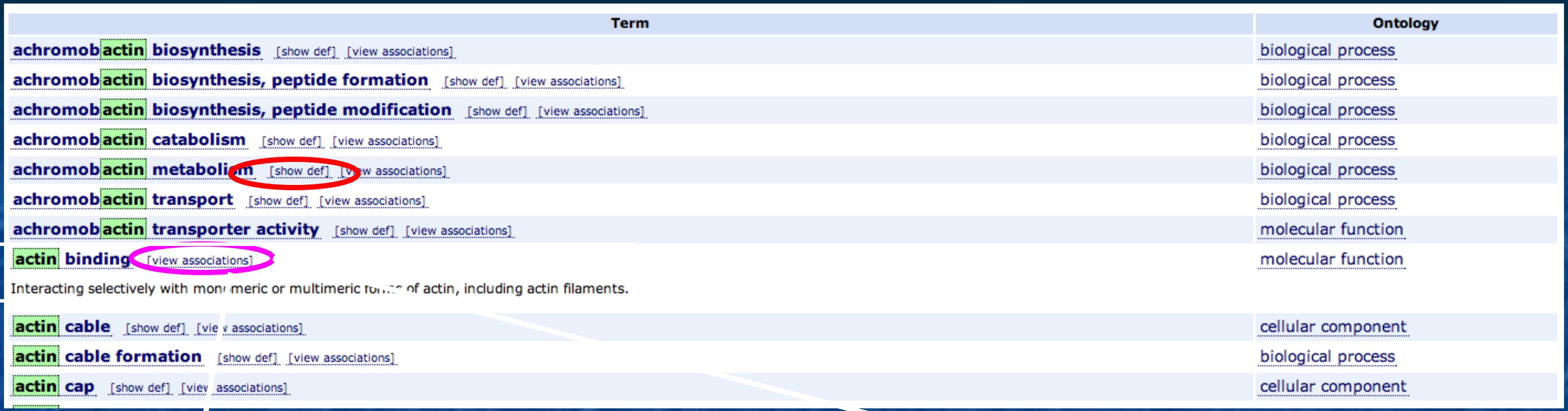


Term Search Results

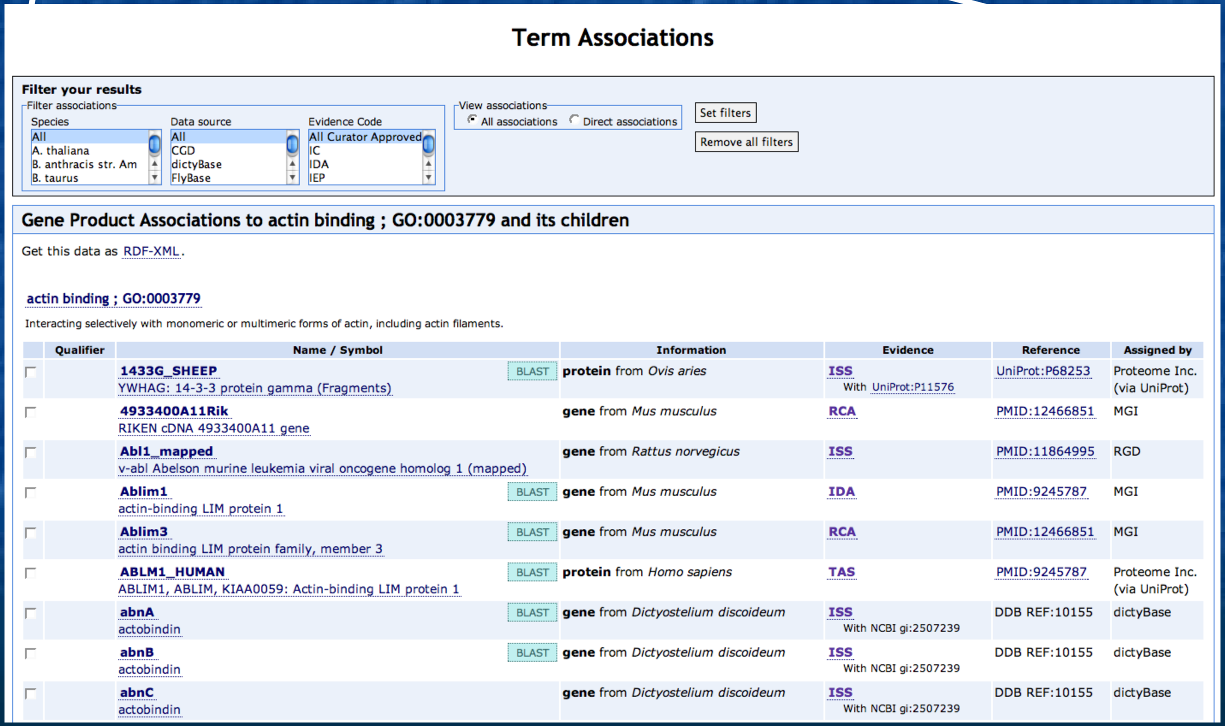
17 results for actin in field(s) **term name, synonyms**

Term	Ontology
achromobactin biosynthesis [view associations] The chemical reactions and pathways resulting in the formation of achromobactin, a citrate siderophore.	biological process
achromobactin biosynthesis, peptide formation [view associations] The chemical reactions and pathways resulting in the formation of the peptide backbone of the siderophore achromobactin.	biological process
achromobactin biosynthesis, peptide modification [show def] [view associations]	biological process
achromobactin catabolism [show def] [view associations]	biological process
achromobactin metabolism [show def] [view associations]	biological process
achromobactin transport [show def] [view associations]	biological process
achromobactin transporter activity [show def] [view associations]	molecular function
actin binding [show def] [view associations]	molecular function
actin cable [show def] [view associations]	cellular component
actin cable formation [show def] [view associations]	biological process
actin cap [show def] [view associations]	cellular component
actin capping protein of dynactin complex [show def] [view associations]	cellular component
actin cortical patch [show def] [view associations]	cellular component
actin cortical patch assembly [show def] [view associations]	biological process
actin cortical patch distribution [show def] [view associations]	biological process
actin cortical patch localization [show def] [view associations]	biological process
actin cross-linking activity To update annotations, use the molecular function terms 'actin filament binding ; GO:0051015' and 'protein binding, bridging ; GO:0030674'.	molecular function

More on term search results



Term	Ontology
achromobactin biosynthesis [show def] [view associations]	biological process
achromobactin biosynthesis, peptide formation [show def] [view associations]	biological process
achromobactin biosynthesis, peptide modification [show def] [view associations]	biological process
achromobactin catabolism [show def] [view associations]	biological process
achromobactin metabolism [show def] [view associations]	biological process
achromobactin transport [show def] [view associations]	biological process
achromobactin transporter activity [show def] [view associations]	molecular function
actin binding [view associations] Interacting selectively with monomeric or multimeric forms of actin, including actin filaments.	molecular function
actin cable [show def] [view associations]	cellular component
actin cable formation [show def] [view associations]	biological process
actin cap [show def] [view associations]	cellular component



Term Associations

Filter your results

Filter associations

Species: All (selected), A. thaliana, B. anthracis str. Am, B. taurus

Data source: All (selected), CGD, dictyBase, FlyBase

Evidence Code: All Curator Approved (selected), IC, IDA, IEP

View associations: ● All associations ○ Direct associations

Gene Product Associations to actin binding ; GO:0003779 and its children

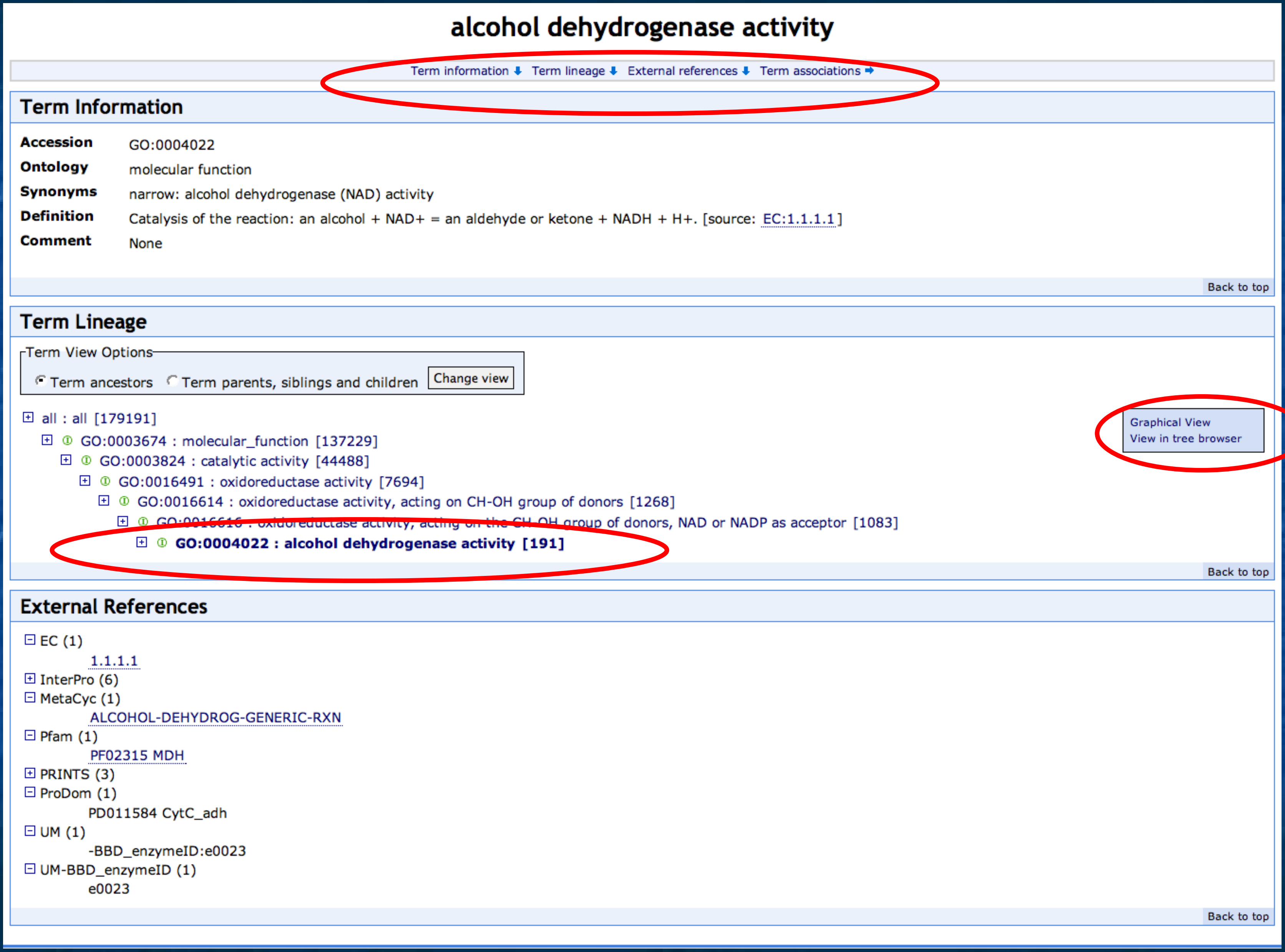
Get this data as RDF-XML.

