

Introduction to the Gene Ontology and GO annotation resources

Rachael Huntley

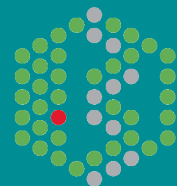
UniProt-GOA

EBI

PAGXX

January 2012

EMBL-EBI



Why do we need GO?



Reasons for the Gene Ontology

- Inconsistency in English language

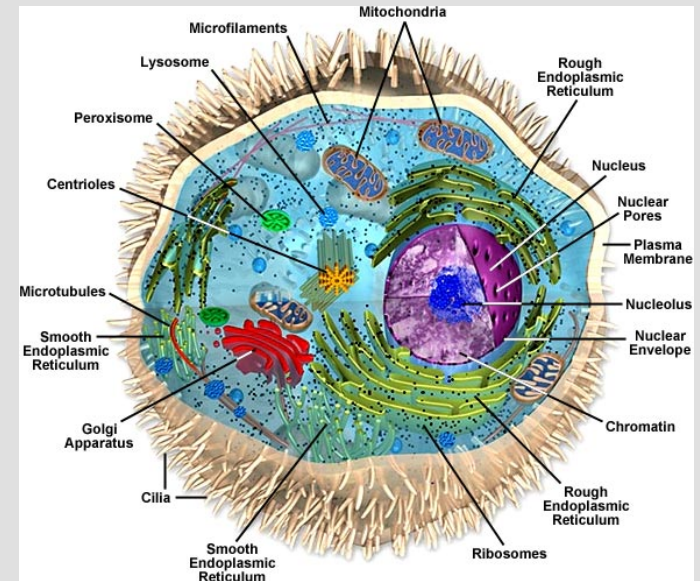
Inconsistency in English language

- Same name for **different** concepts

Cell



or



??

- **Different** names for the **same** concept

Eggplant



Brinjal

Aubergine

Melongene

Same for biological concepts

→ Comparison is difficult – in particular across species or across databases

Just one reason why the Gene Ontology (GO) is needed...



Reasons for the Gene Ontology

- Inconsistency in English language
- Increasing amounts of biological data available
- Increasing amounts of biological data to come

Increasing amounts of biological data available

NCBI Resources How To

PubMed.gov
US National Library of Medicine
National Institutes of Health

PubMed DNA repair Search

RSS Save search Limits Advanced

Display Settings: Summary, 20 per page, Sorted by Recently Added Send to:

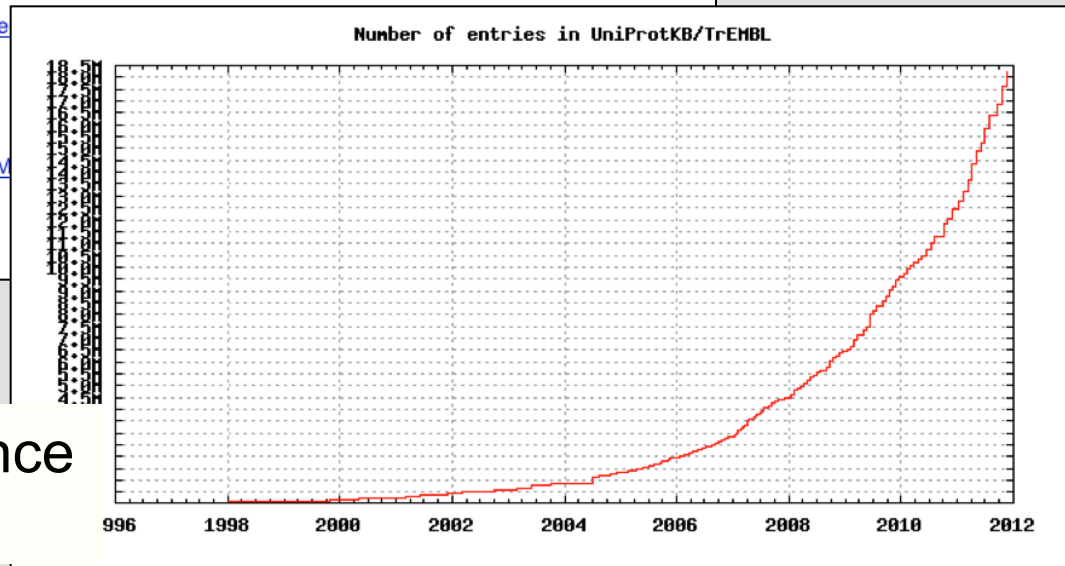
Results: 1 to 20 of 64637

<< First < Prev Page 1 of 3232 Next > Last >>

- ☐ [Germline Stem Cell Gene PIWIL2 Mediates DNA Repair through Relaxation of Chromatin.](#)
1. Yin DT, Wang Q, Chen L, Liu MY, Han C, Yan Q, Shen R, He G, Duan W, Li JJ, Wani A, Gao JX.
PLoS One. 2011;6(11):e27154. Epub 2011 Nov 16.
PMID: 22110608 [PubMed - in process]
- ☐ [An MSI Tumor Specific Frameshift Mutation in a Coding Microsatellite of MSH3 Encodes Epitopes.](#)
2. Garbe Y, Maletzki C, Linnebacher M.
PLoS One. 2011;6(11):e26517. Epub 2011 Nov 14.
PMID: 22110587 [PubMed - in process]
- ☐ [A Review of ERCC1 Gene in Bladder Cancer: Implications for Carcinogenesis.](#)
3. Kawashima A, Takayama H, Tsujimura A.
Adv Urol. 2012;2012:812398. Epub 2011 Oct 26.
PMID: 22110495 [PubMed - as supplied by publisher]
- ☐ [Polymorphisms in DNA Repair Gene XRCC1 and Skin Cancer Risk: A Meta-Analysis.](#)
4. Zhang H, Li W, Franklin MJ, Dudek AZ.
Anticancer Res. 2011 Nov;31(11):3945-52.
PMID: 22110224 [PubMed - in process]

