



# Introduction to the Gene Ontology

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EBI & GO Consortium  
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# Reasons for GO

- The problem: how to
  - ... communicate
  - ... represent biological knowledge in databases
  - ... query databases — find useful answers to biological questions like
    - What does the gene product do?
    - Where and when does it act?
    - Why does it perform these activities?



# The Challenge of Language:

*People call the same thing by different names*





# A Common Vocabulary:

*GO uses one term and many characterized synonyms*

Tactition

Taction

Tactile sense



perception of touch ; GO:0050975





# GO project aims

- Compile structured vocabularies describing aspects of molecular biology
- Describe gene products using vocabulary terms (annotation)
- Provide public resource of data and tools:
  - to query and modify the vocabularies and annotations
  - annotation tools for curators



# GO Scope: 3 domains

- Molecular Function — elemental activity or task
  - *nuclease, DNA binding, transcription factor*
- Biological Process — broad objective or goal
  - *mitosis, signal transduction, metabolism*
- Cellular Component — location or complex
  - *nucleus, ribosome, origin recognition complex*
- \* ‘Normal’ functions and processes only:
  - *No pathological processes*
  - *No experimental conditions*



# GO term features

[Term]

id: GO:0046423

name: allene-oxide cyclase activity

namespace: molecular\_function

def: "Catalysis of the reaction: (9Z)-(13S)-12,13-epoxyoctadeca-9,11,15-trienoate = (15Z)-12-oxophyto-10,15-dienoate." [EC:5.3.99.6]

synonym: "(9Z)-(13S)-12,13-epoxyoctadeca-9,11,15-trienoate isomerase (cyclizing)" EXACT [EC:5.3.99.6]

xref: EC:5.3.99.6

xref: MetaCyc:ALLENE-OXIDE-CYCLASE-RXN

is\_a: GO:0009975 ! cyclase activity

is\_a: GO:0016860 ! intramolecular oxidoreductase activity



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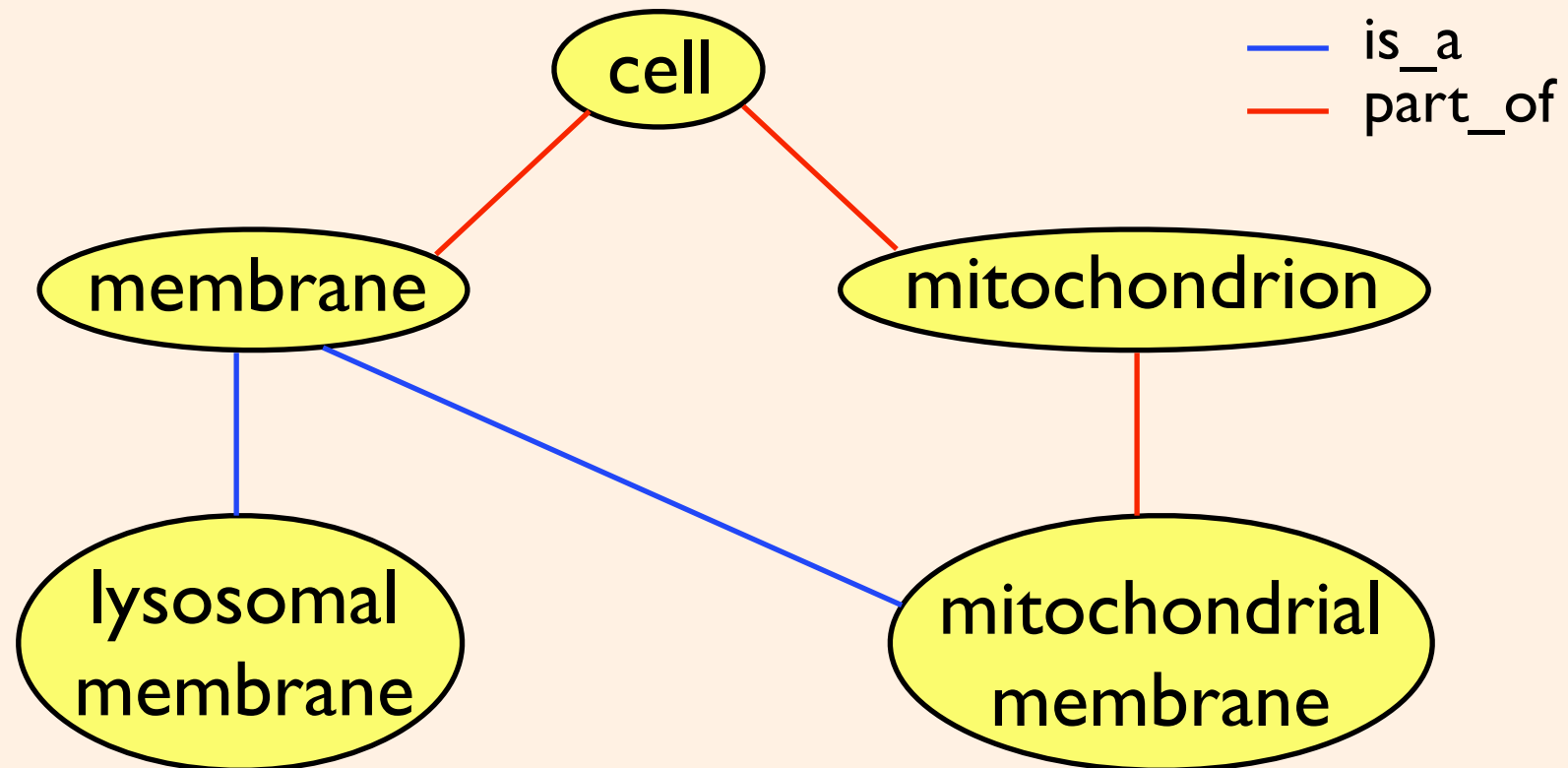
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parents



# GO Structure: DAG



GO is a directed acyclic graph (DAG):  
a term can have one or more parent(s)



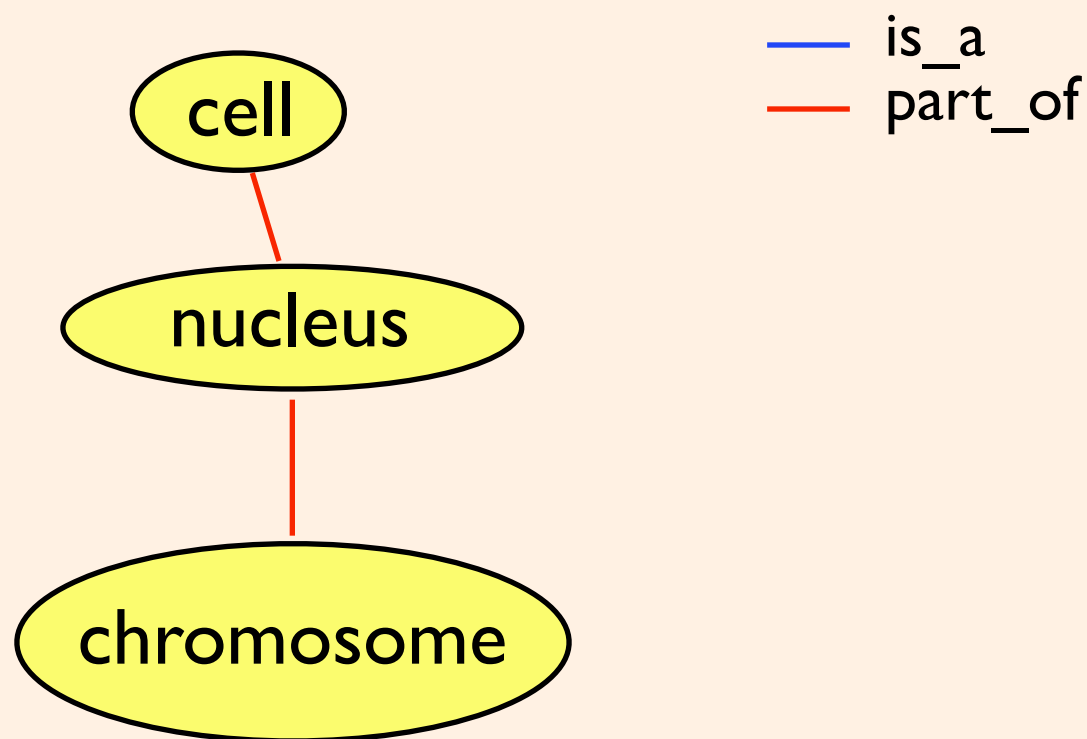
# GO relationships

- now in use:
  - is\_a – subclass; a is a type of b
  - part\_of
    - physical part of (component)
    - subprocess of (process)
- to be added:
  - regulates





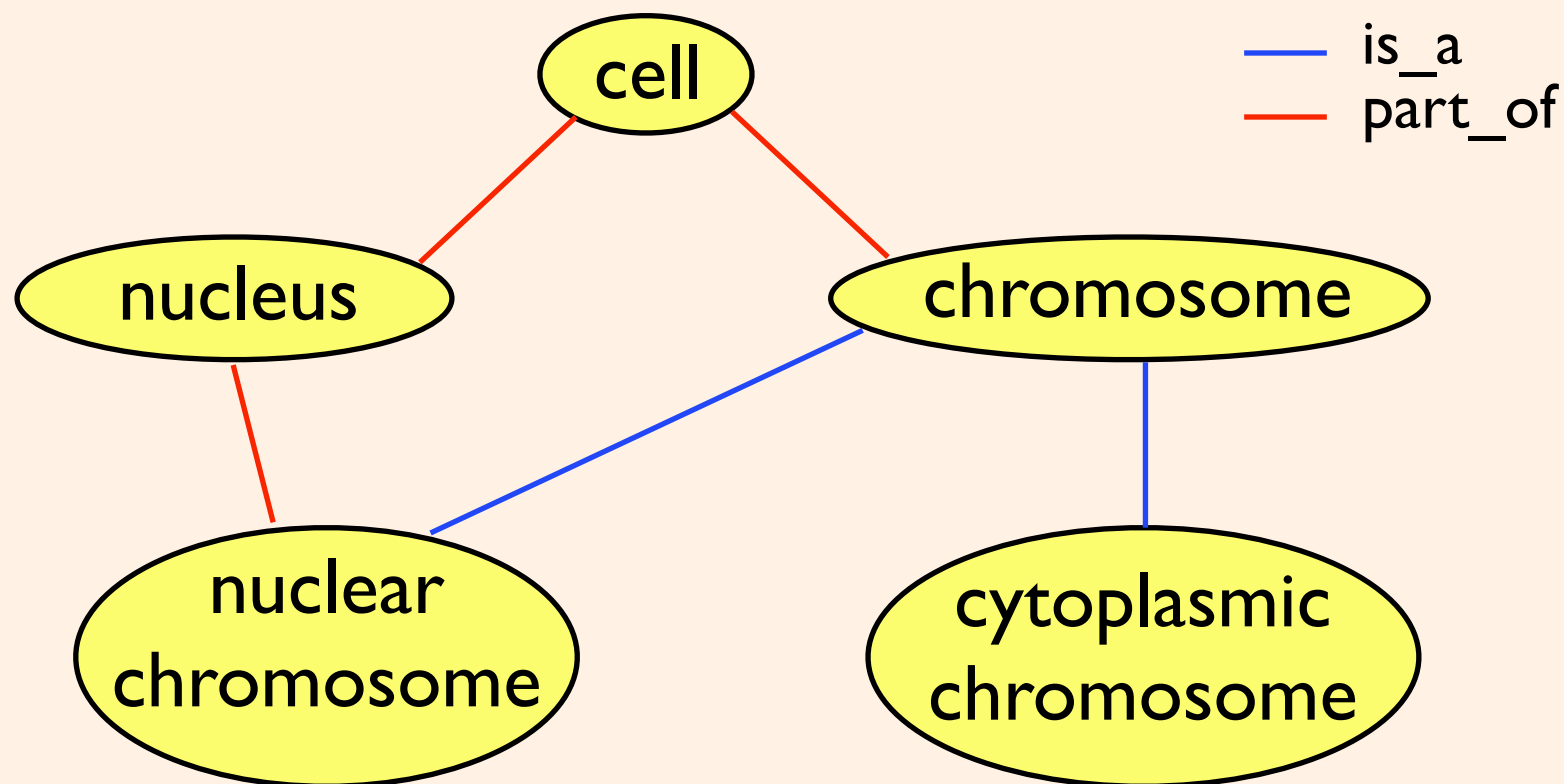
# True Path Rule



But what about bacteria??



# True Path Rule



Resolved structure  
(some terms omitted for clarity)



# Ontology Rules

## (examples)

- Univocity
  - A term (or relationship) should mean the same thing every time it's used
- Positivity
  - Complements of classes are not themselves classes; i.e., terms such as 'non-mammal' or 'non-membrane' do not designate genuine classes
- Objectivity
  - Which classes exist does not depend on our biological knowledge; terms such as 'unknown', 'unclassified' or 'unlocalized' are thus unsuitable

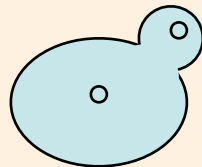


# The Challenge of Univocity:

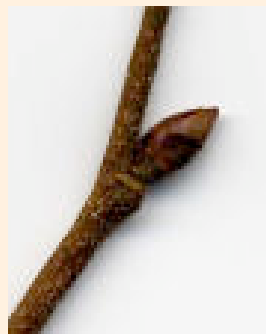
*People use the same words to describe different things*



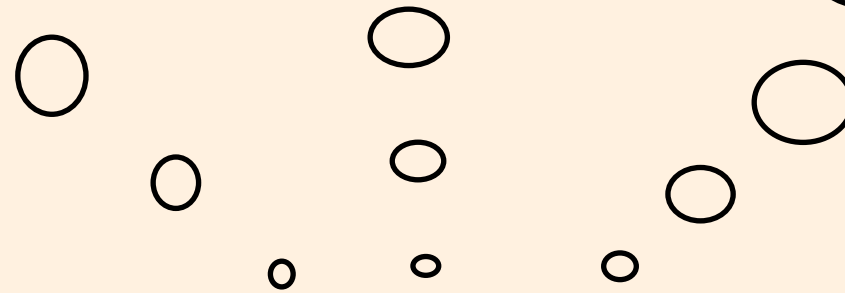
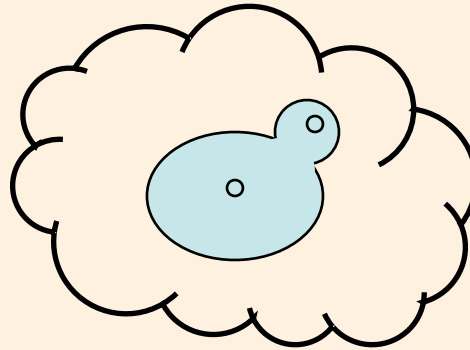
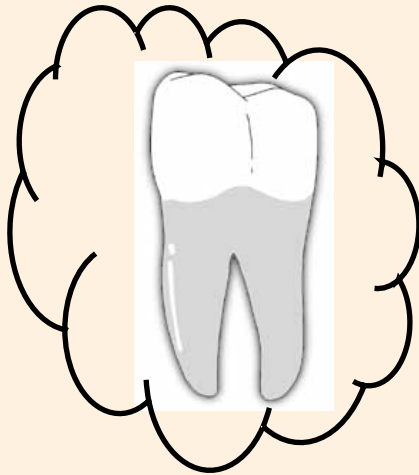
= bud initiation



= bud initiation



= bud initiation



Bud initiation?  
How is a computer  
to know?

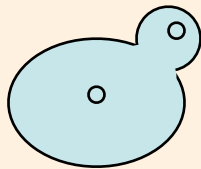


# Univocity:

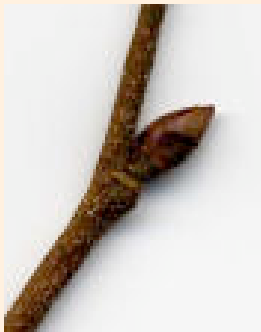
*GO adds descriptors to discriminate among organisms*



= tooth bud initiation



= cellular bud initiation

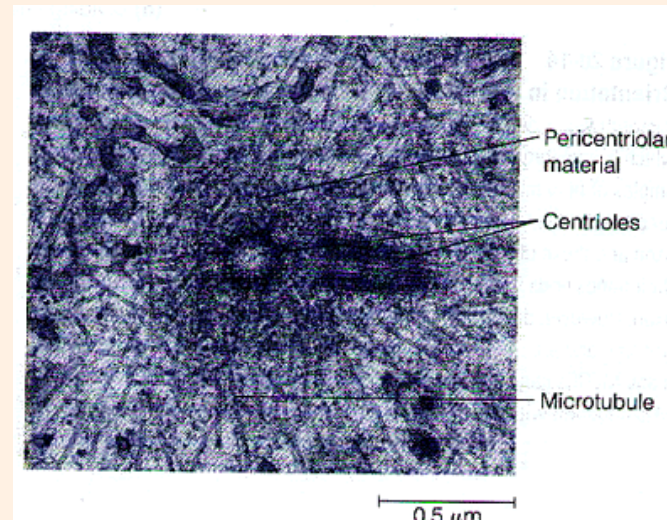


= leaf bud initiation

*note: hypothetical examples*



# The Challenge of Positivity



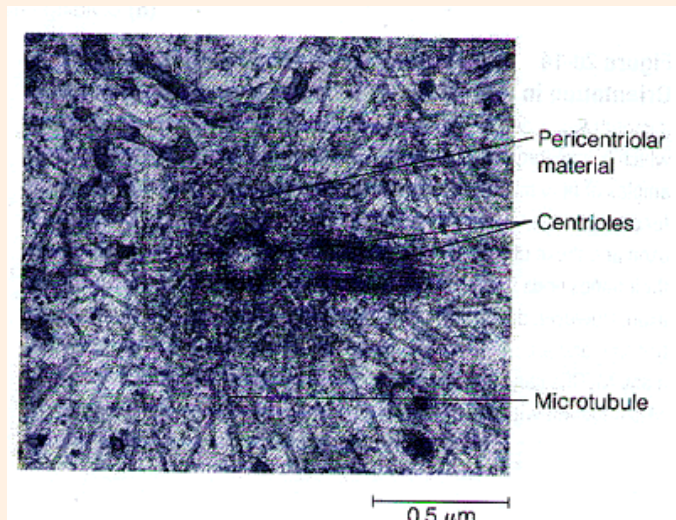
centriole

- Some organelles are membrane-bound.
- A centrosome is not a membrane bound organelle, but it still may be considered an organelle.