actin binding ; GO:0003779

Interacting selectively with monomeric or multimeric forms of actin, including actin filaments.

	Qualifier	Name / Symbol	Information	Evidence	Reference	Assigned by
☐		**1433G_SHEEP** BLAST YWHAG: 14-3-3 protein gamma (Fragments)	**protein** from *Ovis aries*	**ISS** With UniProt:P11576	UniProt:P68253	Proteome Inc. (via UniProt)
☐		**4933400A11Rik** RIKEN cDNA 4933400A11 gene	**gene** from *Mus musculus*	**RCA**	PMID:12466851	MGI
☐		**Abl1_mapped** v-abl Abelson murine leukemia viral oncogene homolog 1 (mapped)	**gene** from *Rattus norvegicus*	**ISS**	PMID:11864995	RGD
☐		**Ablim1** BLAST actin-binding LIM protein 1	**gene** from *Mus musculus*	**IDA**	PMID:9245787	MGI
☐		**Ablim3** BLAST actin binding LIM protein family, member 3	**gene** from *Mus musculus*	**RCA**	PMID:12466851	MGI
☐		**ABLM1_HUMAN** BLAST ABLIM1, ABLIM, KIAA0059: Actin-binding LIM protein 1	**protein** from *Homo sapiens*	**TAS**	PMID:9245787	Proteome Inc. (via UniProt)
☐		**abnA** BLAST actobindin	**gene** from *Dictyostelium discoideum*	**ISS** With NCBI gi:2507239	DDB REF:10155	dictyBase
☐		**abnB** BLAST actobindin	**gene** from *Dictyostelium discoideum*	**ISS** With NCBI gi:2507239	DDB REF:10155	dictyBase
☐		**abnC** actobindin	**gene** from *Dictyostelium discoideum*	**ISS** With NCBI gi:2507239	DDB REF:10155	dictyBase

Term Details Page



alcohol dehydrogenase activity

Term Information

Accession	GO:0004022
Ontology	molecular function
Synonyms	narrow: alcohol dehydrogenase (NAD) activity
Definition	Catalysis of the reaction: an alcohol + NAD+ = an aldehyde or ketone + NADH + H+. [source: EC:1.1.1.1]
Comment	None

Term Lineage

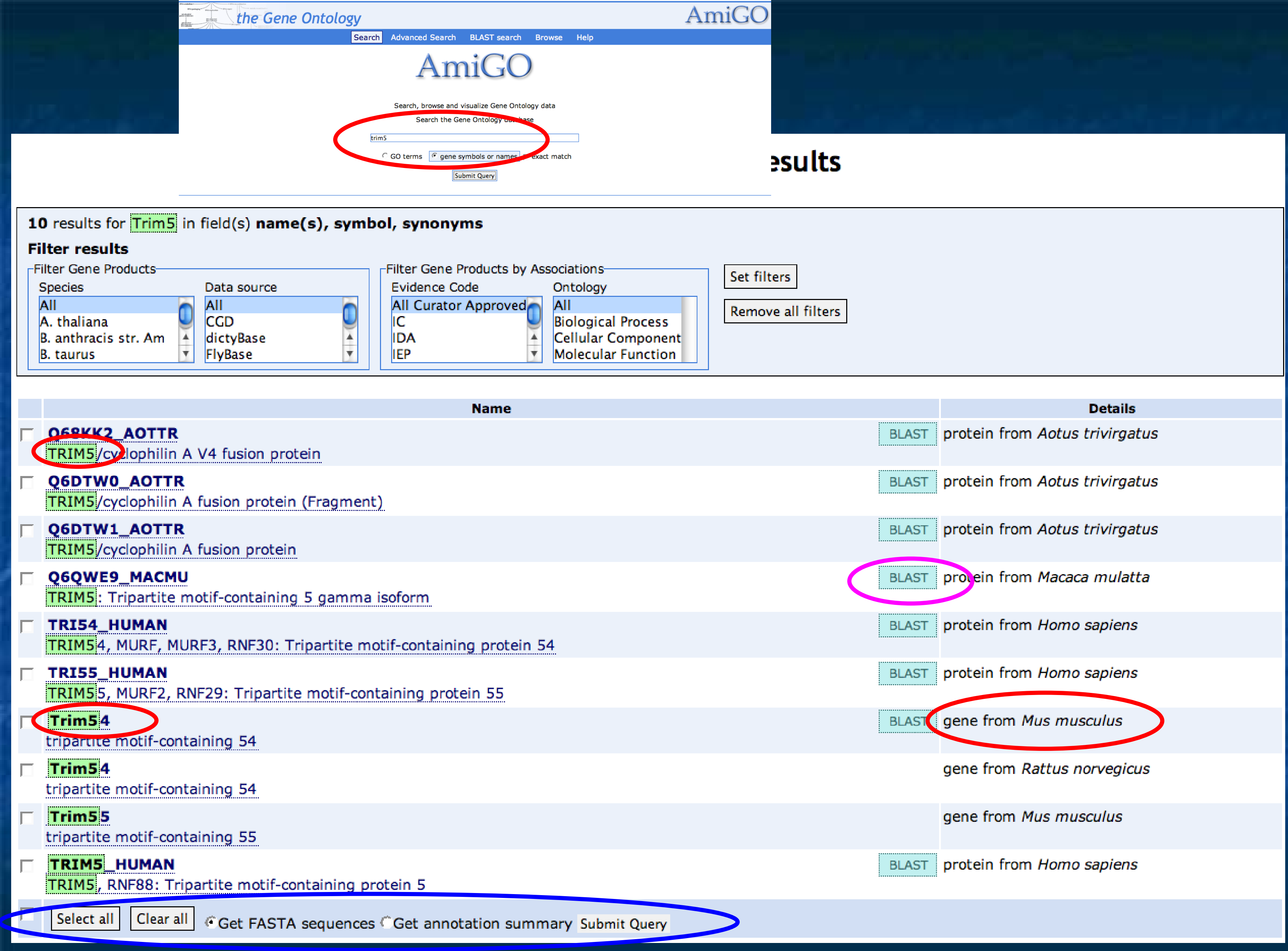
Term View Options

● Term ancestors ○ Term parents, siblings and children

- all : all [179191]
  - GO:0003674 : molecular_function [137229]
    - GO:0003824 : catalytic activity [44488]
      - GO:0016491 : oxidoreductase activity [7694]
        - GO:0016614 : oxidoreductase activity, acting on CH-OH group of donors [1268]
          - GO:0016616 : oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [1083]
            - **GO:0004022 : alcohol dehydrogenase activity [191]**

External References

EC (1)
1.1.1.1
InterPro (6)
MetaCyc (1)
ALCOHOL-DEHYDROG-GENERIC-RXN
Pfam (1)
PF02315 MDH
PRINTS (3)
ProDom (1)
PD011584 CytC_adh
UM (1)
-BBD_enzymeID:e0023
UM-BBD_enzymeID (1)
e0023



AmiGO

Search, browse and visualize Gene Ontology data

Search the Gene Ontology database

trim5

○ GO terms ● gene symbols or names ☐ exact match

Submit Query

esults

10 results for Trim5 in field(s) **name(s), symbol, synonyms**

Filter results

Filter Gene Products

Species	Data source
All	All
A. thaliana	CGD
B. anthracis str. Am	dictyBase
B. taurus	FlyBase

Filter Gene Products by Associations

Evidence Code	Ontology
All Curator Approved	All
IC	Biological Process
IDA	Cellular Component
IEP	Molecular Function

