Extending MediaWiki
for community annotation

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EcoliWiki

TEXAS A&M
UNIVERSITY

Outline

- Using Mediawiki vs. Wikipedia

- TableEdit & Mediawiki tables
  - Background
  - Function
  - Use cases

- Categories
  - As ontologies
  - GONUTS

- Educational Resource
  - Community Assessment of Community Annotation with Ontologies (CACAO)

Using the MediaWiki software

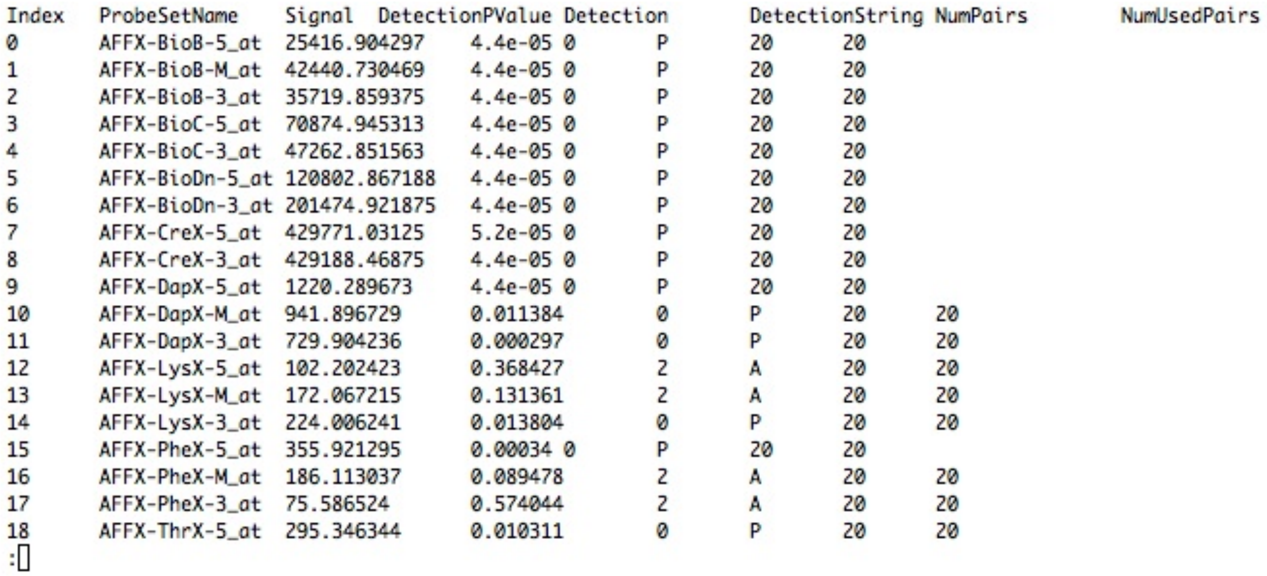
+ Known track record
+ Easy to implement
+ Extensible
+ No/less compromising

+ Established community
+ Easy to maintain
+ Easy to customization

- Smaller audience (experts)
- Specific knowledge about one topic

- No "Google Factor"
- Cost of operation
- Higher barrier to entry

Freeform wikis & tabular data

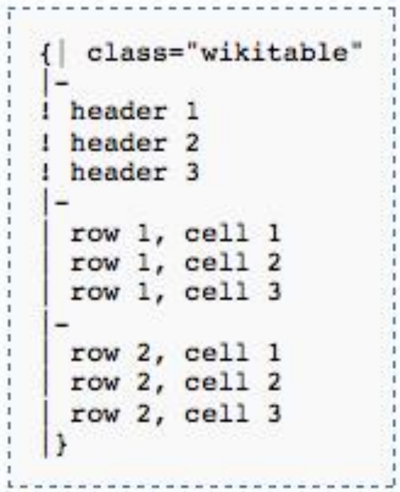


```
Index   ProbeSetName    Signal  DetectionPValue Detection       DetectionString NumPairs        NumUsedPairs
0       AFFX-BioB-5_at  25416.904297    4.4e-05 0       P       20      20
1       AFFX-BioB-M_at  42440.730469    4.4e-05 0       P       20      20
2       AFFX-BioB-3_at  35719.859375    4.4e-05 0       P       20      20
3       AFFX-BioC-5_at  70874.945313    4.4e-05 0       P       20      20
4       AFFX-BioC-3_at  47262.851563    4.4e-05 0       P       20      20
5       AFFX-BioDn-5_at 120802.867188   4.4e-05 0       P       20      20
6       AFFX-BioDn-3_at 201474.921875   4.4e-05 0       P       20      20
7       AFFX-CreX-5_at  429771.03125    5.2e-05 0       P       20      20
8       AFFX-CreX-3_at  429188.46875    4.4e-05 0       P       20      20
9       AFFX-DapX-5_at  1220.289673     4.4e-05 0       P       20      20
10      AFFX-DapX-M_at  941.896729      0.011384        0       P       20      20
11      AFFX-DapX-3_at  729.904236      0.000297        0       P       20      20
12      AFFX-LysX-5_at  102.202423      0.368427        2       A       20      20
13      AFFX-LysX-M_at  172.067215      0.131361        2       A       20      20
14      AFFX-LysX-3_at  224.006241      0.013804        0       P       20      20
15      AFFX-PheX-5_at  355.921295      0.00034 0       P       20      20
16      AFFX-PheX-M_at  186.113037      0.089478        2       A       20      20
17      AFFX-PheX-3_at  75.586524       0.574044        2       A       20      20
18      AFFX-ThrX-5_at  295.346344      0.010311        0       P       20      20
:▯
```

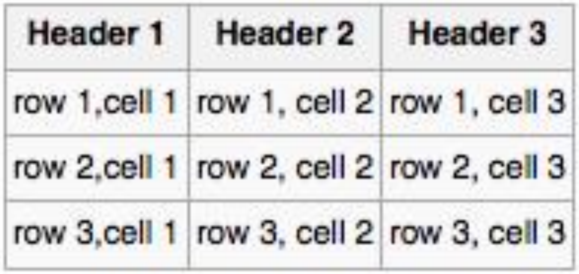
- Typical data for a Model Organism Database:
  - Structural data
  - Microarrays
  - Genomic coordinates / maps
  - Features (genes, ORFs, SNPs, *etc.*)

Wiki tables

- Hard to load data into
- Hard to mine data out-of
- Esoteric markup
  - Not good for the uninitiated
- Semantic tagging
  - More specialized markup



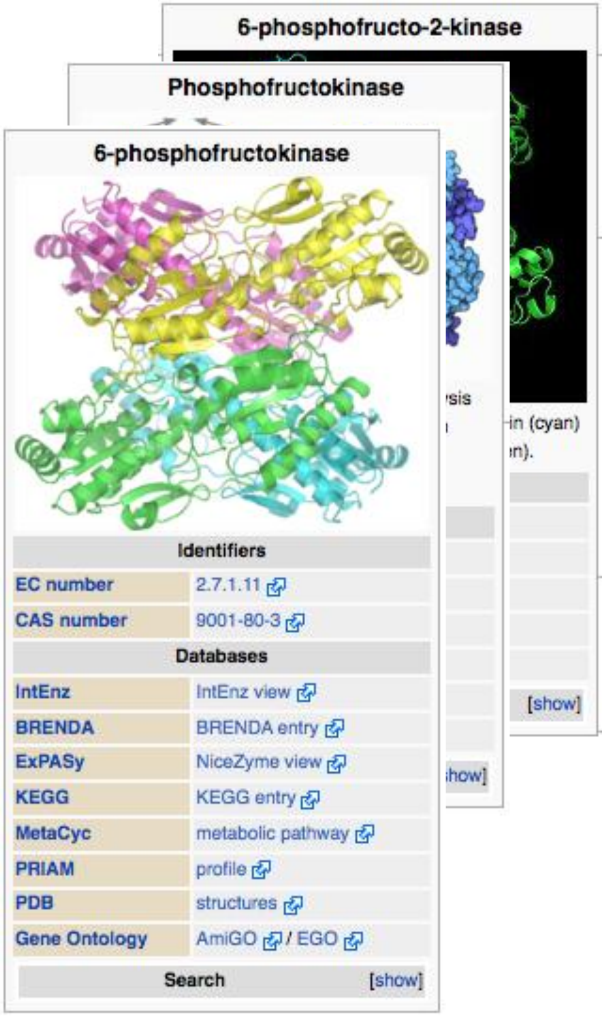
```
{| class="wikitable"
|-
! header 1
! header 2
! header 3
|-
| row 1, cell 1
| row 1, cell 2
| row 1, cell 3
|-
| row 2, cell 1
| row 2, cell 2
| row 2, cell 3
|}
```