Search on 'DNA repair' ...
get almost 65,000 results

Expansion of sequence
information



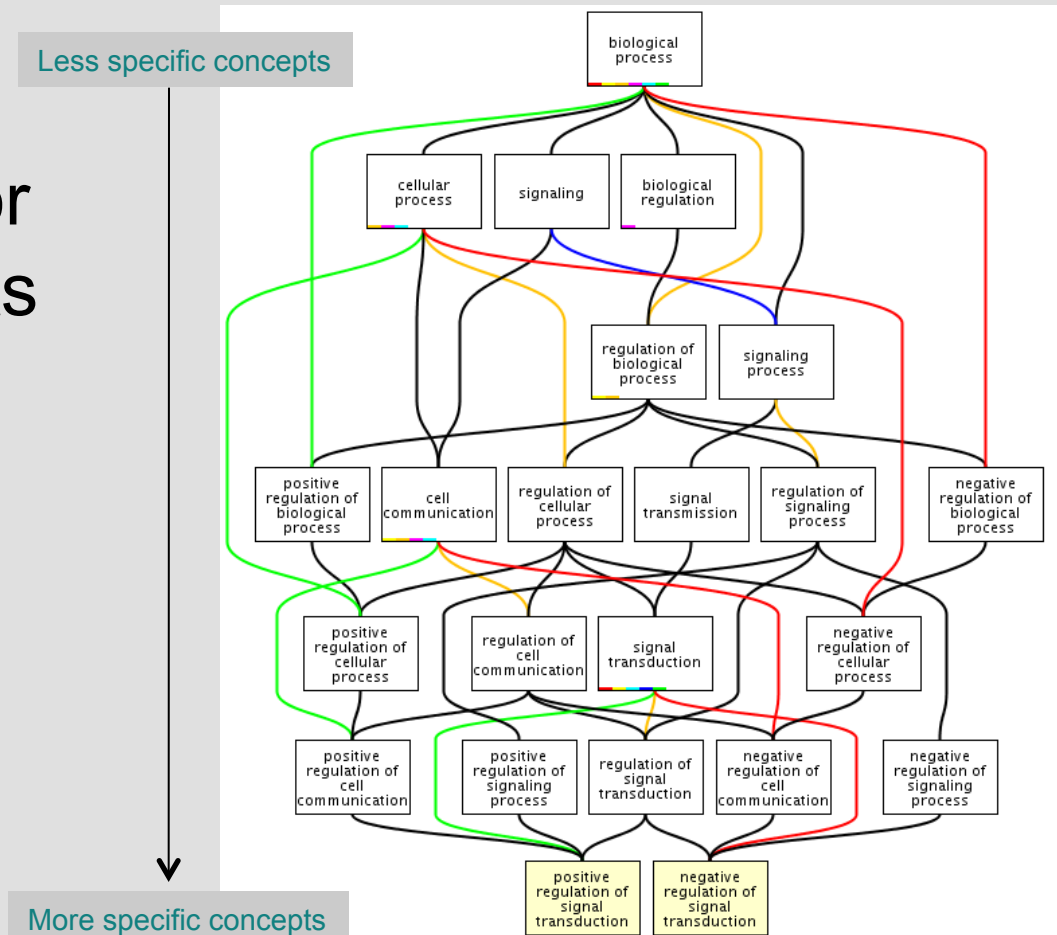


Reasons for the Gene Ontology

- Inconsistency in English language
- Increasing amounts of biological data available
- Increasing amounts of biological data to come
- Large datasets need to be interpreted quickly

The Gene Ontology

- A way to capture biological knowledge for individual gene products in a written and computable form
- A set of concepts and their relationships to each other arranged as a hierarchy

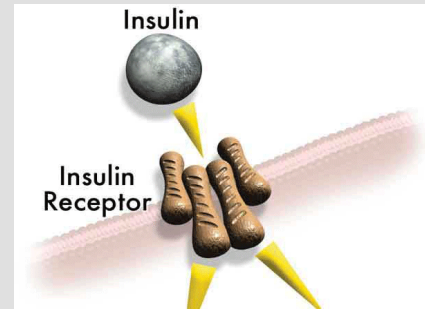


www.ebi.ac.uk/QuickGO

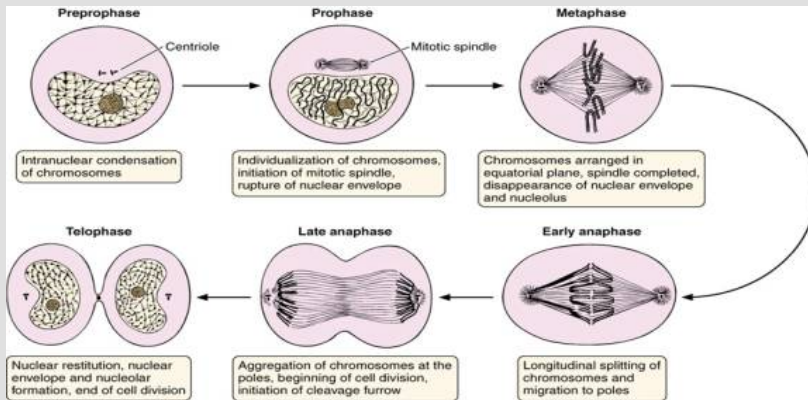
The Concepts in GO

1. Molecular Function

An elemental activity or task or job



- protein kinase activity
- insulin receptor activity



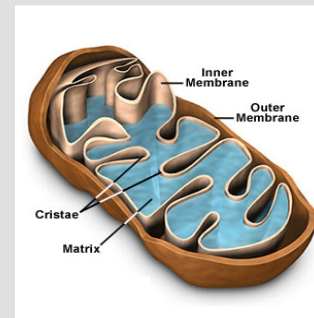
2. Biological Process

A commonly recognised series of events

- cell division

3. Cellular Component

Where a gene product is located



- mitochondrion
- mitochondrial matrix
- mitochondrial inner membrane

Anatomy of a GO term

Unique identifier

Term name

i ID	GO:0005634
i Name	nucleus
i Definition	A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
i Comment	
i Synonyms	
Type	Synonym
exact	cell nucleus
Cross-references associated with this term:	
Database	ID
INTERPRO	IPR000003
INTERPRO	IPR000116
INTERPRO	IPR000135