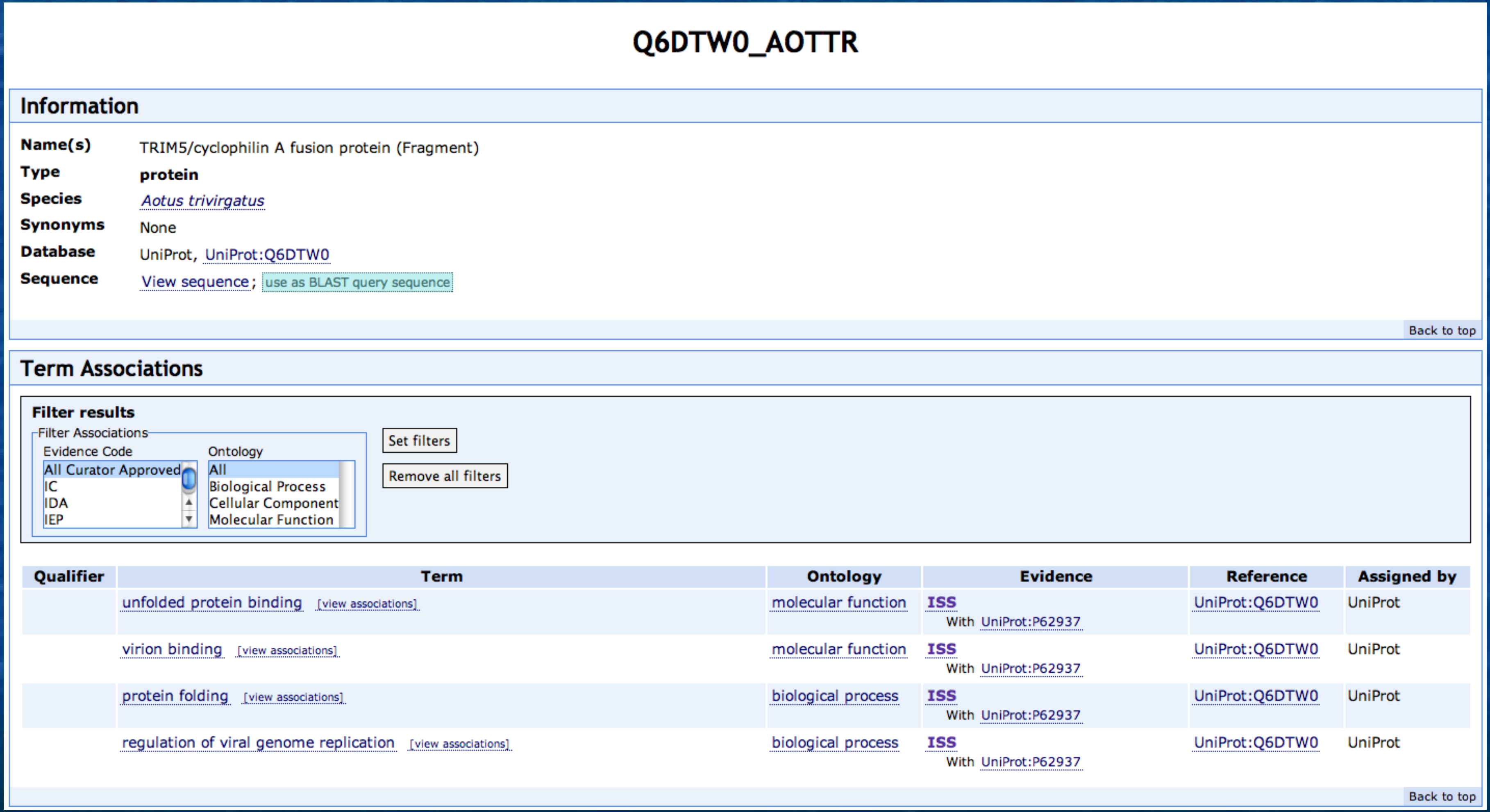
Set filters

Remove all filters

	Name		Details
☐	**Q68KK2_AOTTR** TRIM5/cyclophilin A V4 fusion protein	BLAST	protein from *Aotus trivirgatus*
☐	**Q6DTW0_AOTTR** TRIM5/cyclophilin A fusion protein (Fragment)	BLAST	protein from *Aotus trivirgatus*
☐	**Q6DTW1_AOTTR** TRIM5/cyclophilin A fusion protein	BLAST	protein from *Aotus trivirgatus*
☐	**Q6QWE9_MACMU** TRIM5: Tripartite motif-containing 5 gamma isoform	BLAST	protein from *Macaca mulatta*
☐	**TRI54_HUMAN** TRIM54, MURF, MURF3, RNF30: Tripartite motif-containing protein 54	BLAST	protein from *Homo sapiens*
☐	**TRI55_HUMAN** TRIM55, MURF2, RNF29: Tripartite motif-containing protein 55	BLAST	protein from *Homo sapiens*
☐	**Trim54** tripartite motif-containing 54	BLAST	gene from *Mus musculus*
☐	**Trim54** tripartite motif-containing 54		gene from *Rattus norvegicus*
☐	**Trim55** tripartite motif-containing 55		gene from *Mus musculus*
☐	**TRIM5_HUMAN** TRIM5, RNF88: Tripartite motif-containing protein 5	BLAST	protein from *Homo sapiens*

Select all Clear all ● Get FASTA sequences ○ Get annotation summary Submit Query

Gene Product Details and Annotations



Q6DTW0_AOTTR

Information

Name(s)	TRIM5/cyclophilin A fusion protein (Fragment)
Type	**protein**
Species	*Aotus trivirgatus*
Synonyms	None
Database	UniProt, UniProt:Q6DTW0
Sequence	View sequence; use as BLAST query sequence

Back to top

Term Associations

Filter results

Filter Associations

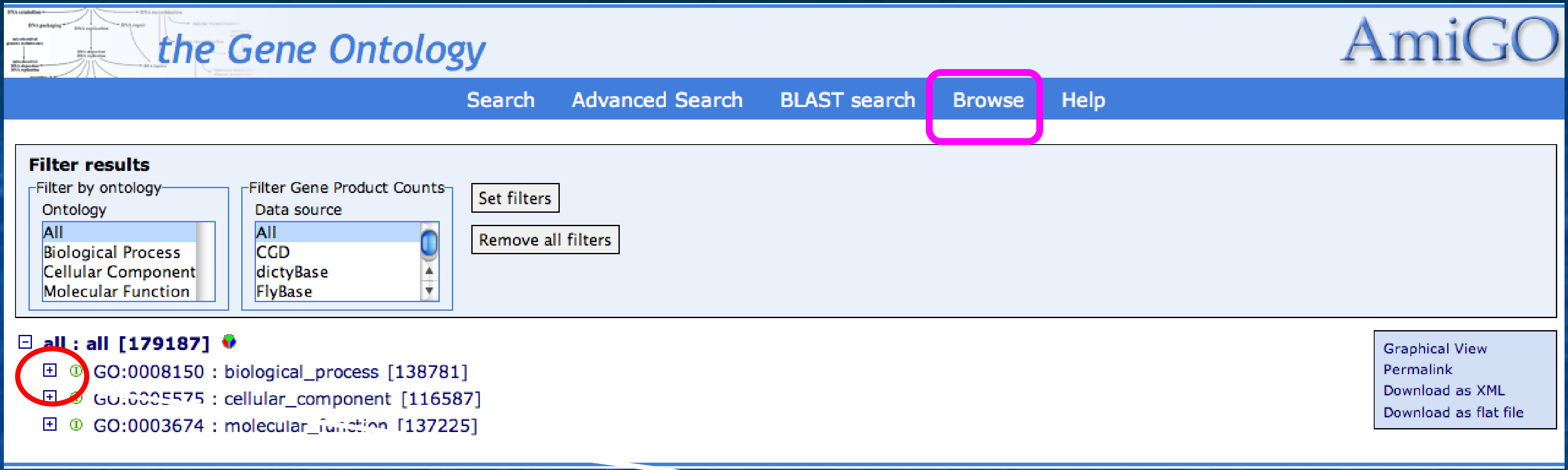
Evidence Code: All Curator Approved, IC, IDA, IEP

Ontology: All, Biological Process, Cellular Component, Molecular Function

Qualifier	Term	Ontology	Evidence	Reference	Assigned by
	unfolded protein binding [view associations]	molecular function	ISS With UniProt:P62937	UniProt:Q6DTW0	UniProt
	virion binding [view associations]	molecular function	ISS With UniProt:P62937	UniProt:Q6DTW0	UniProt
	protein folding [view associations]	biological process	ISS With UniProt:P62937	UniProt:Q6DTW0	UniProt
	regulation of viral genome replication [view associations]	biological process	ISS With UniProt:P62937	UniProt:Q6DTW0	UniProt

Back to top

Browsing the Ontologies



Filter results

Filter by ontology

Ontology: All, Biological Process, Cellular Component, Molecular Function

Filter Gene Product Counts

Data source: All, CGD, dictyBase, FlyBase

⊟ **all : all [179187]** ●

⊞ Ⓘ GO:0008150 : biological_process [138781]

⊞ Ⓘ GO:0005575 : cellular_component [116587]

⊞ Ⓘ GO:0003674 : molecular_function [137225]