Header 1	Header 2	Header 3
row 1,cell 1	row 1, cell 2	row 1, cell 3
row 2,cell 1	row 2, cell 2	row 2, cell 3
row 3,cell 1	row 3, cell 2	row 3, cell 3

Mediawiki Tables

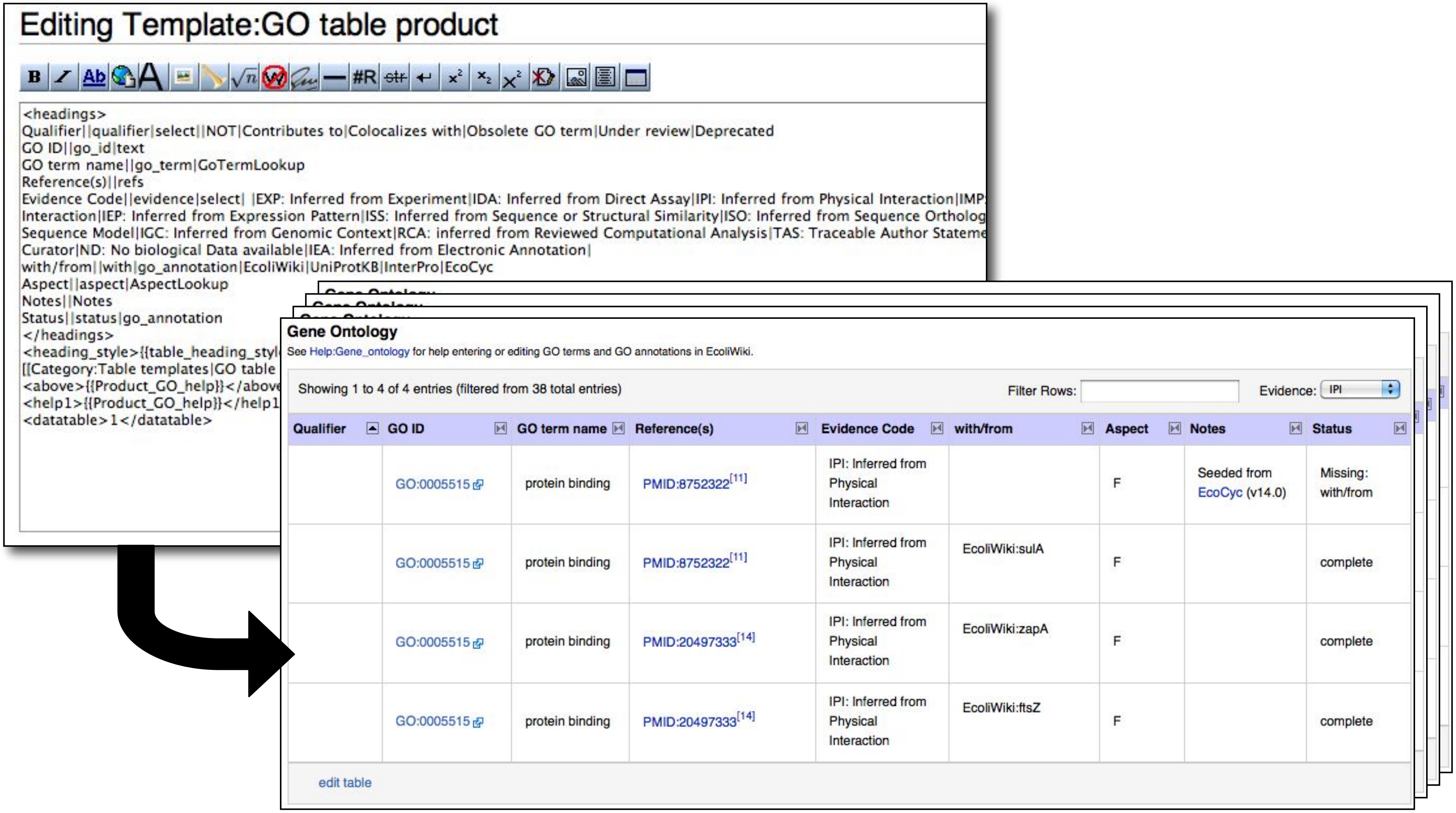
```
{{FixBunching|beg}}
{{enzyme
| Name = 6-phosphofructokinase
| EC_number = 2.7.1.11
| CAS_number = 9001-80-3
| IUBMB_EC_number = 2/7/1/11
| GO_code = 0003872
| image = Phosphofructokinase 6PFK wpmp.png
| width =
| caption =
}}
{{FixBunching|mid}}
{{Infobox protein family
| Symbol = PFK
| Name = Phosphofructokinase
| image = Phosphofructokinase (active vs inactive form).png
| width =
| caption = Bacterial Phosphofructokinase: 3rd glycolysis enzyme (smaller than in
Eukaryotes). In yellow=sugars; in red=ATP-ADP; starred=regulatory sites.<ref
name="pmid6115424">{{PDB|4pfk}}; {{cite journal | author = Evans PR, Farrants GW,
| title = Phosphofructokinase: structure and control | journal = Philos. Trans. R
Lond., B, Biol. Sci. | volume = 293 | issue = 1063 | pages = 53–62 | year = 1981
June | pmid = 6115424 | doi = 10.1098/rstb.1981.0059| laysummary =
http://www.pdb.org/pdb/static.do?p=education_discussion/molecule_of_the_month/pdb
| laysource = PDB Molecule of the Month }}</ref>
| Pfam = PF00365
| Pfam_clan = CL0240
| InterPro = IPR000023
| SMART =
| PROSITE = PDOC00336
| SCOP = 5pfk
| TCDB =
| OPM family =
| OPM protein =
| PDB = {{PDB2|1kzh}}, {{PDB2|1mto}}, {{PDB2|1pfk}}, {{PDB2|1zxx}}, {{PDB2|2f48}}
{{PDB2|2pfk}}, {{PDB2|3pfk}}, {{PDB2|4pfk}}, {{PDB2|6pfk}}
}}
{{FixBunching|end}}
```



6-phosphofructokinase

Identifiers	
EC number	2.7.1.11
CAS number	9001-80-3
Databases	
IntEnz	IntEnz view
BRENDA	BRENDA entry
ExPASy	NiceZyme view
KEGG	KEGG entry
MetaCyc	metabolic pathway
PRIAM	profile
PDB	structures
Gene Ontology	AmiGO / EGO
Search	[show]

TableEdit



Editing Template:GO table product

```
<headings>
Qualifier||qualifier|select||NOT|Contributes to|Colocalizes with|Obsolete GO term|Under review|Deprecated
GO ID||go_id|text
GO term name||go_term|GoTermLookup
Reference(s)||refs
Evidence Code||evidence|select| |EXP: Inferred from Experiment|IDA: Inferred from Direct Assay|IPI: Inferred from Physical Interaction|IMP
Interaction|IEP: Inferred from Expression Pattern|ISS: Inferred from Sequence or Structural Similarity|ISO: Inferred from Sequence Ortholog
Sequence Model|IGC: Inferred from Genomic Context|RCA: inferred from Reviewed Computational Analysis|TAS: Traceable Author Stateme
Curator|ND: No biological Data available|IEA: Inferred from Electronic Annotation|
with/from||with|go_annotation|EcoliWiki|UniProtKB|InterPro|EcoCyc
Aspect||aspect|AspectLookup
Notes||Notes
Status||status|go_annotation
</headings>
<heading_style>{{table_heading_styl
[[Category:Table templates|GO table
<above>{{Product_GO_help}}</above
<help1>{{Product_GO_help}}</help1
<datatable>1</datatable>
```

Gene Ontology

See Help:Gene_ontology for help entering or editing GO terms and GO annotations in EcoliWiki.