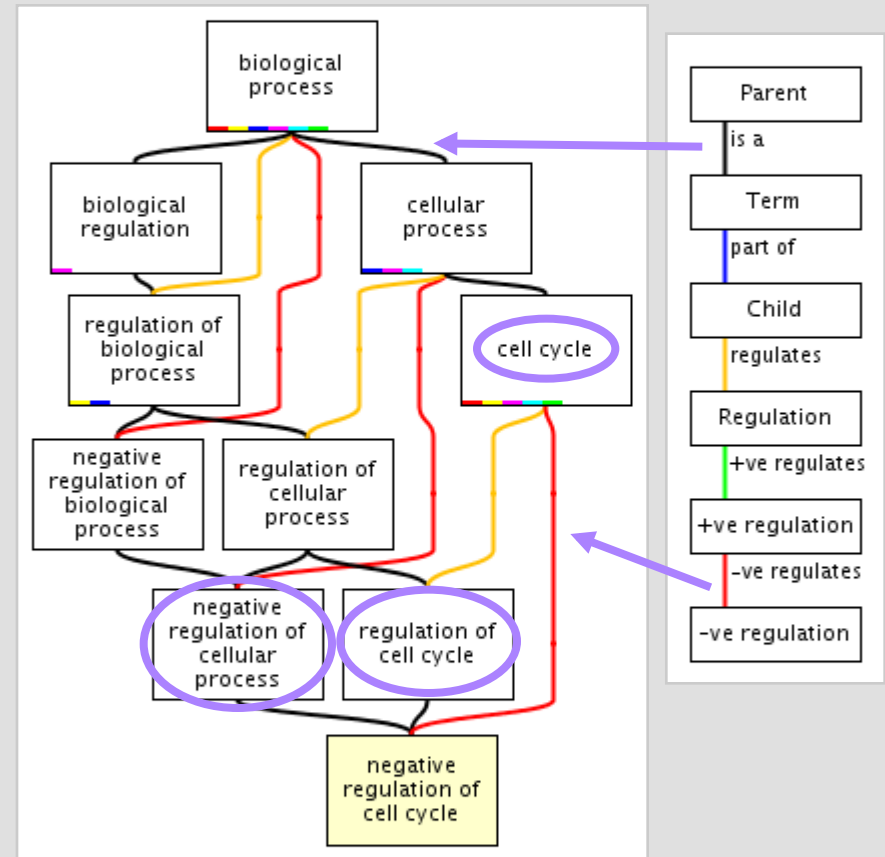
Definition

Synonyms

Cross-references

Ontology structure

- Directed acyclic graph
 - Terms can have more than one parent
- Terms are linked by relationships
 - is_a
 - part_of
 - regulates (and +/- regulates)
 - has_part
 - occurs_in



www.ebi.ac.uk/QuickGO

These relationships allow for complex analysis of large datasets



Reactome



Aims of the GO project

- Compile the ontologies
 - currently over 35,000 terms
 - constantly increasing and improving
- Annotate gene products using ontology terms
 - around 30 groups provide annotations
- Provide a public resource of data and tools
 - regular releases of annotations
 - tools for browsing/querying annotations and editing the ontology

GO Annotation

UniProt-Gene Ontology Annotation (UniProt-GOA) database at the EBI

- Largest open-source contributor of annotations to GO
- Provides annotation for more than 397,000 species
- Our priority is to annotate the human proteome



A GO annotation is ...

...a statement that a gene product;

1. has a particular molecular function
or is involved in a particular biological process
or is located within a certain cellular component
2. as determined by a particular method
3. as described in a particular reference

<i>Accession</i>	<i>Name</i>	<i>GO ID</i>	<i>GO term name</i>	<i>Reference</i>	<i>Evidence code</i>
P00505	GOT2	GO:0004069	aspartate transaminase activity	PMID:2731362	IDA



UniProt-GOA incorporates annotations made using two methods



Electronic Annotation

- Quick way of producing large numbers of annotations
- Annotations use less-specific GO terms
- Only source of annotation for many non-model organism species

Manual Annotation

- Time-consuming process producing lower numbers of annotations
- Annotations tend to use very specific GO terms



Electronic annotation methods

1. Mapping of external concepts to GO terms

e.g. InterPro2GO, UniProt Keyword2GO, Enzyme Commission2GO

UniProt > UniProtKB

P00519 (ABL1_HUMAN) ★ Reviewed, UniProtKB/Swiss-Prot
Last modified October 5, 2010. Version 162. [History...](#)

Clusters with 100%, 90%, 50% identity | Documents (7) | Third-party data

Names · Attributes · General annotation · Ontologies · Interactions · Alt products · Sequence annotation · Sequences