⊞ Node has children, can be clicked to view children

⊟ Node has been opened, can be clicked to close

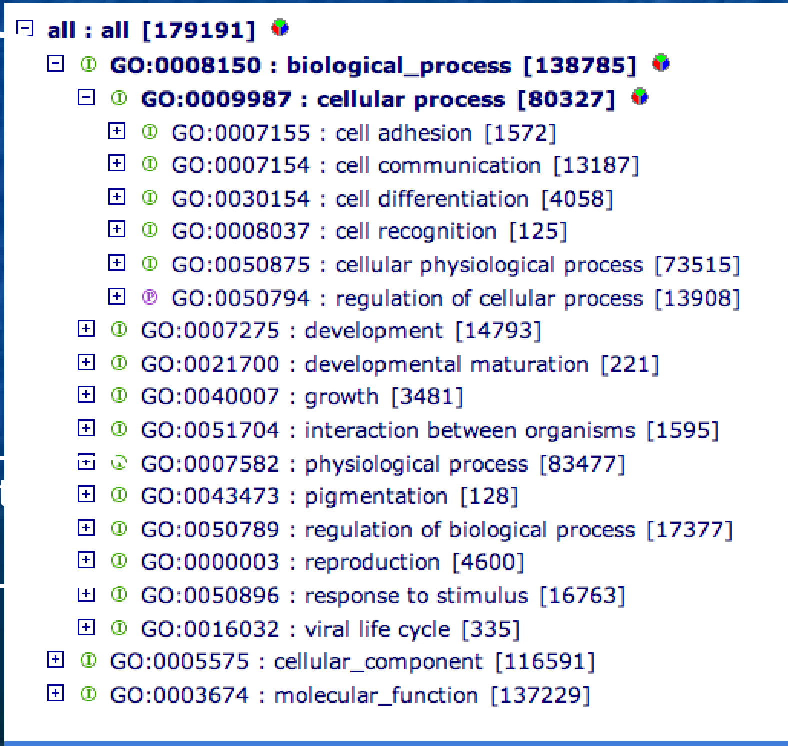
▪ Leaf node or no children

Ⓘ Is_a relationship

Ⓟ Part_of relationship

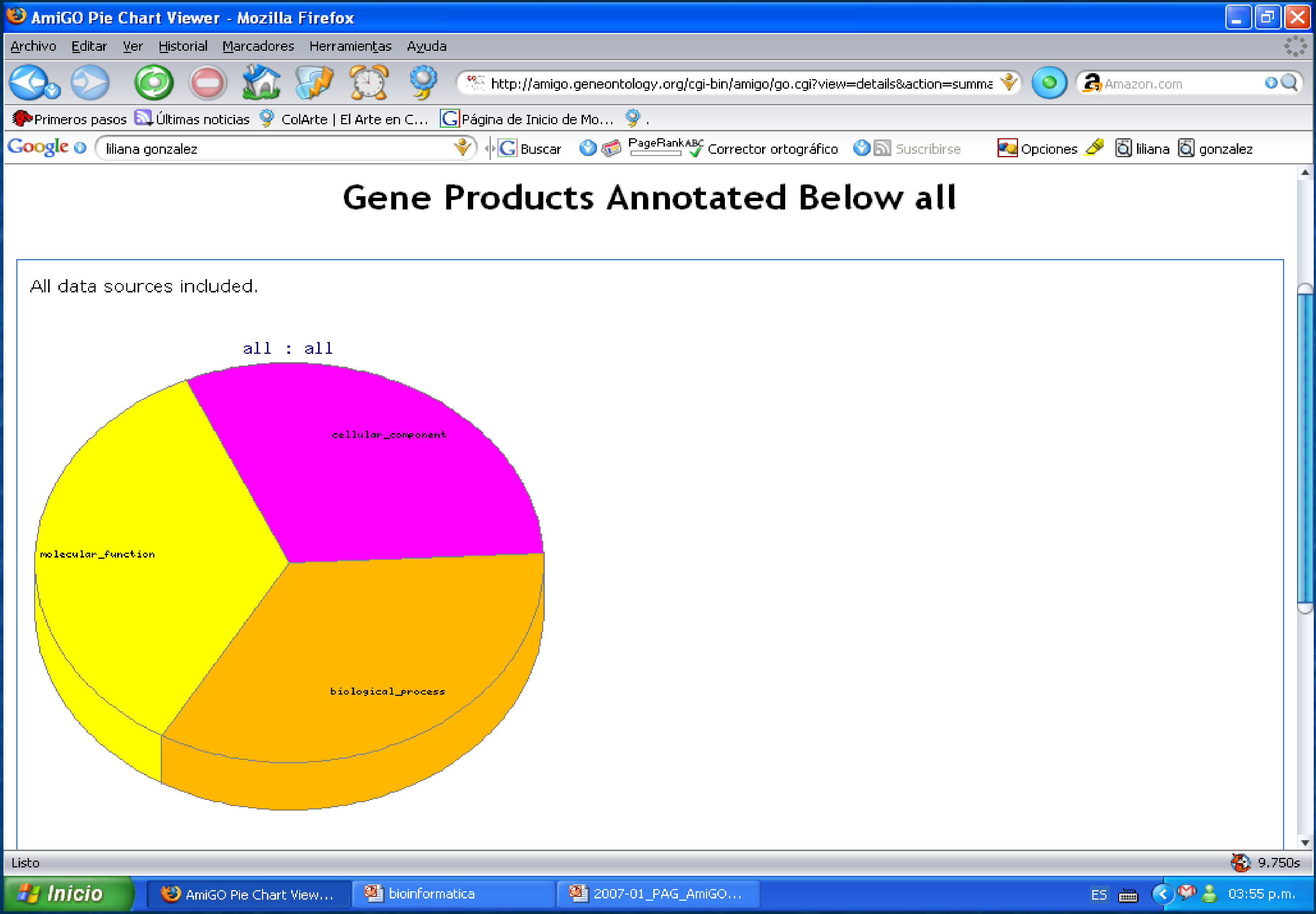
● pie chart summary of the numbers of gene products associated t

any immediate descendants of this term in the tree.



⊟ **all : all [179191]** ●

- ⊟ Ⓘ **GO:0008150 : biological_process [138785]** ●
  - ⊟ Ⓘ **GO:0009987 : cellular process [80327]** ●
    - ⊞ Ⓘ GO:0007155 : cell adhesion [1572]
    - ⊞ Ⓘ GO:0007154 : cell communication [13187]
    - ⊞ Ⓘ GO:0030154 : cell differentiation [4058]
    - ⊞ Ⓘ GO:0008037 : cell recognition [125]
    - ⊞ Ⓘ GO:0050875 : cellular physiological process [73515]
    - ⊞ Ⓟ GO:0050794 : regulation of cellular process [13908]
  - ⊞ Ⓘ GO:0007275 : development [14793]
  - ⊞ Ⓘ GO:0021700 : developmental maturation [221]
  - ⊞ Ⓘ GO:0040007 : growth [3481]
  - ⊞ Ⓘ GO:0051704 : interaction between organisms [1595]
  - ⊞ Ⓘ GO:0007582 : physiological process [83477]
  - ⊞ Ⓘ GO:0043473 : pigmentation [128]
  - ⊞ Ⓘ GO:0050789 : regulation of biological process [17377]
  - ⊞ Ⓘ GO:0000003 : reproduction [4600]
  - ⊞ Ⓘ GO:0050896 : response to stimulus [16763]
  - ⊞ Ⓘ GO:0016032 : viral life cycle [335]
- ⊞ Ⓘ GO:0005575 : cellular_component [116591]
- ⊞ Ⓘ GO:0003674 : molecular_function [137229]

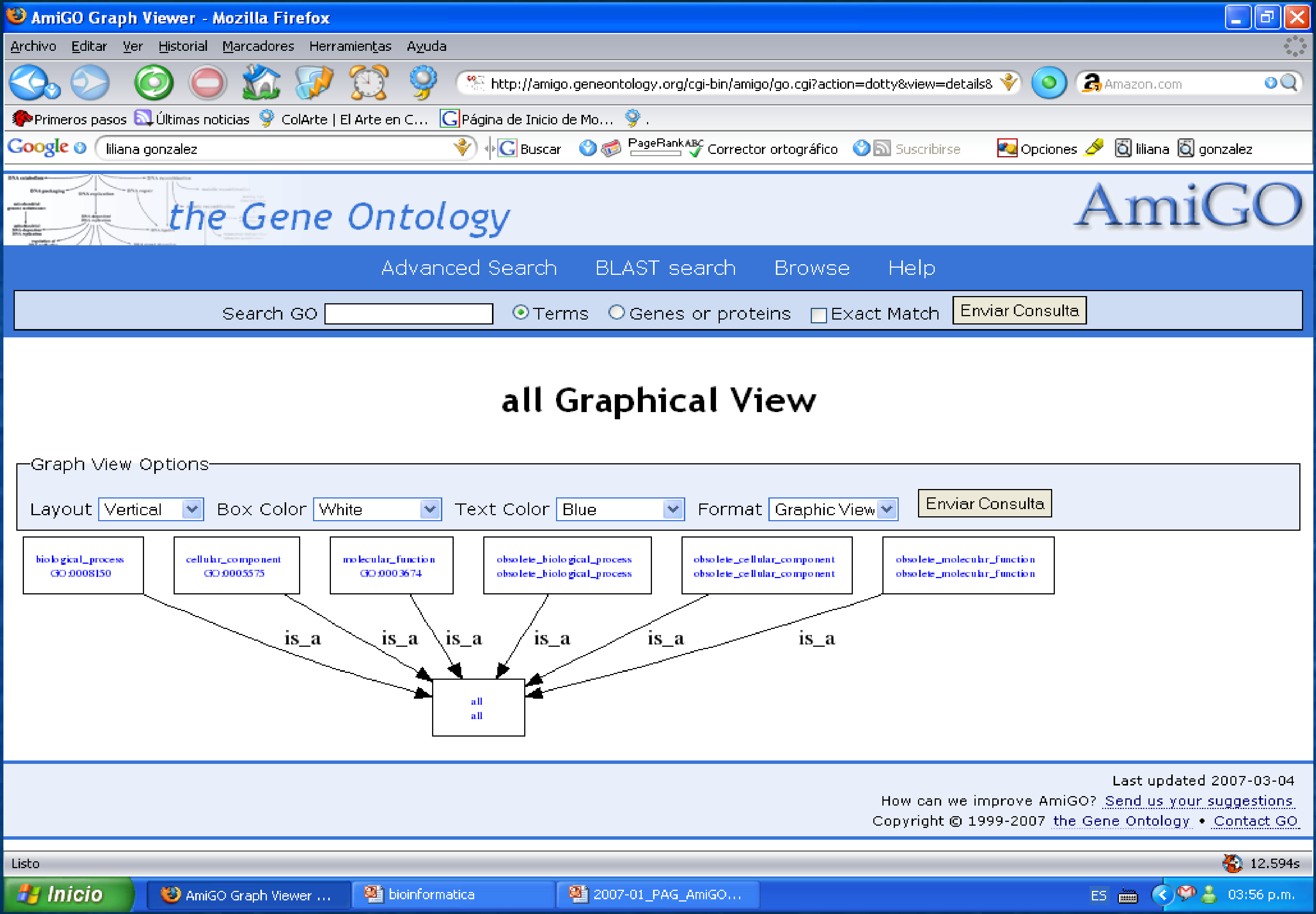


http://amigo.geneontology.org/cgi-bin/amigo/go.cgi?view=details&action=summa

liliana gonzalez

Gene Products Annotated Below all

All data sources included.