Showing 1 to 4 of 4 entries (filtered from 38 total entries)

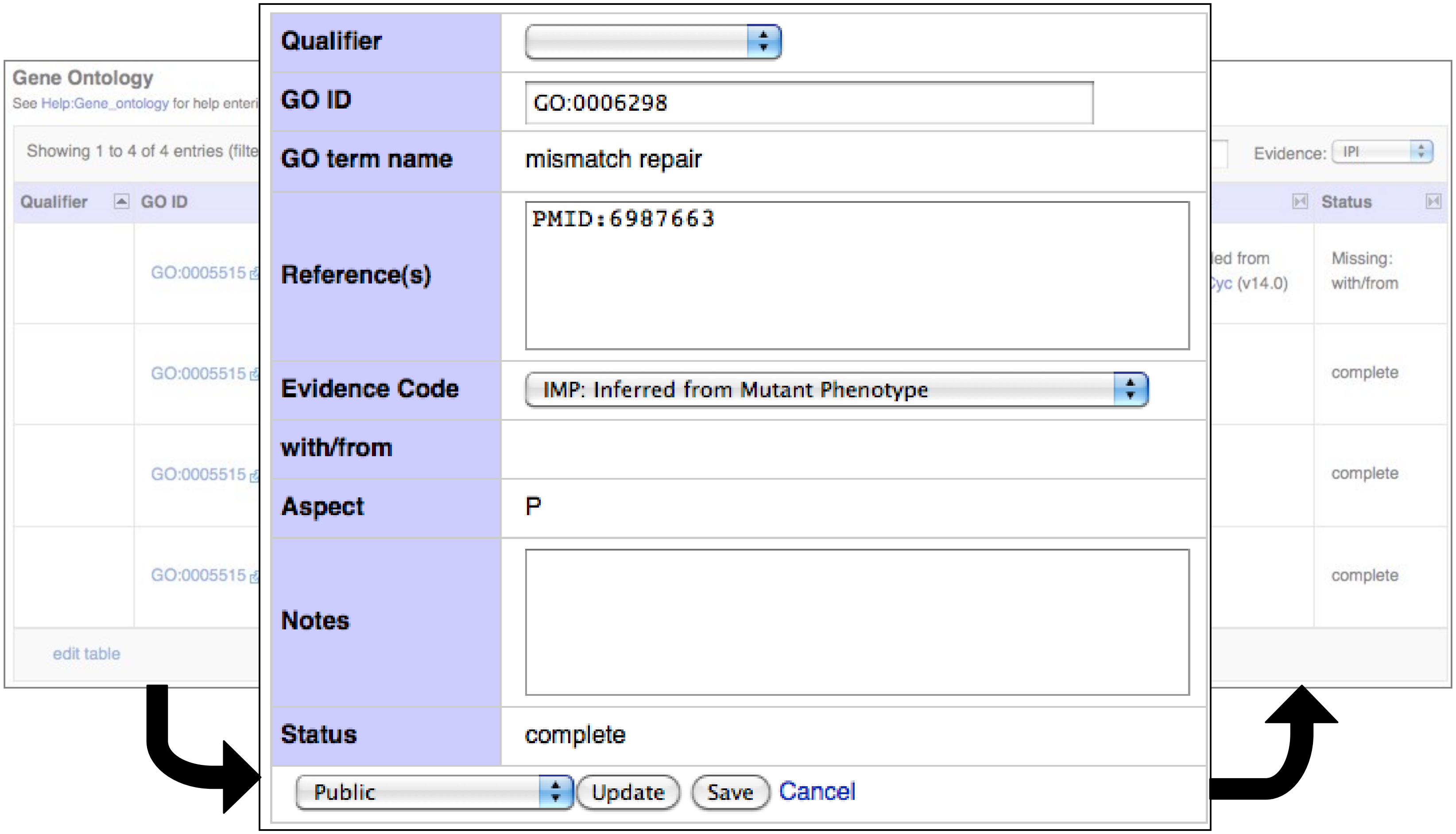
Filter Rows:

Evidence: IPI

Qualifier	GO ID	GO term name	Reference(s)	Evidence Code	with/from	Aspect	Notes	Status
	GO:0005515	protein binding	PMID:8752322[11]	IPI: Inferred from Physical Interaction		F	Seeded from EcoCyc (v14.0)	Missing: with/from
	GO:0005515	protein binding	PMID:8752322[11]	IPI: Inferred from Physical Interaction	EcoliWiki:sulA	F		complete
	GO:0005515	protein binding	PMID:20497333[14]	IPI: Inferred from Physical Interaction	EcoliWiki:zapA	F		complete
	GO:0005515	protein binding	PMID:20497333[14]	IPI: Inferred from Physical Interaction	EcoliWiki:ftsZ	F		complete

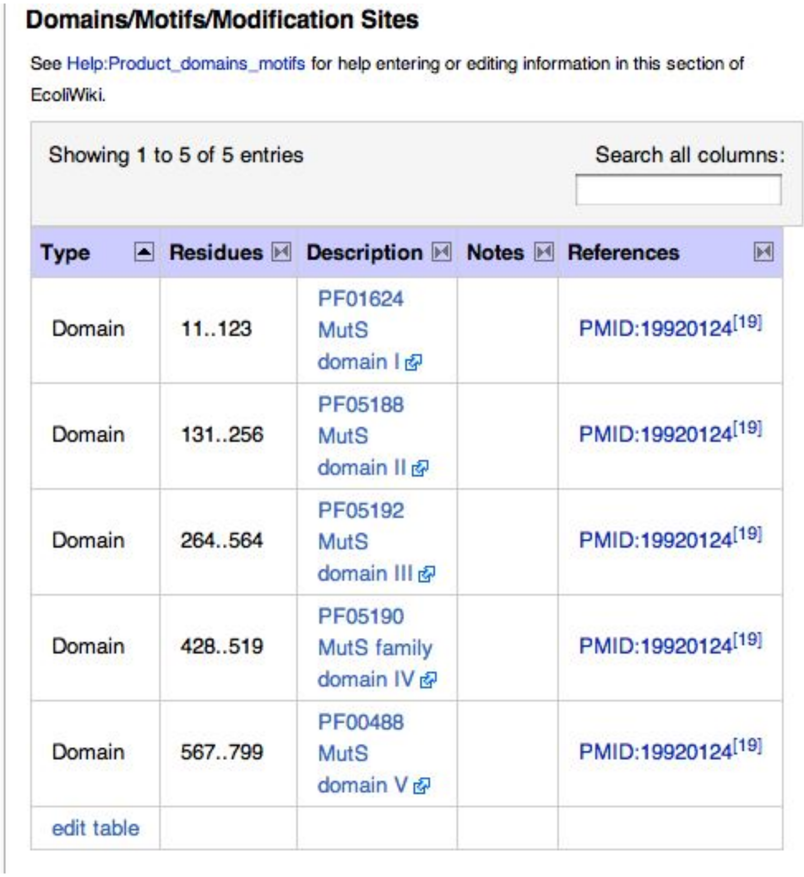
edit table

TableEdit



Qualifier	
GO ID	GO:0006298
GO term name	mismatch repair
Reference(s)	PMID:6987663
Evidence Code	IMP: Inferred from Mutant Phenotype
with/from	
Aspect	P
Notes	
Status	complete

Example: TableEdit
graph generation



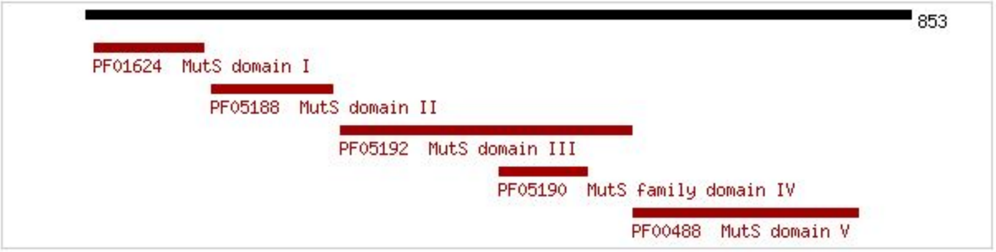
Domains/Motifs/Modification Sites

See Help:Product_domains_motifs for help entering or editing information in this section of EcoliWiki.