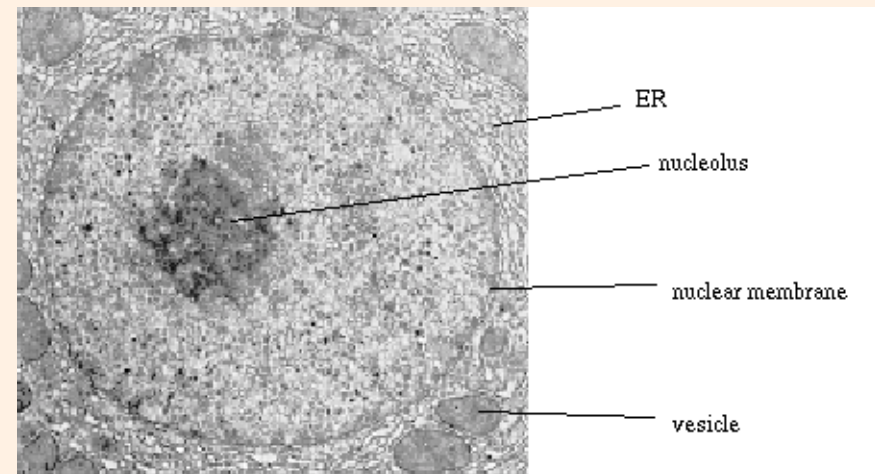
# The Challenge of Positivity:

*Sometimes absence is a distinction in a biologist's mind*



centriole

non-membrane-bound  
organelle GO:0043228



nucleus

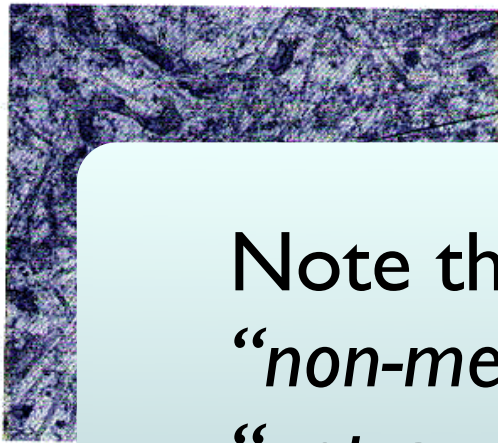
membrane-bound organelle  
GO:0043227





# The Challenge of Positivity:

*Sometimes absence is a distinction in a biologist's mind*



Note the logical difference between  
“*non-membrane-bound organelle*” and  
“*not a membrane-bound organelle*”

The latter includes everything that is  
not a membrane bound organelle!

non  
org

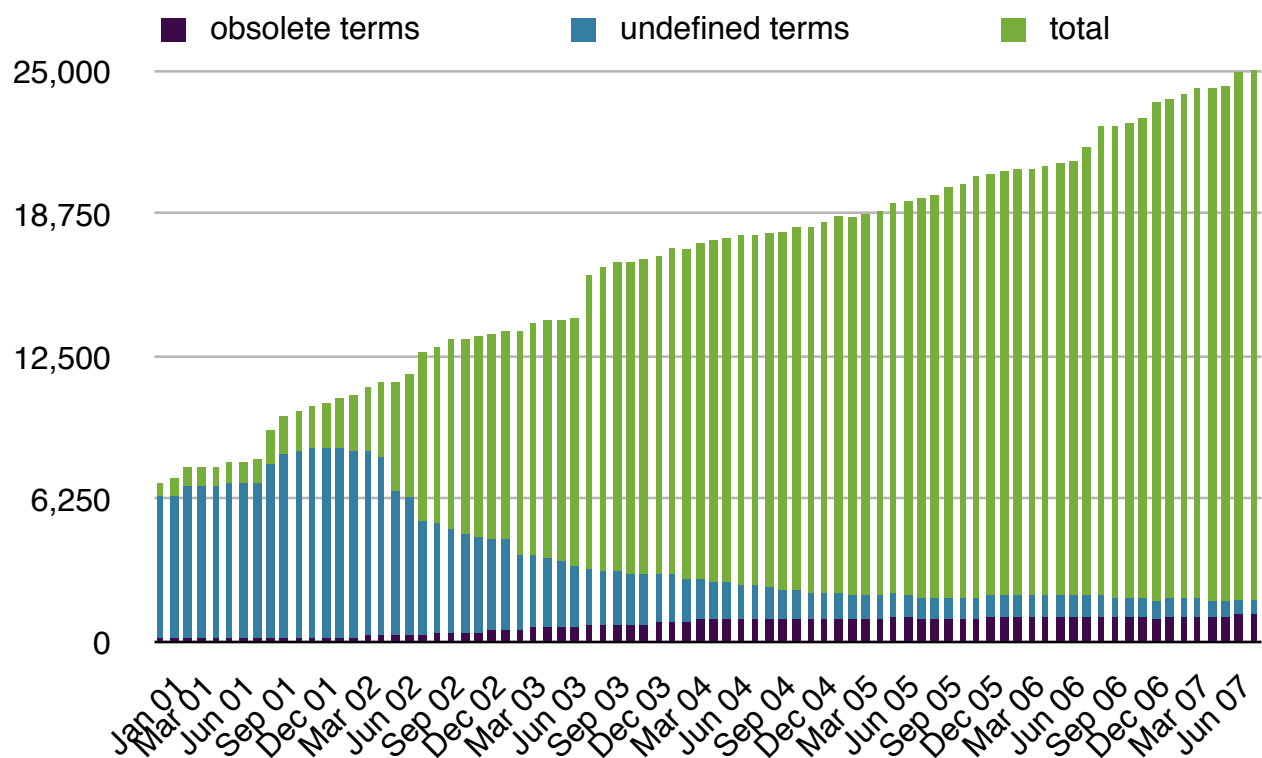
rane

lle



# GO Term History

Jan. 2001–August 2007





# Why GO Changes

- Advances in biology
- New groups join, requiring new terms or different relationships between terms
- Update legacy terms
- Improve logical consistency



# What kinds of changes?

Small or large scale

Biological or logical/structural motivation



# Small-scale Changes

- Individuals (e.g. annotators) request changes
  - Usually one or a few things at a time
  - New terms
  - Path corrections/additions
  - Improved definitions
- Closely coordinated with annotation



# Large-scale Changes

- Improve ontology for a biological topic all at once
  - Motivation: improve usefulness for biologists, especially annotators
  - Usually connected with content meeting
  - Expert biologists involved
- Apply a logical/structural improvement to entire ontology at once
  - Motivation: improve consistency; enhance “computability”
  - Software developers involved



# Applications of GO

- Gene product annotation
  - model organism databases
  - genome sequence analysis
- Expression data analysis
- Text mining
- More ...



# GO Annotation

- What is GO annotation?
  - An annotation is a statement that a gene product ...
    - ... has a particular molecular function
    - ... is involved in a particular biological process
    - ... is located within a certain cellular component
  - ... as determined by a particular method
  - ... as described in a particular reference





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gene  
product



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GO  
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evidence



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Vol. 278, No. 10, Issue of March 7, pp. 8487–8493, 2003  
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## High Conservation of the Set1/Rad6 Axis of Histone 3 Lysine 4 Methylation in Budding and Fission Yeasts\*

Received for publication, September 18, 2002, and in revised form, December 17, 2002  
Published, JBC Papers in Press, December 17, 2002, DOI 10.1074/jbc.M209562200

Assen Roguev†§, Daniel Schacht†§, Anna Shevchenko¶, Rein Aasland¶\*\*, Andrej Shevchenko¶, and A. Francis Stewart\* §§

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Trithorax (4)), a well conserved 150-amino acid domain found in all eukaryotes, which mediates histone methyltransferase activity (5, 6). Trx and Ash1 both contain a SET domain. There is little evidence so far that Trx methylates histones; however, binding to histones has been documented (7). The third trxG3 member, Ash2, does not contain a SET domain but has a PHD finger (8) and a SPRY domain (9).

Although budding yeast does not have a Trx homologue, it has a protein, Set1, with a very similar type of SET domain (10). For this reason, we determined the composition of the Set1 complex, Set1C, and found that it has H3 Lys<sup>4</sup> methyltransferase activity *in vitro* (3). Concomitantly, two other groups have identified most members of Set1C (11, 12). The complete Set1C and the *in vitro* specificity for H3 Lys<sup>4</sup> methylation have since been confirmed (13). The requirement for



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## Conservation of H3 Lys<sup>4</sup> Methylation Axis

a protein that... Thus, in con... contains two

the WD40  $\beta$  pro... Hidden Markov... each of these... ican WD40 re... are significant... *S. cerevisiae* and... man, indicating... not shown).

of *S. cerevisiae*,... Only two other... e evident in the

ponent. We did... Set1 TAP prep-

and poor mass... Sp\_Sdc1 homo-... thus proving its... cant excess of... other proteins,

protein in the... ow similarity to... py-30. The sim-... ization motif

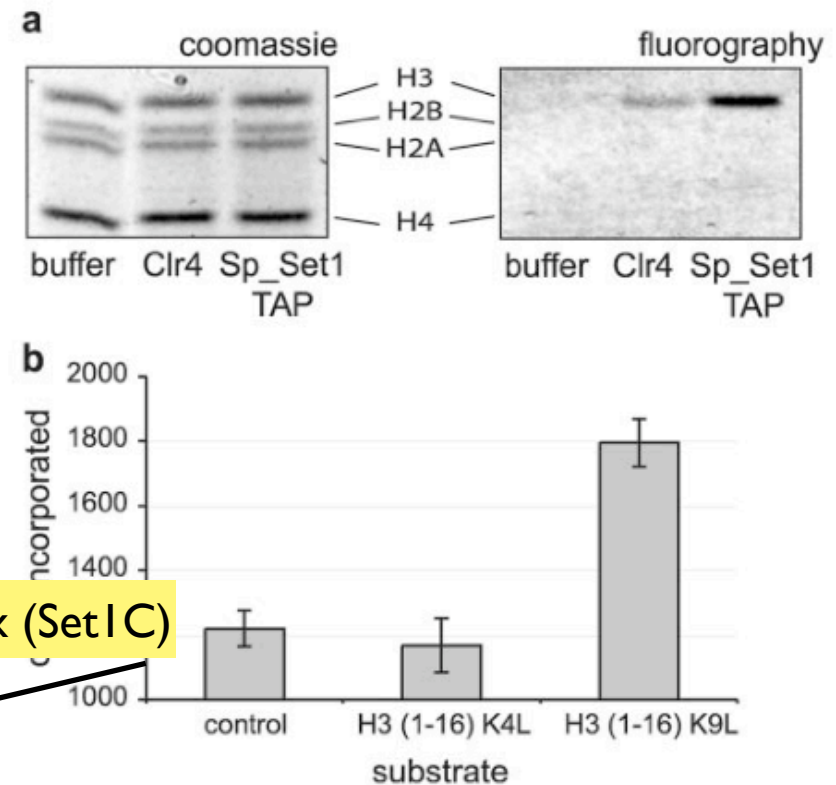


FIG. 3. **Sp\_Set1C methylates histone 3 lysine 4 *in vitro*.** *a*, Sp\_Set1C methyltransferase activity was assayed with Sp\_Set1C-TAP-purified extracts using core histones as substrates in the presence of [<sup>3</sup>H]SAM. Following incubation, the reactions were resolved by SDS-PAGE followed by Coomassie Blue staining and fluorography. *Clr4*, the *S. pombe* H3 Lys<sup>9</sup> methyltransferase was used as a positive control. *b*, Sp\_Set1C has a preference for H3 Lys<sup>4</sup>. The complex isolated from the Sp\_Set1-TAP strain was incubated with H3 N-terminal (1–16) peptides mutated at lysine 4 (K4L) or lysine 9 (K9L) in the presence of [<sup>3</sup>H]SAM, and incorporated <sup>3</sup>H was determined by scintillation counter.



# GO & Text Mining

- GO provides semantic annotation and NLP
- Text mining makes use of semantic annotators

THE JOURNAL OF BIOLOGICAL CHEMISTRY  
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## High Conservation of the Set1/Rad6 Axis of Methylation in Budding and Fission Yeasts

Assen Koguchev<sup>†‡</sup>, Daniel Schaff<sup>†‡</sup>, Anna Shevchenko<sup>¶</sup>, Reinhold A. Francis Stewart<sup>†‡</sup>

From <sup>†</sup>BIOTEC, Technische Universität Dresden, c/o Max Planck Institute for Molecular Cell Biology and Genetics, Pfaffenburger Straße 1, 80509 Dresden, Germany, <sup>‡</sup>Max Planck Institute for Molecular Cell Biology and Genetics, Pfaffenburger Straße 1, 80509 Dresden, Germany, <sup>¶</sup>Department of Molecular Biology, University of Bergen, Thormøhlensgt. 57, 5018 Bergen, Norway, and <sup>§</sup>Department of Molecular Biology, University of Bergen, Thormøhlensgt. 57, 5018 Bergen, Norway

Histone 3 lysine 4 (H3 Lys<sup>4</sup>) methylation in *Saccharomyces cerevisiae* is mediated by the Set1 complex (Set1C) and is dependent upon ubiquitinylation of H2B by Rad6. Mutually exclusive methylation of H3 at Lys<sup>4</sup> or Lys<sup>9</sup> is central to chromatin regulation; however, *S. cerevisiae* lacks Lys<sup>9</sup> methylation. Furthermore, a different H3 Lys<sup>4</sup> methylase, Set7/9, has been identified in mammals, thereby questioning the relevance of the *S. cerevisiae* findings for eukaryotes in general. We report that the majority of Lys<sup>4</sup> methylation in *Schizosaccharomyces pombe*, like in *S. cerevisiae*, is mediated by Set1C and is Rad6-dependent. *S. pombe* Set1C mediates H3 Lys<sup>4</sup> methylation *in vitro* and contains the same eight subunits found in *S. cerevisiae*, including the homologue of the *Drosophila* trithorax Group protein, Ash2. Three additional features of *S. pombe* Set1C each

## Activation of H3 Lys<sup>4</sup> Methylation Axis

a protein that... Thus, in con-... contains two

the WD40  $\beta$  pro-... Hidden Markov... each of these... ican WD40 re-... are significant... *S. cerevisiae* and... man, indicating... not shown).

of *S. cerevisiae*,... Only two other... e evident in the

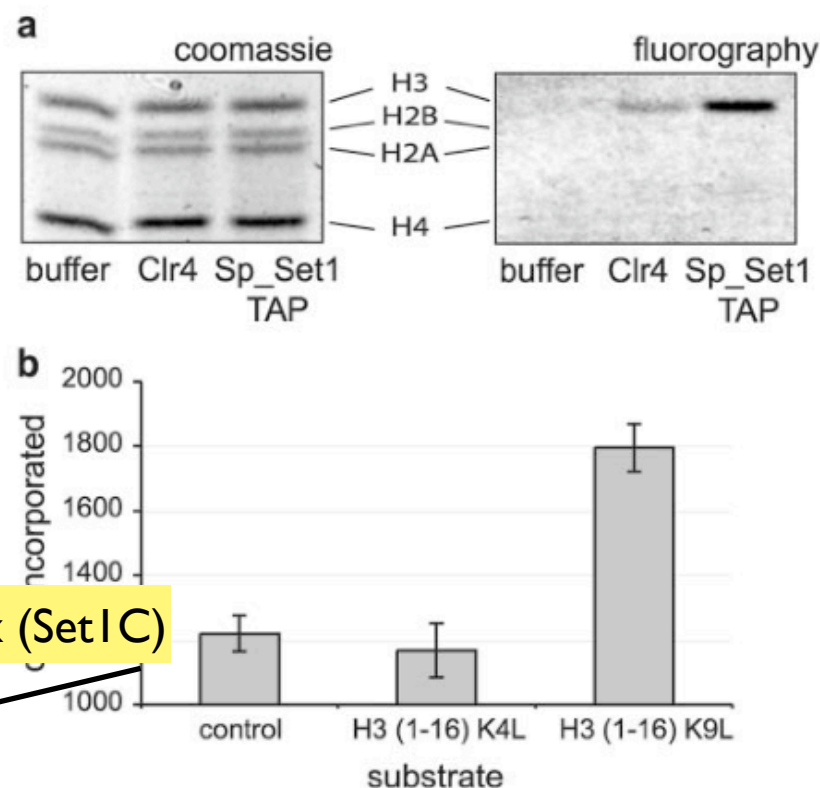


FIG. 3. *Sp\_Set1C* methylates histone 3 lysine 4 *in vitro*. *a*, *Sp\_Set1C* methyltransferase activity was assayed with *Sp\_Set1C*-TAP-purified extracts using core histones as substrates in the presence of [<sup>3</sup>H]SAM. Following incubation, the reactions were resolved by SDS-PAGE followed by Coomassie Blue staining and fluorography. *Clr4*, the *S. pombe* H3 Lys<sup>9</sup> methyltransferase was used as a positive control. *b*, *Sp\_Set1C* has a preference for H3 Lys<sup>4</sup>. The complex isolated from the *Sp\_Set1*-TAP strain was incubated with H3 N-terminal (1–16) peptides mutated at lysine 4 (K4L) or lysine 9 (K9L) in the presence of [<sup>3</sup>H]SAM, and incorporated <sup>3</sup>H was determined by scintillation counter.



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ponent. We did... Set1 TAP prep... and poor mass

Sp\_Sdc1 homo... thus proving its... cant excess of... other proteins... protein in the

ow similarity to... py-30. The sim... ization motif... complete Set1C

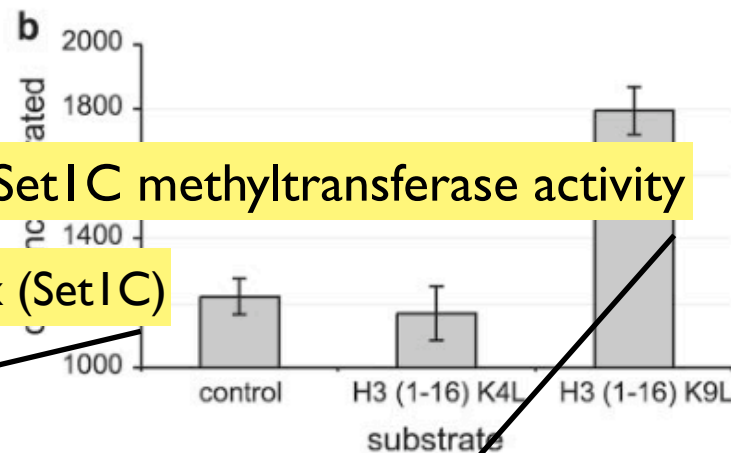
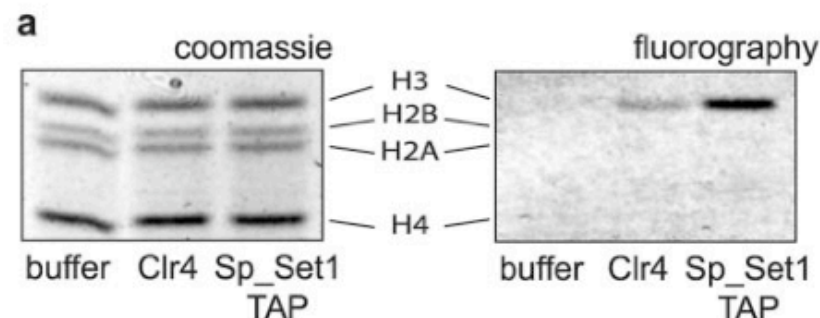


FIG. 3. Sp\_Set1C methylates histone 3 lysine 4 *in vitro*. a, Sp\_Set1C methyltransferase activity was assayed with Sp\_Set1C-TAP-purified extracts using core histones as substrates in the presence of [<sup>3</sup>H]SAM. Following incubation, the reactions were resolved by SDS-PAGE followed by Coomassie Blue staining and fluorography. Clr4, the *S. pombe* H3 Lys<sup>9</sup> methyltransferase was used as a positive control. b, Sp\_Set1C has a preference for H3 Lys<sup>4</sup>. The complex isolated from the Sp\_Set1-TAP strain was incubated with H3 N-terminal (1–16) peptides mutated at lysine 4 (K4L) or lysine 9 (K9L) in the presence of [<sup>3</sup>H]SAM, and incorporated <sup>3</sup>H was determined by scintillation counter.