all Graphical View

Graph View Options

Layout: Vertical
Box Color: White
Text Color: Blue
Format: Graphic View

Last updated 2007-03-04

How can we improve AmiGO? Send us your suggestions

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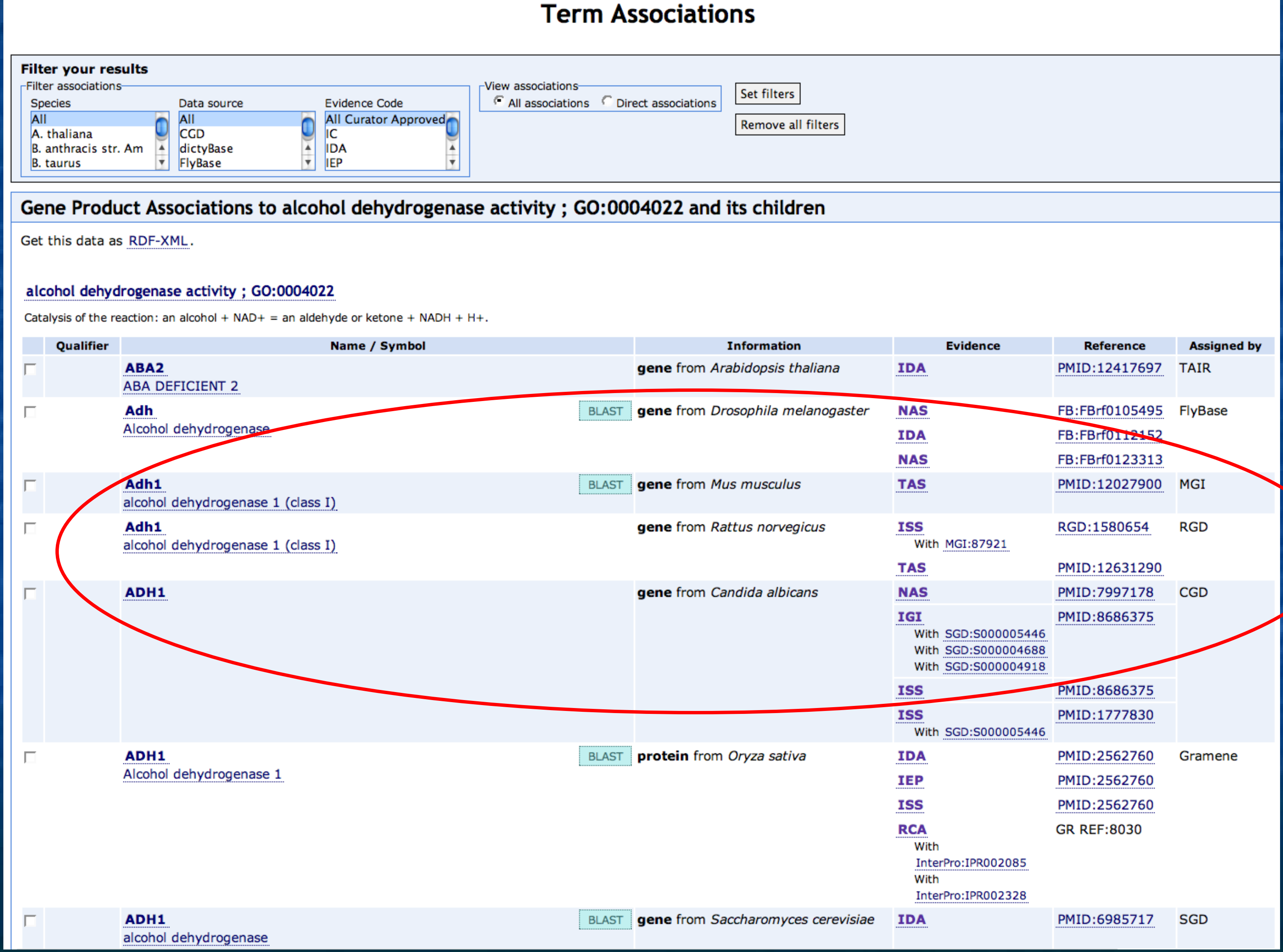
Annotations associated with a term



Term Associations

Filter your results

Filter associations

Species	Data source	Evidence Code
All	All	All Curator Approved
A. thaliana	CGD	IC
B. anthracis str. Am	dictyBase	IDA
B. taurus	FlyBase	IEP

View associations
● All associations ○ Direct associations

Gene Product Associations to alcohol dehydrogenase activity ; GO:0004022 and its children

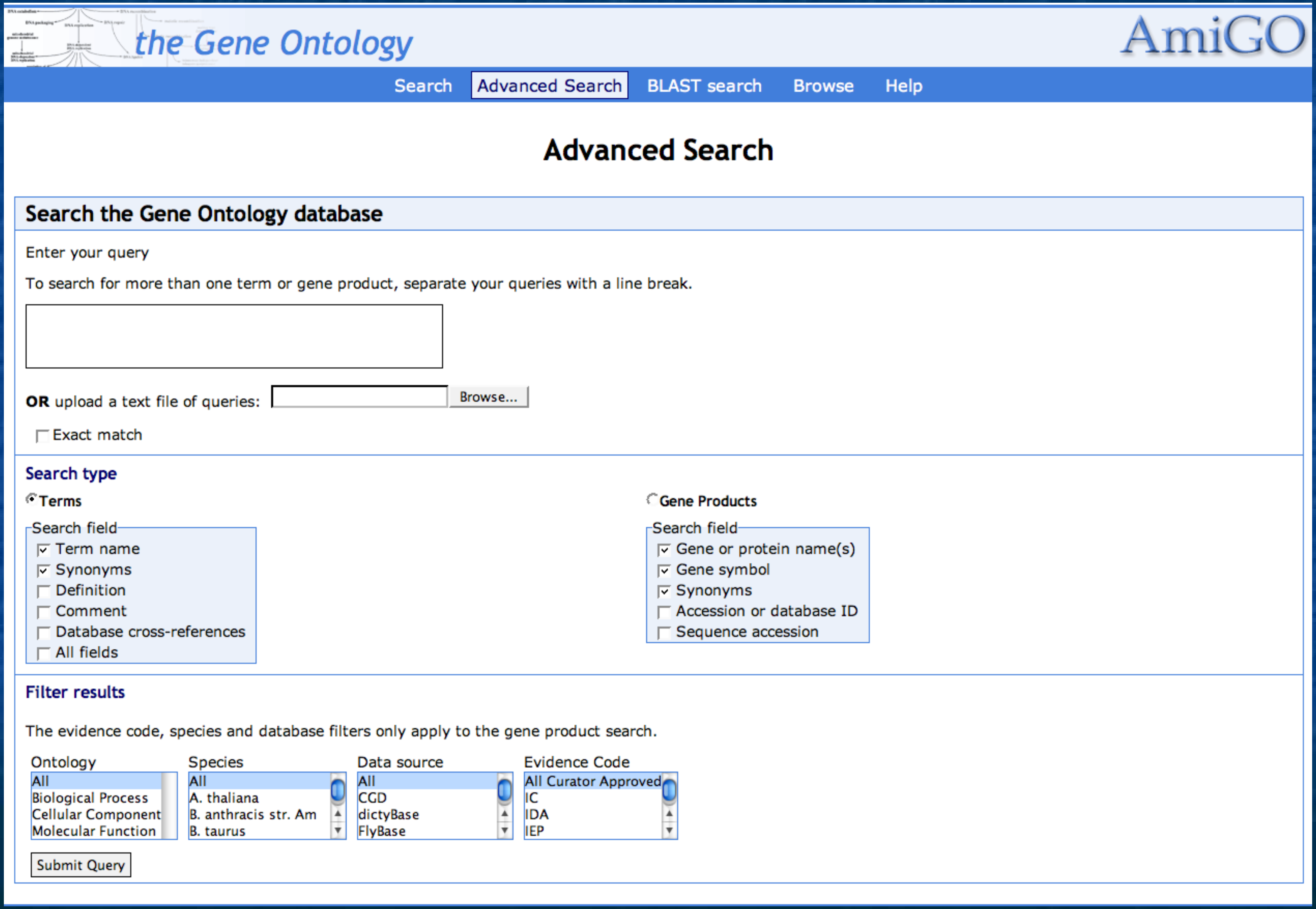
Get this data as RDF-XML.

alcohol dehydrogenase activity ; GO:0004022

Catalysis of the reaction: an alcohol + NAD+ = an aldehyde or ketone + NADH + H+.