Showing 1 to 5 of 5 entries

Search all columns:

Type	Residues	Description	Notes	References
Domain	11..123	PF01624 MutS domain I		PMID:19920124[19]
Domain	131..256	PF05188 MutS domain II		PMID:19920124[19]
Domain	264..564	PF05192 MutS domain III		PMID:19920124[19]
Domain	428..519	PF05190 MutS family domain IV		PMID:19920124[19]
Domain	567..799	PF00488 MutS domain V		PMID:19920124[19]
edit table				

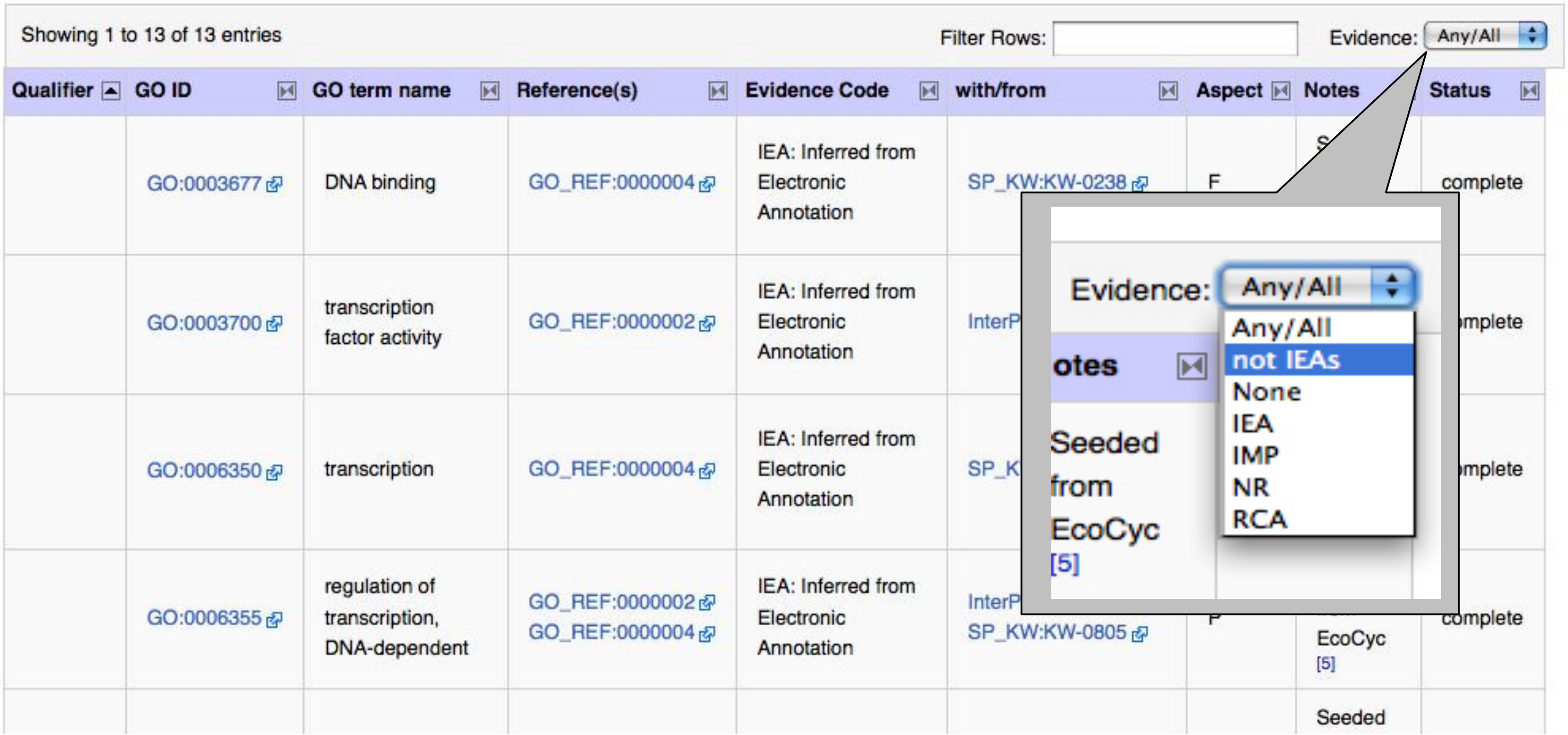


```
if ( defined( 'MW_SUPPORTS_PARSERFIRSTCALLINIT' ) ) {
    $wgHooks['ParserFirstCallInit'][] = 'efMotifMapExtension';
} else {
    $wgExtensionFunctions[] = "efMotifMapExtension";
}

function efMotifMapExtension() {
    global $wgParser;
    $wgParser->setHook( "motif_map", "efRenderMotif_map" );
    return true;
}
```

Example: TableEdit

Javascript, *jQuery*, and *DataTables*



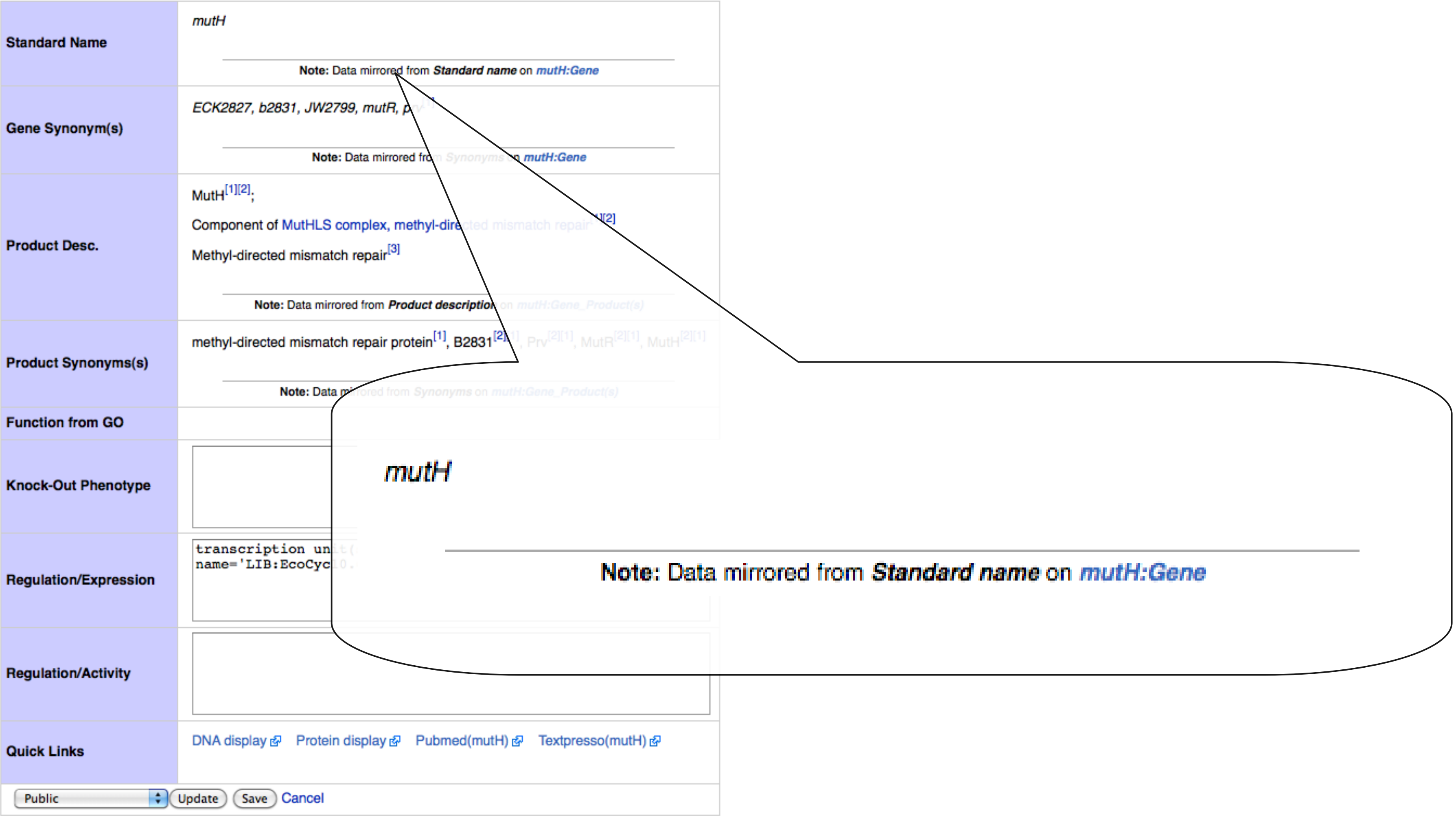
Showing 1 to 13 of 13 entries Filter Rows: Evidence: Any/All