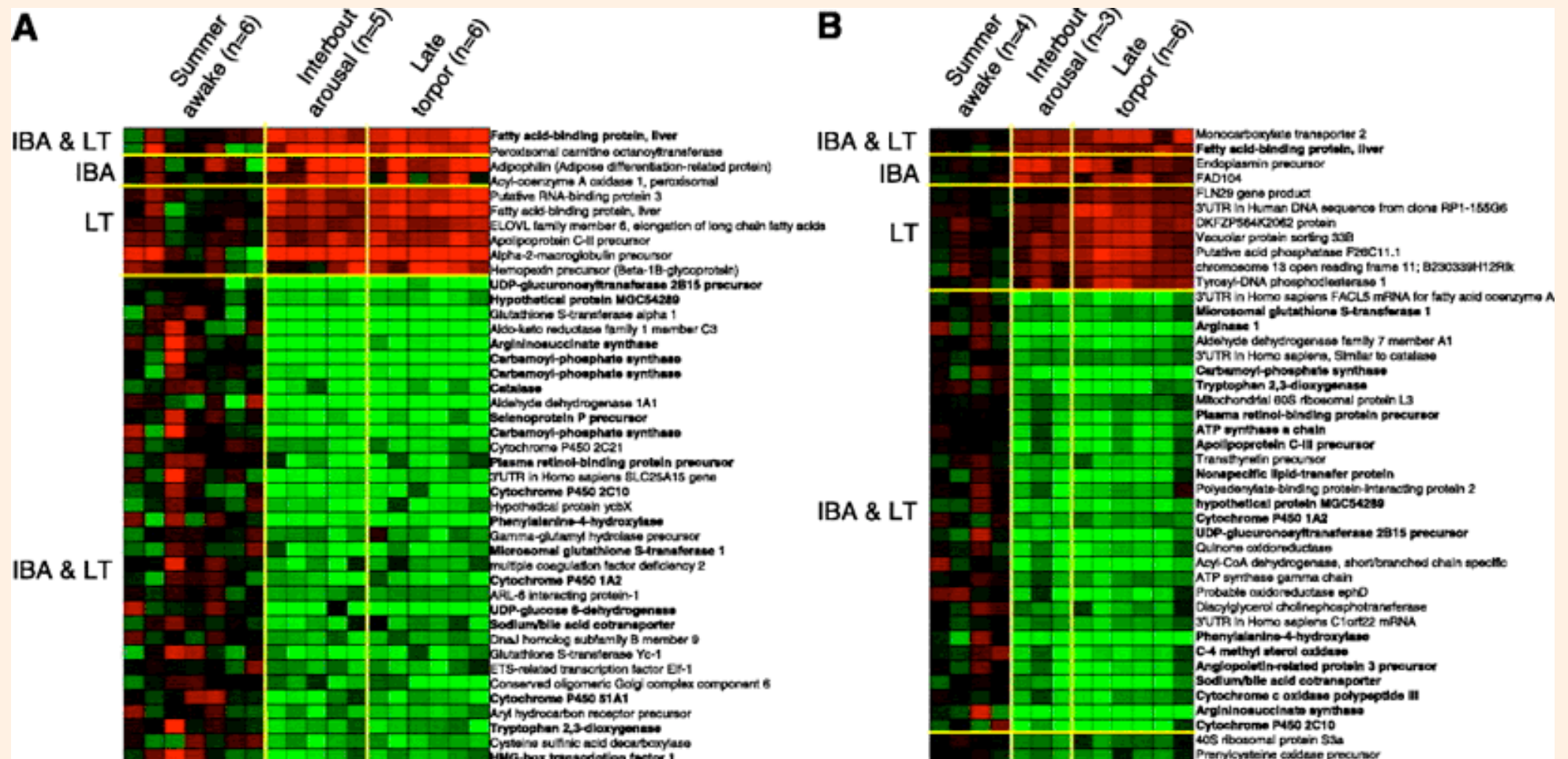


# GO & gene expression



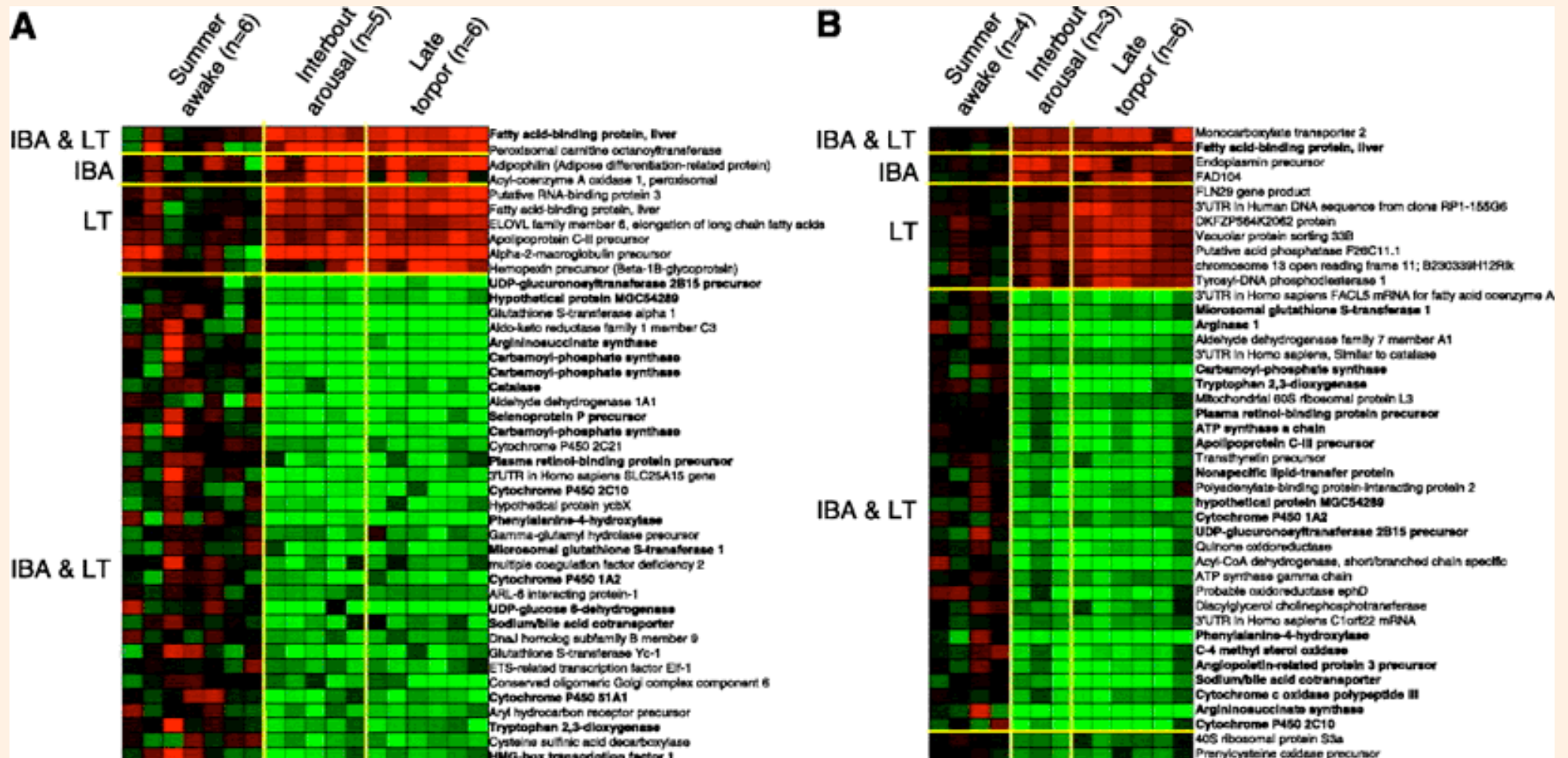


# GO & gene expression

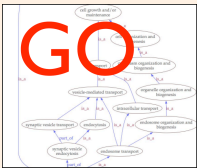




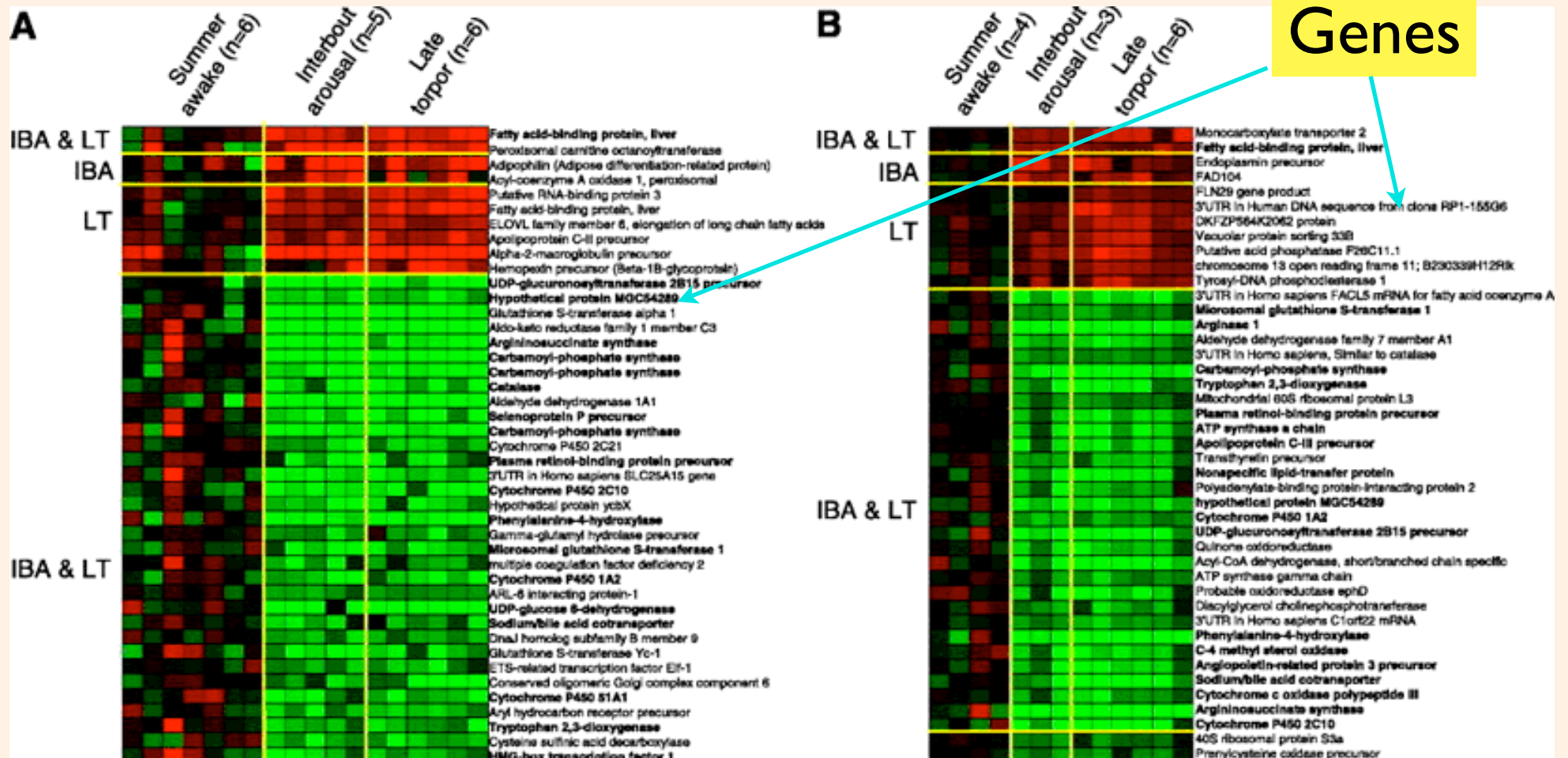
# GO & gene expression



D.R. Williams et al. (2005) *Physiol Genomics* 24(1): 13–22 (Fig. 2)



# GO & gene expression

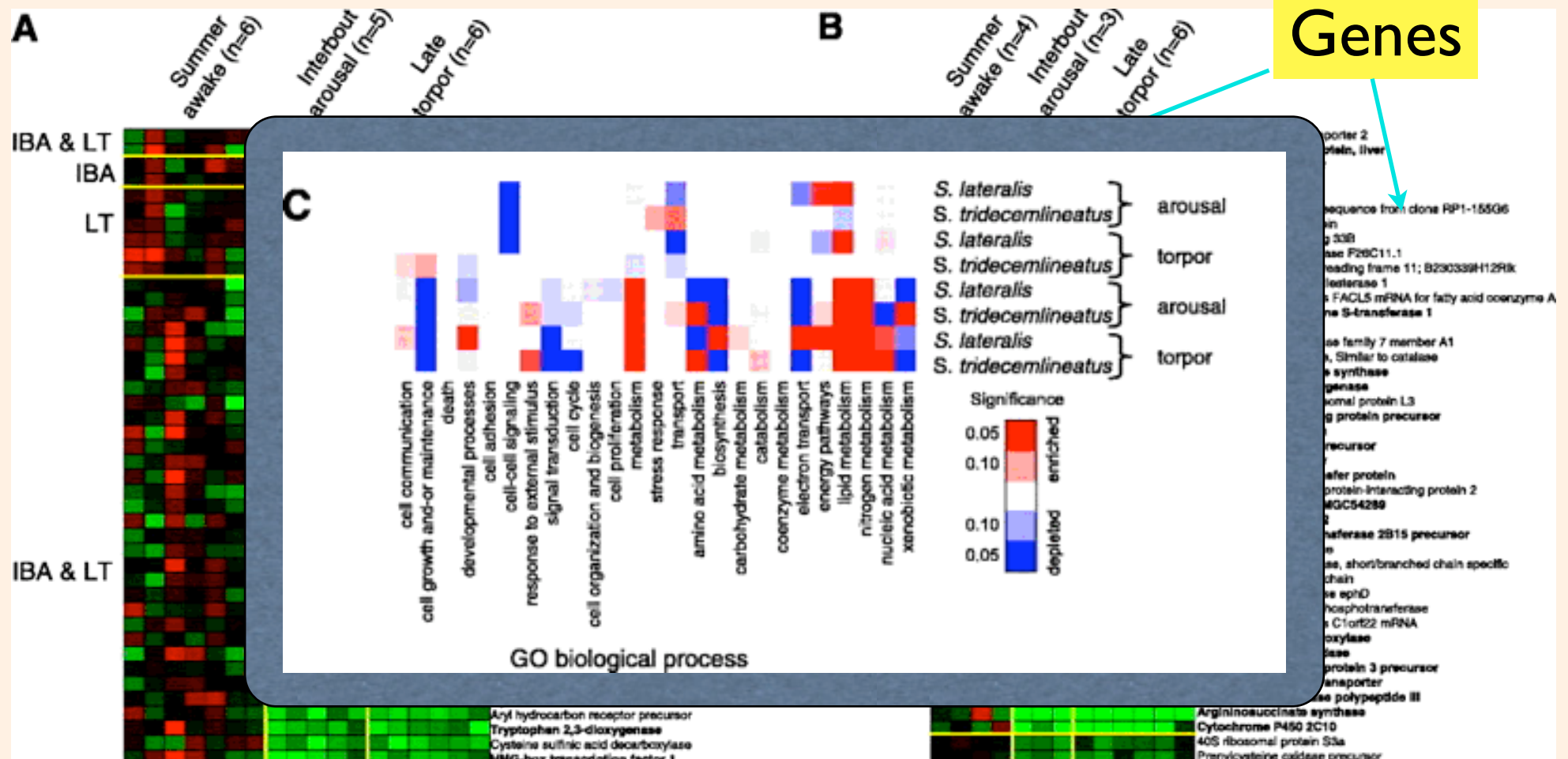


D.R. Williams et al. (2005) *Physiol Genomics* 24(1): 13–22 (Fig. 2)





# GO & gene expression

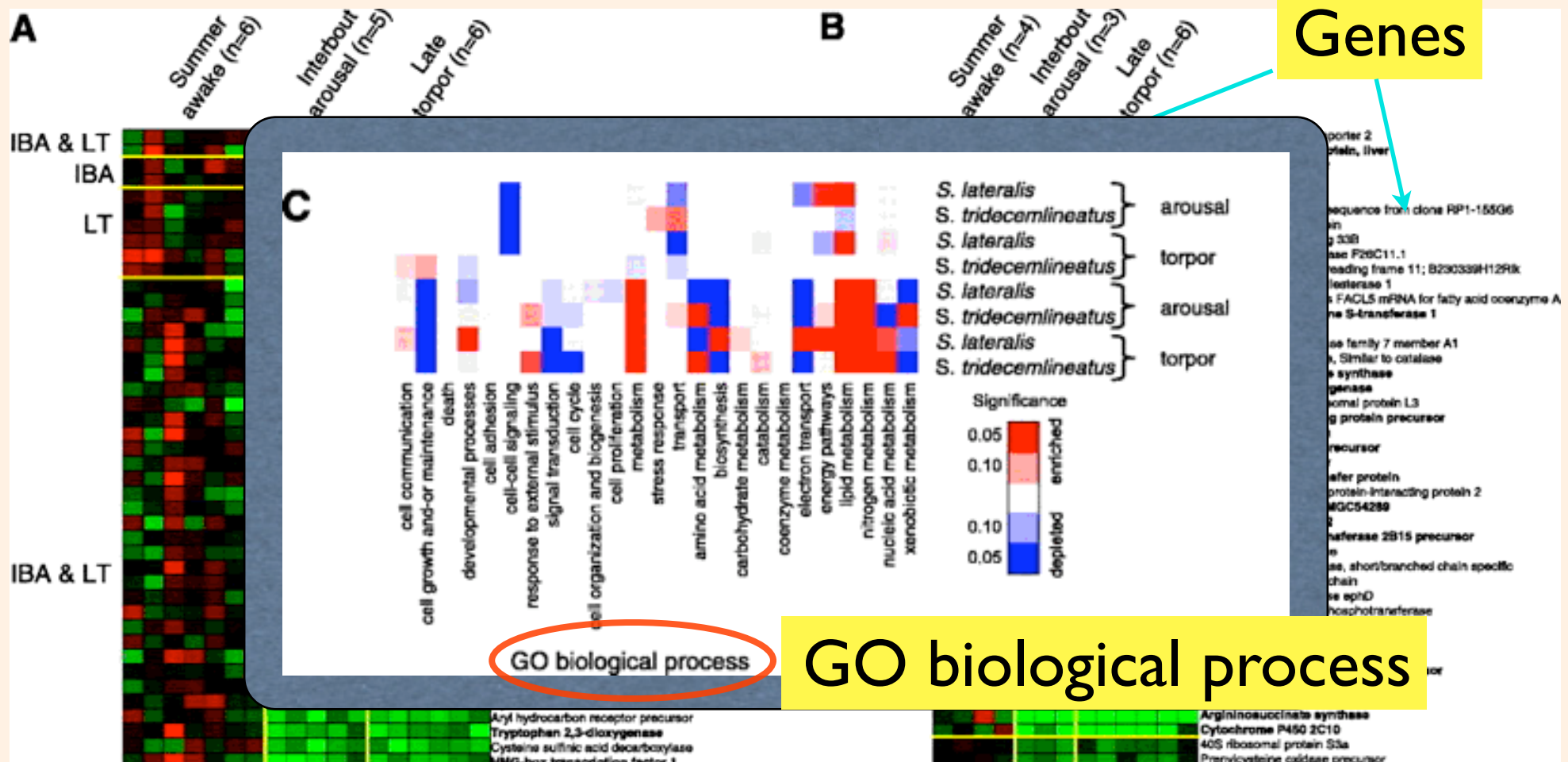


D.R. Williams et al. (2005) *Physiol Genomics* 24(1): 13–22 (Fig. 2)





# GO & gene expression



D.R. Williams et al. (2005) *Physiol Genomics* 24(1): 13–22 (Fig. 2)



# GO Tools

- Database (and schema)
- Perl API
- Browsers, e.g. AmiGO
- Editing tool: OBO-Edit
- Tool collection:
  - Microarray analysis tools
  - Annotation tools
  - others ...