Customize order

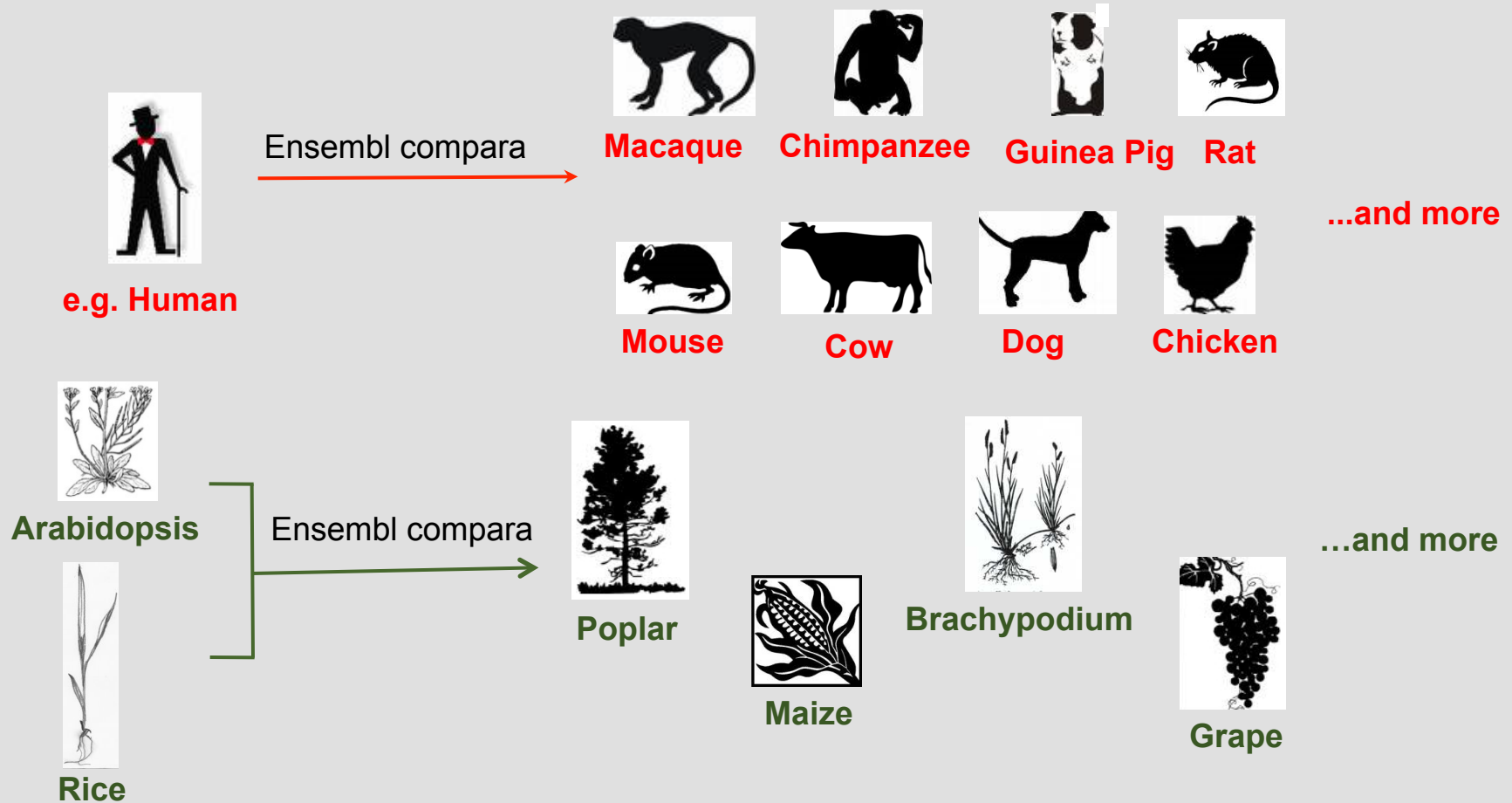
Names and origin

Protein names	<i>Recommended name:</i> Tyrosine-protein kinase ABL1 EC=2.7.10.2 <i>Alternative name(s):</i> Abelson murine leukemia viral oncogene homolog 1 Proto-oncogene c-Abl p150
Gene names	Name: ABL1 Synonyms: ABL, JTK7
Organism	Homo sapiens (Human) [Complete proteome]
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria

GO:0004715 ; non-membrane spanning protein tyrosine kinase activity

Electronic annotation methods

2. Automatic transfer of manual annotations to orthologs



Annotations are high-quality and have an explanation of the method (GO_REF)

Manual annotation by GOA

High–quality, specific annotations made using:

- Full text peer-reviewed papers
- A range of evidence codes to categorise the types of evidence found in a paper
e.g. IDA, IMP, IPI

Number of annotations in UniProt-GOA database

Electronic annotations	110,247,289
Manual annotations*	920,557

Dec 2011 Statistics

* Includes manual annotations integrated from external model organism and specialist groups

How to access and use GO annotation data

Where can you find annotations?

UniProtKB

UniProt > UniProtKB

Search Blast * Align * Retrieve ID Mapping *

Search in **Query**
Protein Knowledgebase (UniProtKB)

P00519 (ABL1_HUMAN) ★ Reviewed, UniProtKB/Swiss-Prot
Last modified October 5, 2010. Version 162. [History...](#)

Clusters with 100%, 90%, 50% identity | Documents (7) | Third-party data

Names · Attributes · General annotation · Ontologies · Interactions · Alt products · Sequences

Customize order

Names and origin

Protein names	Recommended name: Tyrosine-protein kinase ABL1 EC=2.7.10.2 Alternative name(s): Abelson murine leukemia viral oncogene homolog 1 Proto-oncogene c-Abl p150
Gene names	Name: ABL1 Synonyms: ABL, JTK7

Transcript-based displays

- Transcript summary
- Supporting evidence (24)
- Sequence
 - Exons (11)
 - cDNA
 - Protein
- External References
 - General identifiers (105)
 - Oligo probes (38)
 - Gene ontology (48)**
- Genetic Variation
 - Population comparison
 - Comparison image
- Protein Information
 - Protein summary
 - Domains & features (43)
 - Variations (48)

Transcript: ABL1-001 (ENST00000318560)
c-abl oncogene 1, receptor tyrosine kinase [Source:HGNC Symbol;Acc:76]
Location [Chromosome 9: 133,710,453-133,763,062](#) forward strand.
Gene ☐ This transcript is a product of gene [ENSG00000097007](#) - There are 6 transcripts in this gene

Gene ontology [help](#)

The following GO terms have been mapped to this entry via UniProt and/or RefSeq:

GO	GO Term	Evidence	Annotation Source
Accession			
GO:0000115	regulation of transcription involved in S-phase of mitotic cell cycle	TAS	
GO:0000166	nucleotide binding	IEA	
GO:0000267	magnesium ion binding	IDA	
GO:0003677	DNA binding	NAS	
GO:0004672	protein kinase activity	IEA	

Ensembl

Entrez gene

NCBI Resources ☒ How To ☒

Entrez Gene

Genes and mapped phenotypes

Search: [Limits](#) [Advanced search](#) [Help](#)

[Display Settings:](#) ☒ Full Report

ABL1 c-abl oncogene 1, non-receptor tyrosine kinase [*Homo sapiens*]
Gene ID: 25, updated on 5-Oct-2010

Summary

Official Symbol ABL1 provided by [HGNC](#)
Official Full Name c-abl oncogene 1, non-receptor tyrosine kinase provided by [HGNC](#)
Primary source [HGNC:76](#)
Locus tag RP11-83J21.1
See related [Ensembl:ENSG00000097007](#); [HPRD:01809](#); [MIM:189980](#)
Gene type protein coding
RefSeq status REVIEWED

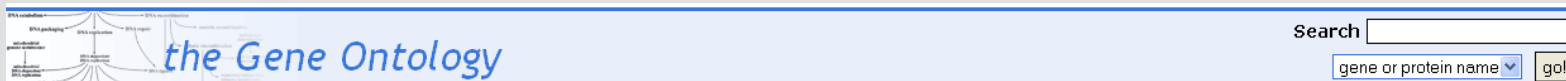
Gene Ontology provided by GOA

Function	Evidence	
	Evidence Code	Pubs
ATP binding	IDA	PubMed
DNA binding	NAS	PubMed
SH3 domain binding	IPI	PubMed
magnesium ion binding	IDA	PubMed
manganese ion binding	IDA	PubMed
non-membrane spanning protein tyrosine kinase activity	IEA	
nucleotide binding	IEA	
proline-rich region binding	IPI	PubMed
protein C-terminus binding	IPI	PubMed
protein binding	IPI	PubMed



Gene Association Files

17 column files containing all information for each annotation



Current Annotations

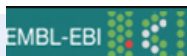
Annotation Details and Downloads

Filtered files
Unfiltered files
gp2protein files

GO Consortium website

Filtered Annotation File Downloads

Species, Database	Gene Products Annotated	Annotations	Submission date MM/DD/YYYY	Download filtered files
<i>Anaplasma phagocytophilum</i> HZ JCVI	1289	3471 (3471 non-IEA)	8/27/2010	annotations [39.7 kb] README
<i>Agrobacterium tumefaciens</i> str. C58 PAMGO	83			
<i>Arabidopsis thaliana</i> TAIR	31339			
<i>Aspergillus nidulans</i> AspGD	11368			
<i>Bacillus anthracis</i> Ames JCVI	5280			



- [UniProtKB-GOA Home](#)
- [New to UniProtKB-GOA?](#)
- [Who uses GO?](#)
- [Downloads](#)
- [Searching UniProtKB-GOA](#)

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[Databases](#) [Tools](#) [Research](#) [Training](#) [Industry](#) [About Us](#) [Help](#) [Site Index](#)

EBI > Databases > Biological Ontologies > UniProtKB-GOA > UniProtKB-GOA Downloads

Query examples - [apoptosis](#), [GO:0006915](#), [tropomyosin](#), [P06727](#).