Qualifier	GO ID	GO term name	Reference(s)	Evidence Code	with/from	Aspect	Notes	Status
	GO:0003677	DNA binding	GO_REF:0000004	IEA: Inferred from Electronic Annotation	SP_KW:KW-0238	F	S	complete
	GO:0003700	transcription factor activity	GO_REF:0000002	IEA: Inferred from Electronic Annotation	InterP			mplete
	GO:0006350	transcription	GO_REF:0000004	IEA: Inferred from Electronic Annotation	SP_K			mplete
	GO:0006355	regulation of transcription, DNA-dependent	GO_REF:0000002 GO_REF:0000004	IEA: Inferred from Electronic Annotation	InterP SP_KW:KW-0805	P	EcoCyc [5]	complete
							Seeded	

Many thanks to Allan Jardine *at* http://datatables.net

Example: TableEdit

Mirroring data



Standard Name	*mutH* **Note:** Data mirrored from ***Standard name*** on ***mutH:Gene***
Gene Synonym(s)	*ECK2827, b2831, JW2799, mutR, prv*[1] **Note:** Data mirrored from *Synonyms* on ***mutH:Gene***
Product Desc.	MutH[1][2]; Component of MutHLS complex, methyl-directed mismatch repair[1][2] Methyl-directed mismatch repair[3] **Note:** Data mirrored from ***Product description*** on *mutH:Gene_Product(s)*
Product Synonyms(s)	methyl-directed mismatch repair protein[1], B2831[2][1], Prv[2][1], MutR[2][1], MutH[2][1] **Note:** Data mirrored from *Synonyms* on *mutH:Gene_Product(s)*
Function from GO	
Knock-Out Phenotype	
Regulation/Expression	transcription un name='LIB:EcoCyc
Regulation/Activity	
Quick Links	DNA display Protein display Pubmed(mutH) Textpresso(mutH)

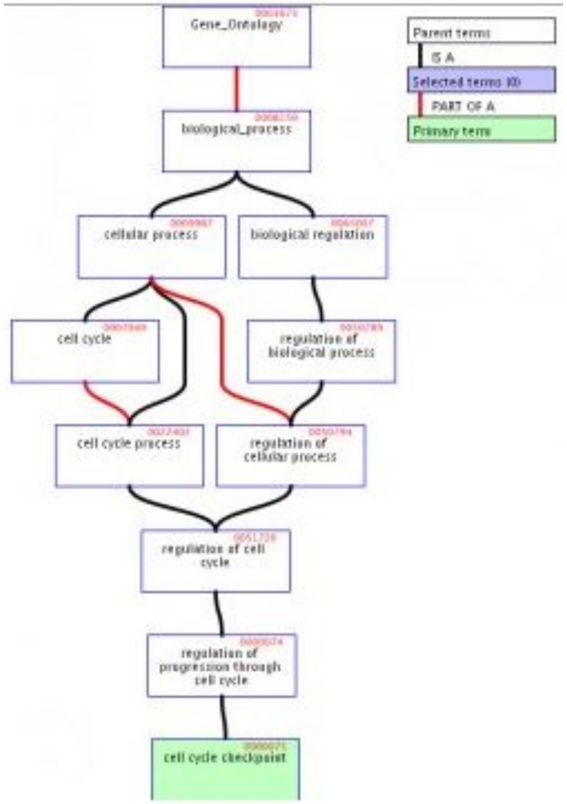
mutH

Note: Data mirrored from ***Standard name*** on ***mutH:Gene***

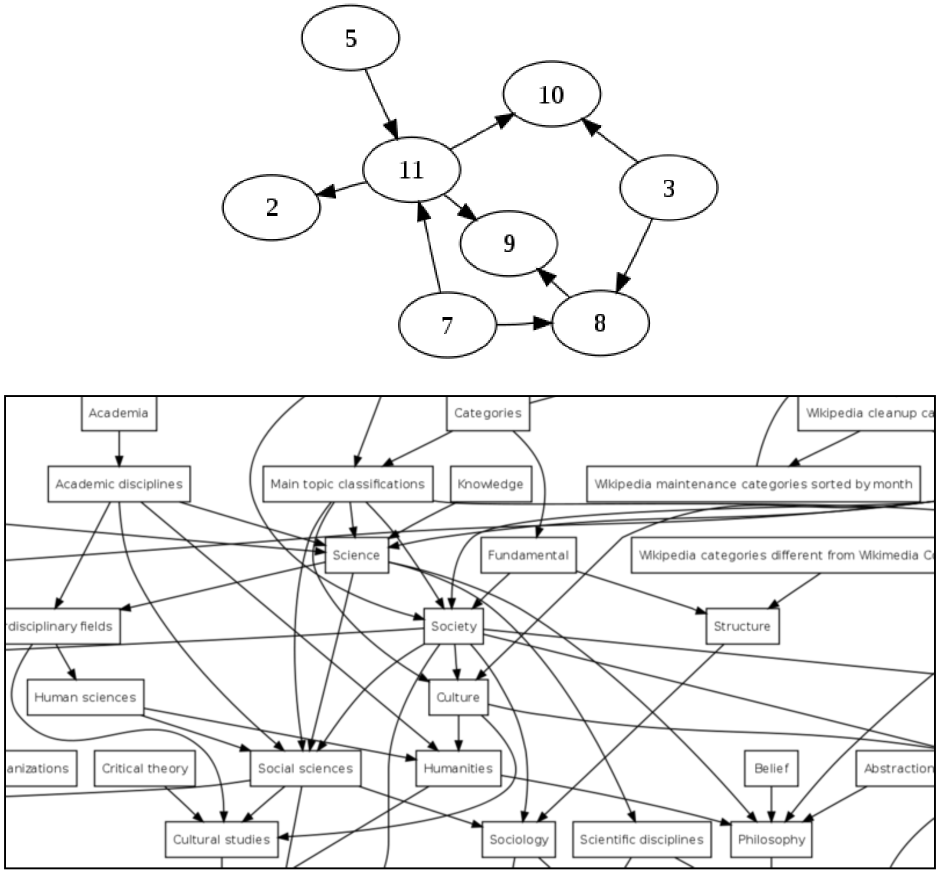
Outline

- Using Mediawiki vs. Wikipedia
- TableEdit & Mediawiki tables
  - Background
  - Function
  - Use cases
- Categories
  - As ontologies
  - GONUTS
- Educational Resource
  - Community Assessment of Community Annotation with Ontologies (CACAO)

Traversing the GO with categories



A typical GO term.



