CACAO Training
part 1

TAMU 2013

BICH489-501/2

Tues Aug 27, 2013

- What are we doing this semester?
- Big picture
- What is CACAO?
- Housekeeping

Overview of the semester

- Training
  - Today: Training
  - Sept 3: Practice papers
- Annotation
  - Sep 8– Nov17: 5 rounds of finding papers, reading, doing annotation
    - Class time for meeting with your team and getting in-person help!
- Conclusion
  - Nov 19-26: Overview of what we did. Prizes?

Big picture

- This class is about understanding how scientists
  - Infer the function of genes
  - Share knowledge with the larger community
- We will learn this by hands-on experience through CACAO
- **Warnings**:
  - This will be confusing at first. Stick with it!
  - Budget your time. This is not a class where you can cram at the end.

What is CACAO?

- **C**ommunity **A**ssessment of **C**ommunity **A**nnotation with **O**ntologies (CACAO)
  - Annotation of gene function
  - Competition
    - Within this class
    - Between TAMU and other schools (BTHO everyone!)
    - Rules next week

Annotation

- Annotation: a note that is made while reading any form of text

- For genome biology,
  - Nucleotide level: Where the genes are in the genome
  - Protein level: What their functions are

From Wikipedia

Annotation

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- For CACAO,
  - ~~Nucleotide level: Where the genes are in the genome~~
  - Protein level: What their functions are

From Wikipedia

Functional Annotation

- Annotation: a note that is made while reading any form of text

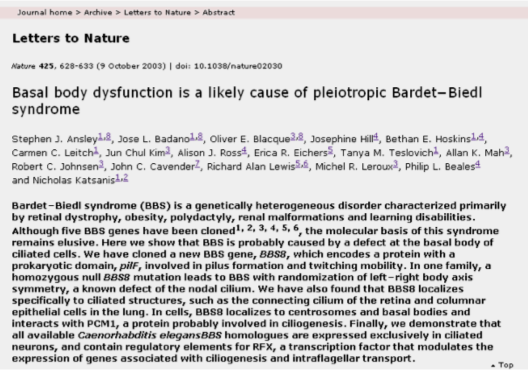
- Functional Annotation: a database entry in a **specific format** that is made based on **evidence** in a peer-reviewed **paper** about the function of a **protein**

Why do functional annotation?

- Allow us to:
  - Infer the function of genes
    - Related by common descent
    - Related by similar expression patterns
    - Related by phylogenetic profiles
    - …

- Allow us to:
  - Understand the capabilities of organisms' genomes
  - Understand patterns of gene expression
    - In different environments
    - In different tissues
    - In disease states
    - …

Where do functional annotations come from?



Journal home > Archive > Letters to Nature > Abstract

Letters to Nature

Nature **425**, 628-633 (9 October 2003) | doi: 10.1038/nature02030

Basal body dysfunction is a likely cause of pleiotropic Bardet–Biedl syndrome

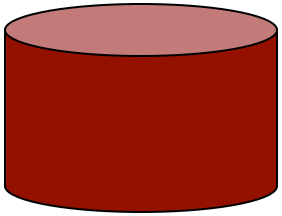
Stephen J. Ansley[1,8], Jose L. Badano[1,8], Oliver E. Blacque[3,8], Josephine Hill[4], Bethan E. Hoskins[1,4], Carmen C. Leitch[1], Jun Chul Kim[3], Alison J. Ross[4], Erica R. Eichers[5], Tanya M. Teslovich[1], Allan K. Mah[3], Robert C. Johnsen[3], John C. Cavender[7], Richard Alan Lewis[5,6], Michel R. Leroux[3], Philip L. Beales[4] and Nicholas Katsanis[1,2]

Bardet–Biedl syndrome (BBS) is a genetically heterogeneous disorder characterized primarily by retinal dystrophy, obesity, polydactyly, renal malformations and learning disabilities. Although five BBS genes have been cloned[1, 2, 3, 4, 5, 6], the molecular basis of this syndrome remains elusive. Here we show that BBS is probably caused by a defect at the basal body of ciliated cells. We have cloned a new BBS gene, *BBS8*, which encodes a protein with a prokaryotic domain, *pilF*, involved in pilus formation and twitching mobility. In one family, a homozygous null *BBS8* mutation leads to BBS with randomization of left–right body axis symmetry, a known defect of the nodal cilium. We have also found that BBS8 localizes specifically to ciliated structures, such as the connecting cilium of the retina and columnar epithelial cells in the lung. In cells, BBS8 localizes to centrosomes and basal bodies and interacts with PCM1, a protein probably involved in ciliogenesis. Finally, we demonstrate that all available *Caenorhabditis elegansBBS* homologues are expressed exclusively in ciliated neurons, and contain regulatory elements for RFX, a transcription factor that modulates the expression of genes associated with ciliogenesis and intraflagellar transport.

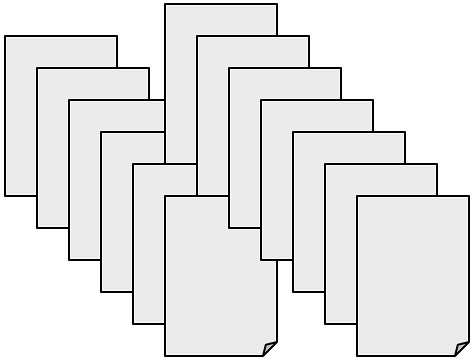
▴ Top

Literature

Biocurators
(rate limiting)



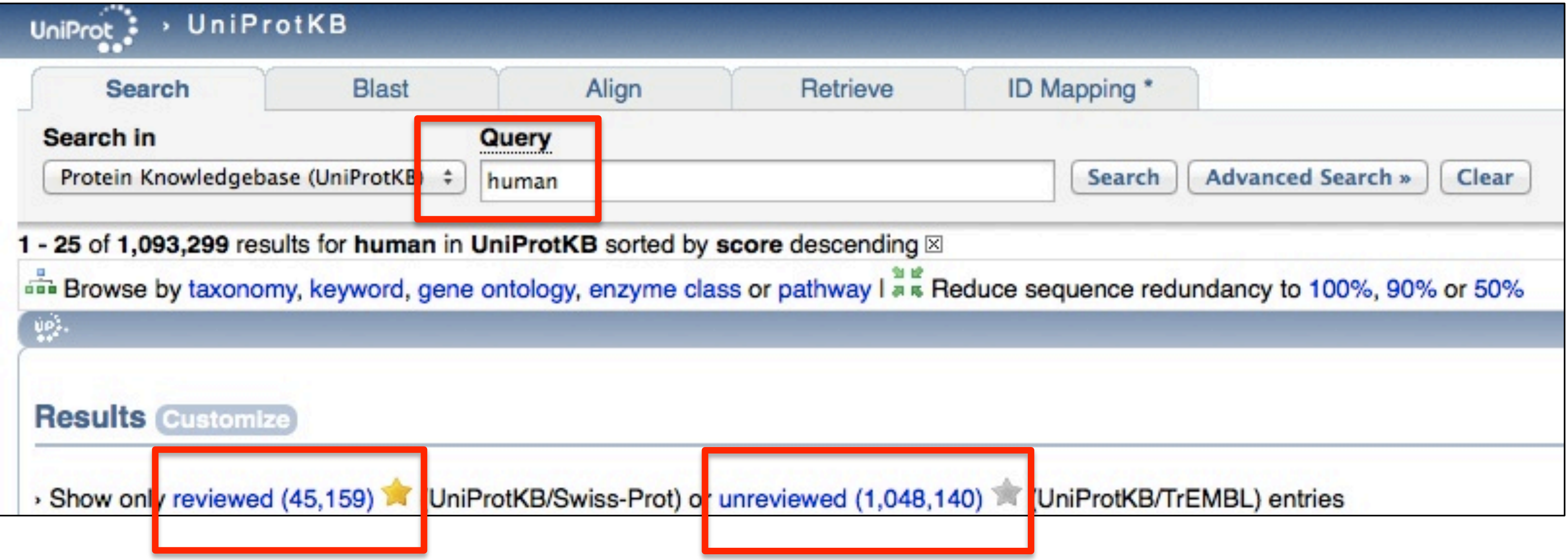
Database



Datasets

Databases need help!

- >21 million peer-reviewed articles in PubMed
- Many millions of proteins recorded in UniProt



Search in: Protein Knowledgebase (UniProtKB)

Query: human

1 - 25 of **1,093,299** results for **human** in **UniProtKB** sorted by **score** descending ☒

Browse by taxonomy, keyword, gene ontology, enzyme class or pathway | Reduce sequence redundancy to 100%, 90% or 50%

Results

› Show only reviewed (45,159) ★ (UniProtKB/Swiss-Prot) or unreviewed (1,048,140) ★ (UniProtKB/TrEMBL) entries

http://www.uniprot.org

Functional Annotation

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What to annotate

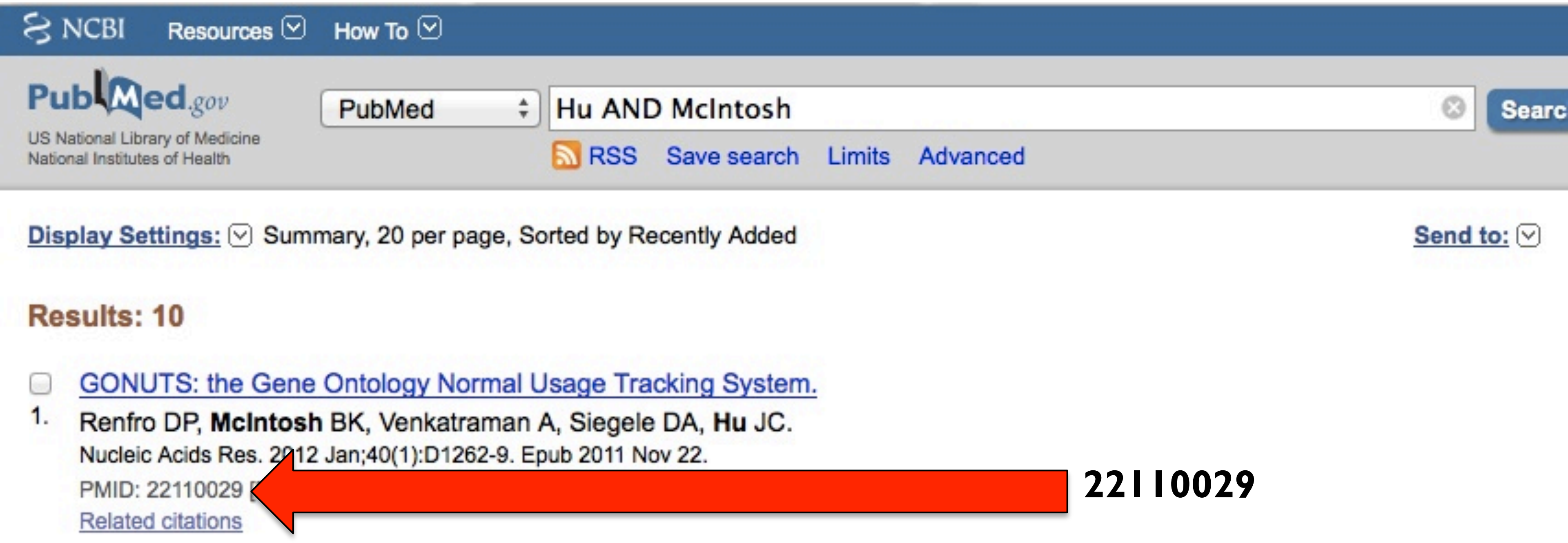
- You can start with a paper
  - Find the proteins discussed
  - Start with a GO term
- You can start with a protein
  - Find papers about the protein
- Either way, don’t get stuck on what you started with
  - Your first paper may not have **experiments** about function
  - Reading about your initial protein may lead you to better information about other proteins