UniProtKB-GOA - Downloads

Set of Proteins	Gene Association File	Identifier Cross-Reference File
UniProtKB	Gene association	UniProtKB ID mapping Readme
Human	Gene association	UniProtKB ID mapping Readme
Mouse	Gene association	UniProtKB ID mapping Readme
Rat	Gene association	UniProtKB ID mapping Readme
Arabidopsis	Gene association	UniProtKB ID mapping Readme
Zebrafish	Gene association	UniProtKB ID mapping Readme
Chicken	Gene association	UniProtKB ID mapping Readme
Cow	Gene association	UniProtKB ID mapping Readme
Proteomes	Gene association Browse	n/a
PDB	Gene association	n/a

UniProt-GOA website

Numerous species-specific files →



<http://www.ebi.ac.uk/GOA/downloads.html>



ABL1

GO browsers

Tyrosine-protein kinase ABL1

protein from *Homo sapiens* (human)

Term associations [Gene product information](#) [Peptide Sequence](#) [Sequence information](#)

Term Associations

Download all association information in: ☐ gene association format ☐ RDF/XML

Accession, Term	Ontology	Qualifier	Evidence	Reference	Assigned by
<input type="checkbox"/> GO:0030036 : actin cytoskeleton organization	2336 gene products view in tree biological process		ISS With UniProtKB:P00520	GO REF:0000024	UniProtKB
<input type="checkbox"/> GO:0007155 : cell adhesion	4735 gene products view in tree biological process		IEA With SP KW:KW-0130	GO REF:0000004	UniProtKB
<input type="checkbox"/> GO:0008630 : DNA damage response, signal transduction resulting in induction of apoptosis	145 gene products view in tree biological process		TAS	PMID:10391249	Proteome Inc.
<input type="checkbox"/> GO:0006298 : mismatch repair					(vis

EMBL-EBI [EB-eye Search](#) All Databases Enter Text Here

Databases Tools EBI Groups Training Industry About Us Help Site Index

EBI > Databases > QuickGO

ABL1 Homo sapiens P00519



QuickGO Click for example search [Web Services](#) [Dataset](#) [Your Terms: 16](#)

Accession [P00519](#)
Gene ABL1
Taxonomy Homo sapiens
Description Tyrosine-protein kinase ABL1

Annotation

Results: 1 to 219 of 219 Page size: Additional filters: None

[Display](#) [ID Mapping](#) [Filter](#) [Statistics](#) [Download](#)

Database ID	Symbol	Qualifier	GO Identifier	GO Term Name	Aspect	Evidence	Reference	With	Taxon	Date	Assigned By	Product ID
Process												
UniProtKB P00519	ABL1		GO:0000115	regulation of transcription involved in S phase of mitotic cell cycle	P	TAS	PMID:8242749		9606	20030904	PINC	
UniProtKB P00519	ABL1		GO:0007185	signal transduction	P	IEA	InterPro2GO	IPR020700	9606	20101009	InterPro	
UniProtKB P00519	ABL1		GO:0051353	positive regulation of oxidoreductase activity	P	IDA	PMID:12893824		9606	20071108	BHF-UCL	
UniProtKB P00519	ABL1		GO:0006468	protein amino acid phosphorylation	P	IEA	InterPro2GO	IPR001245	9606	20101009	InterPro	
UniProtKB P00519	ABL1		GO:0018108	peptidyl-tyrosine phosphorylation	P	IDA	PMID:7590236		9606	20100505	UniProtKB	
UniProtKB P00519	ABL1		GO:0006464	protein modification process	P	NAS	PMID:8242749		9606	20040707	UniProtKB	
UniProtKB P00519	ABL1		GO:0030036	actin cytoskeleton organization	P	ISS	GO_REF:0000024	Abi1 (ABL1_MOUSE)	9606	20061011	UniProtKB	
UniProtKB P00519	ABL1		GO:0006355	regulation of transcription, DNA-dependent	P	TAS	PMID:8242749		9606	20030904	PINC	
UniProtKB P00519	ABL1		GO:0006468	protein amino acid phosphorylation	P	IEA	InterPro2GO	IPR008266	9606	20101009	InterPro	
UniProtKB P00519	ABL1		GO:0018108	peptidyl-tyrosine phosphorylation	P	IEA	InterPro2GO	IPR020700	9606	20101009	InterPro	
UniProtKB P00519	ABL1		GO:0018108	peptidyl-tyrosine phosphorylation	P	IDA	PMID:9144171		9606	20061004	UniProtKB	
UniProtKB P00519	ABL1		GO:0006468	protein amino acid phosphorylation	P	IEA	InterPro2GO	IPR000719	9606	20101009	InterPro	
UniProtKB P00519	ABL1		GO:0006298	mismatch repair	P	TAS	PMID:10391249		9606	20030904	PINC	
UniProtKB P00519	ABL1		GO:0008630	DNA damage response, signal transduction resulting in induction of apoptosis	P	TAS	PMID:10391249		9606	20030904	PINC	

The EBI's QuickGO browser

The screenshot shows the EBI QuickGO web interface. At the top is a navigation bar with 'EMBL-EBI' and 'EB-eye Search' logos, a search input field, and buttons for 'Go', 'Reset', and 'Give us feedback'. Below this is a menu with 'Databases', 'Tools', 'EBI Groups', 'Training', 'Industry', 'About Us', and 'Help'. A left sidebar contains links for 'QuickGO', 'Help', 'Reference', and 'FAQs'. The main content area is titled 'QuickGO' and includes a description: 'QuickGO is a fast web-based browser for Gene Ontology terms and annotations, which is provided by the UniProtKB-GOA group at the EBI.' Below the description is a search box with the placeholder 'Click for example search' and a 'Search!' button. To the right of the search box are links for 'Web Services', 'Dataset', and 'Your Terms: 16'. Further down, there are three main sections: 'Search and Filter GO annotation sets' (highlighted with a red box and an arrow from the text 'Find sets of GO annotations'), 'Investigate GO slims', and 'Example queries'. The 'Example queries' section lists three search methods: by keyword or ID, by protein name or accession, and by ontology. On the right side of the interface, there are two boxes: 'QuickGO Tips' with two bullet points about customizing GO slims and using the search facility, and a 'Tutorial' box with a link to 'Try an interactive demo'. On the left side, two text boxes with arrows point to the search box and the 'Search and Filter GO annotation sets' section, with the text 'Search GO terms or proteins' and 'Find sets of GO annotations' respectively.