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



# GO Tools page

Gene Ontology Tools

http://www.geneontology.org/GO.tools.shtml?all

Search

gene or protein name

## the Gene Ontology

Close menus

Home

**Downloads**

- Ontologies
- Annotations
- Database
- Mappings to GO
- Teaching Resources
- Monthly Reports

**GO Tools**

- Browsers
- Microarray tools
- Annotation tools
- Other tools
- Submit New Tools

**Documentation**

- FAQ
- Introduction
- Annotation Guide
- Evidence Code Guide
- File Format Guide
- Editorial Style Guide
- Component Ontology
- Function Ontology
- Process Ontology
- GO Slim Guide
- Meeting minutes




**About GO**

- GO Consortium
- Publications
- Citation Policy

## Gene Ontology Tools

**Consortium Tools**  
**Non-Consortium Tools**

**Key**

 web-based tool	 downloadable tool	 compatible OSs (for downloadable tools)
---	---	---

### Consortium Tools

The tools below are developed within the Gene Ontology Consortium. They continue to be improved and expanded and you can receive support in using these tools by writing to the [GO mailing list](#).

The tools on this page are free to academics.

#### AmiGO

[Berkeley Drosophila Genome Project](#)

No abstract available

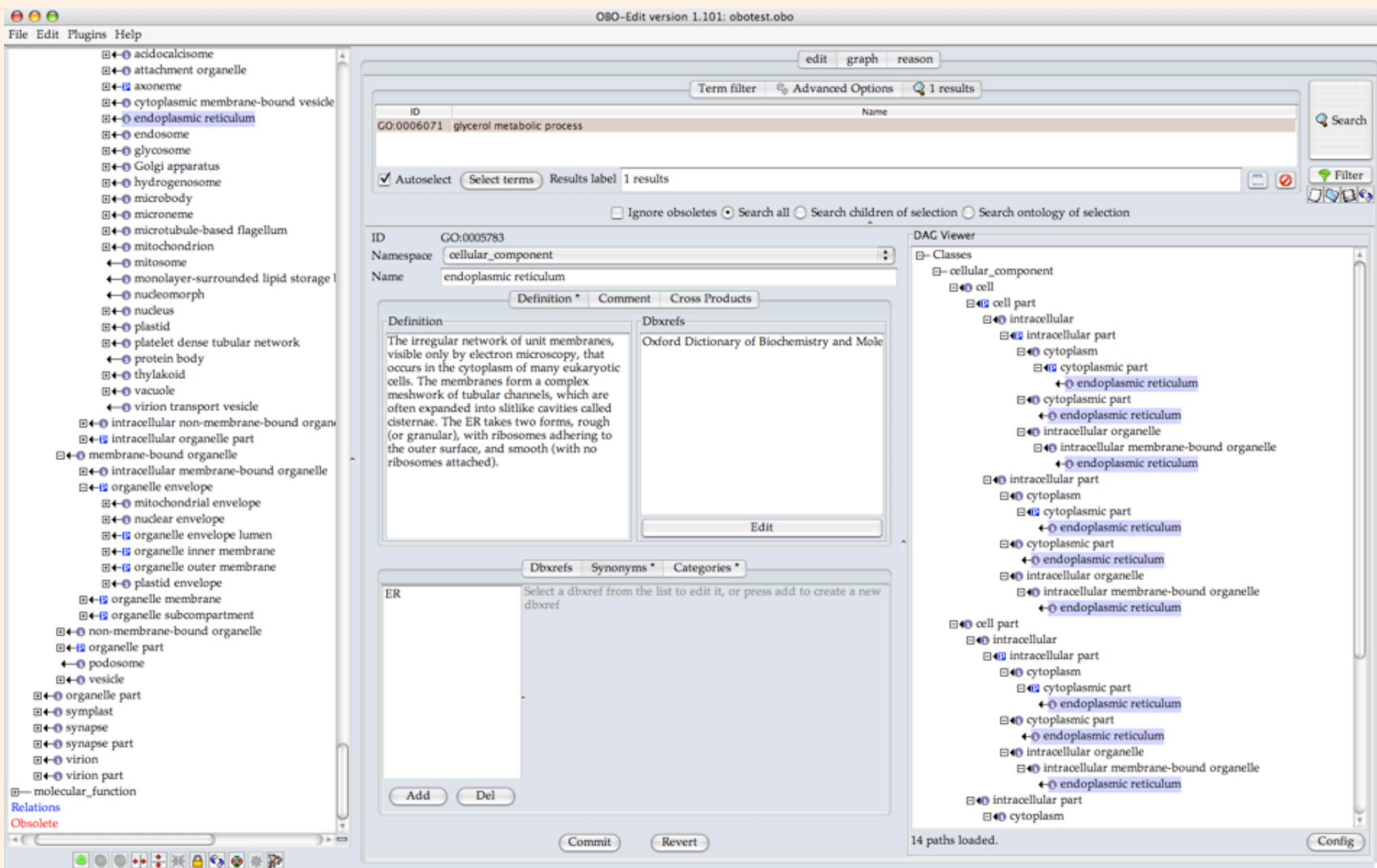
[AmiGO](#) allows you to search for a GO term and view all gene products annotated to it, or search for a gene product and view all its associations. You can also browse the ontologies to view relationships between terms as well as the number of gene products annotated to a given term. AmiGO accesses the GO MySQL database (see below); the browser and documentation are available from <http://www.godatabase.org/dev/>.

AmiGO uses the GO database, which is updated monthly.

#### DAG-Edit (also known as OBO-Edit)



# OBO-Edit





# OBO-Edit

OBO-Edit version 1.101: obotest.obo

File Edit Plugins Help

edit graph reason

Term filter Advanced Options 1 results

search

ID GO:0006071 glycerol metabolic process

Autoselect Select terms Results label 1 results

Ignore obsoletes Search all Search children of selection Search ontology of selection

ID GO:0005783  
Namespace cellular\_component  
Name endoplasmic reticulum

Definition \* Comment Cross Products

Definition  
The irregular network of unit membranes, visible only by electron microscopy, that occurs in the cytoplasm of many eukaryotic cells. The membranes form a complex meshwork of tubular channels, which are often expanded into slitlike cavities called cisternae. The ER takes two forms, rough (or granular), with ribosomes adhering to the outer surface, and smooth (with no ribosomes attached).

Dbxrefs  
Oxford Dictionary of Biochemistry and Mole

Edit

Dbxrefs Synonyms \* Categories \*

ER  
Select a dbxref from the list to edit it, or press add to create a new dbxref

Add Del

Commit Revert

DAG Viewer

Classes

- cellular\_component
  - cell
    - cell part
      - intracellular
        - intracellular part
          - cytoplasm
            - cytoplasmic part
              - endoplasmic reticulum

- intracellular part
- cytoplasm
  - cytoplasmic part
    - endoplasmic reticulum
- intracellular organelle
- intracellular membrane-bound organelle
  - endoplasmic reticulum
- cell part
- intracellular
  - intracellular part
    - cytoplasm
      - cytoplasmic part
        - endoplasmic reticulum

14 paths loaded.

Config

Relations  
Obsolete





# OBO-Edit

OBO-Edit version 1.101: obotest.obo

File Edit Plugins Help

edit graph reason

Term filter Advanced Options 1 results

search

tree view & editing

GO:0006071 glycerol metabolic process

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DAG Viewer

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14 paths loaded.

Config



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OBO-Edit version 1.101: obotest.obo

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Dbxrefs Synonyms \* Categories \*

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Select a dbxref from the list to edit it, or press add to create a new dbxref

Add Del

Commit Revert

search

tree view & editing

text editing

DAG Viewer

Classes

cellular\_component

cell

cell part

intracellular

intracellular part

cytoplasm

cytoplasmic part

endoplasmic reticulum

cytoplasmic part

endoplasmic reticulum

intracellular organelle

intracellular membrane-bound organelle

endoplasmic reticulum

intracellular part

cytoplasm

cytoplasmic part

endoplasmic reticulum

cytoplasmic part

endoplasmic reticulum

intracellular organelle

intracellular membrane-bound organelle

endoplasmic reticulum

cell part

intracellular

intracellular part

cytoplasm

cytoplasmic part

endoplasmic reticulum

cytoplasmic part

endoplasmic reticulum

intracellular organelle

intracellular membrane-bound organelle

endoplasmic reticulum

intracellular part

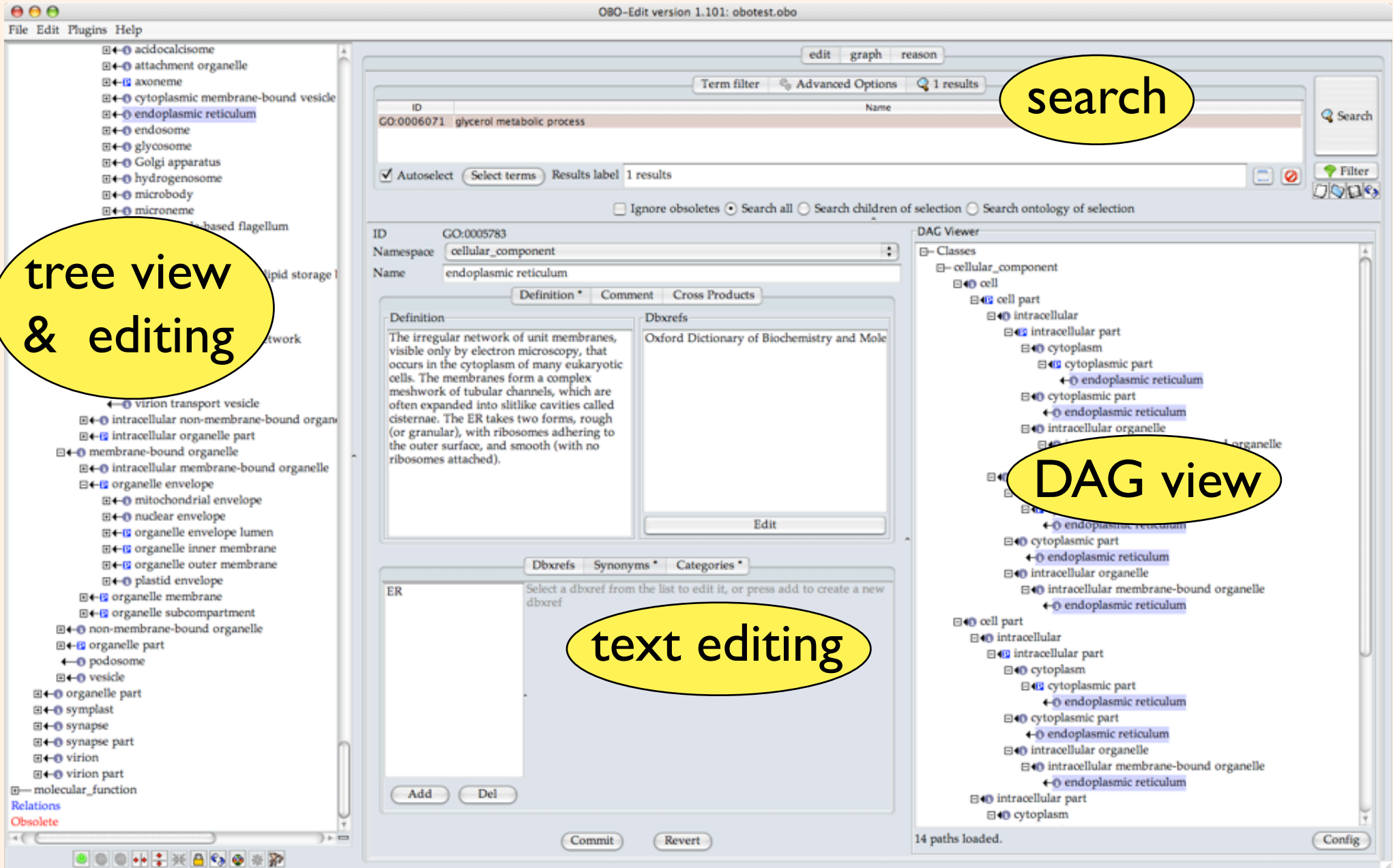
cytoplasm

14 paths loaded.

Config



# OBO-Edit



search

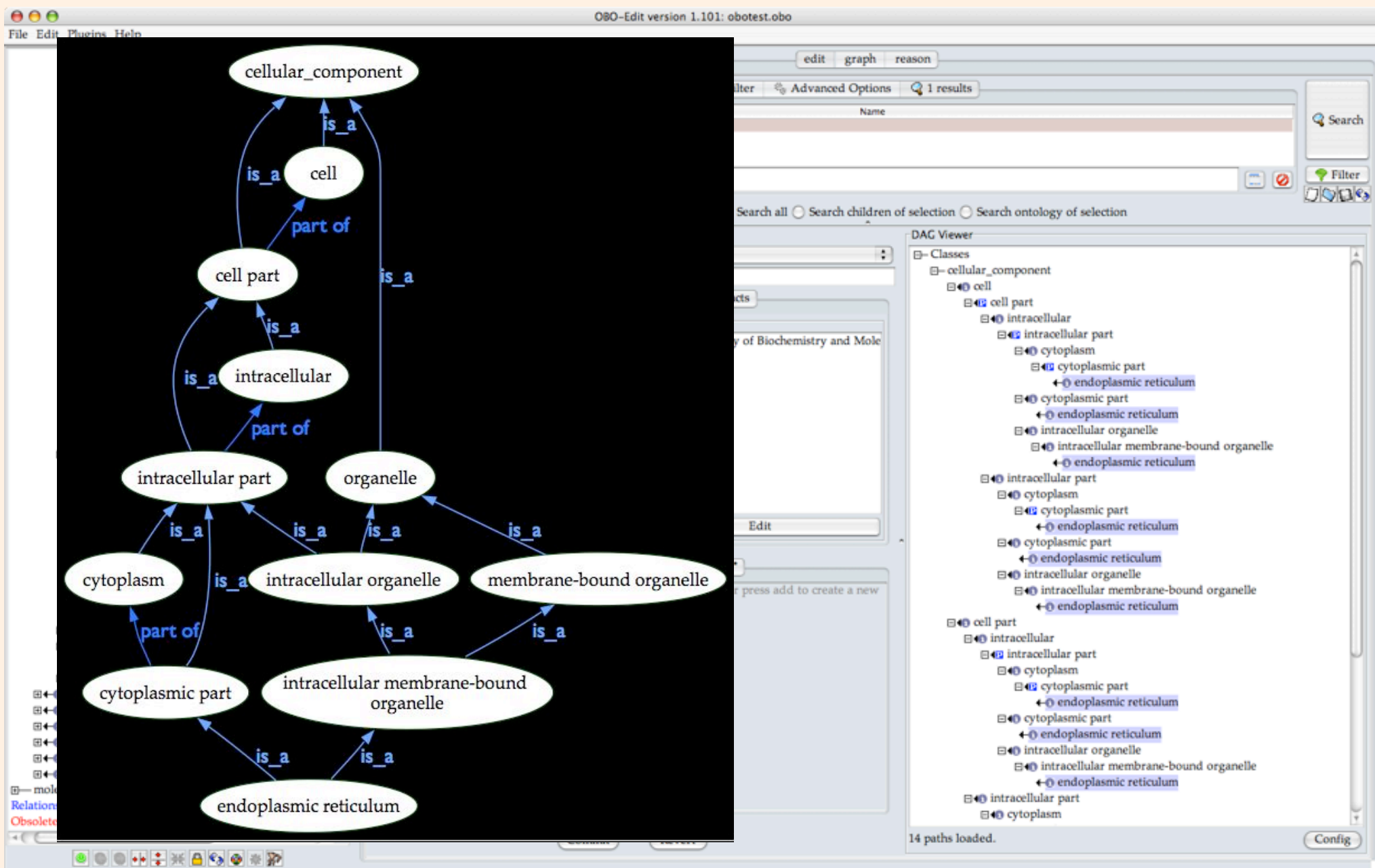
## DAG view

text editing



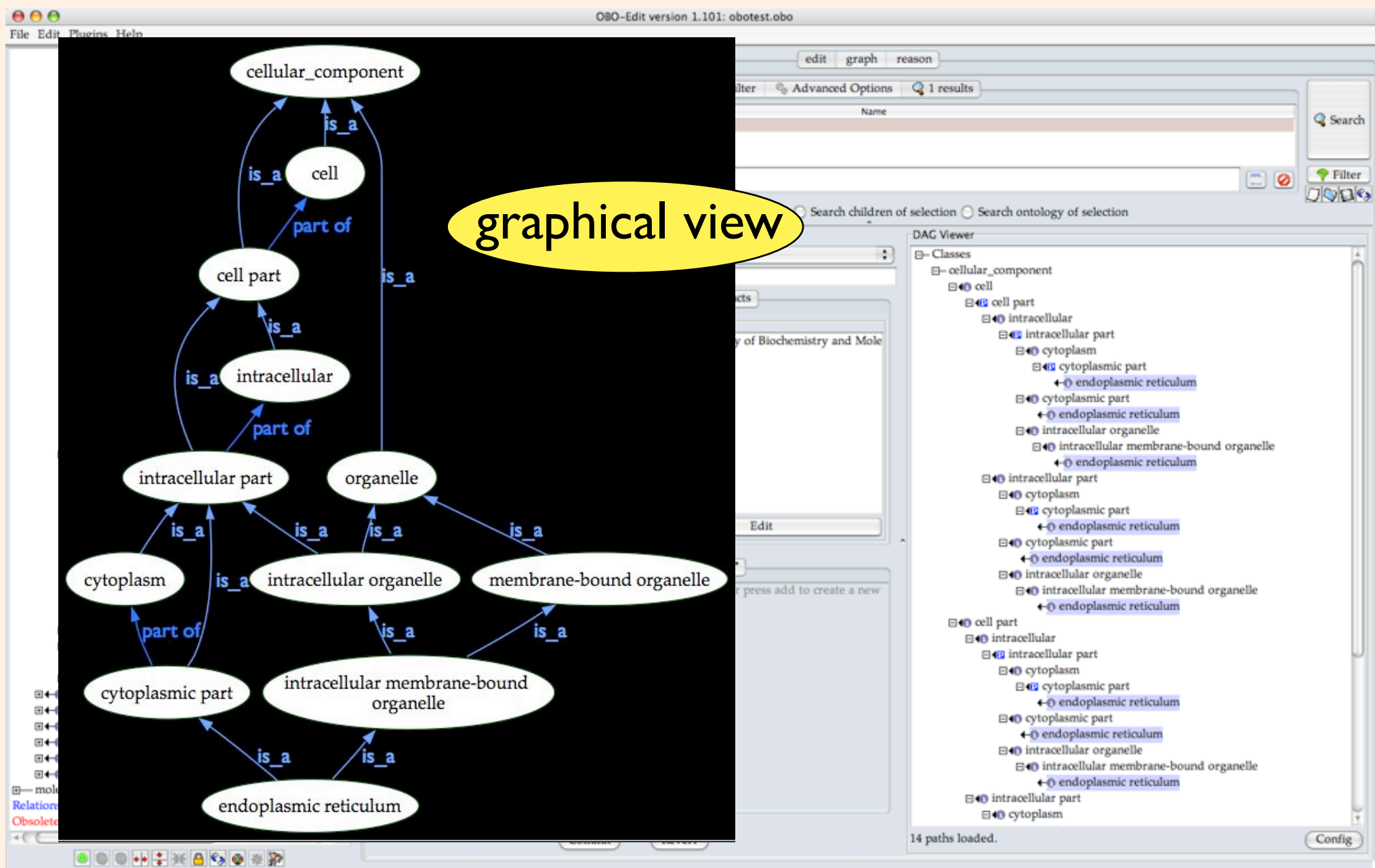


# OBO-Edit





# OBO-Edit





# OBO-Edit

OBO-Edit version 1.101: obotest.obo

File Edit Plugins Help

edit graph reason

Filter Advanced Options 1 results

graphical view

cellular\_component

cell

cell part

intracellular

intracellular part

cytoplasm

cytoplasmic part

endoplasmic reticulum

intracellular organelle

membrane-bound organelle

organelle

Verification Plugin

Configuration Verification Results

Check Name	On text edit?	On reasoner?	On save?	On load?	On manual?	Configure
Comment checks	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Cycle Check	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Dangling Inters...	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Dbxref check	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Definition checks	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Disjointness ...	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Name Redund...	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Name checks	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Synonym checks	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
isac	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
ns	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Con...