Starting with a paper

- Need a scientific paper with experimental data
  - – No review articles, no books, no textbooks, no wikipedia articles, no class notes…
  - – BUT you should start with those!
  - – DON’T start with a random PubMed search

Starting with a paper

- Need a scientific paper with experimental data
  - You will need the PMID number



Hu AND McIntosh

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

Results: 10

☐ 1. GONUTS: the Gene Ontology Normal Usage Tracking System.
Renfro DP, **McIntosh** BK, Venkatraman A, Siegele DA, **Hu** JC.
Nucleic Acids Res. 2012 Jan;40(1):D1262-9. Epub 2011 Nov 22.
PMID: 22110029

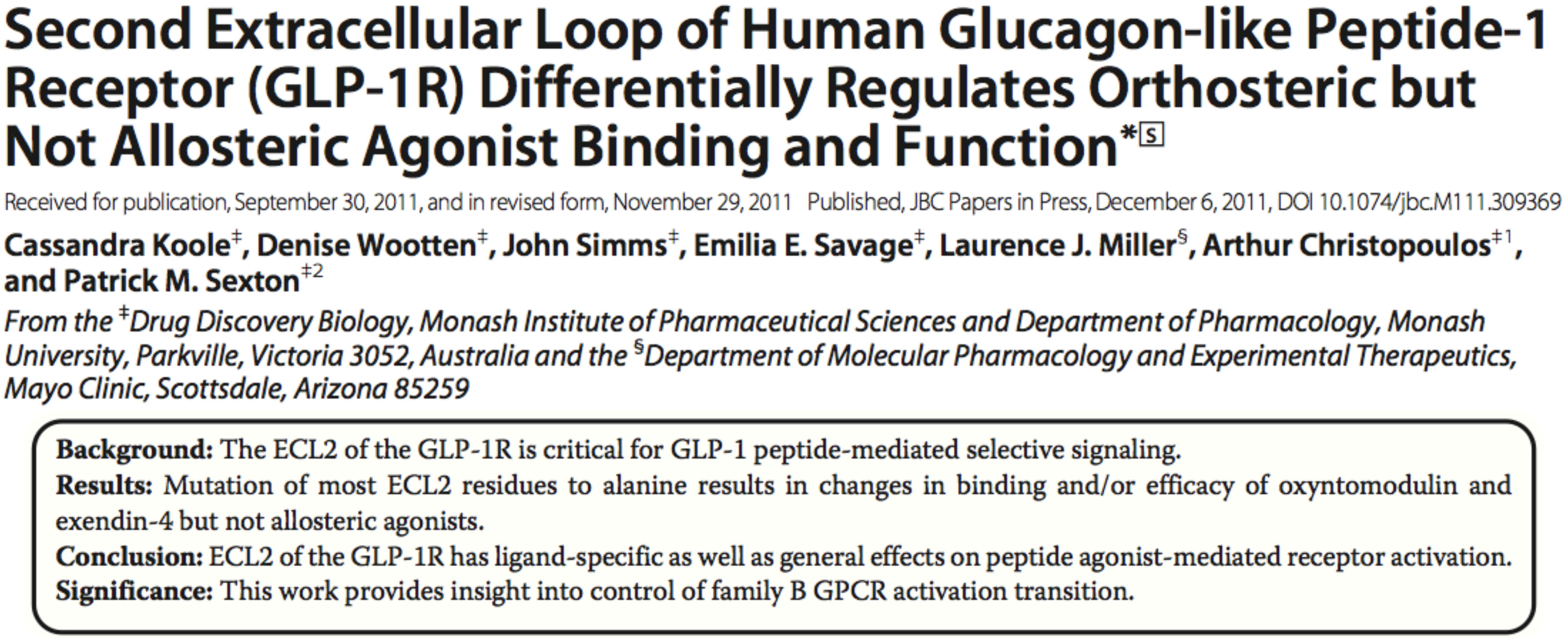
22110029

Getting the full text

- The abstract is not enough
  - But may be enough to reject a paper!!!
- Some papers are open access
  - Pubmed Central
  - Journal sites
    - TAMU pays for lots of subscriptions
    - Access from off campus via http://library.tamu.edu
      - E-journals
      - Citation search takes PMIDs

Beware!

- Good science ≠ good for annotation



Second Extracellular Loop of Human Glucagon-like Peptide-1 Receptor (GLP-1R) Differentially Regulates Orthosteric but Not Allosteric Agonist Binding and Function[*][S]

Received for publication, September 30, 2011, and in revised form, November 29, 2011 Published, JBC Papers in Press, December 6, 2011, DOI 10.1074/jbc.M111.309369

Cassandra Koole[‡], Denise Wootten[‡], John Simms[‡], Emilia E. Savage[‡], Laurence J. Miller[§], Arthur Christopoulos[‡1], and Patrick M. Sexton[‡2]

From the [‡]Drug Discovery Biology, Monash Institute of Pharmaceutical Sciences and Department of Pharmacology, Monash University, Parkville, Victoria 3052, Australia and the [§]Department of Molecular Pharmacology and Experimental Therapeutics, Mayo Clinic, Scottsdale, Arizona 85259

Background: The ECL2 of the GLP-1R is critical for GLP-1 peptide-mediated selective signaling.
Results: Mutation of most ECL2 residues to alanine results in changes in binding and/or efficacy of oxyntomodulin and exendin-4 but not allosteric agonists.
Conclusion: ECL2 of the GLP-1R has ligand-specific as well as general effects on peptide agonist-mediated receptor activation.
Significance: This work provides insight into control of family B GPCR activation transition.

Beware!

- Good science ≠ good for annotation

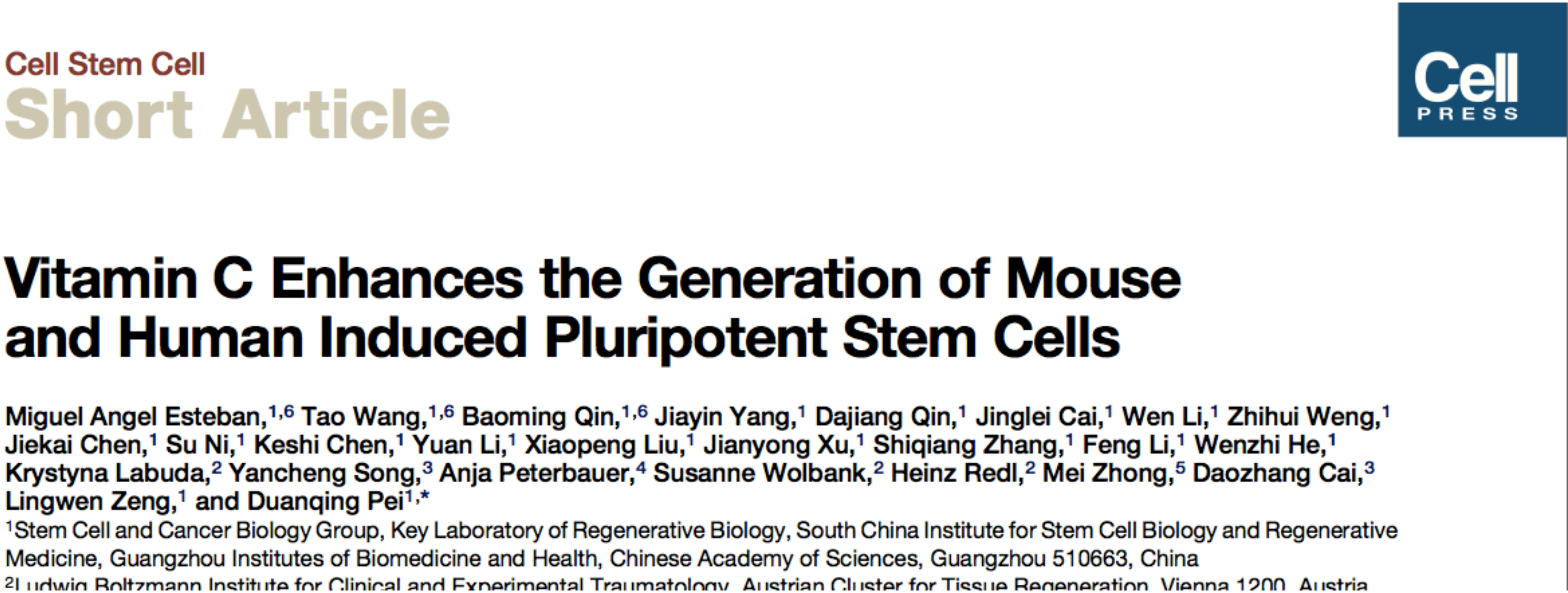
Robust design and optimization of retroaldol enzymes

Eric A. Althoff,[1,2] Ling Wang,[1] Lin Jiang,[1,3] Lars Giger,[4] Jonathan K. Lassila,[5] Zhizhi Wang,[1] Matthew Smith,[1] Sanjay Hari,[1] Peter Kast,[4] Daniel Herschlag,[5] Donald Hilvert,[4] and David Baker[1]*

[1]Department of Biochemistry, University of Washington and HHMI, Seattle, Washington 98195
[2]Arzeda Corp., Seattle, Washington 98102
[3]Department of Biological Chemistry, UCLA, Los Angeles, California 90095
[4]Laboratory of Organic Chemistry, ETH Zurich, 8093 Zurich, Switzerland
[5]Department of Biochemistry, Stanford University, Stanford, California 94305

Beware!

- Good science ≠ good for annotation



Cell Stem Cell

Short Article

Vitamin C Enhances the Generation of Mouse and Human Induced Pluripotent Stem Cells

Miguel Angel Esteban,[1,6] Tao Wang,[1,6] Baoming Qin,[1,6] Jiayin Yang,[1] Dajiang Qin,[1] Jinglei Cai,[1] Wen Li,[1] Zhihui Weng,[1] Jiekai Chen,[1] Su Ni,[1] Keshi Chen,[1] Yuan Li,[1] Xiaopeng Liu,[1] Jianyong Xu,[1] Shiqiang Zhang,[1] Feng Li,[1] Wenzhi He,[1] Krystyna Labuda,[2] Yancheng Song,[3] Anja Peterbauer,[4] Susanne Wolbank,[2] Heinz Redl,[2] Mei Zhong,[5] Daozhang Cai,[3] Lingwen Zeng,[1] and Duanqing Pei[1,*]

[1] Stem Cell and Cancer Biology Group, Key Laboratory of Regenerative Biology, South China Institute for Stem Cell Biology and Regenerative Medicine, Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou 510663, China

[2] Ludwig Boltzmann Institute for Clinical and Experimental Traumatology, Austrian Cluster for Tissue Regeneration, Vienna 1200, Austria

Beware!