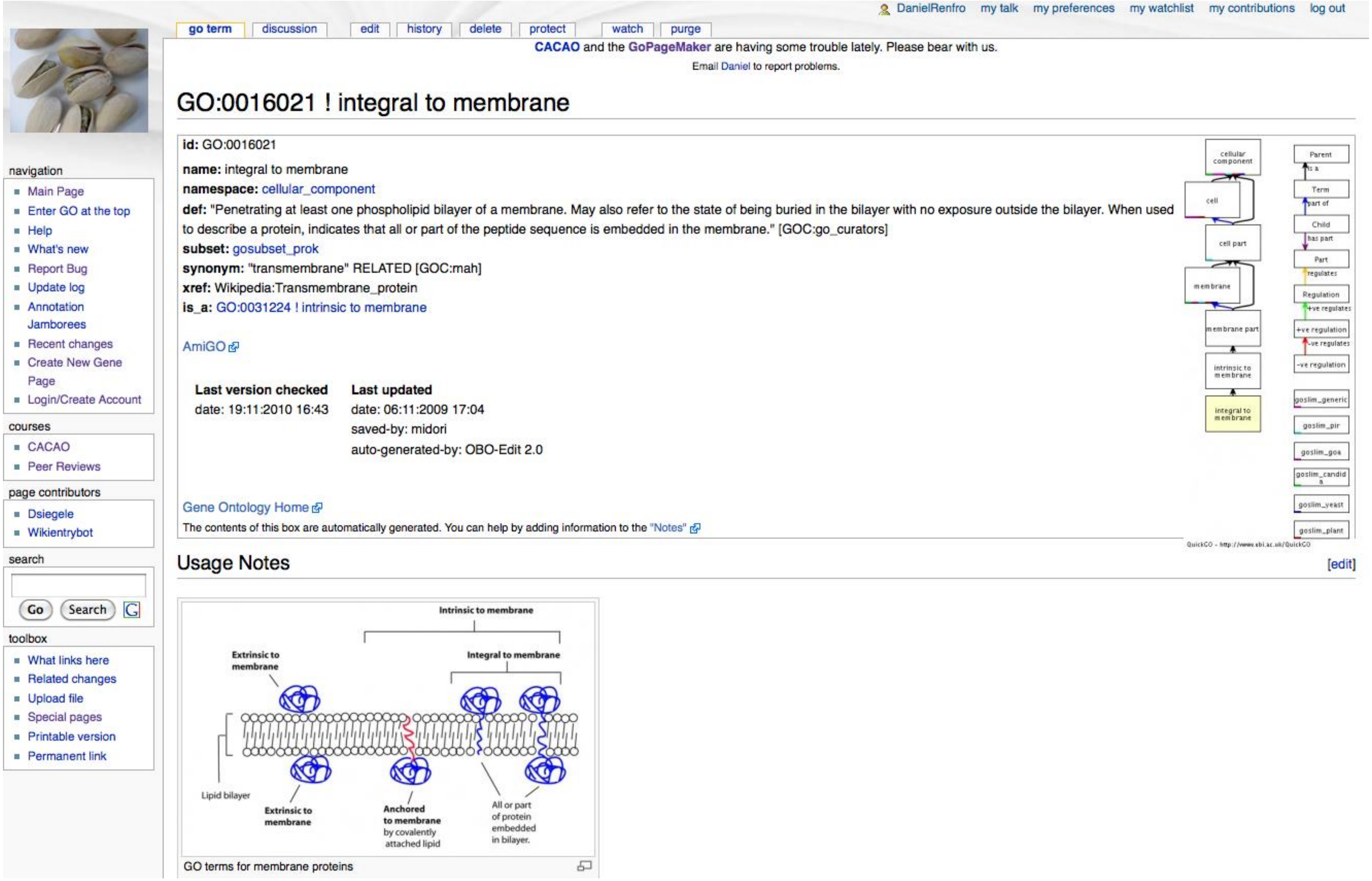
Two directed acyclic graphs (DAGs)

A wiki for Gene Ontology

GONUTS

- Gene Ongology Normal Usage Tracking System
- Finding the right GO term (out of ~285,000 terms)
- Best practices, user notes, *etc.*
- Annotating any gene in UniProt
- Example annotations from MGI, FlyBase, WormBase, dictyBase…

(http://gowiki.tamu.edu)



CACAO and the **GoPageMaker** are having some trouble lately. Please bear with us.

Email Daniel to report problems.

GO:0016021 ! integral to membrane

id: GO:0016021

name: integral to membrane

namespace: cellular_component

def: "Penetrating at least one phospholipid bilayer of a membrane. May also refer to the state of being buried in the bilayer with no exposure outside the bilayer. When used to describe a protein, indicates that all or part of the peptide sequence is embedded in the membrane." [GOC:go_curators]

subset: gosubset_prok

synonym: "transmembrane" RELATED [GOC:mah]

xref: Wikipedia:Transmembrane_protein

is_a: GO:0031224 ! intrinsic to membrane

AmiGO

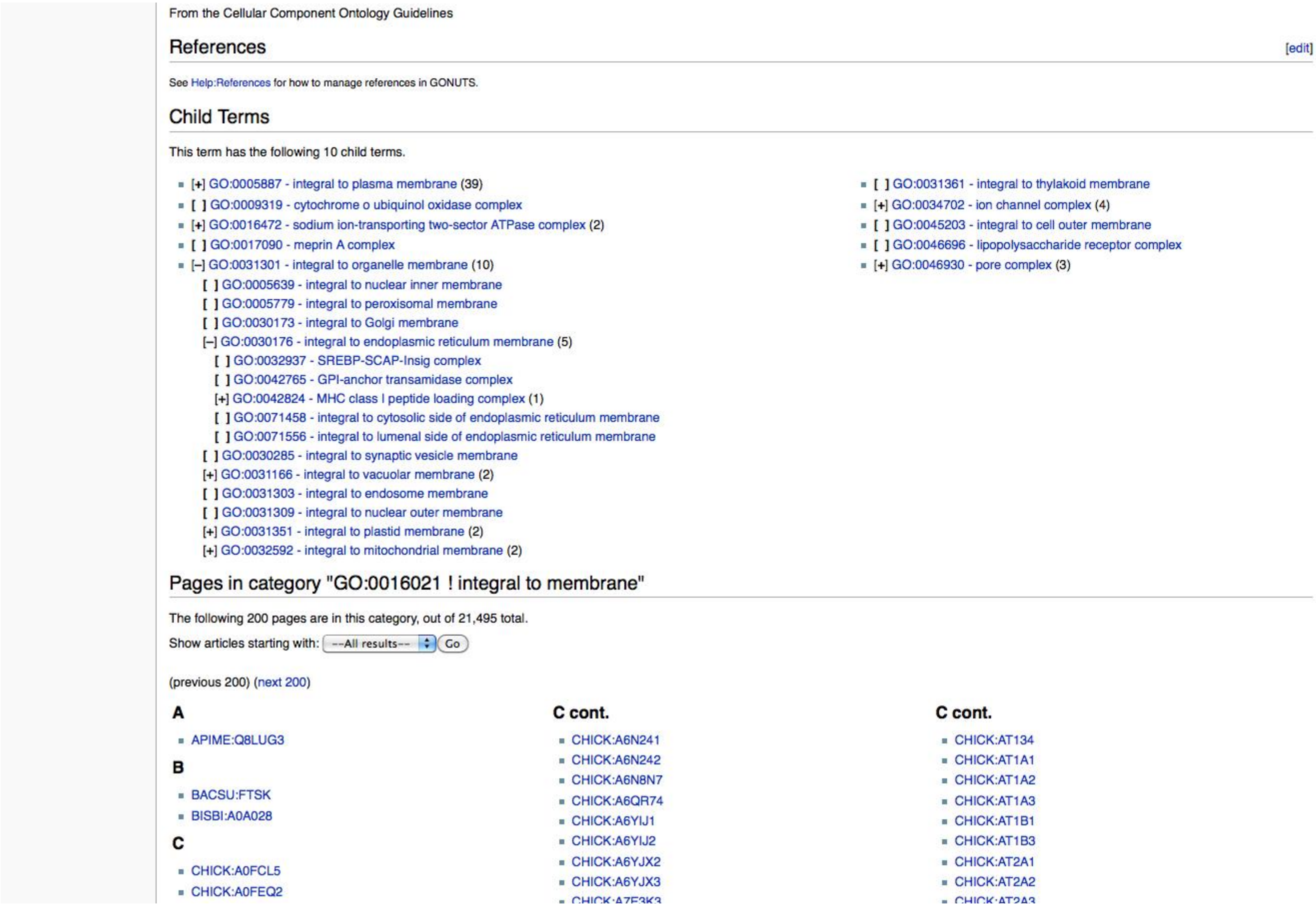
Last version checked	**Last updated**
date: 19:11:2010 16:43	date: 06:11:2009 17:04 saved-by: midori auto-generated-by: OBO-Edit 2.0

Gene Ontology Home

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

Usage Notes

GO terms for membrane proteins



From the Cellular Component Ontology Guidelines

References

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

Child Terms

This term has the following 10 child terms.