	Qualifier	Name / Symbol	Information	Evidence	Reference	Assigned by
☐		**ABA2** ABA DEFICIENT 2	**gene** from *Arabidopsis thaliana*	IDA	PMID:12417697	TAIR
☐		**Adh** Alcohol dehydrogenase BLAST	**gene** from *Drosophila melanogaster*	NAS IDA NAS	FB:FBrf0105495 FB:FBrf0112152 FB:FBrf0123313	FlyBase
☐		**Adh1** alcohol dehydrogenase 1 (class I) BLAST	**gene** from *Mus musculus*	TAS	PMID:12027900	MGI
☐		**Adh1** alcohol dehydrogenase 1 (class I)	**gene** from *Rattus norvegicus*	ISS With MGI:87921 TAS	RGD:1580654 PMID:12631290	RGD
☐		**ADH1**	**gene** from *Candida albicans*	NAS IGI With SGD:S000005446 With SGD:S000004688 With SGD:S000004918 ISS ISS With SGD:S000005446	PMID:7997178 PMID:8686375 PMID:8686375 PMID:1777830	CGD
☐		**ADH1** Alcohol dehydrogenase 1 BLAST	**protein** from *Oryza sativa*	IDA IEP ISS RCA With InterPro:IPR002085 With InterPro:IPR002328	PMID:2562760 PMID:2562760 PMID:2562760 GR REF:8030	Gramene
☐		**ADH1** alcohol dehydrogenase BLAST	**gene** from *Saccharomyces cerevisiae*	IDA	PMID:6985717	SGD

Advanced search



Advanced Search

Search the Gene Ontology database

Enter your query

To search for more than one term or gene product, separate your queries with a line break.

OR upload a text file of queries: Browse...

☐ Exact match

Search type

● **Terms**

Search field
- ☑ Term name
- ☑ Synonyms
- ☐ Definition
- ☐ Comment
- ☐ Database cross-references
- ☐ All fields

○ **Gene Products**

Search field
- ☑ Gene or protein name(s)
- ☑ Gene symbol
- ☑ Synonyms
- ☐ Accession or database ID
- ☐ Sequence accession

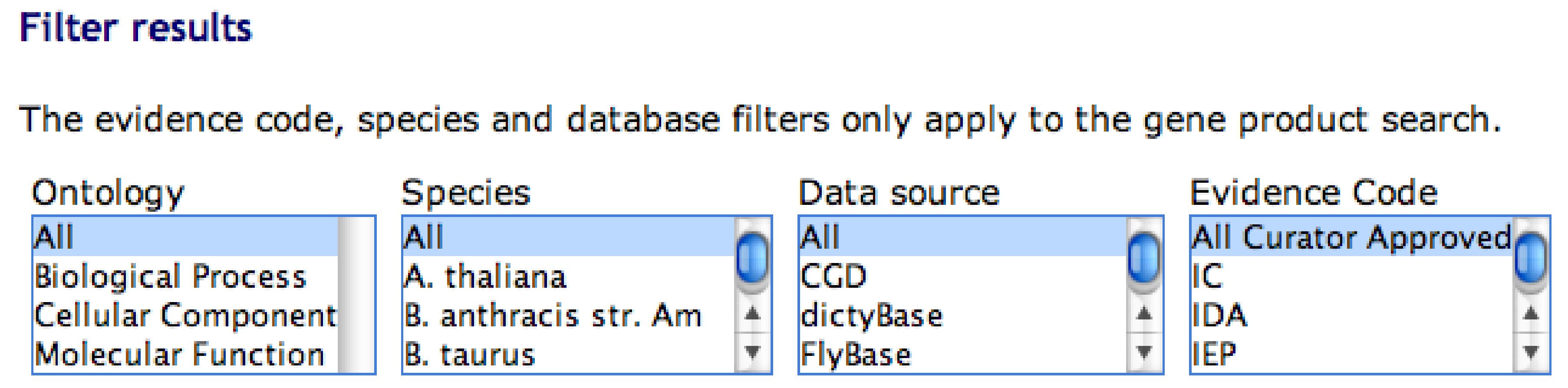
Filter results

The evidence code, species and database filters only apply to the gene product search.

Ontology	Species	Data source	Evidence Code
All	All	All	All Curator Approved
Biological Process	A. thaliana	CGD	IC
Cellular Component	B. anthracis str. Am	dictyBase	IDA
Molecular Function	B. taurus	FlyBase	IEP

Submit Query

Filters



Filter results

The evidence code, species and database filters only apply to the gene product search.

Ontology
- All
- Biological Process
- Cellular Component
- Molecular Function

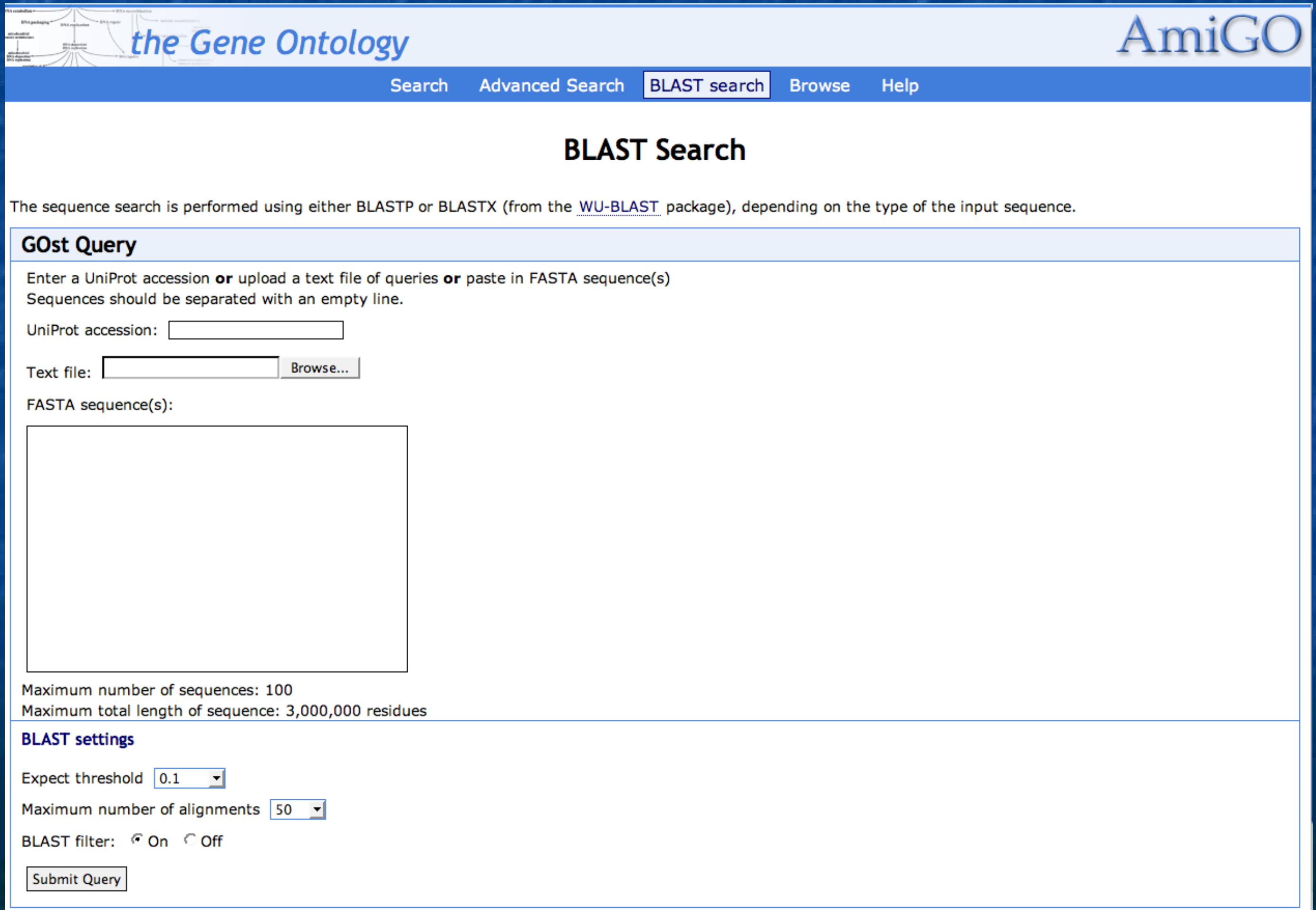
Species
- All
- A. thaliana
- B. anthracis str. Am
- B. taurus

Data source
- All
- CGD
- dictyBase
- FlyBase

Evidence Code
- All Curator Approved
- IC
- IDA
- IEP

GOST-Gene Ontology blaST

- Blast a protein sequence against all gene products that have a GO annotation
- Can be accessed from the AmiGO Home page (front page)



BLAST Search

The sequence search is performed using either BLASTP or BLASTX (from the WU-BLAST package), depending on the type of the input sequence.

GOst Query

Enter a UniProt accession **or** upload a text file of queries **or** paste in FASTA sequence(s)
Sequences should be separated with an empty line.