- Good science ≠ good for annotation

10624 • The Journal of Neuroscience, August 11, 2010 • 30(32):10624–10638

Neurobiology of Disease

Excess Phosphoinositide 3-Kinase Subunit Synthesis and Activity as a Novel Therapeutic Target in Fragile X Syndrome

Christina Gross,[1] Mika Nakamoto,[2*] Xiaodi Yao,[1*] Chi-Bun Chan,[3] So Y. Yim,[1] Keqiang Ye,[3] Stephen T. Warren,[2,4,5] and Gary J. Bassell[1,6]
Departments of [1]Cell Biology, [2]Human Genetics, [3]Pathology and Laboratory Medicine, [4]Biochemistry, [5]Pediatrics, and [6]Neurology, Emory University School of Medicine, Atlanta, Georgia 30322

Suggested papers

- We will post some suggested papers to use as starting points
  - Not required
  - Use if you are struggling or try these first before tackling more complicated/interesting things

Finding proteins

- Search UniProt for something interesting
- Look in UniProt for the protein(s) in the paper you are reading.

No matter what, you will need to find the protein's accession on UniProt (http://uniprot.org)

⬇

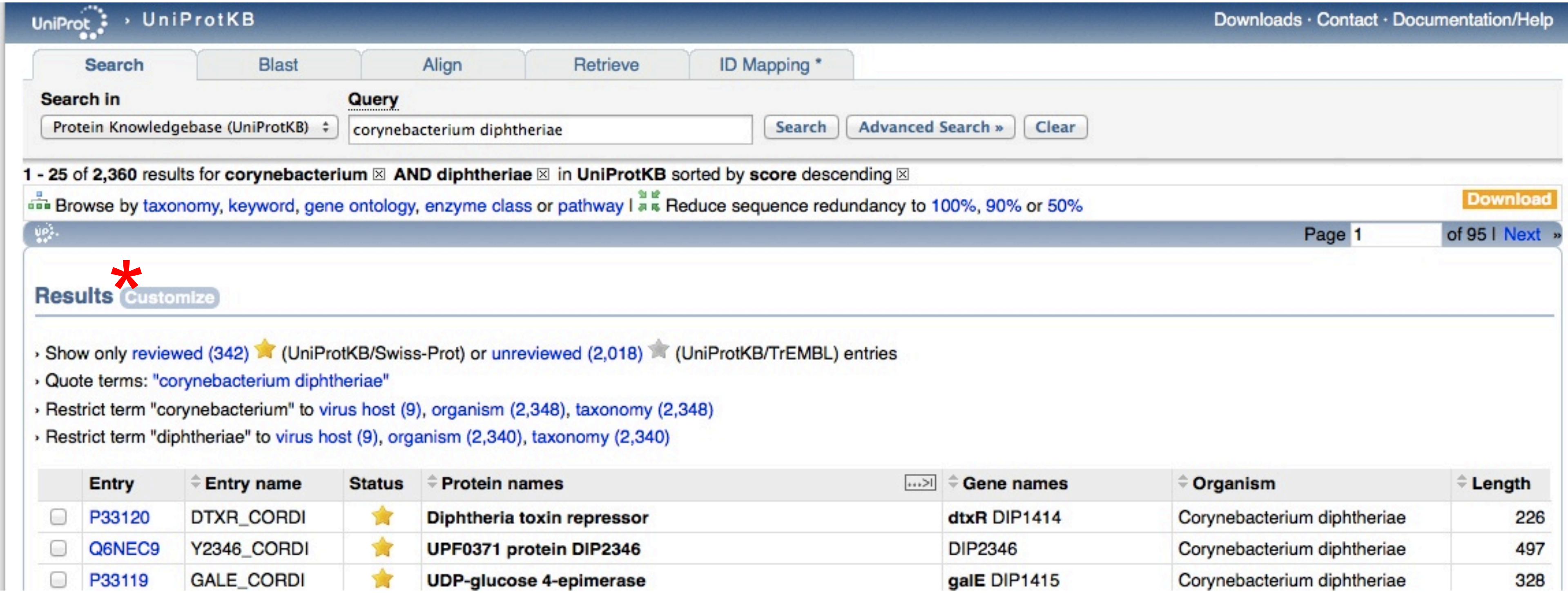
Use that accession to make a page for that protein on GONUTS (http://gowiki.tamu.edu)

⬇

Add your GO annotations to the protein's page on GONUTS

UniProt (http://www.uniprot.org)

- If you have a paper, look for an accession
- Otherwise, search by name/keyword



corynebacterium diphtheriae

1 - 25 of 2,360 results for **corynebacterium** ☒ **AND diphtheriae** ☒ in **UniProtKB** sorted by **score** descending ☒

Browse by taxonomy, keyword, gene ontology, enzyme class or pathway | Reduce sequence redundancy to 100%, 90% or 50%

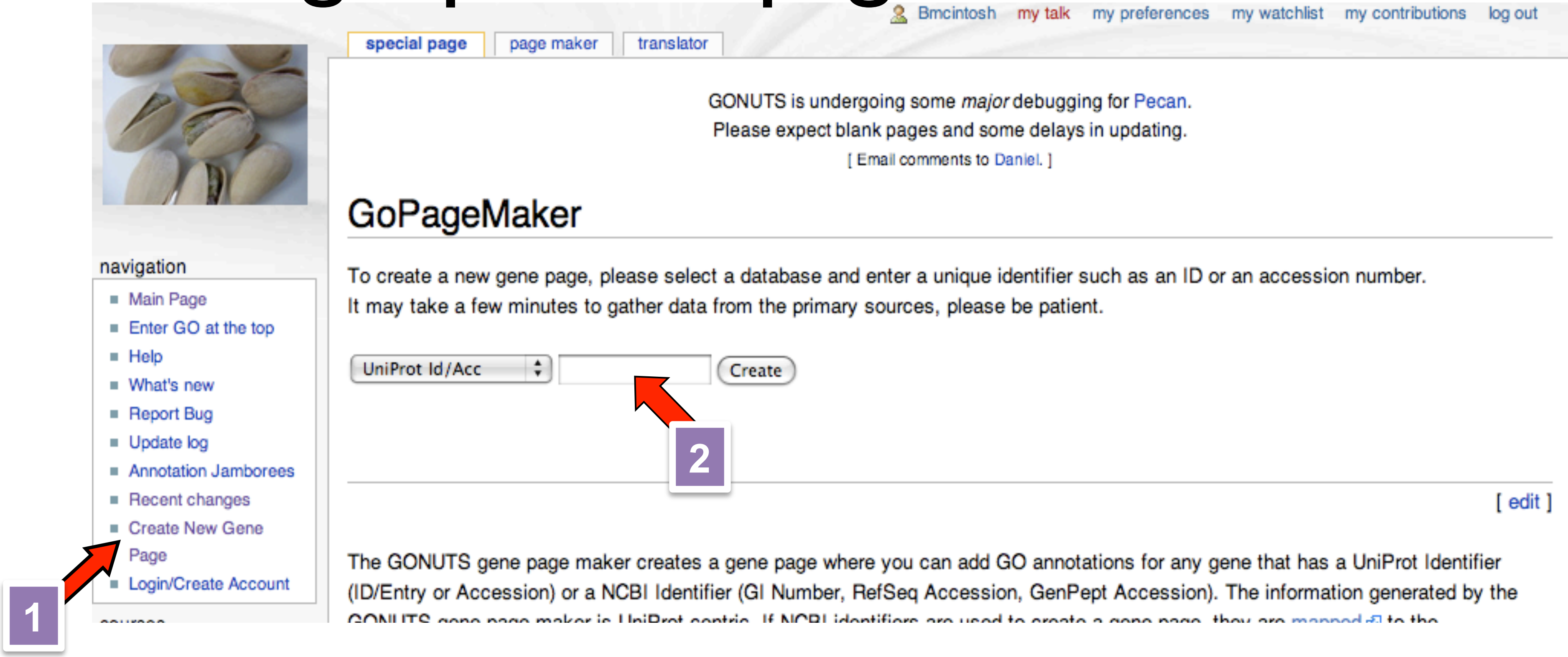
- Show only reviewed (342) ★ (UniProtKB/Swiss-Prot) or unreviewed (2,018) ★ (UniProtKB/TrEMBL) entries
- Quote terms: "corynebacterium diphtheriae"
- Restrict term "corynebacterium" to virus host (9), organism (2,348), taxonomy (2,348)
- Restrict term "diphtheriae" to virus host (9), organism (2,340), taxonomy (2,340)

	Entry	Entry name	Status	Protein names	Gene names	Organism	Length
☐	P33120	DTXR_CORDI	★	**Diphtheria toxin repressor**	**dtxR** DIP1414	Corynebacterium diphtheriae	226
☐	Q6NEC9	Y2346_CORDI	★	**UPF0371 protein DIP2346**	DIP2346	Corynebacterium diphtheriae	497
☐	P33119	GALE_CORDI	★	**UDP-glucose 4-epimerase**	**galE** DIP1415	Corynebacterium diphtheriae	328

Make sure you have the right protein

- Right species/strain
- Not a fragment
- Sometimes UniProt has multiple entries for the same protein
    - Gold star = SwissProt = reviewed
    - Blank star = TrEMBL = computational entry
- Sometimes the protein you want is not in UniProt
    - May want to find another paper/protein
- Ask for help
    - OK to email the UniProt help desk
    - check your reasoning with us!

Making a protein page in GONUTS



GONUTS is undergoing some *major* debugging for Pecan.
Please expect blank pages and some delays in updating.
[Email comments to Daniel.]