Show warnings

☒ On text edits? ☒ On reasoner? ☒ On save? ☒ On load? ☒ On manual?

☐ Check obsoletes?

Add check Remove check

Run Manual Check

endoplasmic reticulum

intracellular part

cytoplasm

14 paths loaded.

Config



# OBO-Edit

OBO-Edit version 1.101: obotest.obo

File Edit Plugins Help

edit graph reason

filter Advanced Options 1 results

graphical view

verification

cellular\_component

cell

cell part

intracellular

intracellular part

organelle

cytoplasm

intracellular organelle

membrane-bound organelle

cytoplasmic part

intracellular membrane-bound organelle

endoplasmic reticulum

is\_a

part of

Check Name	On text edit?	On reasoner?	On save?	On load?	On manual?	Configure
Comment checks	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Cycle Check	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Dangling Inter...	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Dbxref check	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Definition checks	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Disjointness ...	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Name Redund...	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Name checks	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
Synonym checks	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
isac	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	Con...
ns	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Con...

Show warnings

☒ On text edits? ☒ On reasoner? ☒ On save? ☒ On load? ☒ On manual?

☐ Check obsoletes?

Add check Remove check

Run Manual Check

endoplasmic reticulum

intracellular part

cytoplasm

14 paths loaded.

Config





# OBO-Edit 2.0

OBO-Edit version 2.000-beta16: obotest.obo

File Edit View

### Ontology Editor Panel

- glycerol catabolic process
  - propanediol catabolic process
    - propanediol metabolic process
      - sphingosine metabolic process
      - sterol metabolic process
      - triethanolamine metabolic process
    - aldehyde metabolic process
      - acetaldehyde metabolic process
      - aldehyde biosynthetic process
      - aldehyde catabolic process
      - formaldehyde metabolic process
      - glyceraldehyde-3-phosphate metabolic process
        - glyceraldehyde-3-phosphate biosynthetic process
        - glyceraldehyde-3-phosphate catabolic process
      - isopentenyl diphosphate biosynthetic process, meval
      - glyoxylate metabolic process
      - hexadecanal metabolic process

### Search Panel

Search results: name contains "kinase activity" and definition\_dbxref starts with "MetaCyc" Search

Matches all ☐ Matches any ☐

Select terms that have a Name that contains the value catabolic

Select terms that have a Dbxref that starts with the value MetaCyc

name contains "catabolic" and dbxref starts with "MetaCyc"

☒ Show debugging hints Search

### Text Editor

ID: GO:0019563  
Namespace: biological\_process  
Name: glycerol catabolic process

Definition \* Comment Cross Products

Definition: The chemical reactions and pathways resulting in the breakdown of glycerol, 1,2,3-propanetriol, a sweet, hygroscopic, viscous liquid, widely distributed in nature as a constituent of many lipids.

Dbxrefs: GOC:go\_curators  
ISBN:0198506732  
Oxford Dictionary of Biochemistry and Molecular Biology

Dbxrefs \* Synonyms \* Categories \*

MetaCyc:PWY-4261  
MetaCyc:PWY0-381

### Graph Editor



# OBO-Edit 2.0

The screenshot displays the OBO-Edit version 2.000-beta16 interface. The main window is divided into several panels:

- Ontology Editor Panel (Top Left):** Shows a hierarchical tree view of the ontology. A yellow oval highlights the text "tree view & editing" over this panel. The tree structure includes terms like "glycerol catabolic process", "propanediol catabolic process", "propanediol metabolic process", "sphingosine metabolic process", "sterol metabolic process", "gonolamine metabolic process", "bolic process", "le metabolic process", "synthetic process", "bolic process", "yde metabolic process", "aldehyde-3-phosphate metabolic process", "glyceraldehyde-3-phosphate biosynthetic process", "glyceraldehyde-3-phosphate catabolic process", "isopentenyl diphosphate biosynthetic process, meval", "glyoxylate metabolic process", and "hexadecanal metabolic process".
- Graph Editor (Bottom Left):** Displays a graphical representation of the ontology structure. It shows a network of terms connected by arrows, including "alcohol metabolic process", "polyol metabolic process", "glycerol metabolic process", "polyol catabolic process", and "glycerol catabolic process".
- Search Panel (Top Right):** Contains search results for the query "name contains 'kinase activity' and definition\_dbxref starts with 'MetaCyc'". It shows two matches: "Select terms that have a Name that contains the value catabolic" and "Select terms that have a Dbxref that starts with the value MetaCyc".
- Text Editor (Bottom Right):** Displays the details for the selected term "glycerol catabolic process". It includes fields for ID (GO:0019563), Namespace (biological\_process), and Name (glycerol catabolic process). The Definition tab is active, showing the text: "The chemical reactions and pathways resulting in the breakdown of glycerol, 1,2,3-propanetriol, a sweet, hygroscopic, viscous liquid, widely distributed in nature as a constituent of many lipids." The Dbxrefs tab is also visible, showing references like "GOC:go\_curators" and "ISBN:0198506732 Oxford Dictionary of Biochemistry and Molecular Biology".



# OBO-Edit 2.0

OBO-Edit version 2.000-beta16: obotest.obo

File Edit View

**tree view & editing**

**graphical editing**

**Search Panel** Search results: name contains "kinase activity" and definition\_dbxref starts with "MetaCyc" Search

**Search Panel** Matches all Matches any

Select terms that have a Name that contains the value catabolic

Select terms that have a Dbxref that starts with the value MetaCyc

name contains "catabolic" and dbxref starts with "MetaCyc"

☒ Show debugging hints Search

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Dbxrefs

GOC:go\_curators

ISBN:0198506732  
Oxford Dictionary of Biochemistry and Molecular Biology

Dbxrefs \* Synonyms \* Categories \*

MetaCyc:PWY-4261

MetaCyc:PWY0-381

Graph Editor

alcohol metabolic process

polyol metabolic process

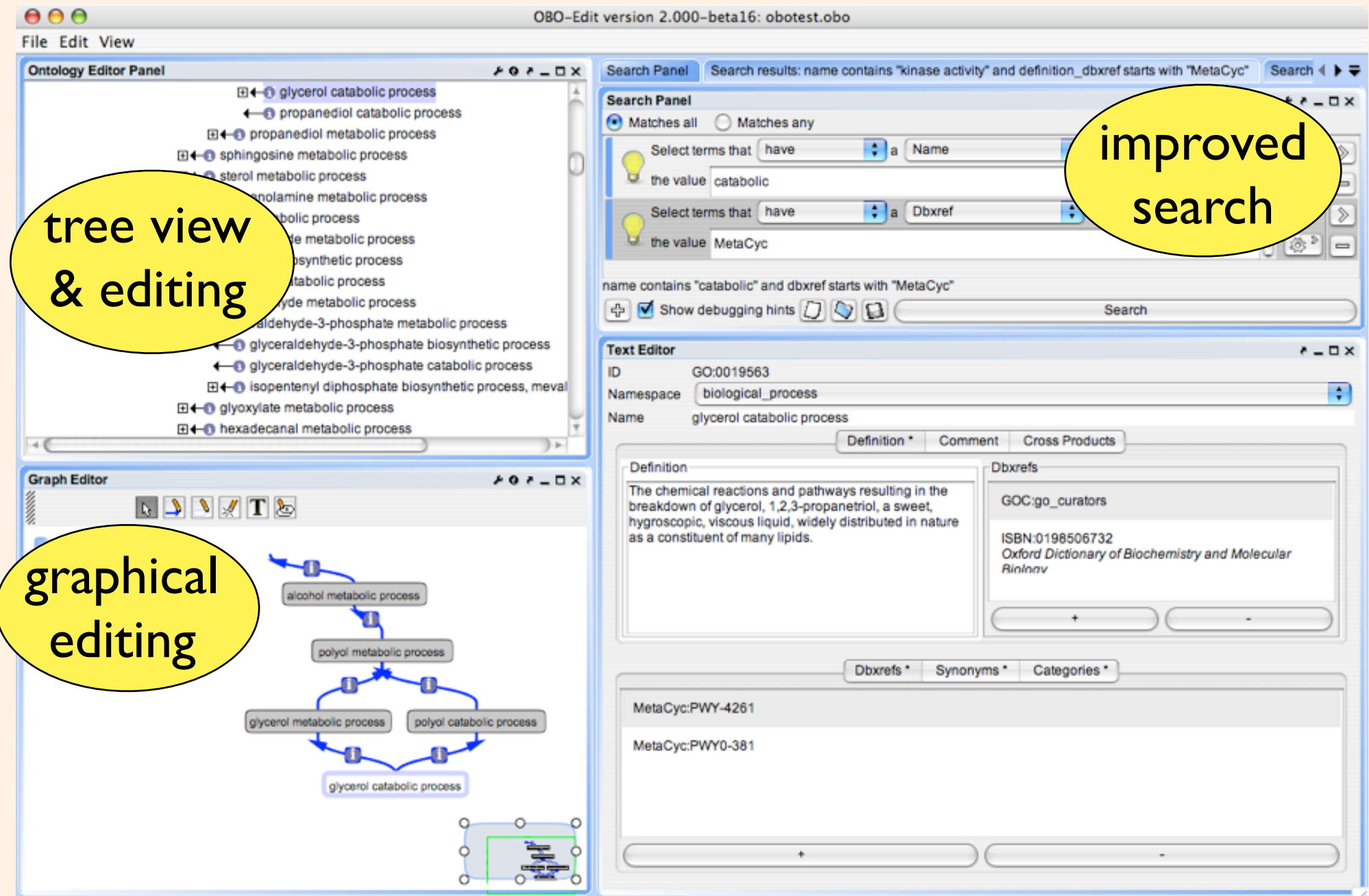
glycerol metabolic process

polyol catabolic process

glycerol catabolic process



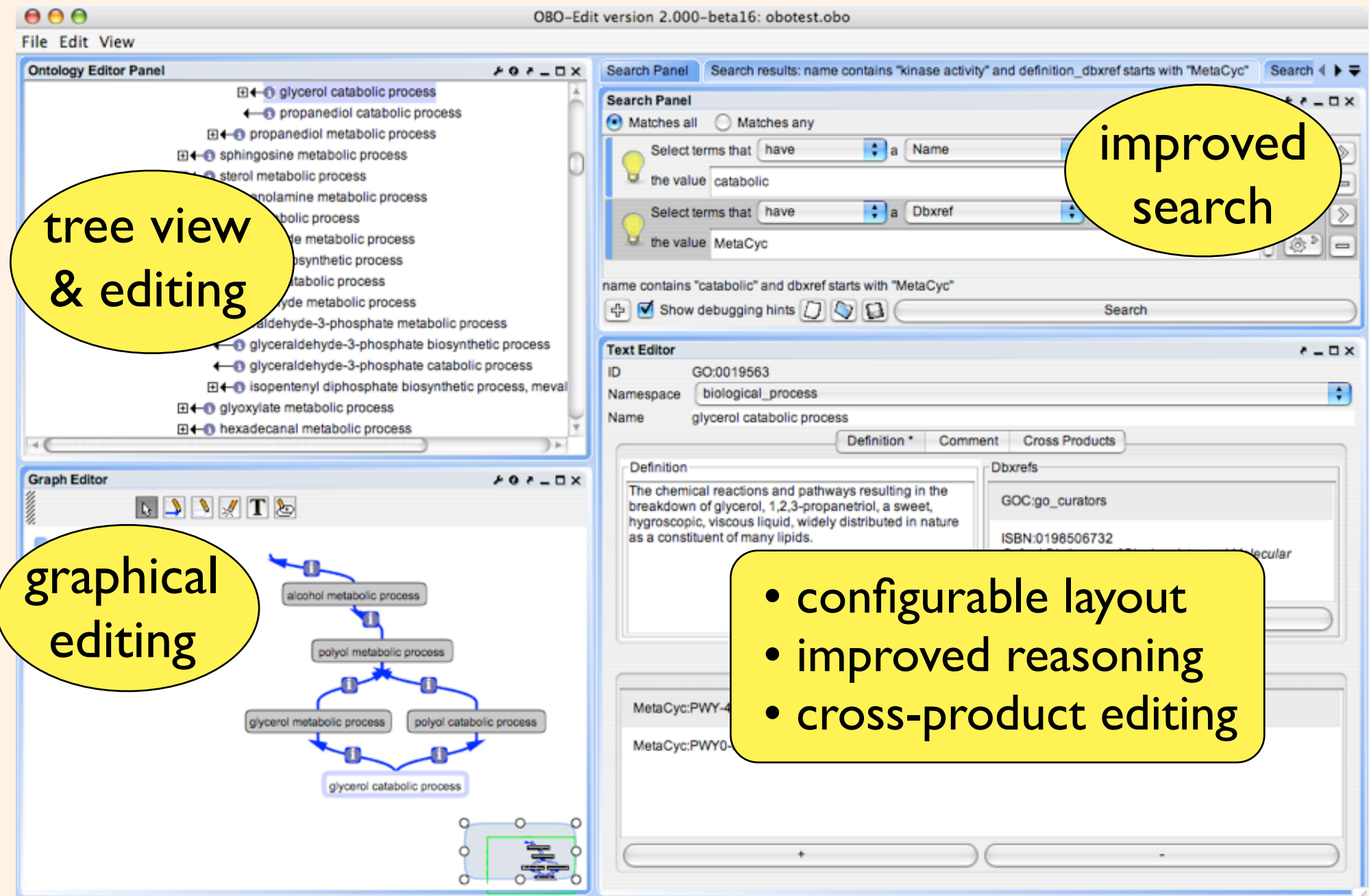
# OBO-Edit 2.0







# OBO-Edit 2.0



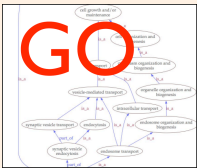
improved  
search

graphical editing

- configurable layout
- improved reasoning
- cross-product editing



# AmiGO



# AmiGO

AmiGO: Term Details

http://amigo.geneontology.org/cgi-bin/amigo/go.cgi?view=details&search\_constraint=terms&d Google

*the Gene Ontology* AmiGO

Advanced Search BLAST search Browse Help

Search GO  ☒ Terms ☐ Genes or proteins ☐ Exact Match

## glycerol biosynthetic process

Term information Term lineage External references Term associations

### Term Information

**Accession** GO:0006114

**Ontology** biological process

**Synonyms**  
exact: glycerol anabolism  
exact: glycerol biosynthesis  
exact: glycerol formation  
exact: glycerol synthesis

**Definition** The chemical reactions and pathways resulting in the formation of glycerol, 1,2,3-propanetriol, a sweet, hygroscopic, viscous liquid, widely distributed in nature as a constituent of many lipids. [source: GOC:aj, ISBN:0198506732]

**Comment** None

[Back to top](#)

### Term Lineage

**Filter tree view**

Filter Gene Product Counts

Data source

- All
- CGD
- dictyBase
- FlyBase

Term View Options

☒ Term ancestors ☐ Term parents, siblings and children

[all : all \[219941\]](#) [Graphical View](#)



# AmiGO

AmiGO: Term Details

http://amigo.geneontology.org/cgi-bin/amigo/go.cgi?view=details&search\_constraint=terms&d Google

the Gene Ontology AmiGO

Advanced Search BLAST search Browse Help

Search GO GO:0006114

all : all [219941]

**glycerol biosynthetic process**

Term information Term lineage

**Term Information**

**Accession** GO:0006114

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**Comment** None

**Term Lineage**

**Filter tree view**

Filter Gene Product Counts

Data source

All  
CGD  
dictyBase  
FlyBase

Term View Options

☒ Term ancestors ☐ Term

all : all [219941]

all : all [219941]  
GO:0008150 : biological\_process [140556]  
GO:0009987 : cellular process [71496]  
GO:0044237 : cellular metabolic process [48331]  
GO:0006066 : alcohol metabolic process [1827]  
GO:0046165 : alcohol biosynthetic process [300]  
GO:0046173 : polyol biosynthetic process [11]  
**GO:0006114 : glycerol biosynthetic process [8]**  
GO:0019751 : polyol metabolic process [155]  
GO:0006071 : glycerol metabolic process [122]  
**GO:0006114 : glycerol biosynthetic process [8]**  
GO:0046173 : polyol biosynthetic process [11]  
**GO:0006114 : glycerol biosynthetic process [8]**  
GO:0044249 : cellular biosynthetic process [12620]  
GO:0046165 : alcohol biosynthetic process [300]  
GO:0046173 : polyol biosynthetic process [11]  
**GO:0006114 : glycerol biosynthetic process [8]**  
GO:0008152 : metabolic process [55902]  
GO:0009058 : biosynthetic process [15503]  
GO:0044240 : cellular biosynthetic process [12620]



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AmiGO: Term Details

http://amigo.geneontology.org/cgi-bin/amigo/go.cgi?view=details&search\_constraint=terms&d Google

the Gene Ontology AmiGO

Advanced Search BLAST search Browse Help

Search GO GO:0006114 all : all [219941]

**glycerol biosynthetic process**

Term information Term lineage

**Term Information**

**Accession** GO:0006114

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Filter Gene Product Counts

Data source

All  
CGD  
dictyBase  
FlyBase

Term View Options

☒ Term ancestors ☐ Term

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- GO:0008150 : biological\_process [140556]
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- GO:0046173 : polyol biosynthetic process [11]
- GO:0006114 : glycerol biosynthetic process [8]**
- GO:0008152 : metabolic process [55902]
- GO:0009058 : biosynthetic process [15503]

Graphical View

More about AmiGO later!