Search GO terms or proteins

Find sets of GO annotations

QuickGO

QuickGO is a fast web-based browser for [Gene Ontology](#) terms and annotations, which is provided by the [UniProtKB-GOA group](#) at the EBI.

Click for example search Search!

Web Services Dataset Your Terms: 16

Search and Filter GO annotation sets

Extensive filters are available from this page to allow the generation of specific subsets of GO annotations, mapped to sequence identifiers of your choice.

Investigate GO slims

GO slims are lists of GO terms that have been selected from the full set of terms available from the Gene Ontology project.

GO slims can be used to generate a focused view of part of the GO, or with annotation data they can be used to see how a set of proteins/genes can be broadly categorized (using annotation data and the relationships that exist between terms in the ontologies).

Further information on GO slims can be found at the [GO Consortium web site](#).

Example queries

QuickGO can be queried for both **GO terms** and **proteins**:

- Search for terms by keyword or ID: [apoptosis](#), [GO:0006915](#)
- Search for proteins by name or accession: [tropomyosin](#), [P06727](#)
- List all terms in an ontology: [Biological Process](#), [Molecular Function](#), [Cellular Component](#)

QuickGO Tips

- QuickGO can help make customized GO slims, which can be used to 'map up' your gene/protein identifiers to broadly categorise their functions or subcellular locations. Click [here](#) for more information.
- QuickGO's search facility can be used to find information on GO terms as well as information on annotation to distinct proteins. Just type a partial GO term name/synonym or a gene symbol, protein name or sequence identifier into the Search box.

Tutorial

[Try an interactive demo](#)

How scientists use the GO

- Access gene product functional information
- Analyse high-throughput genomic or proteomic datasets
- Validation of experimental techniques
- Get a broad overview of a proteome
- Obtain functional information for novel gene products

Some examples...

Term enrichment

- Most popular type of GO analysis
- Determines which GO terms are more often associated with a specified list of genes/proteins compared with a control list or rest of genome
- Many tools available to do this analysis
- User must decide which is best for their analysis

Numerous Third Party Tools



Tools for Searching and Browsing GO

The following tools make use of the GO ontologies or the gene associations provided by Consortium members. Being listed on this page does not represent an endorsement by the GO Consortium, nor has the Consortium tested the tool or found that it uses the Consortium information accurately. This page is provided to promote an exchange of information between users and software developers.



web-based tool

Tools for Analysis of Data Sets, e.g. gene expression / microarray data

The following tools make use of the GO ontologies or the gene associations provided by Consortium members. Being listed on this page does not represent an endorsement by the GO Consortium, nor has the Consortium tested the tool or found that it uses the Consortium information accurately. This page is provided to promote an exchange of information between users and software developers.

Unless stated otherwise, tools are free for academic use.

AmiGO

[The Gene Ontology Consortium](#)

No publication

AmiGO provides an interface to search and browse GO terms and view the terms with which they are associated; it also provides gene product annotations. AmiGO also provides a way to submit gene product annotations annotated to a GO term and submitted to the GO Consortium.

Key



web-based tool



downloadable tool



compatible OSs (for downloadable tools)

Unless stated otherwise, tools are free for academic use.

Avadis

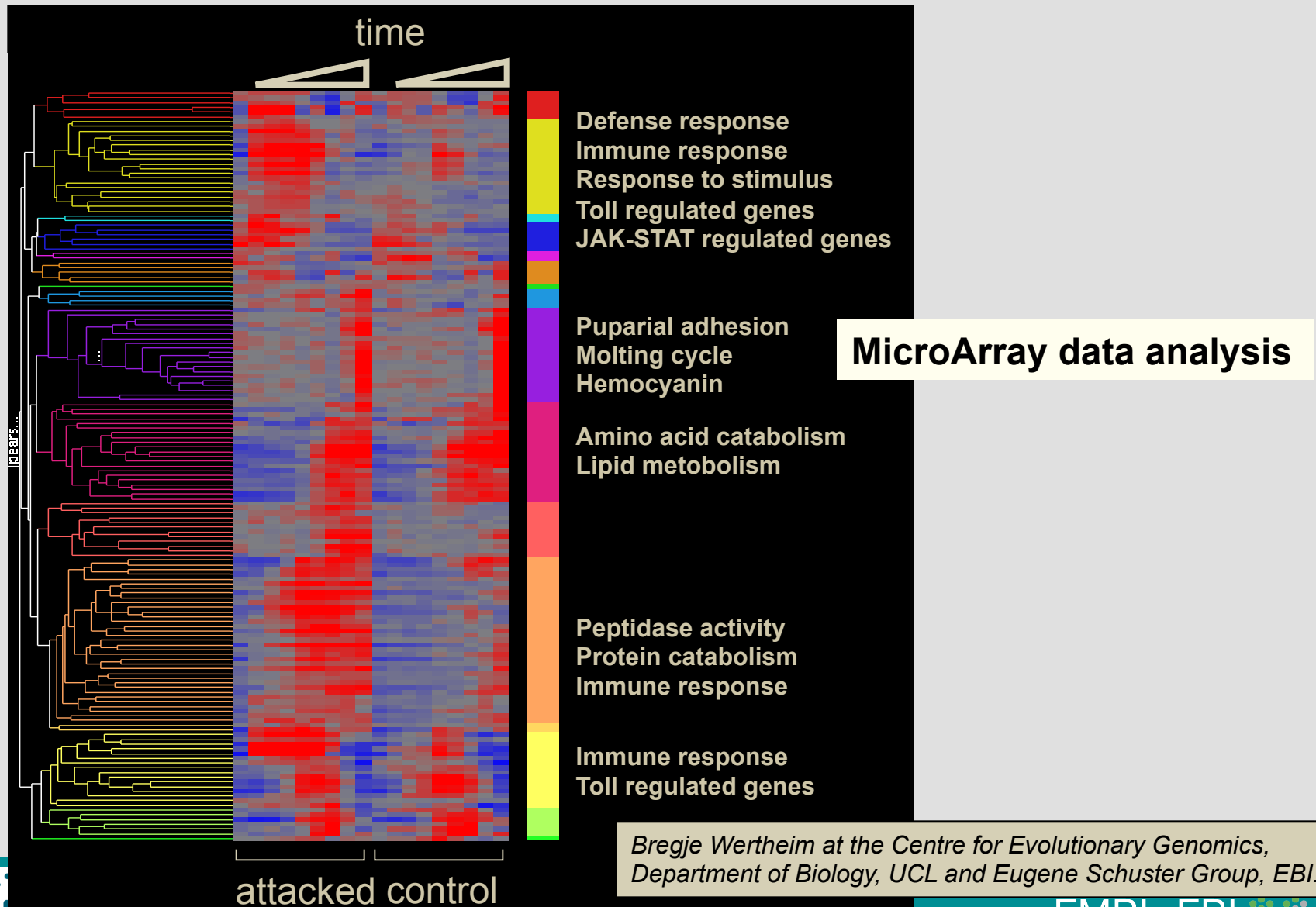
[Strand Genomics](#)