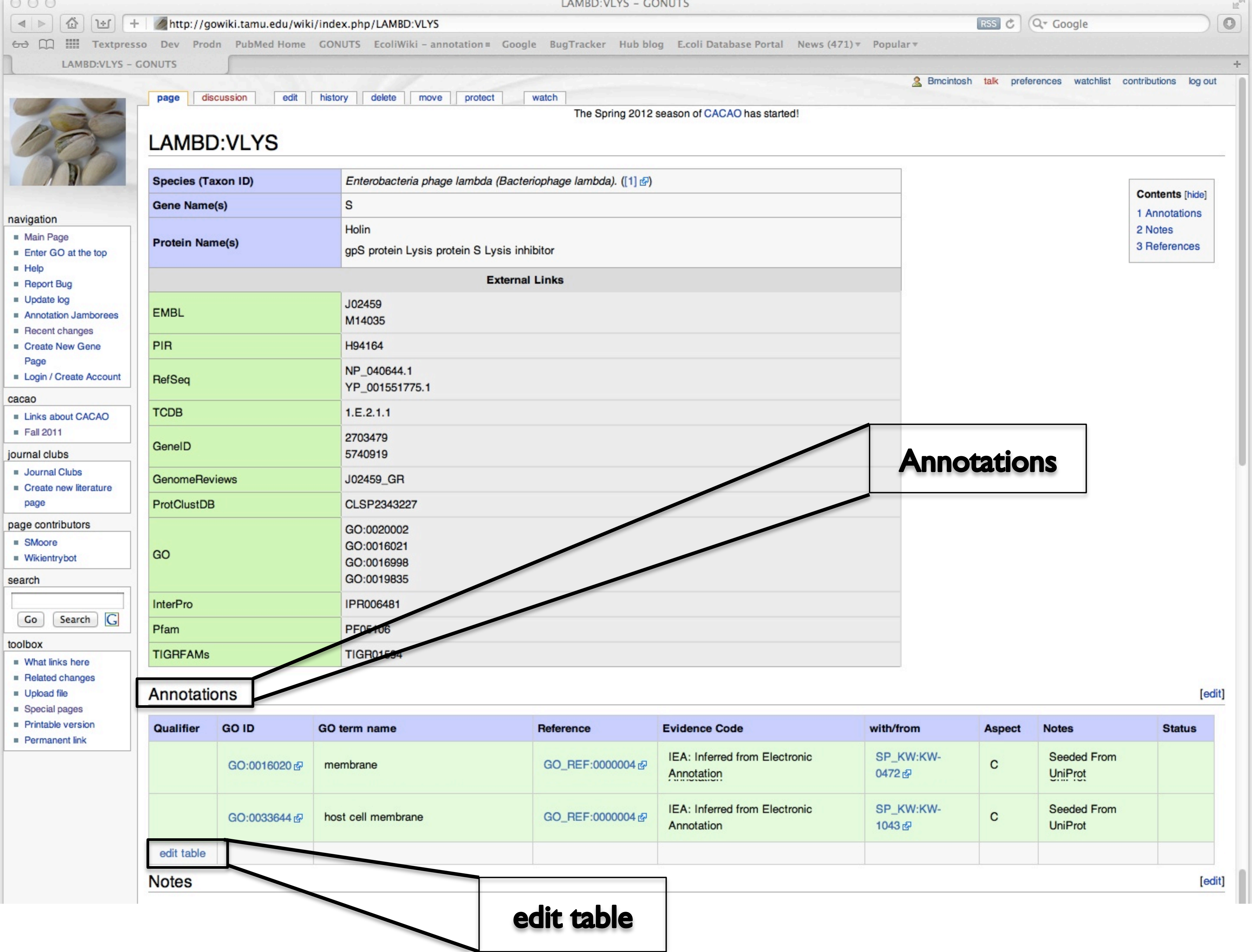
GoPageMaker

To create a new gene page, please select a database and enter a unique identifier such as an ID or an accession number.
It may take a few minutes to gather data from the primary sources, please be patient.

The GONUTS gene page maker creates a gene page where you can add GO annotations for any gene that has a UniProt Identifier (ID/Entry or Accession) or a NCBI Identifier (GI Number, RefSeq Accession, GenPept Accession). The information generated by the GONUTS gene page maker is UniProt centric. If NCBI identifiers are used to create a gene page, they are mapped to the

- GoPageMaker will:
  - Check if the page exists in GONUTS & take you there if it does.
  - Make a page if it does not exist in GONUTS already & pull all of the annotations from UniProt into a table that you can edit.

- Make as many protein pages as you would like!



The Spring 2012 season of CACAO has started!

LAMBD:VLYS

Species (Taxon ID)	*Enterobacteria phage lambda (Bacteriophage lambda).* ([1])
Gene Name(s)	S
Protein Name(s)	Holin gpS protein Lysis protein S Lysis inhibitor
External Links	
EMBL	J02459 M14035
PIR	H94164
RefSeq	NP_040644.1 YP_001551775.1
TCDB	1.E.2.1.1
GeneID	2703479 5740919
GenomeReviews	J02459_GR
ProtClustDB	CLSP2343227
GO	GO:0020002 GO:0016021 GO:0016998 GO:0019835
InterPro	IPR006481
Pfam	PF05106
TIGRFAMs	TIGR01594

Annotations

[edit]

Qualifier	GO ID	GO term name	Reference	Evidence Code	with/from	Aspect	Notes	Status
	GO:0016020	membrane	GO_REF:0000004	IEA: Inferred from Electronic Annotation	SP_KW:KW-0472	C	Seeded From UniProt	
	GO:0033644	host cell membrane	GO_REF:0000004	IEA: Inferred from Electronic Annotation	SP_KW:KW-1043	C	Seeded From UniProt	
edit table								

Notes

[edit]

Annotations

edit table

Functional Annotation

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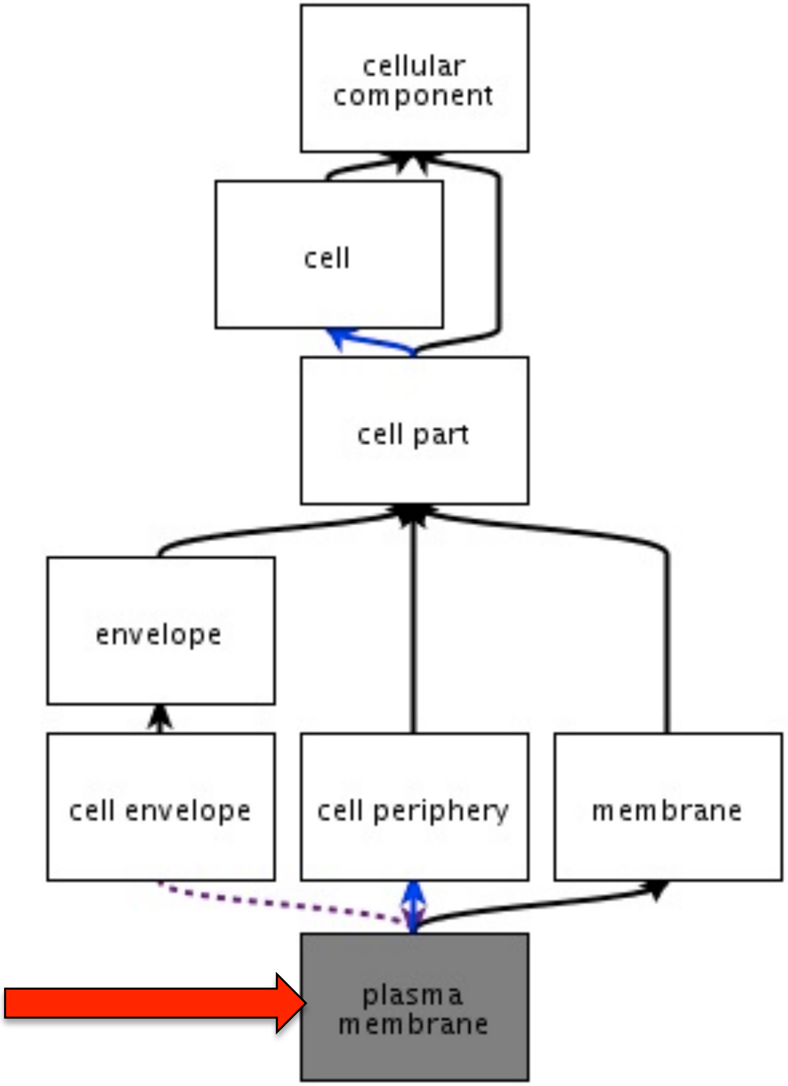
GO (Gene Ontology) Annotations

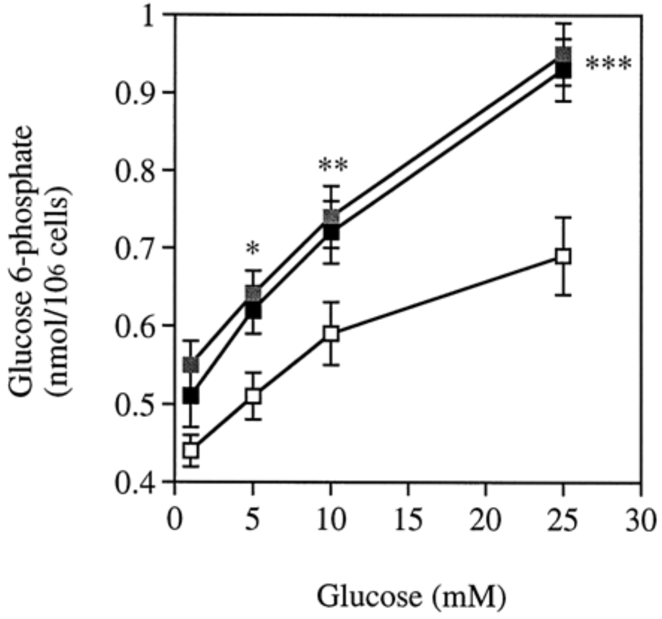
- 3 aspects (ontologies) :
  - Molecular Function
  - Biological Process
  - Cellular Component
- Controlled vocabulary
  - ID number for computers
  - Name and definition for humans
- Relationships