UniProt accession:

Text file:

FASTA sequence(s):

Maximum number of sequences: 100
Maximum total length of sequence: 3,000,000 residues

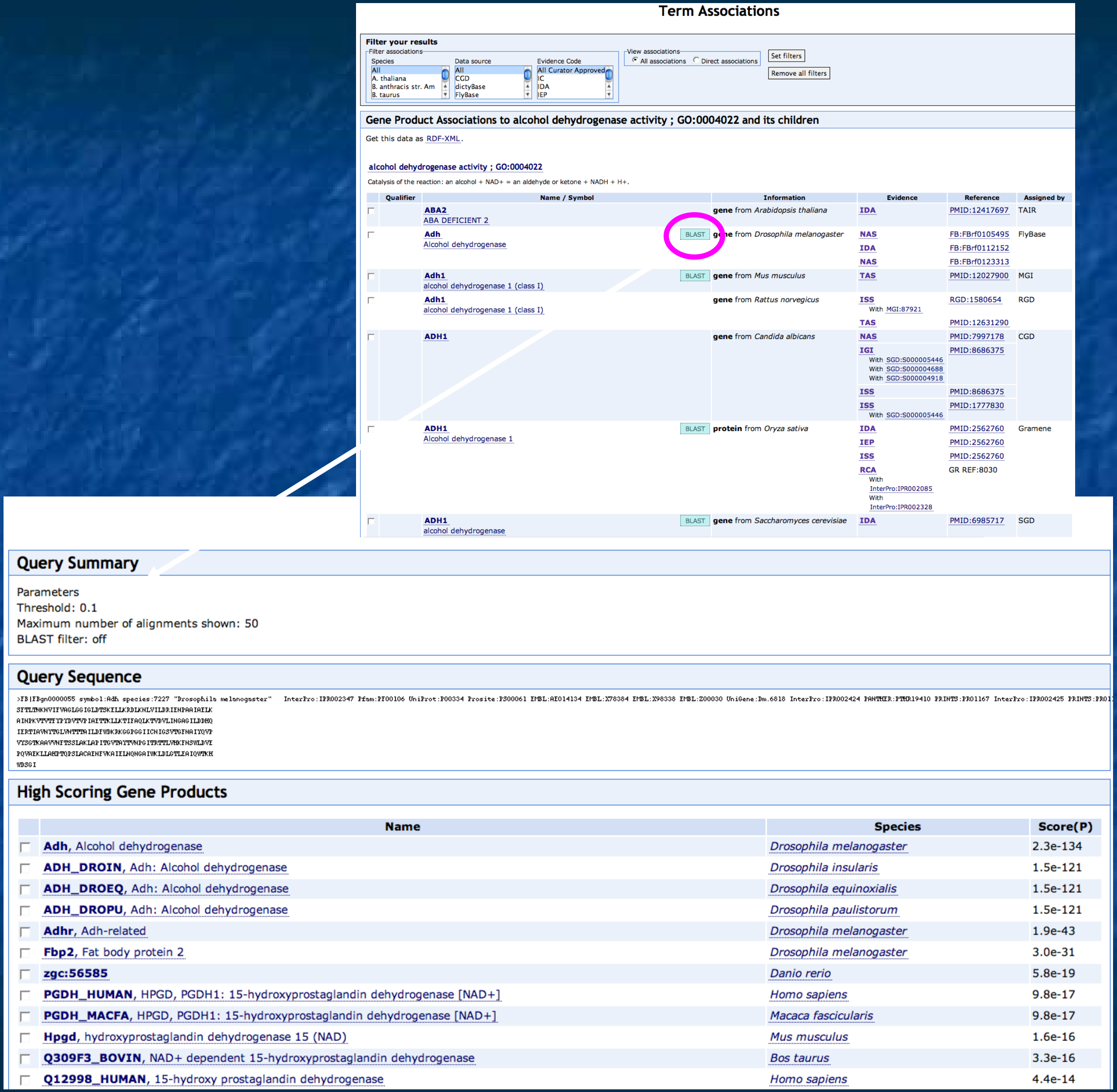
BLAST settings

Expect threshold 0.1

Maximum number of alignments 50

BLAST filter: ● On ○ Off

GOst can also be accessed from the annotations section



Term Associations

Filter your results

Filter associations

Species: All, A. thaliana, B. anthracis str. Am, B. taurus

Data source: All, CGD, dictyBase, FlyBase

Evidence Code: All Curator Approved, IC, IDA, IEP

View associations: ● All associations ○ Direct associations

Gene Product Associations to alcohol dehydrogenase activity ; GO:0004022 and its children

Get this data as RDF-XML.

alcohol dehydrogenase activity ; GO:0004022

Catalysis of the reaction: an alcohol + NAD+ = an aldehyde or ketone + NADH + H+.

	Qualifier	Name / Symbol		Information	Evidence	Reference	Assigned by
☐		**ABA2** ABA DEFICIENT 2		**gene** from *Arabidopsis thaliana*	IDA	PMID:12417697	TAIR
☐		**Adh** Alcohol dehydrogenase	BLAST	**gene** from *Drosophila melanogaster*	NAS IDA NAS	FB:FBrf0105495 FB:FBrf0112152 FB:FBrf0123313	FlyBase
☐		**Adh1** alcohol dehydrogenase 1 (class I)	BLAST	**gene** from *Mus musculus*	TAS	PMID:12027900	MGI
☐		**Adh1** alcohol dehydrogenase 1 (class I)		**gene** from *Rattus norvegicus*	ISS With MGI:87921 TAS	RGD:1580654 PMID:12631290	RGD
☐		**ADH1**		**gene** from *Candida albicans*	NAS IGI With SGD:S000005446 With SGD:S000004688 With SGD:S000004918 ISS ISS With SGD:S000005446	PMID:7997178 PMID:8686375 PMID:8686375 PMID:1777830	CGD
☐		**ADH1** Alcohol dehydrogenase 1	BLAST	**protein** from *Oryza sativa*	IDA IEP ISS RCA With InterPro:IPR002085 With InterPro:IPR002328	PMID:2562760 PMID:2562760 PMID:2562760 GR REF:8030	Gramene
☐		**ADH1** alcohol dehydrogenase	BLAST	**gene** from *Saccharomyces cerevisiae*	IDA	PMID:6985717	SGD

Query Summary

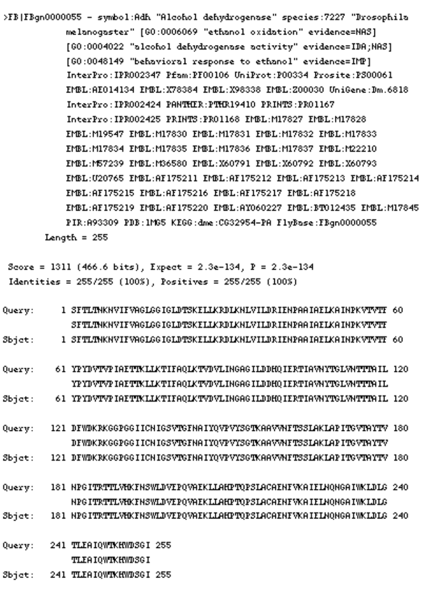
Parameters
Threshold: 0.1
Maximum number of alignments shown: 50
BLAST filter: off

Query Sequence

```
>FB|FBgn0000055 symbol:Adh species:7227 "Drosophila melanogaster"   InterPro:IPR002347 Pfam:PF00106 UniProt:P00334 Prosite:PS00061 EMBL:AE014134 EMBL:X78384 EMBL:X98338 EMBL:Z00030 UniGene:Dm.6818 InterPro:IPR002424 PANTHER:PTHR19410 PRINTS:PR01167 InterPro:IPR002425 PRINTS:PR01
SFTLTNKNVIFVAGLGGIGLDTSKELLKRDLKNLVILDRIENPAAIAELK
AINPKVTVTFYPYDVTVPIAETTKLLKTIFAQLKTVDVLINGAGILDDHQ
IERTIAVNYTGLVNTTTAILDFWDKRKGGPGGIICNIGSVTGFNAIYQVP
VYSGTKAAVVNFTSSLAKLAPITGVTAYTVNPGITRTTLVHKFNSWLDVE
PQVAEKLLAHPTQPSLACAENFVKAIELNQNGAIWKLDLGTLEAIQWTKH
WDSGI
```