- [+] GO:0005887 - integral to plasma membrane (39)
- [ ] GO:0009319 - cytochrome o ubiquinol oxidase complex
- [+] GO:0016472 - sodium ion-transporting two-sector ATPase complex (2)
- [ ] GO:0017090 - meprin A complex
- [–] GO:0031301 - integral to organelle membrane (10)
  - [ ] GO:0005639 - integral to nuclear inner membrane
  - [ ] GO:0005779 - integral to peroxisomal membrane
  - [ ] GO:0030173 - integral to Golgi membrane
  - [–] GO:0030176 - integral to endoplasmic reticulum membrane (5)
    - [ ] GO:0032937 - SREBP-SCAP-Insig complex
    - [ ] GO:0042765 - GPI-anchor transamidase complex
    - [+] GO:0042824 - MHC class I peptide loading complex (1)
    - [ ] GO:0071458 - integral to cytosolic side of endoplasmic reticulum membrane
    - [ ] GO:0071556 - integral to lumenal side of endoplasmic reticulum membrane
  - [ ] GO:0030285 - integral to synaptic vesicle membrane
  - [+] GO:0031166 - integral to vacuolar membrane (2)
  - [ ] GO:0031303 - integral to endosome membrane
  - [ ] GO:0031309 - integral to nuclear outer membrane
  - [+] GO:0031351 - integral to plastid membrane (2)
  - [+] GO:0032592 - integral to mitochondrial membrane (2)
- [ ] GO:0031361 - integral to thylakoid membrane
- [+] GO:0034702 - ion channel complex (4)
- [ ] GO:0045203 - integral to cell outer membrane
- [ ] GO:0046696 - lipopolysaccharide receptor complex
- [+] GO:0046930 - pore complex (3)

Pages in category "GO:0016021 ! integral to membrane"

The following 200 pages are in this category, out of 21,495 total.

Show articles starting with:

(previous 200) (next 200)

A

- APIME:Q8LUG3

B

- BACSU:FTSK
- BISBI:A0A028

C

- CHICK:A0FCL5
- CHICK:A0FEQ2

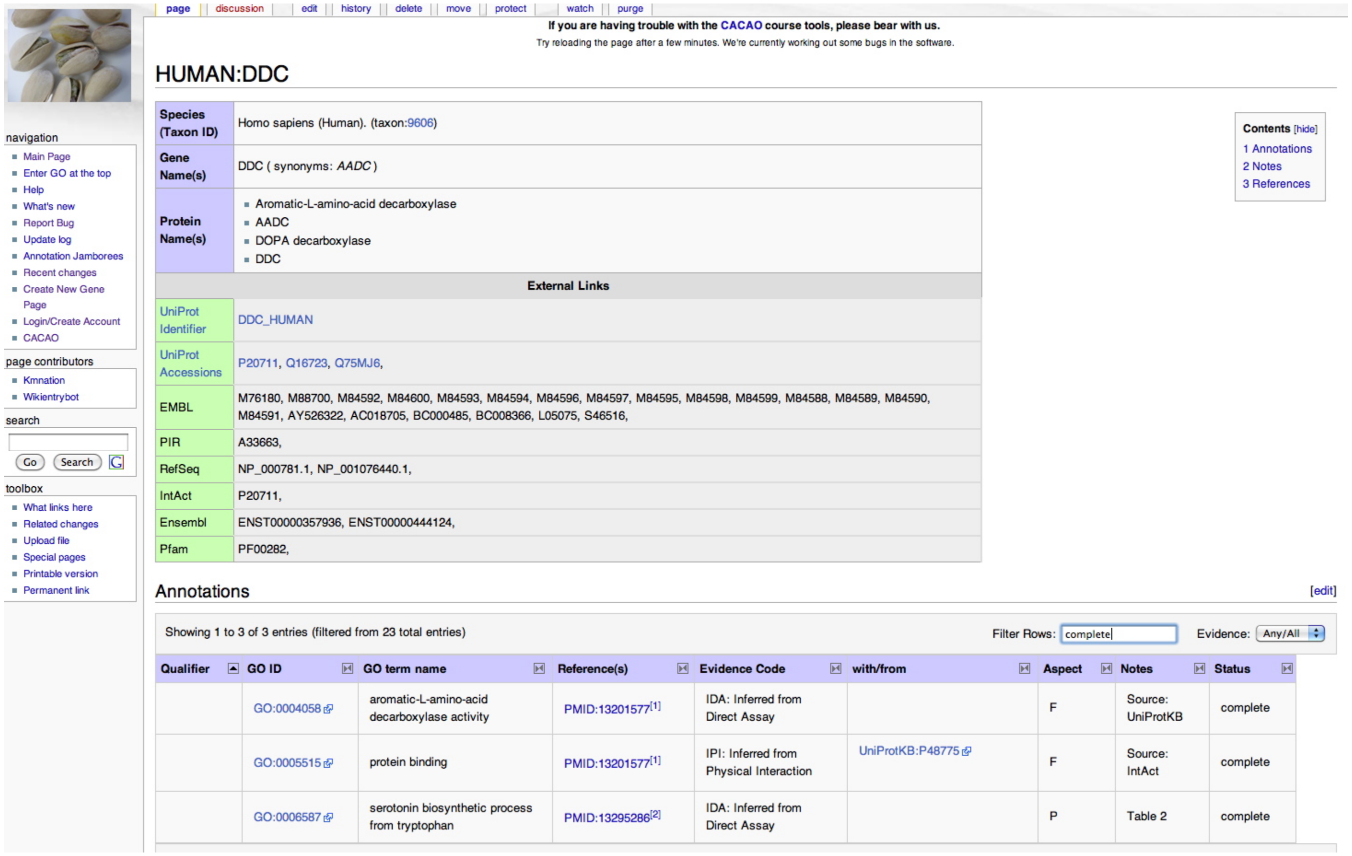
C cont.

- CHICK:A6N241
- CHICK:A6N242
- CHICK:A6N8N7
- CHICK:A6QR74
- CHICK:A6YIJ1
- CHICK:A6YIJ2
- CHICK:A6YJX2
- CHICK:A6YJX3

C cont.

- CHICK:AT134
- CHICK:AT1A1
- CHICK:AT1A2
- CHICK:AT1A3
- CHICK:AT1B1
- CHICK:AT1B3
- CHICK:AT2A1
- CHICK:AT2A2

Annotation on GONUTS



If you are having trouble with the CACAO course tools, please bear with us.

Try reloading the page after a few minutes. We're currently working out some bugs in the software.