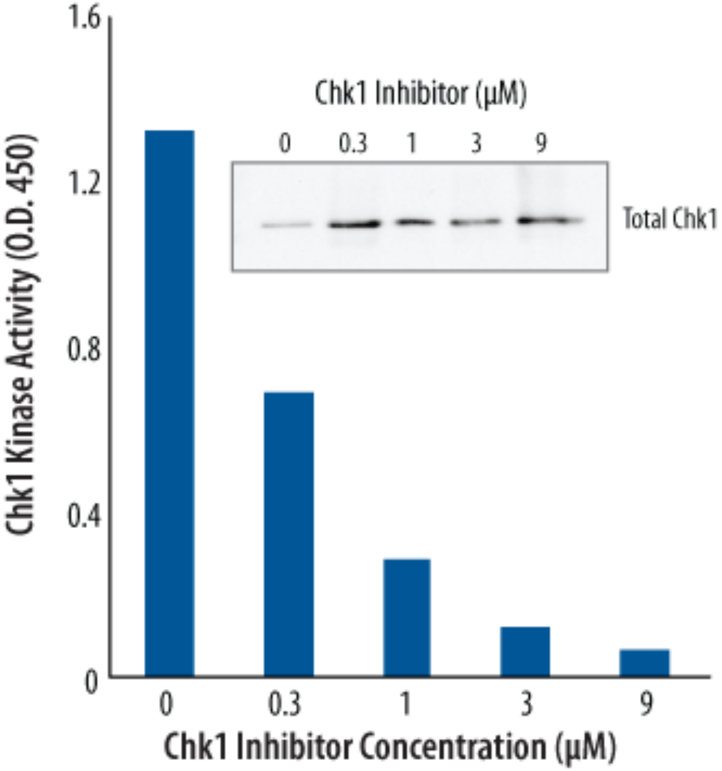
QuickGO - http://www.ebi.ac.uk/QuickGO

Molecular Function

- activities or what a protein can do by itself



GO:0004347 hexokinase activity

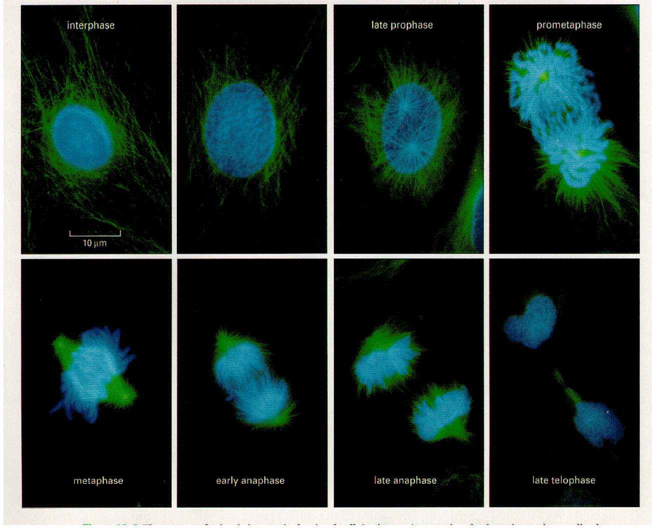


GO:0016301 Kinase activity

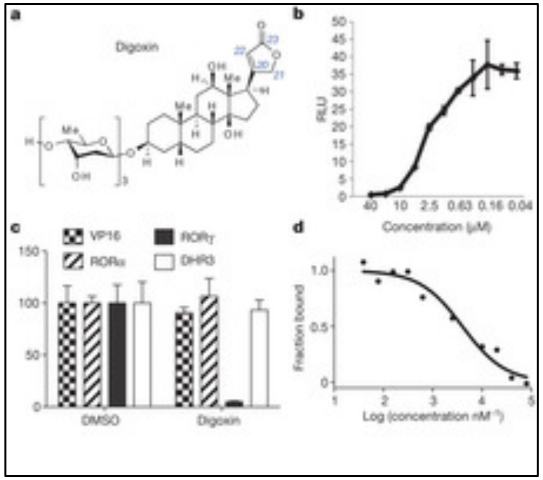
From PMID:9341134, rndsystems.com

Biological Process

- a commonly recognized series of events
  - Including, but not just biochemical pathways



GO:0051301 cell division



GO:0006351 transcription, DNA dependent

Fig. 3. **Multiple sand flea lesions at the fingertips**

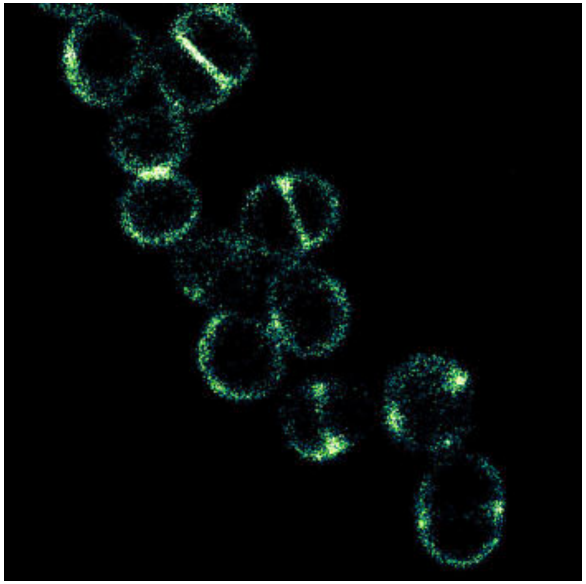
GO:0009405 pathogenesis

From ridge.icu.ac.jp, edtech.clas.pdx.edu, scielosp.org

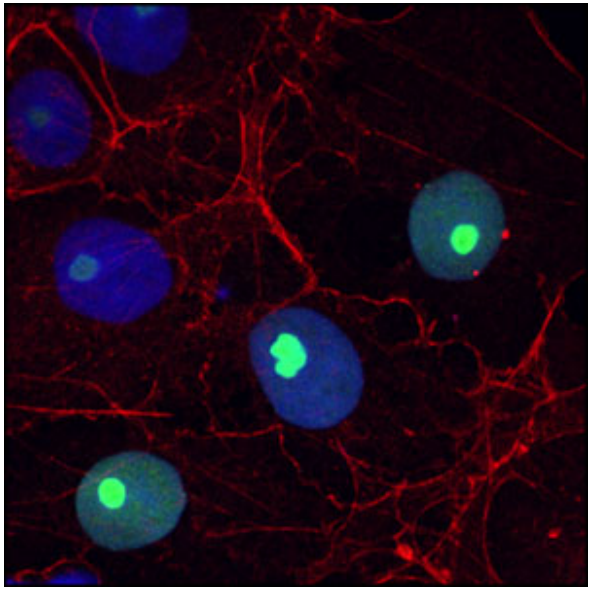
Cellular Component

- where a gene product acts
  - Subcellular location
  - Multicomponent complex

GO:0005739
mitochondrion



GO:0009274
peptidoglycan-based cell wall

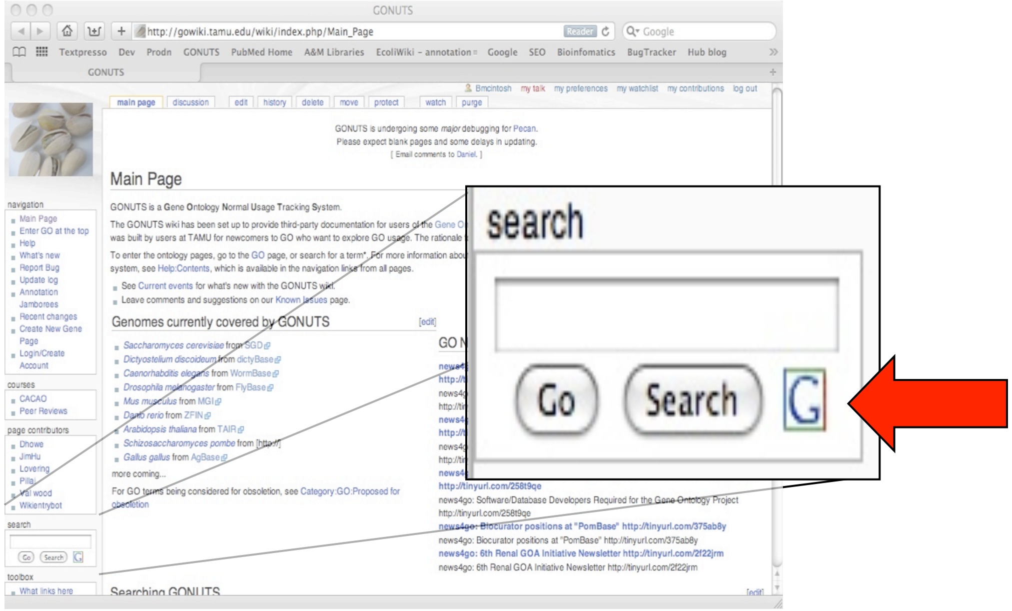


GO:0005840
ribosome

From visualphotos.com, epmm.group.shef.ac.uk, http://www.cellsignal.com/products/2415.html

Finding GO terms

- GONUTS: http://gowiki.tamu.edu
- QuickGO: http://www.ebi.ac.uk/QuickGO
- AmiGO: http://amigo.geneontology.org



GONUTS is undergoing some *major* debugging for Pecan.
Please expect blank pages and some delays in updating.
[Email comments to Daniel.]

Main Page

GONUTS is a **G**ene **O**ntology **N**ormal **U**sage **T**racking **S**ystem.

The GONUTS wiki has been set up to provide third-party documentation for users of the Gene O
was built by users at TAMU for newcomers to GO who want to explore GO usage. The rationale

To enter the ontology pages, go to the GO page, or search for a term*. For more information abou
system, see Help:Contents, which is available in the navigation links from all pages.

- See Current events for what's new with the GONUTS wiki.
- Leave comments and suggestions on our Known Issues page.

Genomes currently covered by GONUTS [edit]

- *Saccharomyces cerevisiae* from SGD
- *Dictyostelium discoideum* from dictyBase
- *Caenorhabditis elegans* from WormBase
- *Drosophila melanogaster* from FlyBase
- *Mus musculus* from MGI
- *Danio rerio* from ZFIN
- *Arabidopsis thaliana* from TAIR
- *Schizosaccharomyces pombe* from [http://]
- *Gallus gallus* from AgBase

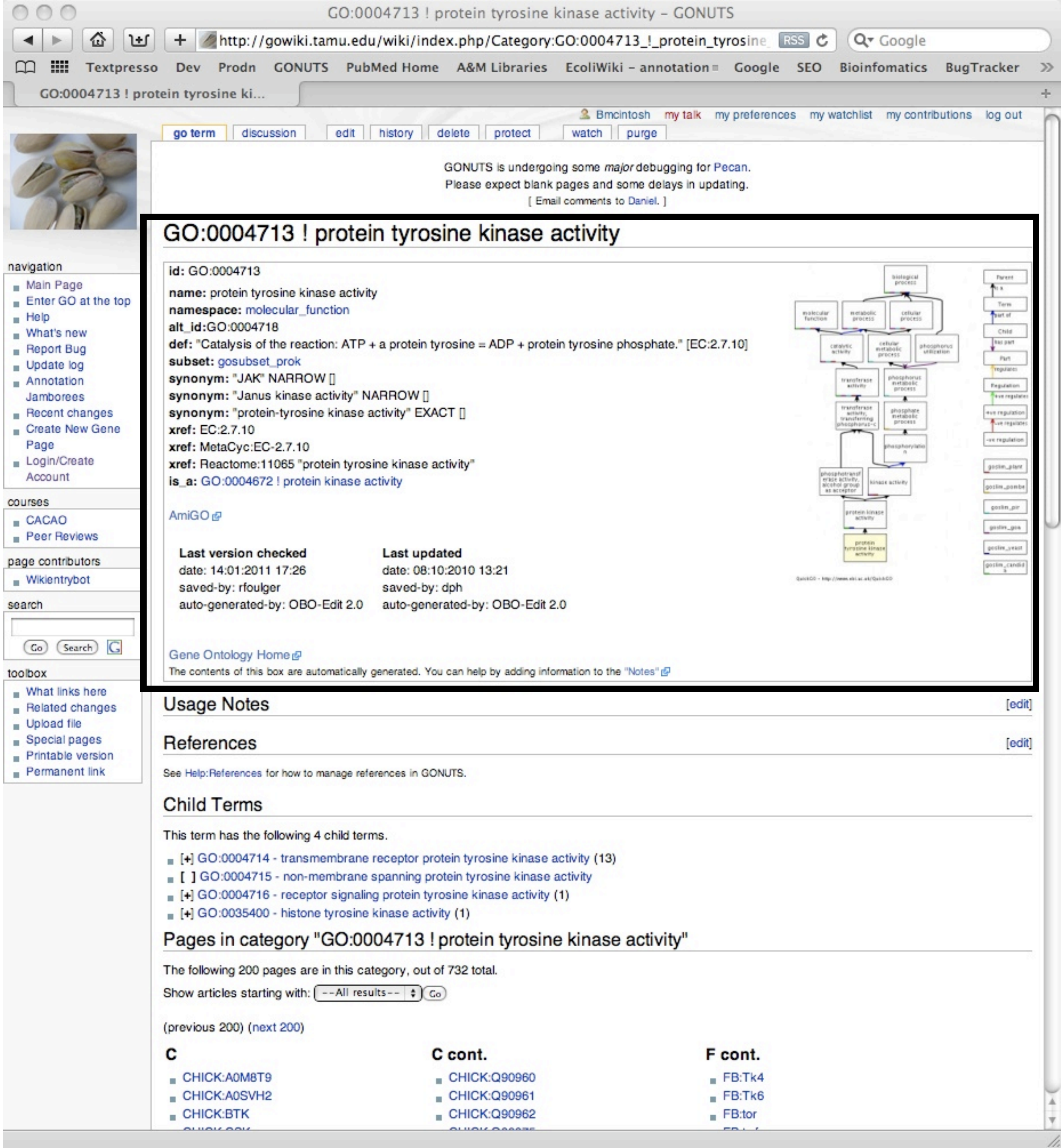
more coming...