# GO and Other Ontologies



# Ontologies and Experiments

human lung fibroblasts  
treated with cycloheximide



# Ontologies and Experiments

human lung fibroblasts  
treated with cycloheximide





# Ontologies and Experiments

↑  
human lung fibroblasts  
treated with cycloheximide



# Ontologies and Experiments

taxonomy

human lung fibroblasts  
treated with cycloheximide



# Ontologies and Experiments

taxonomy

human lung fibroblasts  
treated with cycloheximide



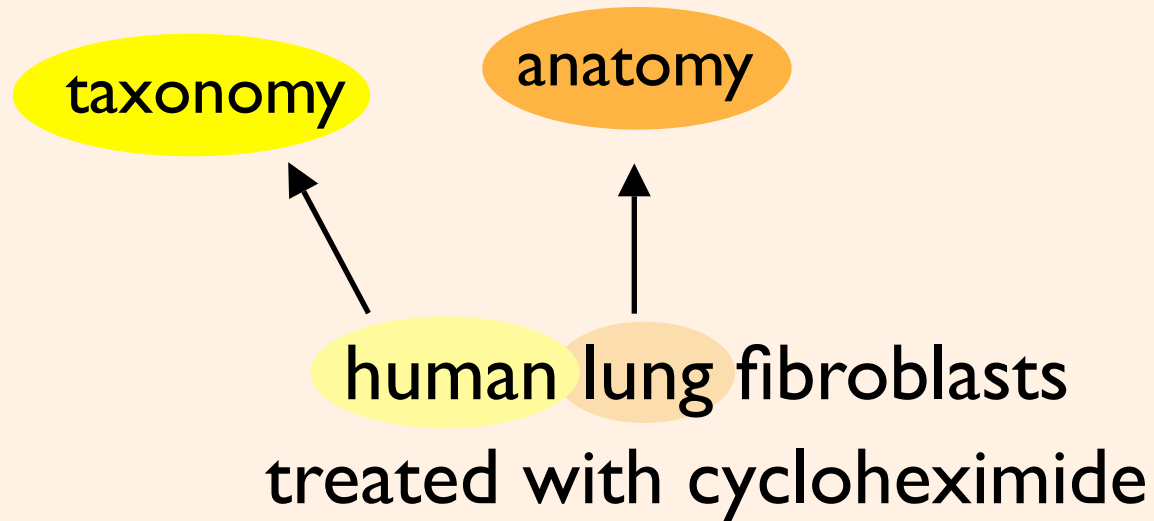
# Ontologies and Experiments

taxonomy

human lung fibroblasts  
treated with cycloheximide

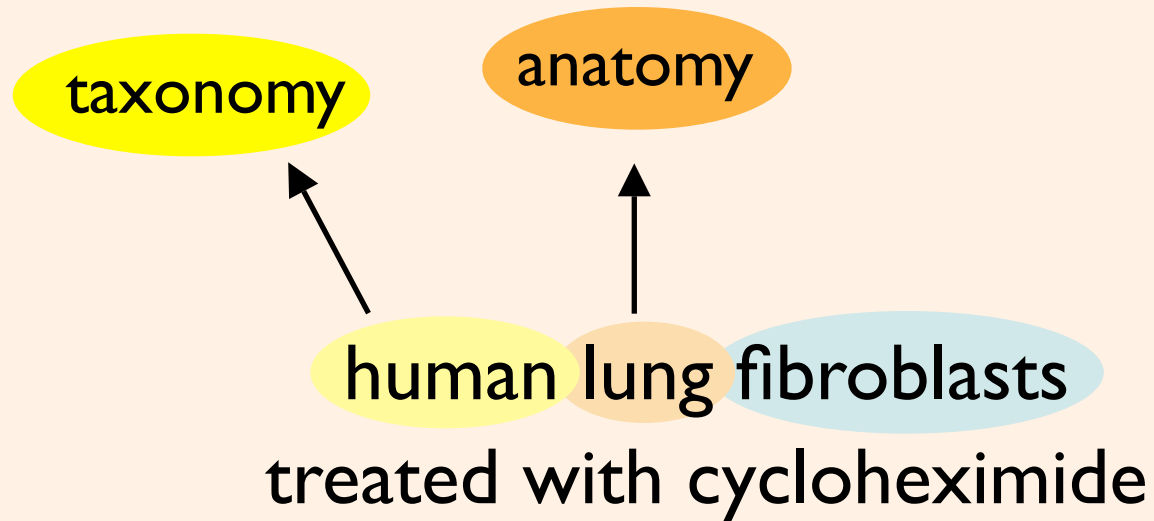


# Ontologies and Experiments



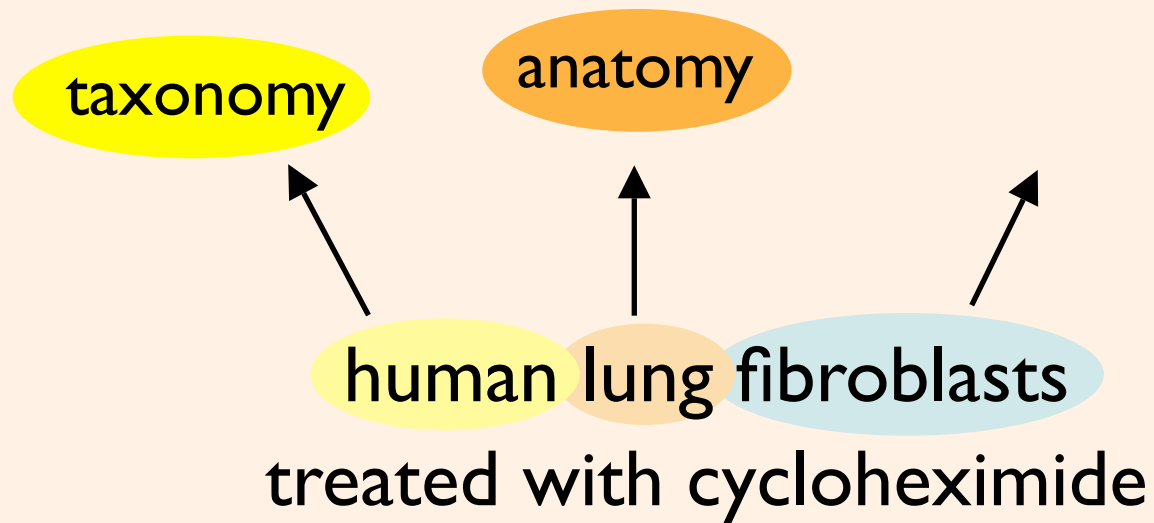


# Ontologies and Experiments





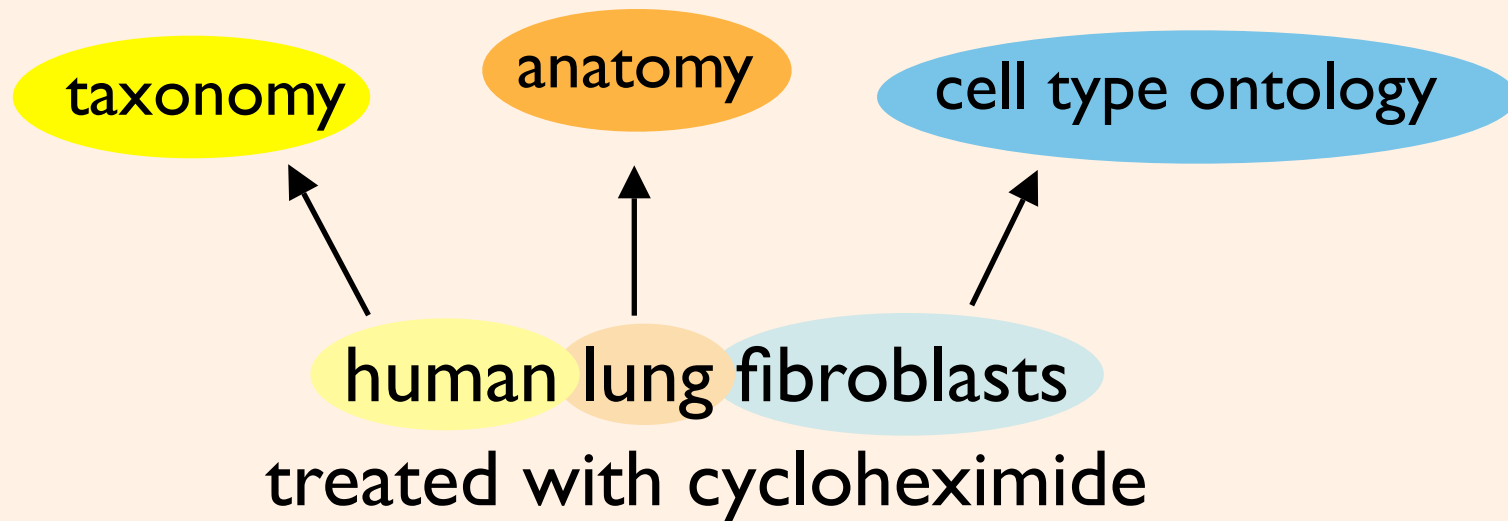
# Ontologies and Experiments





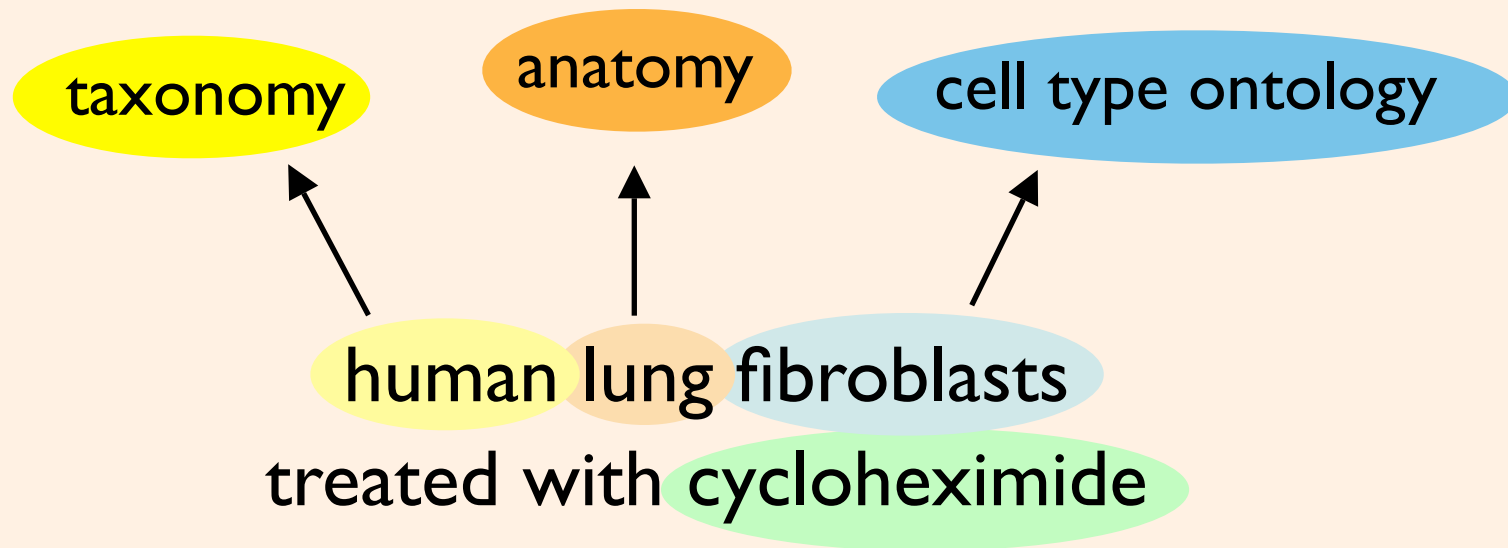


# Ontologies and Experiments



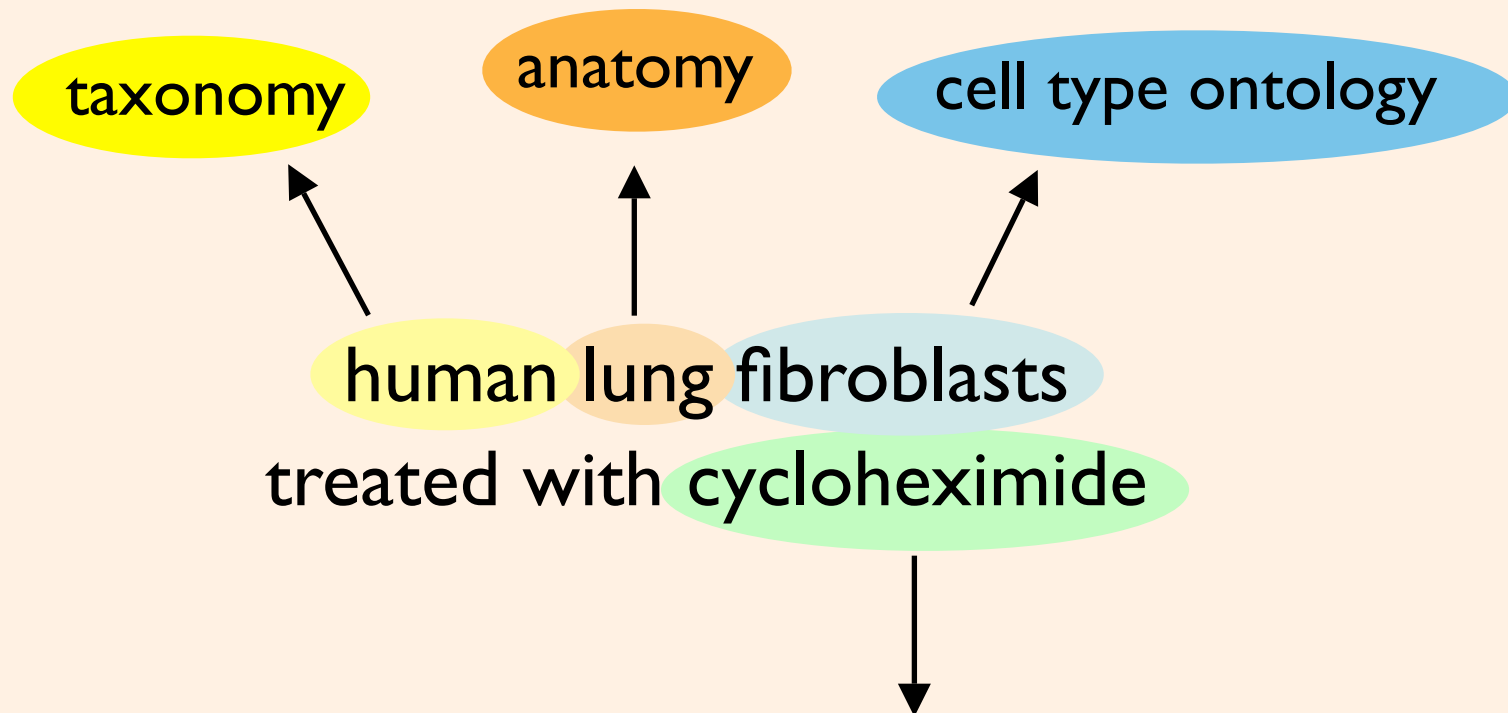


# Ontologies and Experiments



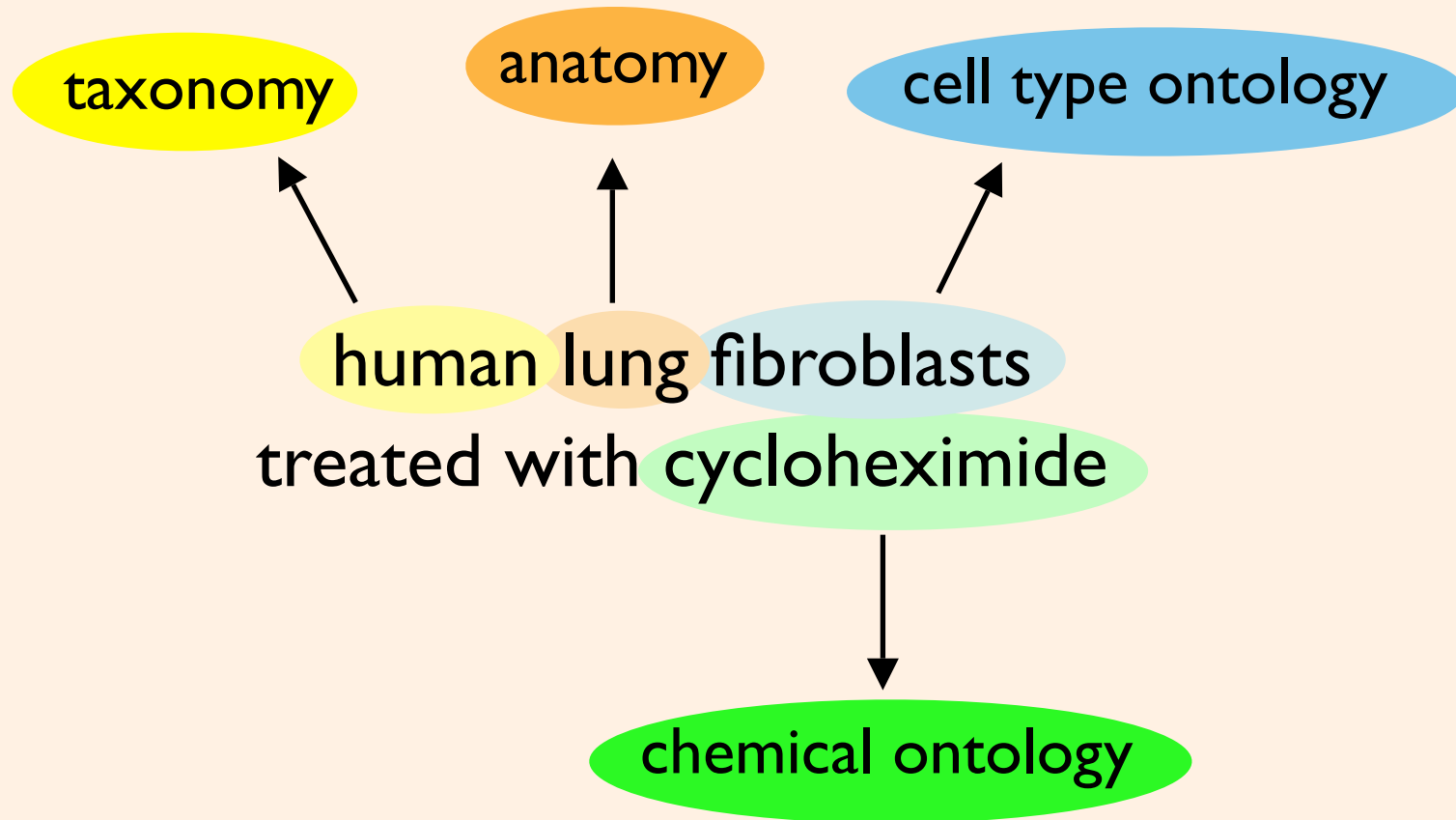


# Ontologies and Experiments





# Ontologies and Experiments





# OBO Foundry

- Open Biomedical Ontologies
  - Collection of shared genomics and proteomics vocabularies
  - Principles:
    - Open source
    - Common syntax (e.g. OWL or OBO)
    - Orthogonal; avoid duplication
    - Share ID space
    - Define terms
    - Involve the community



# OBO Foundry

OBO Foundry Ontologies

http://obofoundry.org/

OBO FOUNDRY

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Ontologies Resources Participate About

Welcome to the OBO Foundry Ontologies

Domain	Prefix	Files	Format	Foundry	OBO CVS
<a href="#">Animal natural history and life history</a>	ADW	<a href="#">protege_source</a>	<a href="#">Protege</a>	no	no
<a href="#">Biological imaging methods</a>	FBbi	<a href="#">image.obo</a>	<a href="#">OBO</a>	no	yes
<a href="#">Biological process</a>	GO	<a href="#">gene_ontology.obo</a>	<a href="#">OBO</a>	yes	yes
<a href="#">BRENDA tissue / enzyme source</a>	BTO	<a href="#">BrendaTissue.obo</a>	<a href="#">OBO</a>	no	yes
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<a href="#">C. elegans gross anatomy</a>	WBbt		<a href="#">OBO</a>	no	no
<a href="#">C. elegans phenotype</a>	WBPhenotype	<a href="#">phenotype_ontology_obo.cgi</a>	<a href="#">OBO</a>	no	no
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<a href="#">Dictyostelium discoideum anatomy</a>	DDANAT	<a href="#">dictyostelium_anatomy.obo</a>	<a href="#">OBO</a>	no	yes
<a href="#">Drosophila development</a>	FBdv	<a href="#">fly_development.obo</a>	<a href="#">OBO</a>	no	yes
<a href="#">Drosophila gross</a>	FBht	<a href="#">fly_anatomy.obo</a>	<a href="#">OBO</a>	no	yes

**Other Ontology Lists**

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- ★ [Ontology Lookup Service \(OLS\)](#) (OBO Foundry term lookup)

**Quick Links**

- ★ [Mappings between ontologies](#)
- ★ [How to join](#)
- ★ [Download alternate formats](#)

**News**

**2007/06/21: New OBO Foundry Site**

This site contains OBO Foundry ontologies and points to some other related efforts. It also provides discussion fora, technical infrastructure, and other services to facilitate ontology development. Please contribute, we welcome feedback and encourage participation.