No publication

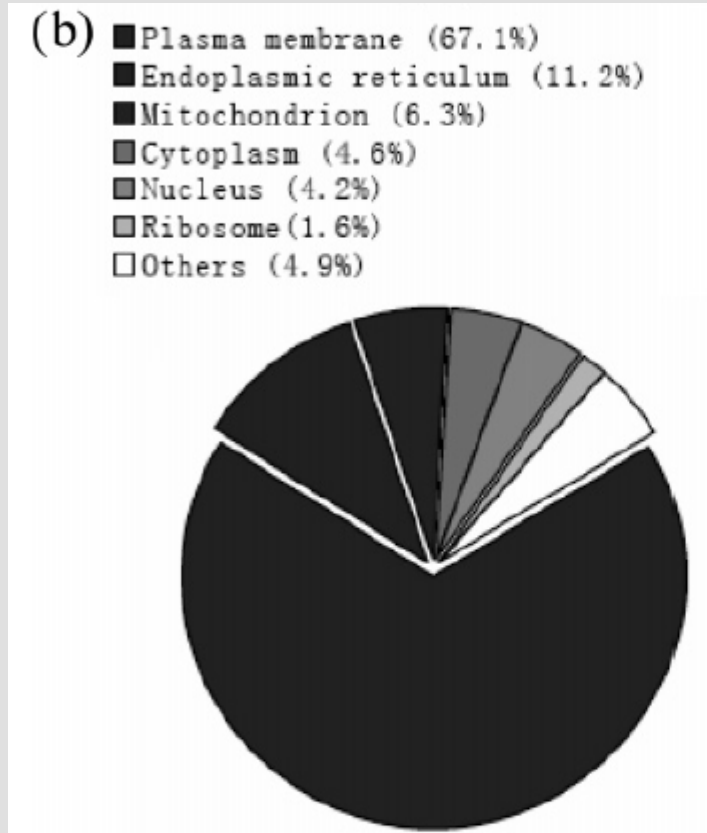
Avadis is a data analysis and visualization tool for gene expression data. Avadis has a built-in Gene Ontology browser to view ontology hierarchies. There are common ontology paths for multiple genes. Genes can be clustered based on ontology terms to identify functional signatures in gene expression clusters.



Analysis of high-throughput genomic datasets



Validation of experimental techniques



Rat liver plasma membrane isolation

(Cao *et al.*, Journal of Proteome Research 2006)

Annotating novel sequences

- Can use BLAST queries to find similar sequences with GO annotation which can be transferred to the new sequence
- Two tools currently available;