For GO terms being considered for obsoletion, see Category:GO:Proposed for obsoletion

GO N

http://tinyurl.com/258t9qe
news4go: Software/Database Developers Required for the Gene Ontology Project
http://tinyurl.com/258t9qe
news4go: Biocurator positions at "PomBase" http://tinyurl.com/375ab8y
news4go: Biocurator positions at "PomBase" http://tinyurl.com/375ab8y
news4go: 6th Renal GOA Initiative Newsletter http://tinyurl.com/2f22jrm
news4go: 6th Renal GOA Initiative Newsletter http://tinyurl.com/2f22jrm

Searching GONUTS [edit]



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[Email comments to Daniel.]

GO:0004713 ! protein tyrosine kinase activity

id: GO:0004713
name: protein tyrosine kinase activity
namespace: molecular_function
alt_id:GO:0004718
def: "Catalysis of the reaction: ATP + a protein tyrosine = ADP + protein tyrosine phosphate." [EC:2.7.10]
subset: gosubset_prok
synonym: "JAK" NARROW []
synonym: "Janus kinase activity" NARROW []
synonym: "protein-tyrosine kinase activity" EXACT []
xref: EC:2.7.10
xref: MetaCyc:EC-2.7.10
xref: Reactome:11065 "protein tyrosine kinase activity"
is_a: GO:0004672 ! protein kinase activity

AmiGO

Last version checked	**Last updated**
date: 14:01:2011 17:26	date: 08:10:2010 13:21
saved-by: rfoulger	saved-by: dph
auto-generated-by: OBO-Edit 2.0	auto-generated-by: OBO-Edit 2.0

Gene Ontology Home
The contents of this box are automatically generated. You can help by adding information to the "Notes"

Usage Notes

[edit]

References

[edit]

See Help:References for how to manage references in GONUTS.

Child Terms

This term has the following 4 child terms.

- [+] GO:0004714 - transmembrane receptor protein tyrosine kinase activity (13)
- [ ] GO:0004715 - non-membrane spanning protein tyrosine kinase activity
- [+] GO:0004716 - receptor signaling protein tyrosine kinase activity (1)
- [+] GO:0035400 - histone tyrosine kinase activity (1)

Pages in category "GO:0004713 ! protein tyrosine kinase activity"

The following 200 pages are in this category, out of 732 total.

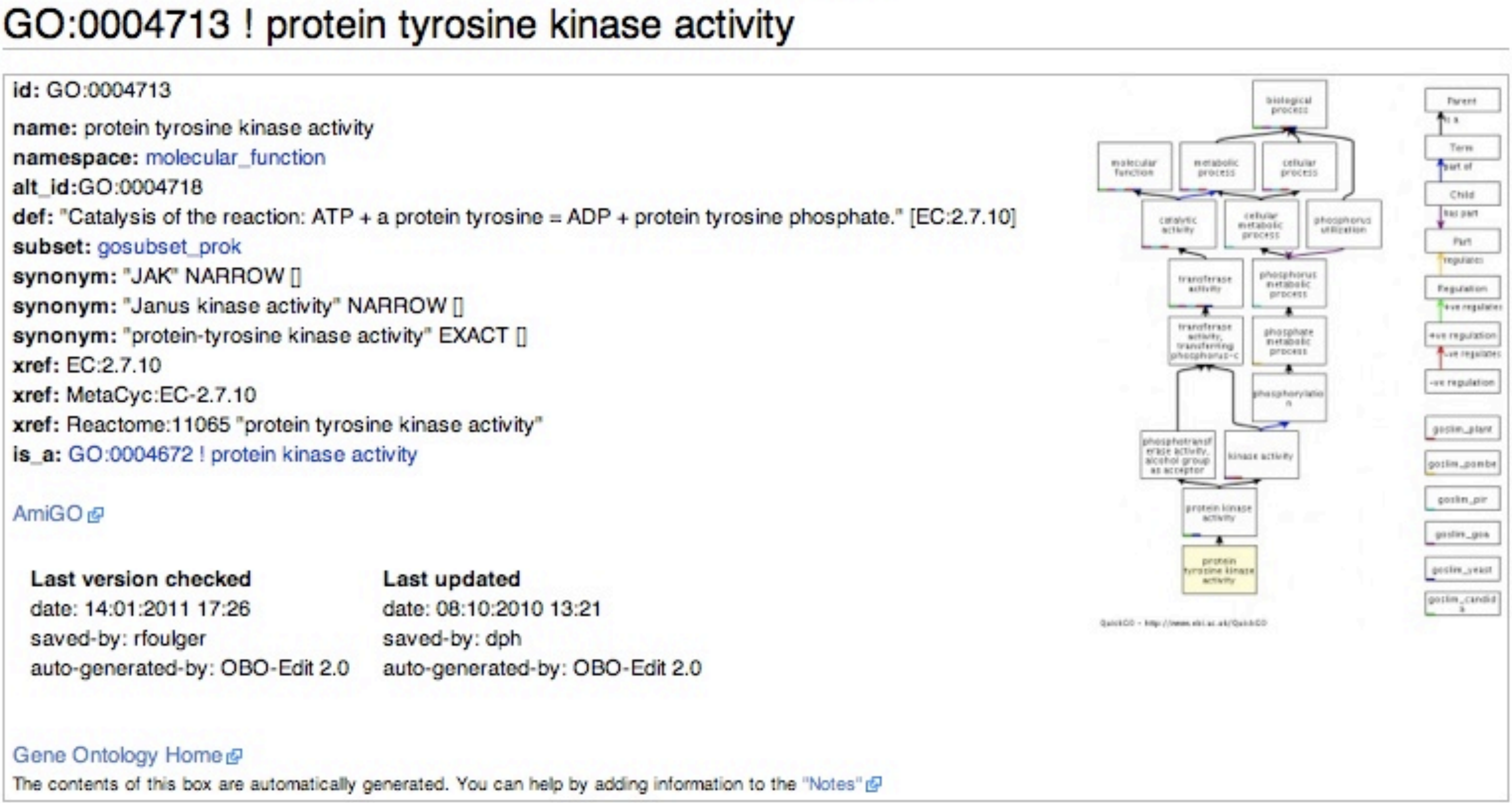
Show articles starting with: --All results-- Go

(previous 200) (next 200)

C
- CHICK:A0M8T9
- CHICK:A0SVH2
- CHICK:BTK

C cont.
- CHICK:Q90960
- CHICK:Q90961
- CHICK:Q90962

F cont.
- FB:Tk4
- FB:Tk6
- FB:tor



GO:0004713 ! protein tyrosine kinase activity

id: GO:0004713

name: protein tyrosine kinase activity

namespace: molecular_function

alt_id:GO:0004718

def: "Catalysis of the reaction: ATP + a protein tyrosine = ADP + protein tyrosine phosphate." [EC:2.7.10]

subset: gosubset_prok

synonym: "JAK" NARROW []

synonym: "Janus kinase activity" NARROW []

synonym: "protein-tyrosine kinase activity" EXACT []

xref: EC:2.7.10

xref: MetaCyc:EC-2.7.10

xref: Reactome:11065 "protein tyrosine kinase activity"

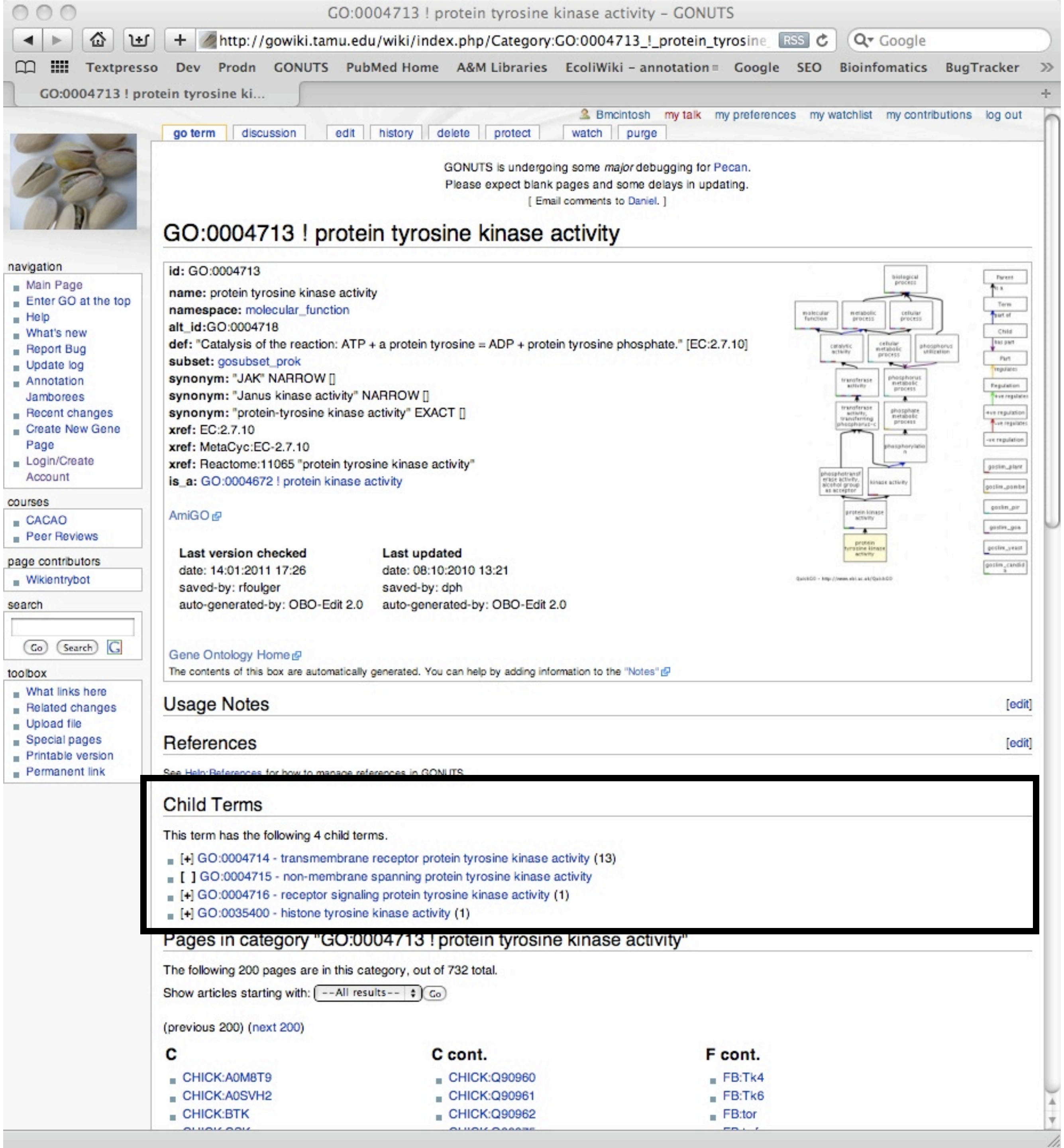
is_a: GO:0004672 ! protein kinase activity