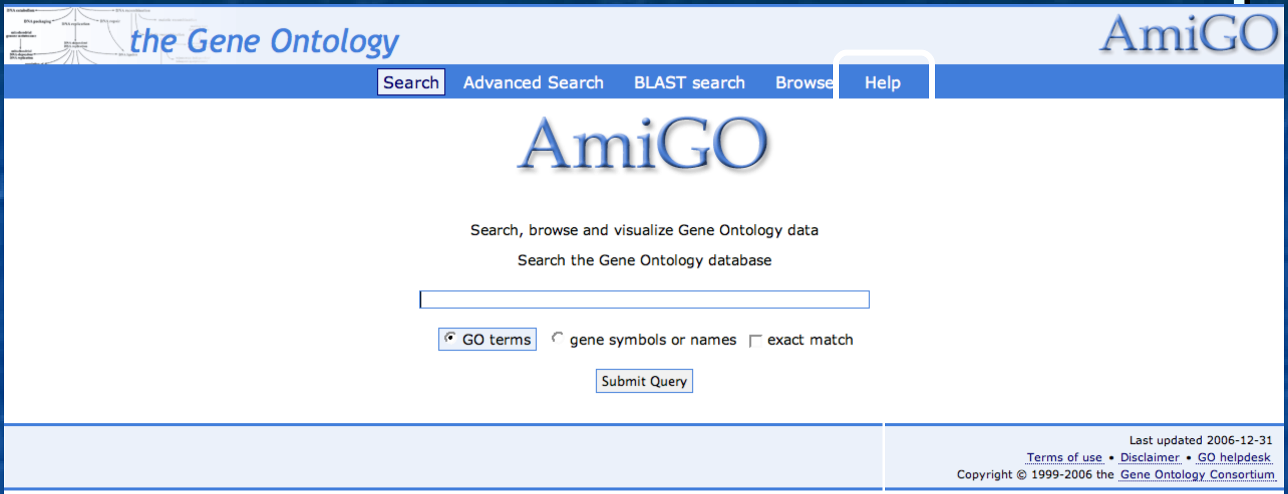
High Scoring Gene Products

	Name	Species	Score(P)
☐	**Adh**, Alcohol dehydrogenase	*Drosophila melanogaster*	2.3e-134
☐	**ADH_DROIN**, Adh: Alcohol dehydrogenase	*Drosophila insularis*	1.5e-121
☐	**ADH_DROEQ**, Adh: Alcohol dehydrogenase	*Drosophila equinoxialis*	1.5e-121
☐	**ADH_DROPU**, Adh: Alcohol dehydrogenase	*Drosophila paulistorum*	1.5e-121
☐	**Adhr**, Adh-related	*Drosophila melanogaster*	1.9e-43
☐	**Fbp2**, Fat body protein 2	*Drosophila melanogaster*	3.0e-31
☐	**zgc:56585**	*Danio rerio*	5.8e-19
☐	**PGDH_HUMAN**, HPGD, PGDH1: 15-hydroxyprostaglandin dehydrogenase [NAD+]	*Homo sapiens*	9.8e-17
☐	**PGDH_MACFA**, HPGD, PGDH1: 15-hydroxyprostaglandin dehydrogenase [NAD+]	*Macaca fascicularis*	9.8e-17
☐	**Hpgd**, hydroxyprostaglandin dehydrogenase 15 (NAD)	*Mus musculus*	1.6e-16
☐	**Q309F3_BOVIN**, NAD+ dependent 15-hydroxyprostaglandin dehydrogenase	*Bos taurus*	3.3e-16
☐	**Q12998_HUMAN**, 15-hydroxy prostaglandin dehydrogenase	*Homo sapiens*	4.4e-14



```
>FB|FBgn0000055 - symbol:Adh "Alcohol dehydrogenase" species:7227 "Drosophila
          melanogaster" [GO:0006069 "ethanol oxidation" evidence=NAS]
          [GO:0004022 "alcohol dehydrogenase activity" evidence=IDA;NAS]
          [GO:0048149 "behavioral response to ethanol" evidence=IMP]
          InterPro:IPR002347 Pfam:PF00106 UniProt:P00334 Prosite:PS00061
          EMBL:AE014134 EMBL:X78384 EMBL:X98338 EMBL:Z00030 UniGene:Dm.6818
          InterPro:IPR002424 PANTHER:PTHR19410 PRINTS:PR01167
          InterPro:IPR002425 PRINTS:PR01168 EMBL:M17827 EMBL:M17828
          EMBL:M19547 EMBL:M17830 EMBL:M17831 EMBL:M17832 EMBL:M17833
          EMBL:M17834 EMBL:M17835 EMBL:M17836 EMBL:M17837 EMBL:M22210
          EMBL:M57239 EMBL:M36580 EMBL:X60791 EMBL:X60792 EMBL:X60793
          EMBL:U20765 EMBL:AF175211 EMBL:AF175212 EMBL:AF175213 EMBL:AF175214
          EMBL:AF175215 EMBL:AF175216 EMBL:AF175217 EMBL:AF175218
          EMBL:AF175219 EMBL:AF175220 EMBL:AY060227 EMBL:BT012435 EMBL:M17845
          PIR:A93309 PDB:1MG5 KEGG:dme:CG32954-PA FlyBase:FBgn0000055
       Length = 255

 Score = 1311 (466.6 bits), Expect = 2.3e-134, P = 2.3e-134
 Identities = 255/255 (100%), Positives = 255/255 (100%)

Query:     1 SFTLTNKNVIFVAGLGGIGLDTSKELLKRDLKNLVILDRIENPAAIAELKAINPKVTVTF 60
             SFTLTNKNVIFVAGLGGIGLDTSKELLKRDLKNLVILDRIENPAAIAELKAINPKVTVTF
Sbjct:     1 SFTLTNKNVIFVAGLGGIGLDTSKELLKRDLKNLVILDRIENPAAIAELKAINPKVTVTF 60

Query:    61 YPYDVTVPIAETTKLLKTIFAQLKTVDVLINGAGILDDHQIERTIAVNYTGLVNTTTAIL 120
             YPYDVTVPIAETTKLLKTIFAQLKTVDVLINGAGILDDHQIERTIAVNYTGLVNTTTAIL
Sbjct:    61 YPYDVTVPIAETTKLLKTIFAQLKTVDVLINGAGILDDHQIERTIAVNYTGLVNTTTAIL 120

Query:   121 DFWDKRKGGPGGIICNIGSVTGFNAIYQVPVYSGTKAAVVNFTSSLAKLAPITGVTAYTV 180
             DFWDKRKGGPGGIICNIGSVTGFNAIYQVPVYSGTKAAVVNFTSSLAKLAPITGVTAYTV
Sbjct:   121 DFWDKRKGGPGGIICNIGSVTGFNAIYQVPVYSGTKAAVVNFTSSLAKLAPITGVTAYTV 180

Query:   181 NPGITRTTLVHKFNSWLDVEPQVAEKLLAHPTQPSLACAENFVKAIELNQNGAIWKLDLG 240
             NPGITRTTLVHKFNSWLDVEPQVAEKLLAHPTQPSLACAENFVKAIELNQNGAIWKLDLG
Sbjct:   181 NPGITRTTLVHKFNSWLDVEPQVAEKLLAHPTQPSLACAENFVKAIELNQNGAIWKLDLG 240

Query:   241 TLEAIQWTKHWDSGI 255
             TLEAIQWTKHWDSGI
Sbjct:   241 TLEAIQWTKHWDSGI 255
```

AmiGO Help



Search, browse and visualize Gene Ontology data

Search the Gene Ontology database

Last updated 2006-12-31

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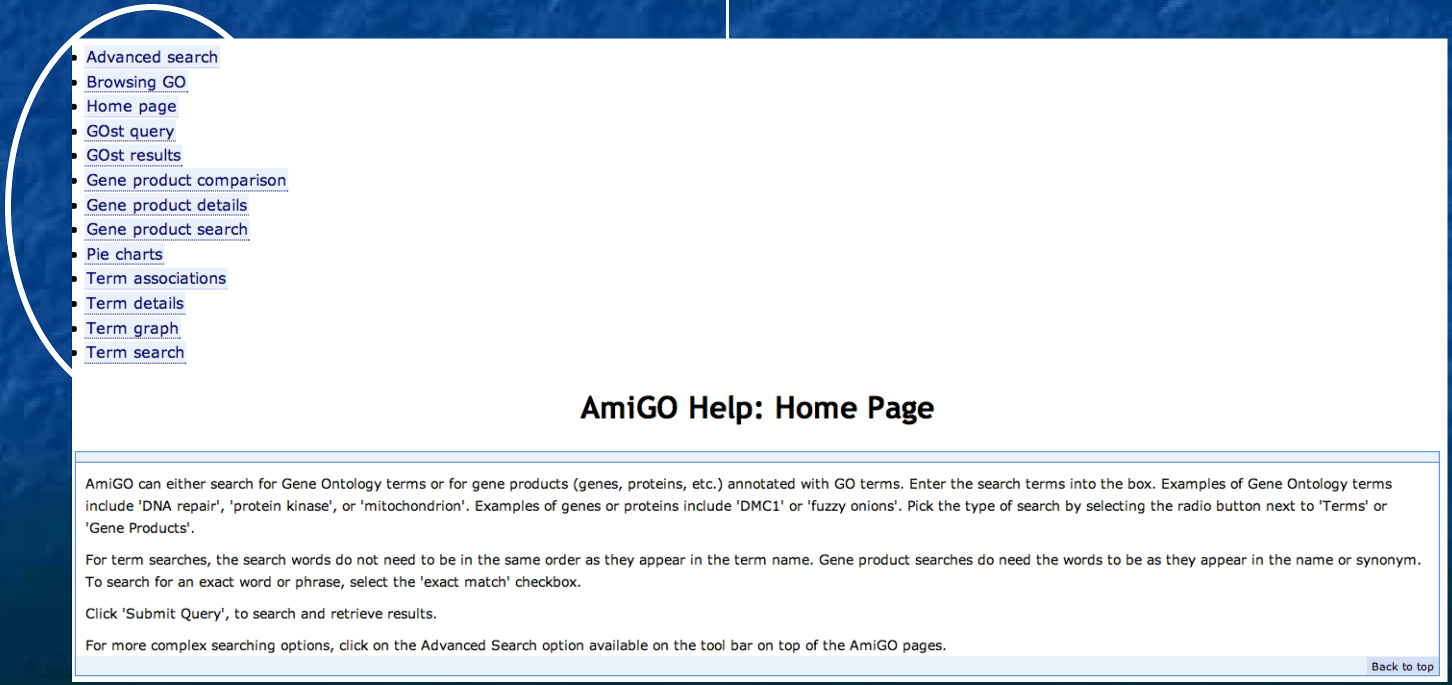

- Advanced search
- Browsing GO
- Home page
- GOst query
- GOst results
- Gene product comparison
- Gene product details
- Gene product search
- Pie charts
- Term associations
- Term details
- Term graph
- Term search

AmiGO Help: Home Page

AmiGO can either search for Gene Ontology terms or for gene products (genes, proteins, etc.) annotated with GO terms. Enter the search terms into the box. Examples of Gene Ontology terms include 'DNA repair', 'protein kinase', or 'mitochondrion'. Examples of genes or proteins include 'DMC1' or 'fuzzy onions'. Pick the type of search by selecting the radio button next to 'Terms' or 'Gene Products'.

For term searches, the search words do not need to be in the same order as they appear in the term name. Gene product searches do need the words to be as they appear in the name or synonym. To search for an exact word or phrase, select the 'exact match' checkbox.

Click 'Submit Query', to search and retrieve results.

For more complex searching options, click on the Advanced Search option available on the tool bar on top of the AmiGO pages.