# OBO Foundry

OBO Foundry Ontologies

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OBO FOUNDRY

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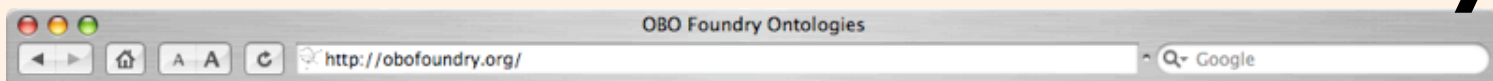
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obofoundry.org





# OBO Foundry



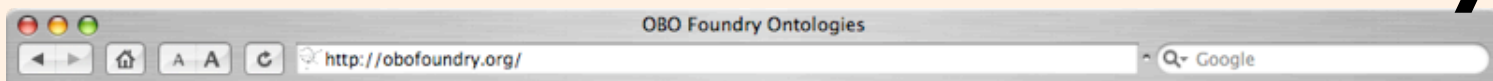
OBO FOUNDRY		
Ontologies	Resources	Participat
Welcome to the OBO Fou		
Domain	Prefix	File
<a href="#">Animal natural history and life history</a>	ADW	<a href="#">protege_source</a>
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<a href="#">Drosophila development</a>	FBdv	<a href="#">fly developmen</a>
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OBO Download Matrix		
Main Criteria <b>Ontologies</b> Browse Project CVS Subscribe Contact		
<b>OBO Download Matrix</b>		
<p>This page is for downloading OBO ontologies in a variety of formats, and for downloading reports from each of the ontologies. The data below is derived automatically from the primary sources, available from the main OBO website. The status of this page is EXPERIMENTAL. See below for caveats.</p> <p>This page will be retired when the current functionality is subsumed by the BioPortal resource developed by the NCBO</p> <p>Ontologies Logical Definitions Mappings Format Guide Metadata Reports FTP Archive Statistics</p>		
Ontologies		
Ontology	ID Prefix	Files
adult_mouse_anatomy:Mouse adult gross anatomy	MA	obo_xml[595 kb] -- obo[285 kb] -- go_ont[169 kb] -- owl[1311 kb] -- chadoxml[1614 kb] -- godb_prestore[1498 kb] -- rdf[830 kb] -- tbl[93 kb] -- prolog[676 kb] -- validation_report[2 kb] -- stats[2 kb] -- pellet_report[0 kb] -- obo.html[1737 kb] --
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biological_process:Biological process	GO	obo_xml[19969 kb] -- obo[6909 kb] -- obo_xml[12263 kb] -- obo[6909 kb] -- go_ont[2987 kb] -- owl[25382 kb] -- chadoxml[31966 kb] -- godb_prestore[26749 kb] -- rdf[11461 kb] -- tbl[4304 kb] -- prolog[13859 kb] -- validation_report[0 kb] -- stats[2 kb] -- pellet_report[0 kb] -- obo.html[26513 kb] --
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caro:Common Anatomy Reference Ontology	CARO	obo_xml[18 kb] -- obo[10 kb] -- go_ont[2 kb] -- owl[54 kb] -- chadoxml[47 kb] -- godb_prestore[37 kb] -- rdf[20 kb] -- tbl[6 kb] -- prolog[18 kb] -- validation_report[0 kb] -- stats[2 kb] -- pellet_report[14 kb] -- obo.html[44 kb] --
cell:Cell type	CL	obo_xml[351 kb] -- obo[200 kb] -- go_ont[66 kb] -- owl[783 kb] -- chadoxml[978 kb] -- godb_prestore[830 kb] -- rdf[409 kb] -- tbl[102 kb] --

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# OBO Foundry



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OBO Download Matrix		
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brei		obo_xml[0 kb] -- obo[2 kb] -- owl[2 kb] -- chadoxml[2 kb] -- godb_prestore[1 kb] -- rdf[0 kb] -- prolog[0 kb] -- validation_report[0 kb] -- stats[0 kb] -- pellet_report[0 kb] -- obo.html[0 kb] --
caro:Common Anatomy Reference Ontology	CARO	obo_xml[18 kb] -- obo[10 kb] -- go_ont[2 kb] -- owl[54 kb] -- chadoxml[47 kb] -- godb_prestore[37 kb] -- rdf[20 kb] -- tbl[6 kb] -- prolog[18 kb] -- validation_report[0 kb] -- stats[2 kb] -- pellet_report[14 kb] -- obo.html[44 kb] --
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obofoundry.org



# Cross-products in GO

- Explicit links between one GO term and another ontology term

# Many GO terms are *implicitly* composite

- [cysteine](#) biosynthesis
- [myoblast](#) fusion
- [ATP](#) synthesis coupled [proton](#) transport (ChEBI)
- [snoRNA](#) catabolism
- [wing disc](#) pattern formation
- [epidermal cell](#) differentiation
- regulation of [flower](#) development
- [interleukin-18](#) receptor complex
- [B-cell](#) differentiation
- [dorsal](#) ectoderm

# Opaque references to other **OBO** ontologies

- [cysteine](#) biosynthesis (ChEBI)
- [myoblast](#) fusion (Cell Type Ontology)
- [ATP](#) synthesis coupled [proton](#) transport (ChEBI)
- [snoRNA](#) catabolism (Sequence Ontology)
- [wing disc](#) pattern formation (*Drosophila* anatomy)
- [epidermal cell](#) differentiation (Cell Type Ontology)
- regulation of [flower](#) development (*Plant* anatomy)
- [interleukin-18](#) receptor complex (not yet in OBO)
- [B-cell](#) differentiation (Cell Type Ontology)
- [dorsal](#) ectoderm (Spatial Qualifiers)

# Methodology

- Make opaque references explicit
- Use OBO ontologies
  - ChEBI
  - Cell
  - PATO (qualities)
  - Anatomy/CARO