AmiGO

Last version checked	**Last updated**
date: 14:01:2011 17:26	date: 08:10:2010 13:21
saved-by: rfoulger	saved-by: dph
auto-generated-by: OBO-Edit 2.0	auto-generated-by: OBO-Edit 2.0

Gene Ontology Home

The contents of this box are automatically generated. You can help by adding information to the "Notes"



GONUTS is undergoing some *major* debugging for Pecan.
Please expect blank pages and some delays in updating.
[Email comments to Daniel.]

GO:0004713 ! protein tyrosine kinase activity

id: GO:0004713
name: protein tyrosine kinase activity
namespace: molecular_function
alt_id:GO:0004718
def: "Catalysis of the reaction: ATP + a protein tyrosine = ADP + protein tyrosine phosphate." [EC:2.7.10]
subset: gosubset_prok
synonym: "JAK" NARROW []
synonym: "Janus kinase activity" NARROW []
synonym: "protein-tyrosine kinase activity" EXACT []
xref: EC:2.7.10
xref: MetaCyc:EC-2.7.10
xref: Reactome:11065 "protein tyrosine kinase activity"
is_a: GO:0004672 ! protein kinase activity

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Usage Notes

[edit]

References

[edit]

See Help:References for how to manage references in GONUTS.

Child Terms

This term has the following 4 child terms.

- [+] GO:0004714 - transmembrane receptor protein tyrosine kinase activity (13)
- [ ] GO:0004715 - non-membrane spanning protein tyrosine kinase activity
- [+] GO:0004716 - receptor signaling protein tyrosine kinase activity (1)
- [+] GO:0035400 - histone tyrosine kinase activity (1)

Pages in category "GO:0004713 ! protein tyrosine kinase activity"

The following 200 pages are in this category, out of 732 total.

Show articles starting with:

(previous 200) (next 200)

C	C cont.	F cont.
CHICK:A0M8T9	CHICK:Q90960	FB:Tk4
CHICK:A0SVH2	CHICK:Q90961	FB:Tk6
CHICK:BTK	CHICK:Q90962	FB:tor

Strategies

- Search for a keyword and browse the ontology for the right term
- Look at terms suggested by others for your protein
  - Computational with the IEA evidence code
  - Curators with TAS or IC
- Look at terms used for homologous proteins in model organisms

Functional Annotation

- Annotation: a note that is made while reading any form of text

- Functional Annotation: a database entry in a **specific format** that is made based on **evidence** in a peer-reviewed **paper** about the function of a **protein**

Evidence Codes for CACAO

- Evidence codes describe the type of work or analysis done by the authors
  - IDA: Inferred from Direct Assay
  - IMP: Inferred from Mutant Phenotype
  - IGI: Inferred from Genetic Interaction
  - ISO: Inferred from Sequence Orthology
  - ISA: Inferred from Sequence Alignment
  - ISM: Inferred from Sequence Model
  - IGC: Inferred from Genomic Context

- Expert biocurators get to use others, but we restrict them for CACAO. If it's not one of these 7, your annotation is incorrect!!!

- http://gowiki.tamu.edu/wiki/index.php/evidence_codes

Evidence Codes for CACAO

- Picking the right evidence code is important
- Use the evidence code decision tree
- Use the evidence code guidelines at the GO consortium website:
  - http://www.geneontology.org/GO.evidence.shtml
- Discuss!

Functional Annotation

- Annotation: a note that is made while reading any form of text

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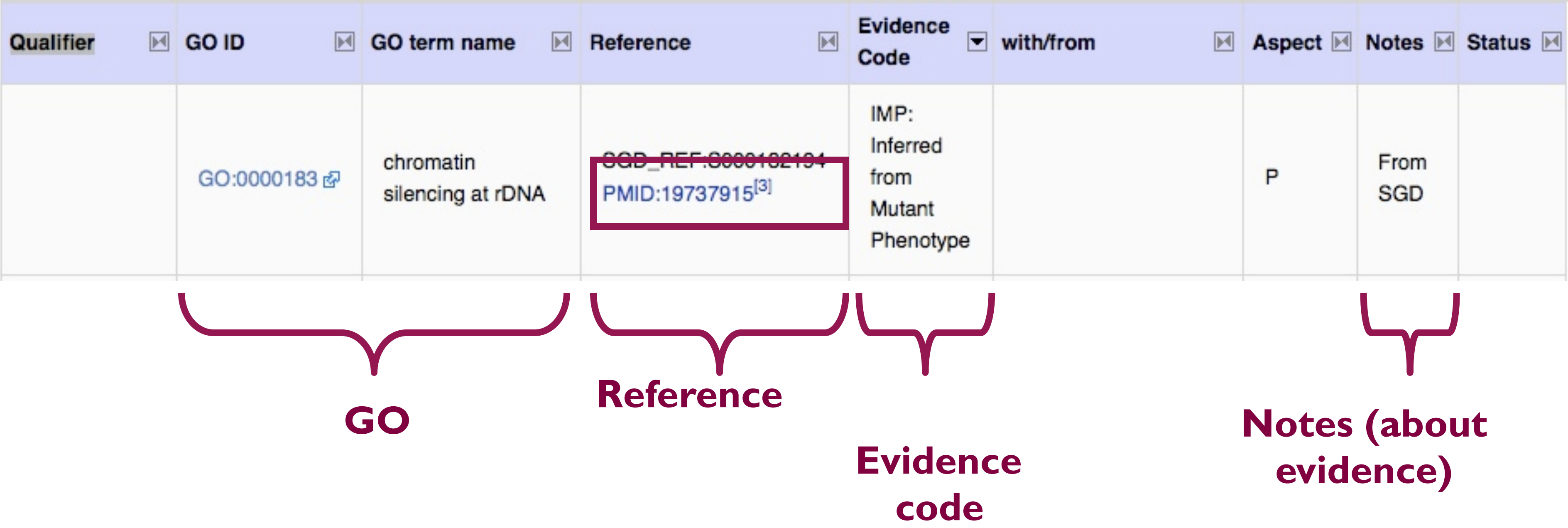
4 REQUIRED parts of EVERY GO annotation



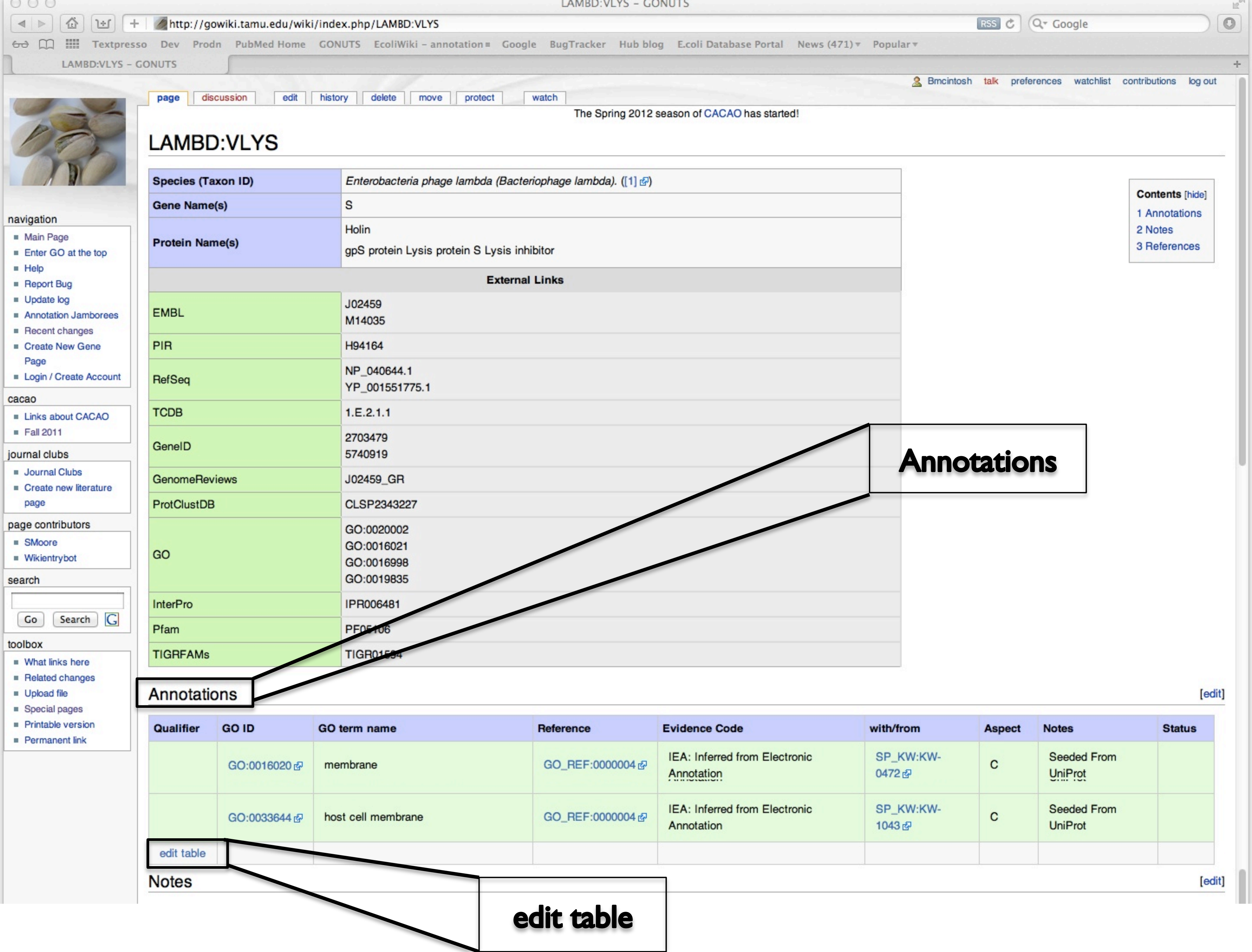
Qualifier	GO ID	GO term name	Reference	Evidence Code	with/from	Aspect	Notes	Status
	GO:0000183	chromatin silencing at rDNA	SGD_REF:S000182194 PMID:19737915[3]	IMP: Inferred from Mutant Phenotype		P	From SGD	

GO

Reference

Evidence code

Notes (about evidence)



The Spring 2012 season of CACAO has started!