AmiGO BLAST – searches the GO Consortium database

BLAST2GO – searches the NCBI database

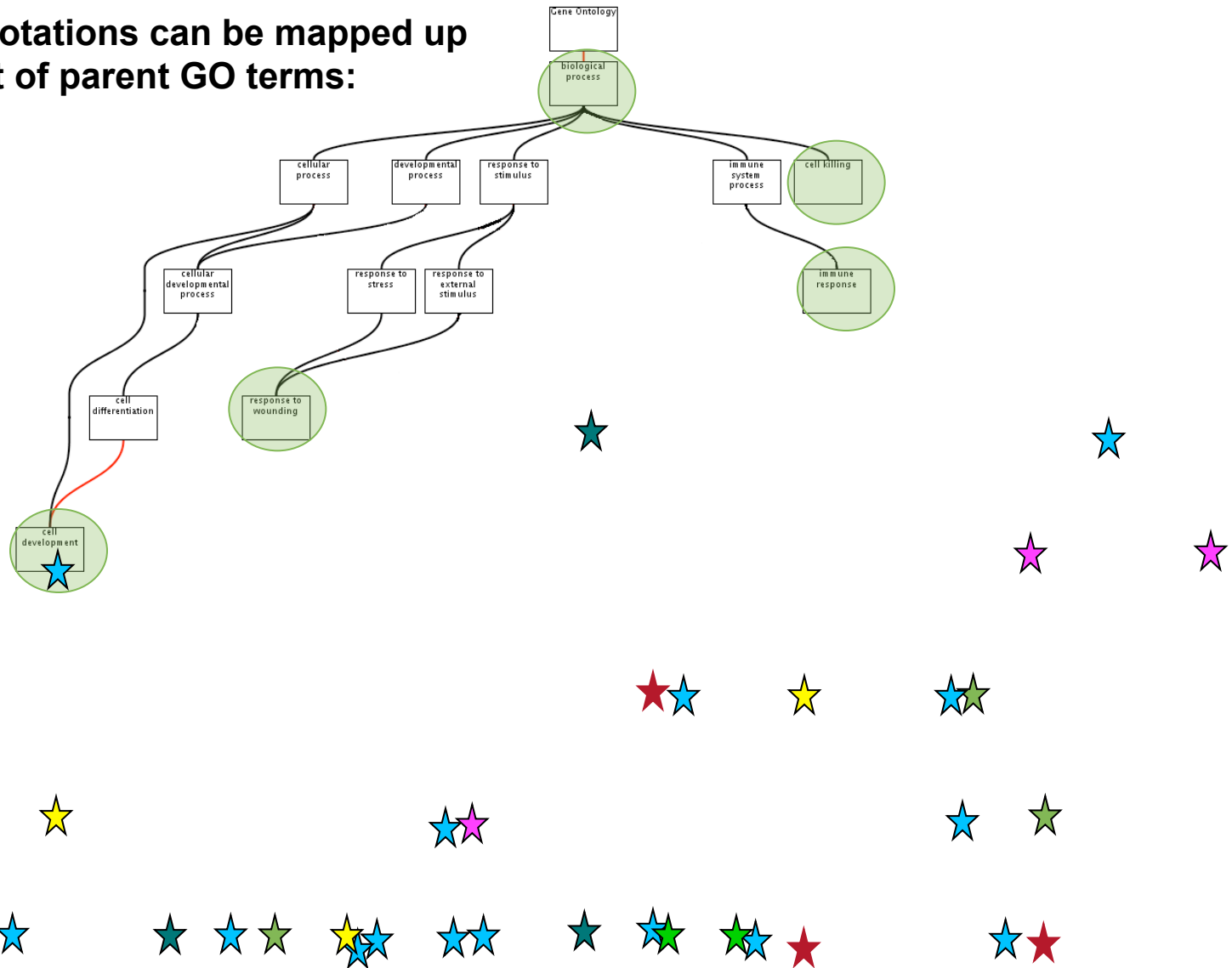


Using the GO to provide a functional overview for a large dataset

- Many GO analysis tools use GO slims to give a broad overview of the dataset
- GO slims are cut-down versions of the GO and contain a subset of the terms in the whole GO
- GO slims usually contain less-specialised GO terms

Slimming the GO using the 'true path rule'

...however annotations can be mapped up to a smaller set of parent GO terms:



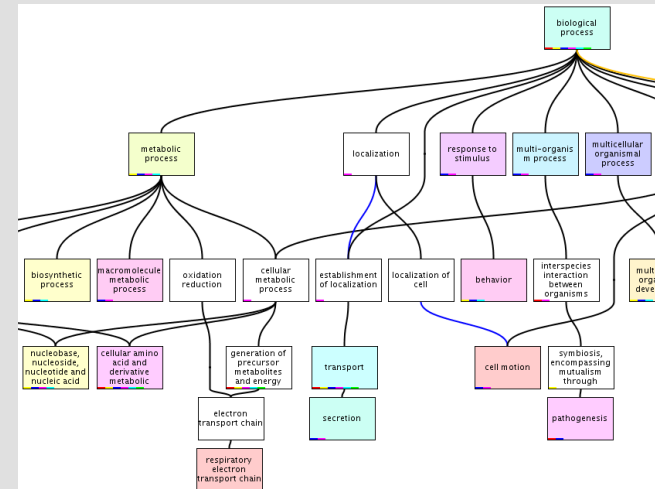
GO slims

Custom slims are available for download;

<http://www.geneontology.org/GO.slims.shtml>

or you can make your own using;

- QuickGO
<http://www.ebi.ac.uk/QuickGO>
- AmiGO's GO slimmer
<http://amigo.geneontology.org/cgi-bin/amigo/slimmer>



The EBI's QuickGO browser

The screenshot shows the EBI QuickGO browser interface. At the top is a navigation bar with 'EMBL-EBI' logo, 'EB-eye Search' button, a search input field with 'All Databases' dropdown, and buttons for 'Go', 'Reset', 'Advanced Search', and 'Give us feedback'. Below this is a menu with 'Databases', 'Tools', 'EBI Groups', 'Training', 'Industry', 'About Us', and 'Help'. A sidebar on the left contains 'QuickGO', 'Help', 'Reference', and 'FAQs'. The main content area shows the 'QuickGO' page with a breadcrumb 'EBI > Databases > QuickGO'. Three callout boxes on the left point to specific features: 'Search GO terms or proteins' points to the search input; 'Find sets of GO annotations' points to the 'Search and Filter GO annotation sets' section; 'Map-up annotations with GO slims' points to the 'Investigate GO slims' section. The 'Search and Filter GO annotation sets' section describes extensive filters for generating subsets of GO annotations. The 'Investigate GO slims' section explains that GO slims are lists of terms selected from the full set and can be used to generate a focused view or categorize proteins/genes. Below these is an 'Example queries' section with three bullet points: searching by keyword or ID (e.g., 'apoptosis', 'GO:0006915'), searching by protein name or accession (e.g., 'tropomyosin', 'P06727'), and listing all terms in an ontology (e.g., 'Biological Process', 'Molecular Function', 'Cellular Component'). On the right, a 'QuickGO Tips' box provides two tips: using QuickGO to make customized GO slims and using the search facility to find information on GO terms and proteins. Below the tips is a 'Tutorial' box with a link to 'Try an interactive demo'.

Search GO terms or proteins

Find sets of GO annotations

Map-up annotations with GO slims

Questions on how to use QuickGO? Contact goa@ebi.ac.uk

Search and Filter GO annotation sets

Extensive filters are available from this page to allow the generation of specific subsets of GO annotations, mapped to sequence identifiers of your choice.

Investigate GO slims

GO slims are lists of GO terms that have been selected from the full set of terms available from the Gene Ontology project.

GO slims can be used to generate a focused view of part of the GO, or with annotation data they can be used to see how a set of proteins/genes can be broadly categorized (using annotation data and the relationships that exist between terms in the ontologies).

Further information on GO slims can be found at the [GO Consortium web site](#).

Example queries

QuickGO can be queried for both **GO terms** and **proteins**:

- Search for terms by keyword or ID: [apoptosis](#), [GO:0006915](#)
- Search for proteins by name or accession: [tropomyosin](#), [P06727](#)
- List all terms in an ontology: [Biological Process](#), [Molecular Function](#), [Cellular Component](#)

QuickGO Tips

- QuickGO can help make customized GO slims, which can be used to 'map up' your gene/protein identifiers to broadly categorise their functions or subcellular locations. Click [here](#) for more information.
- QuickGO's search facility can be used to find information on GO terms as well as information on annotation to distinct proteins. Just type a partial GO term name/synonym or a gene symbol, protein name or sequence identifier into the Search box.

Tutorial

[Try an interactive demo](#)

The UniProt-GOA group

Curators:

Emily Dimmer
Rachael Huntley
Yasmin Alam-Faruque
Prudence Mutowo

Software developer:

Tony Sawford

Team leaders:

Rolf Apweiler
Claire O' Donovan

Email: goa@ebi.ac.uk



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