# GO: now

GO

amino acid  
metabolism

GABA  
metabolism

amino acid  
biosynthesis

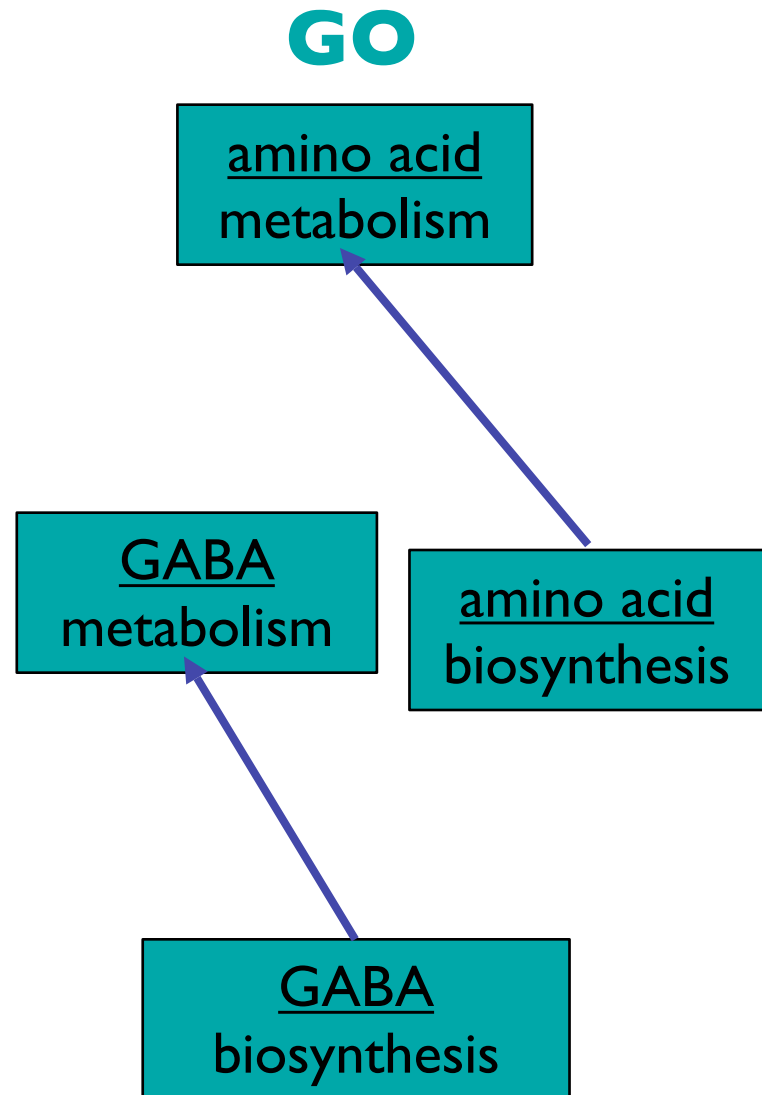
GABA  
biosynthesis

↑  
*is\_a*

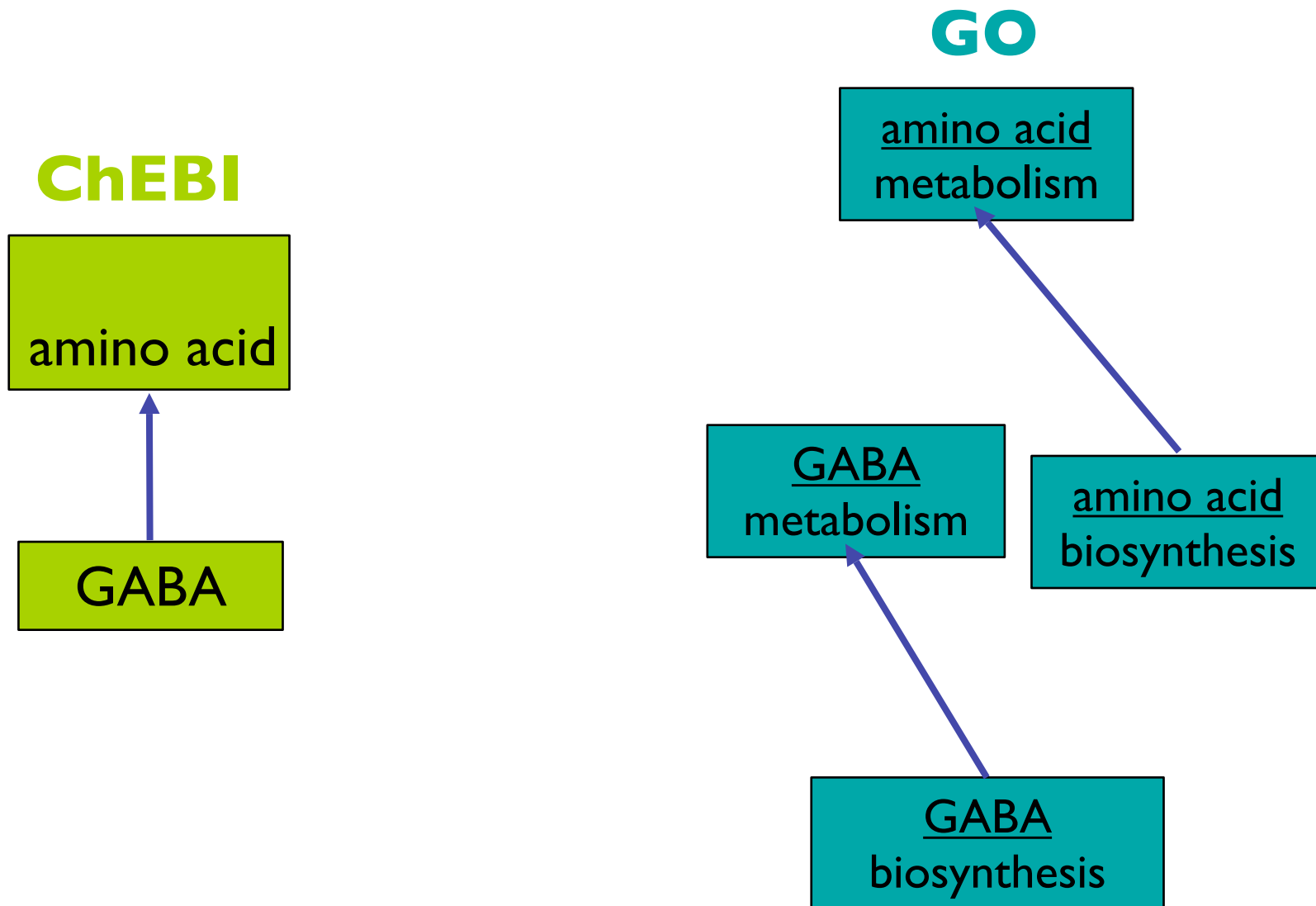


# GO+ChEBI: now

↑  
*is\_a*

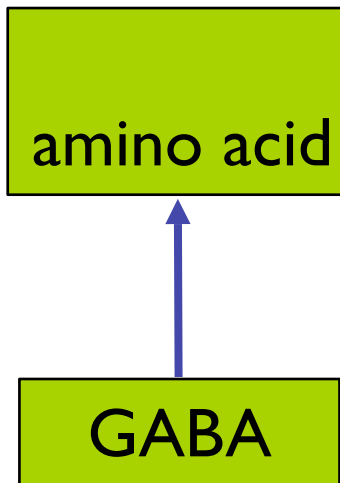


# GO+ChEBI: now

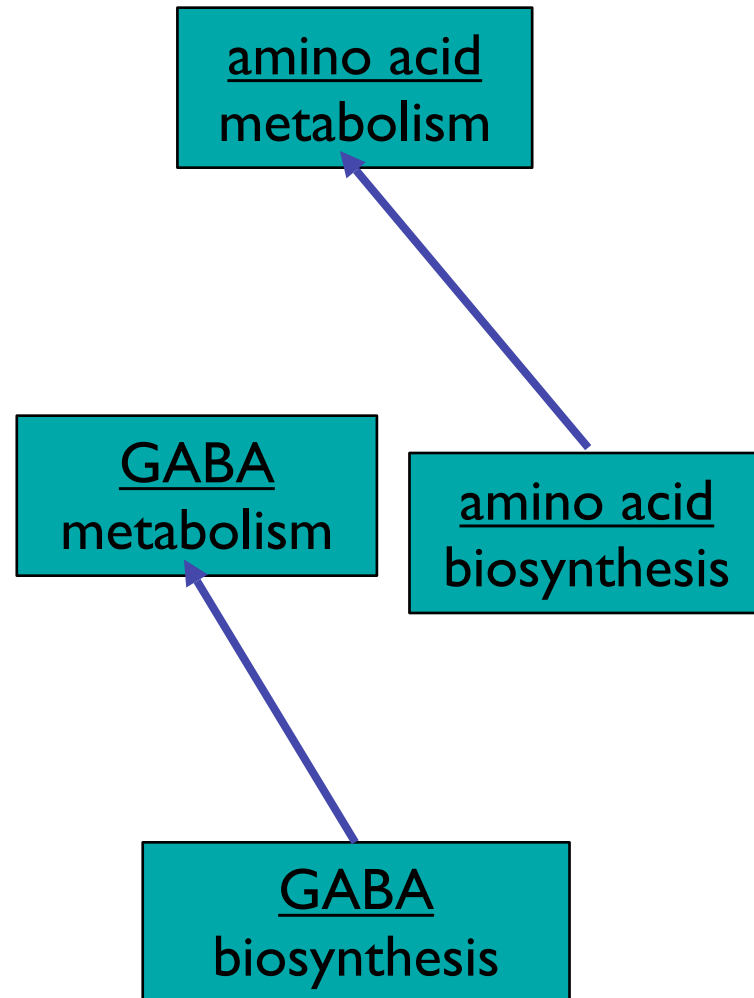


# Linking GO to ChEBI

**ChEBI**

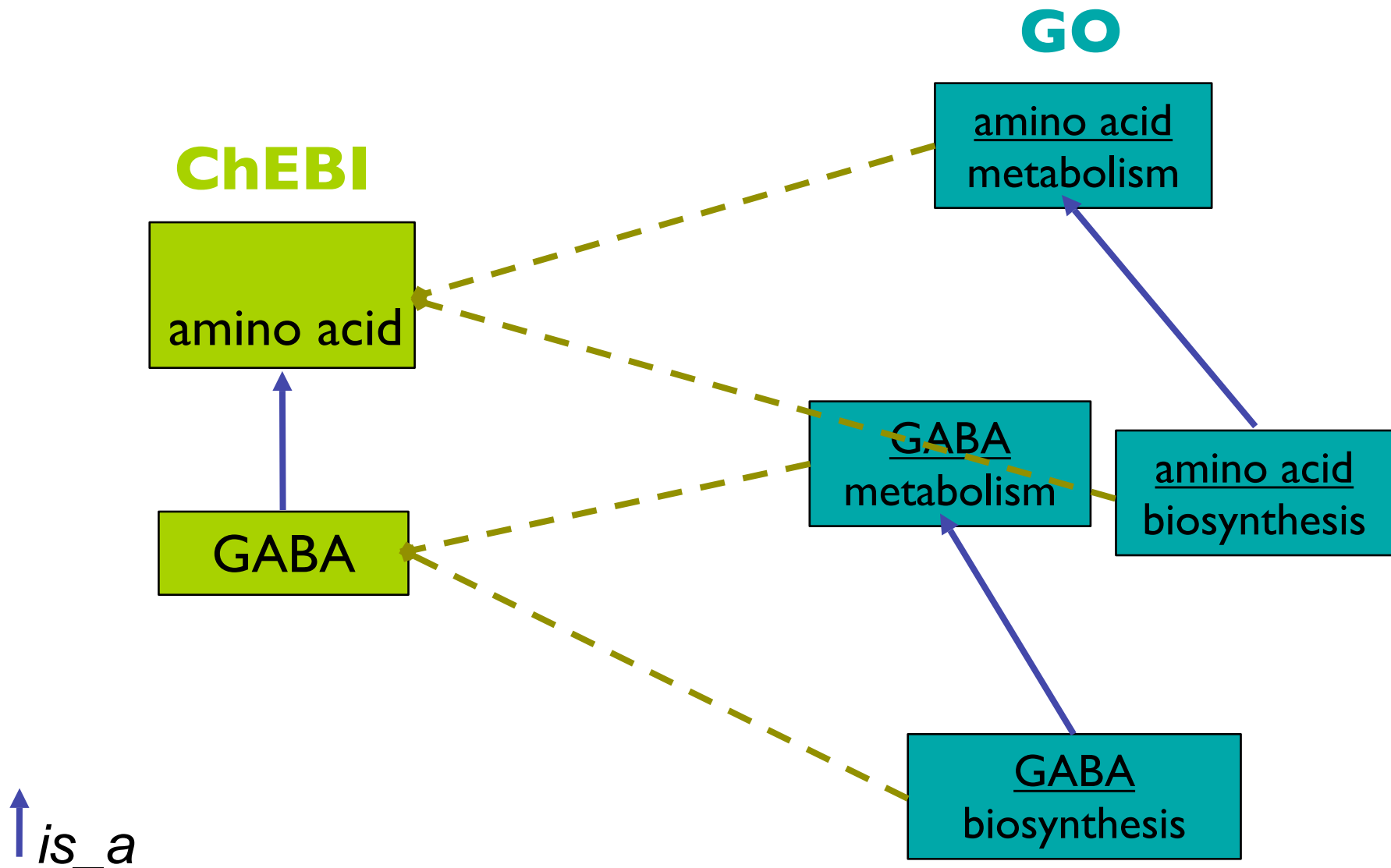


**GO**

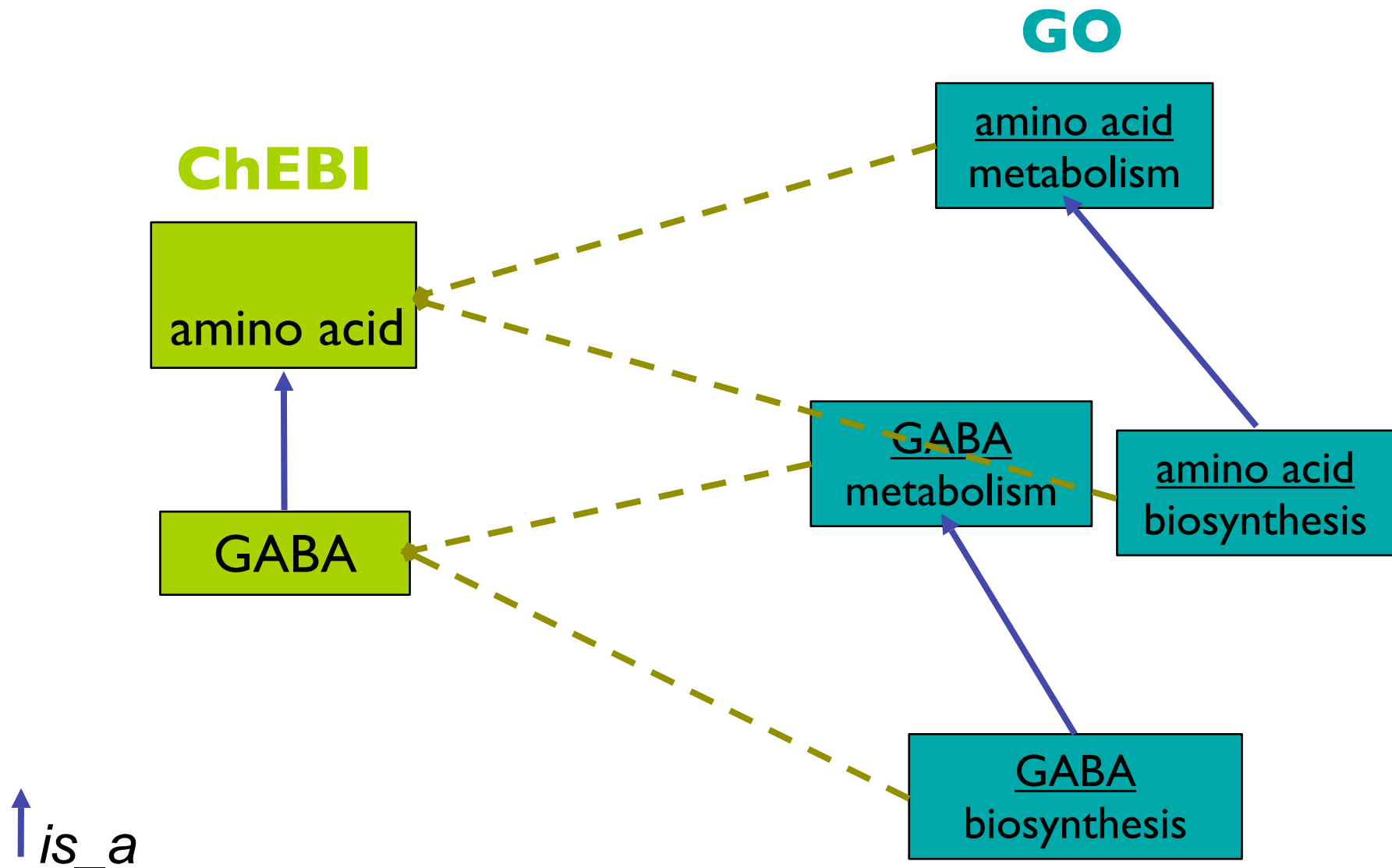


↑  
*is\_a*

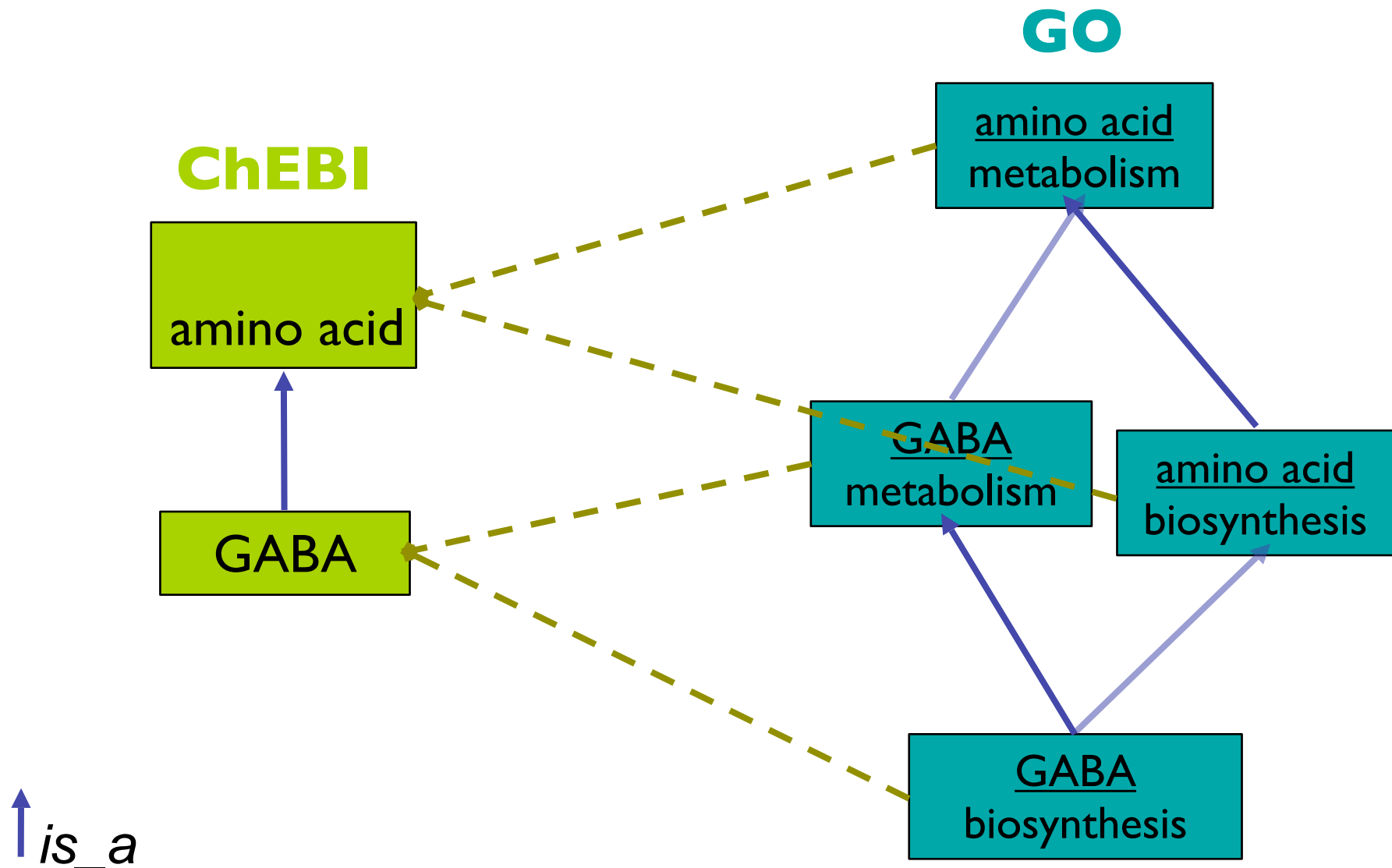
# Linking GO to ChEBI



# Can we find missing links?



# Can we find missing links?



# Simple DAGs are not enough

- We want to define GO terms using ChEBI terms
- DAGs give necessary conditions
- We want to give necessary and sufficient conditions
- Solution:
  - Genus-differentia definitions
  - Aka cross-products, aka intersections



# Example genus-differentia definition

- A **GABA metabolic process** is:
  - A **metabolic process**
    - That *has\_participant* **GABA**
- This is saying more than simply adding a DAG link between GABA metabolic process and GABA
  - It allows us to do powerful reasoning
    - Keeps ontologies in sync

[Term]

id: GO:0009447

name: putrescine catabolic process

intersection\_of: GO:0009056 ! catabolism

intersection\_of: results\_in\_division\_of CHEBI:17148 ! putrescine

[Term]

id: GO:0009448

name: gamma-aminobutyric acid metabolic process

intersection\_of: GO:0008152 ! metabolism

intersection\_of: has\_participant CHEBI:16865 ! gamma-aminobutyric acid

[Term]

id: GO:0009449

name: gamma-aminobutyric acid biosynthetic process

intersection\_of: GO:0009058 ! biosynthesis

intersection\_of: results\_in\_change\_to CHEBI:16865 ! gamma-aminobutyric acid

[Term]

id: GO:0009450

name: gamma-aminobutyric acid catabolic process

intersection\_of: GO:0009056 ! catabolism

intersection\_of: results\_in\_division\_of CHEBI:16865 ! gamma-aminobutyric acid



# GO and Phenotypes

- Phenotype annotation uses GO — and other OBO ontologies — in combination with qualities from PATO
- An *entity* (GO, anatomy, etc. term) has a *quality* (PATO term)
- Example: decreased rate of sucrose synthesis



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GO:0005986



# GO and Phenotypes

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- An *entity* (GO, anatomy, etc. term) has a *quality* (PATO term)
- Example: decreased rate of sucrose synthesis

PATO:0000911

GO:0005986



# Phenote

- Java application for annotating phenotypes using biological ontologies
- Uses any ontology in OBO format



# Phenote

The screenshot shows the Phenote 1.4 software interface. It features a window with a title bar and several input fields. The 'Pub' field contains the text 'example'. The 'Genotype' field is empty. The 'Entity' field has a dropdown menu open, showing options: 'ALL', 'FMA', 'GO' (highlighted), 'CL', 'SO', 'CHEBI', and 'ALL'. The 'Quality' field is empty. The 'Add'l Entity' field has a dropdown menu open, showing options: 'ALL', 'FMA', 'GO' (highlighted), 'CL', 'SO', 'CHEBI', and 'ALL'. The 'Time' field is empty. The 'Count' field is empty. The 'Unit' field has a dropdown menu open, showing options: 'ALL', 'FMA', 'GO' (highlighted), 'CL', 'SO', 'CHEBI', and 'ALL'. The 'Abnormal' field has a dropdown menu open, showing options: 'ALL', 'FMA', 'GO' (highlighted), 'CL', 'SO', 'CHEBI', and 'ALL'. The 'Description' field is empty. There are 'Comp' buttons next to the 'Entity' and 'Add'l Entity' dropdowns.

ting phenotypes

- Uses any ontology in OBO format





# Phenote

Phenote 1.4

Pub

Genotype

Genetic Context

Entity

Quality

Add'l Entity

Time

Count

Unit

Abnormal

Description

**Term Info**

**sucrose biosynthetic process** ☒

**ONTOLOGY** biological\_process

**ID** GO:0005986

**Exact** sucrose anabolism

**Synonyms:** sucrose biosynthesis  
sucrose formation  
sucrose synthesis

**X-refs** MetaCyc:14466

**Definition** The chemical reactions and pathways resulting in the formation of sucrose, the disaccharide fructofuranosyl-glucopyranoside.

**Superclass** [disaccharide biosynthetic process](#)  
[sucrose metabolic process](#)

Pub	Genotype	Genetic Context	Entity	Quality	Add'l Entity	Time
example			sucrose biosynthetic pr...			

Filter:



# Phenote

Phenote 1.4

Pub

Genotype

Genetic Context

Entity

Quality

Add'l Entity

Time

Count

Unit

Abnormal

Description

Term Info

**decreased rate**

ONTOLOGY quality

ID PATO:0000911

Exact slow rate

Synonyms:

Definition A rate which is relative low.

Superclass [rate](#)

Pub	Genotype	Genetic Context	Entity	Quality	Add'l Entity	Time
example			sucrose biosynthetic pr...	decreased rate		

Filter:



# Acknowledgements

- The GO Editorial Office
  - Jane Lomax
  - Amelia Ireland
  - Jennifer Deegan
- GO Consortium members
- Funding:

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# The GO Consortium



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## Current GO Consortium Members

**Berkeley Bioinformatics and Ontology Project (BBOP)** [↗](#): *Drosophila* informatics; development of GO database and software; Sequence Ontology development; National Center for Biomedical Ontology biomedical informatics research

**dictyBase** [↗](#): informatics resource for the slime mold *Dictyostelium discoideum*

**FlyBase** [↗](#): database for the fruitfly *Drosophila melanogaster*

**GeneDB** [↗](#) (part of the Pathogen Sequencing Unit [↗](#) at the Wellcome Trust Sanger Institute): includes databases for the fission yeast *Schizosaccharomyces pombe* [↗](#) and several [↗](#) protozoan parasites [↗](#), including *Plasmodium falciparum*, *Leishmania major* and *Trypanosoma brucei*.

**Gene Ontology Annotation @ EBI (GOA)** [↗](#): annotation of [↗](#) UniProt Knowledgebase [↗](#) (Swiss-Prot/TrEMBL/PIR-PSD) and [↗](#) InterPro [↗](#) databases

**Gramene** [↗](#): a comparative mapping resource for grains, including rice (*Oryza*)

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**Reactome** [↗](#): a knowledgebase of biological processes (formerly Genome Knowledgebase)

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**The Arabidopsis Information Resource (TAIR)** [↗](#): database for the brassica family plant *Arabidopsis thaliana*

**The J. Craig Venter Institute (JCVI)** [↗](#) [formerly The Institute for Genomic Research (TIGR)]: databases on several bacterial species

**WormBase** [↗](#): database for the nematode *Caenorhabditis elegans*

**Zebrafish Information Network (ZFIN)** [↗](#): reference datasets and information on *Danio rerio*



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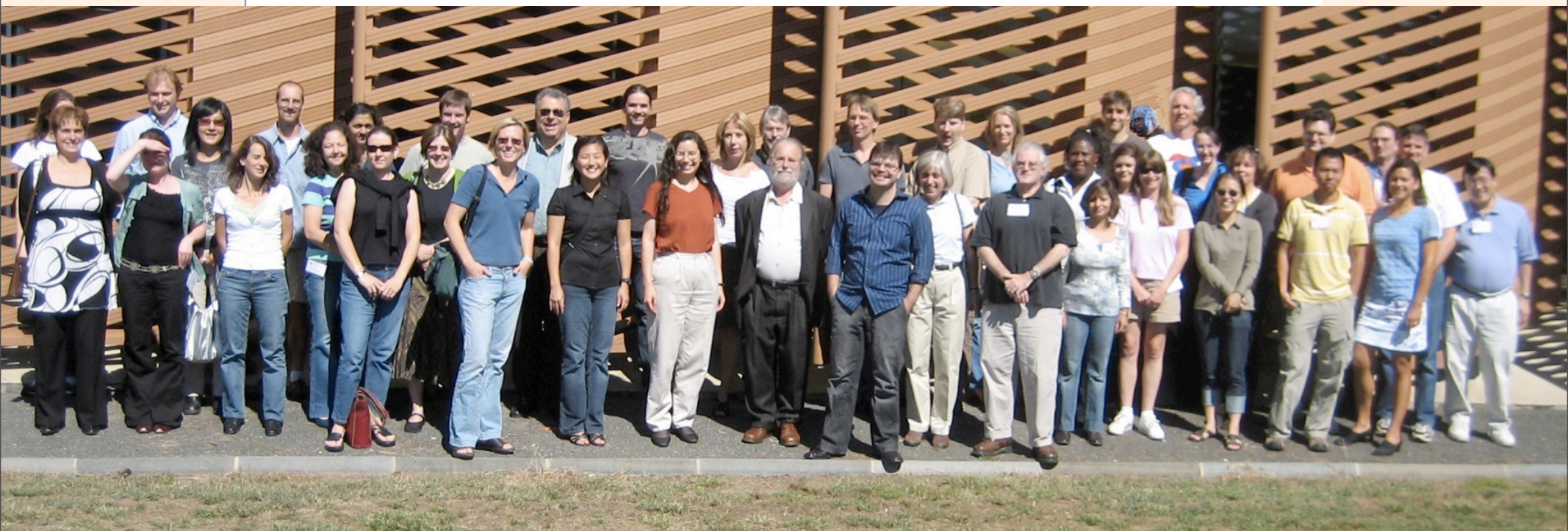


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
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