LAMBD:VLYS

Contents [hide]
1 Annotations
2 Notes
3 References

Species (Taxon ID)	*Enterobacteria phage lambda (Bacteriophage lambda).* ([1])
Gene Name(s)	S
Protein Name(s)	Holin gpS protein Lysis protein S Lysis inhibitor
External Links	
EMBL	J02459 M14035
PIR	H94164
RefSeq	NP_040644.1 YP_001551775.1
TCDB	1.E.2.1.1
GeneID	2703479 5740919
GenomeReviews	J02459_GR
ProtClustDB	CLSP2343227
GO	GO:0020002 GO:0016021 GO:0016998 GO:0019835
InterPro	IPR006481
Pfam	PF05106
TIGRFAMs	TIGR01594

Annotations

Annotations

[edit]

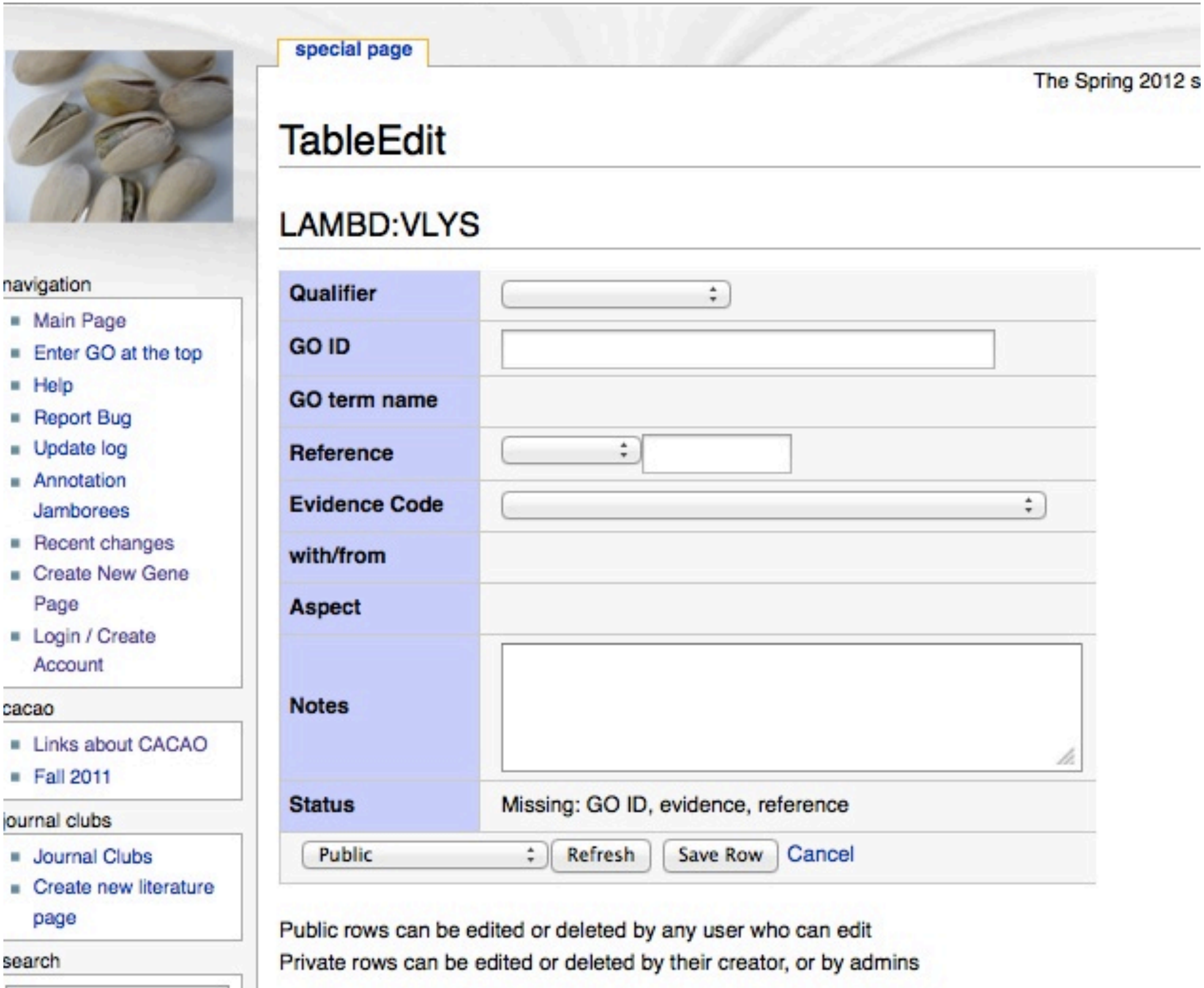
Qualifier	GO ID	GO term name	Reference	Evidence Code	with/from	Aspect	Notes	Status
	GO:0016020	membrane	GO_REF:0000004	IEA: Inferred from Electronic Annotation	SP_KW:KW-0472	C	Seeded From UniProt	
	GO:0033644	host cell membrane	GO_REF:0000004	IEA: Inferred from Electronic Annotation	SP_KW:KW-1043	C	Seeded From UniProt	
edit table								

Notes

[edit]

edit table

Entering/editing annotations



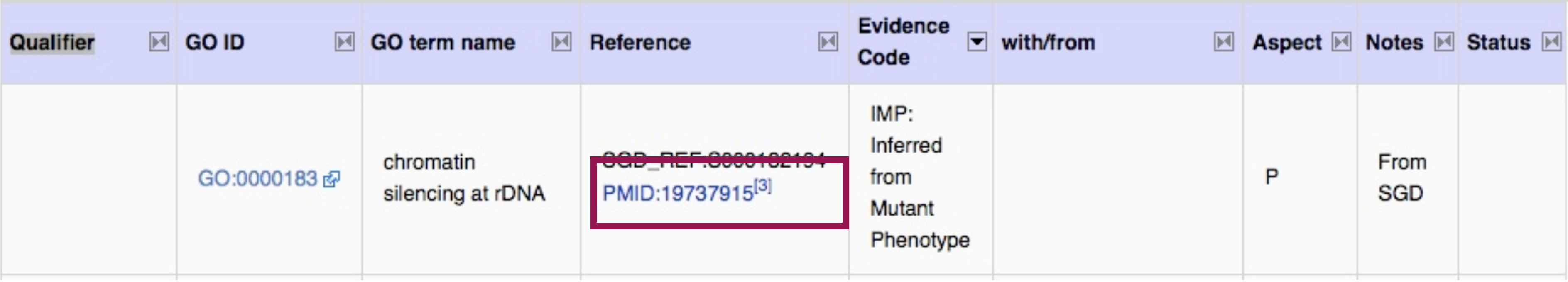
TableEdit

LAMBD:VLYS

Qualifier	
GO ID	
GO term name	
Reference	
Evidence Code	
with/from	
Aspect	
Notes	
Status	Missing: GO ID, evidence, reference

Public rows can be edited or deleted by any user who can edit
Private rows can be edited or deleted by their creator, or by admins

4 REQUIRED parts of EVERY GO annotation



Qualifier	GO ID	GO term name	Reference	Evidence Code	with/from	Aspect	Notes	Status
	GO:0000183	chromatin silencing at rDNA	SGD_REF:S000132194 PMID:19737915[3]	IMP: Inferred from Mutant Phenotype		P	From SGD	

GO

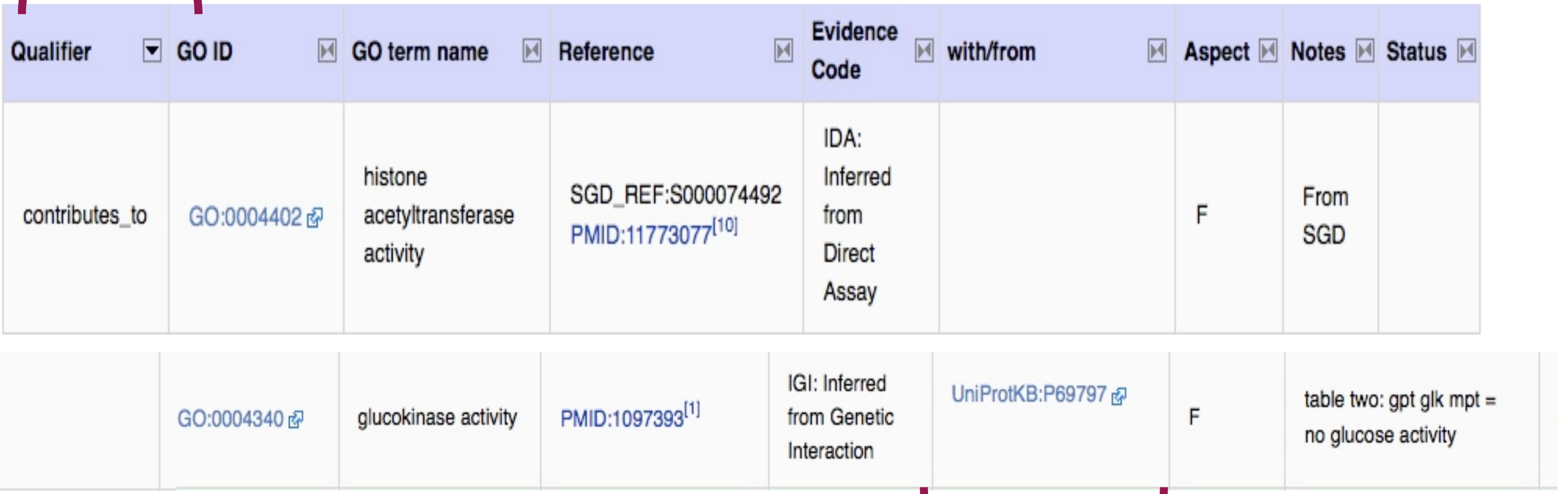
Reference

Evidence code

Notes (about evidence)

2 other parts that may be required…

Qualifier



Qualifier	GO ID	GO term name	Reference	Evidence Code	with/from	Aspect	Notes	Status
contributes_to	GO:0004402	histone acetyltransferase activity	SGD_REF:S000074492 PMID:11773077[10]	IDA: Inferred from Direct Assay		F	From SGD	
	GO:0004340	glucokinase activity	PMID:1097393[1]	IGI: Inferred from Genetic Interaction	UniProtKB:P69797	F	table two: gpt glk mpt = no glucose activity	

With/From

Example paper

http://www.ncbi.nlm.nih.gov/pubmed/8227000