HUMAN:DDC

Species (Taxon ID)	Homo sapiens (Human). (taxon:9606)
Gene Name(s)	DDC (synonyms: *AADC*)
Protein Name(s)	Aromatic-L-amino-acid decarboxylase AADC DOPA decarboxylase DDC
External Links	
UniProt Identifier	DDC_HUMAN
UniProt Accessions	P20711, Q16723, Q75MJ6,
EMBL	M76180, M88700, M84592, M84600, M84593, M84594, M84596, M84597, M84595, M84598, M84599, M84588, M84589, M84590, M84591, AY526322, AC018705, BC000485, BC008366, L05075, S46516,
PIR	A33663,
RefSeq	NP_000781.1, NP_001076440.1,
IntAct	P20711,
Ensembl	ENST00000357936, ENST00000444124,
Pfam	PF00282,

Annotations

Showing 1 to 3 of 3 entries (filtered from 23 total entries)

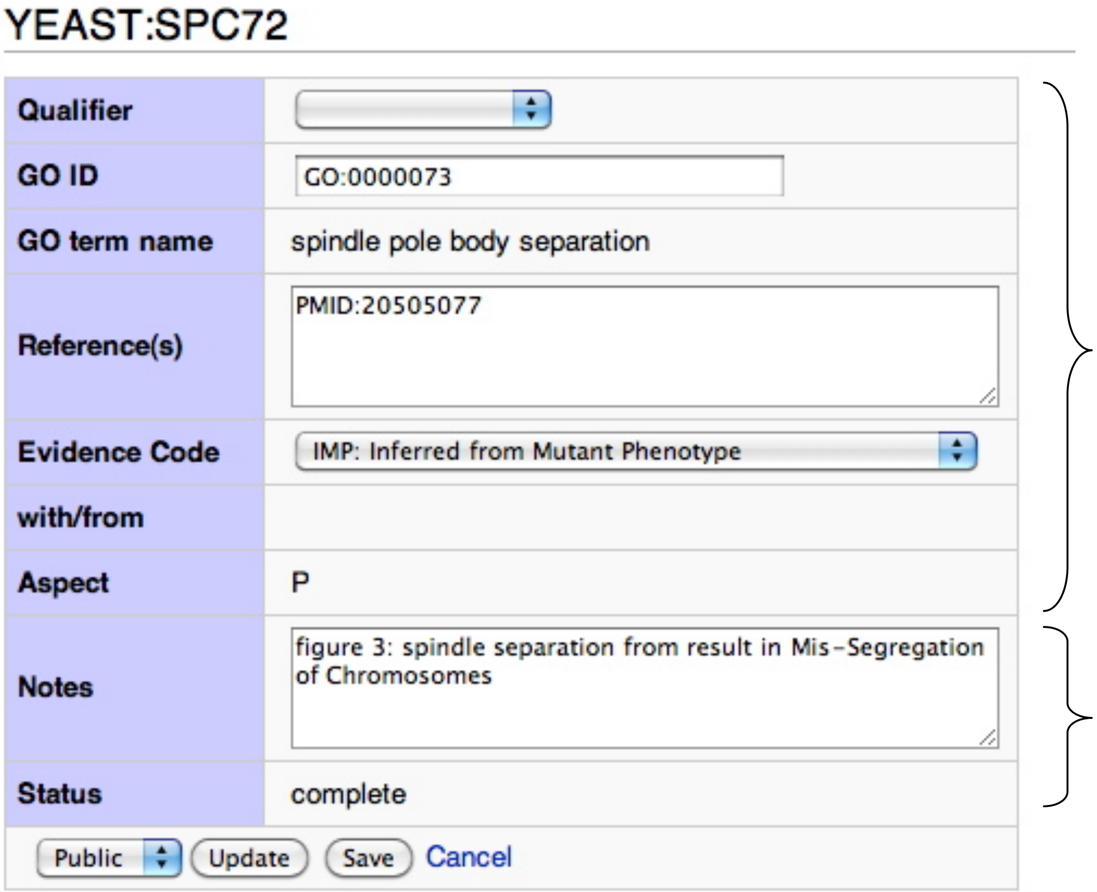
Filter Rows: complete

Evidence: Any/All

Qualifier	GO ID	GO term name	Reference(s)	Evidence Code	with/from	Aspect	Notes	Status
	GO:0004058	aromatic-L-amino-acid decarboxylase activity	PMID:13201577[1]	IDA: Inferred from Direct Assay		F	Source: UniProtKB	complete
	GO:0005515	protein binding	PMID:13201577[1]	IPI: Inferred from Physical Interaction	UniProtKB:P48775	F	Source: IntAct	complete
	GO:0006587	serotonin biosynthetic process from tryptophan	PMID:13295286[2]	IDA: Inferred from Direct Assay		P	Table 2	complete

- Users can create gene pages for anything in UniProt.
    - New gene pages are populated with information, including previous GO annotations.

Annotation on GONUTS



YEAST:SPC72

Qualifier	
GO ID	GO:0000073
GO term name	spindle pole body separation
Reference(s)	PMID:20505077
Evidence Code	IMP: Inferred from Mutant Phenotype
with/from	
Aspect	P
Notes	figure 3: spindle separation from result in Mis-Segregation of Chromosomes
Status	complete

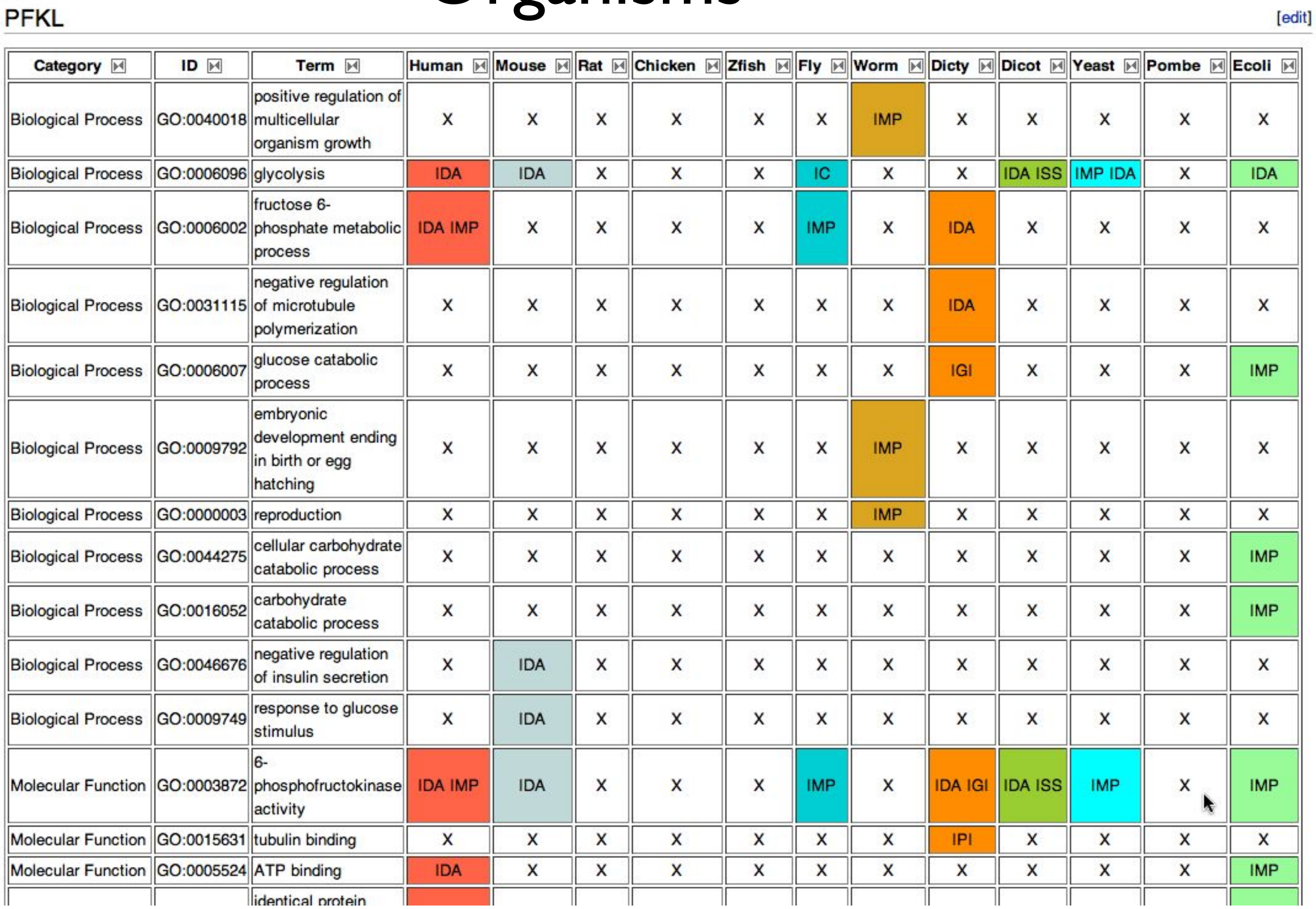
Submitted to
GO consortium

Viewable on
GONUTS

Comparing annotations

Organisms →

GO Terms ↓



PFKL

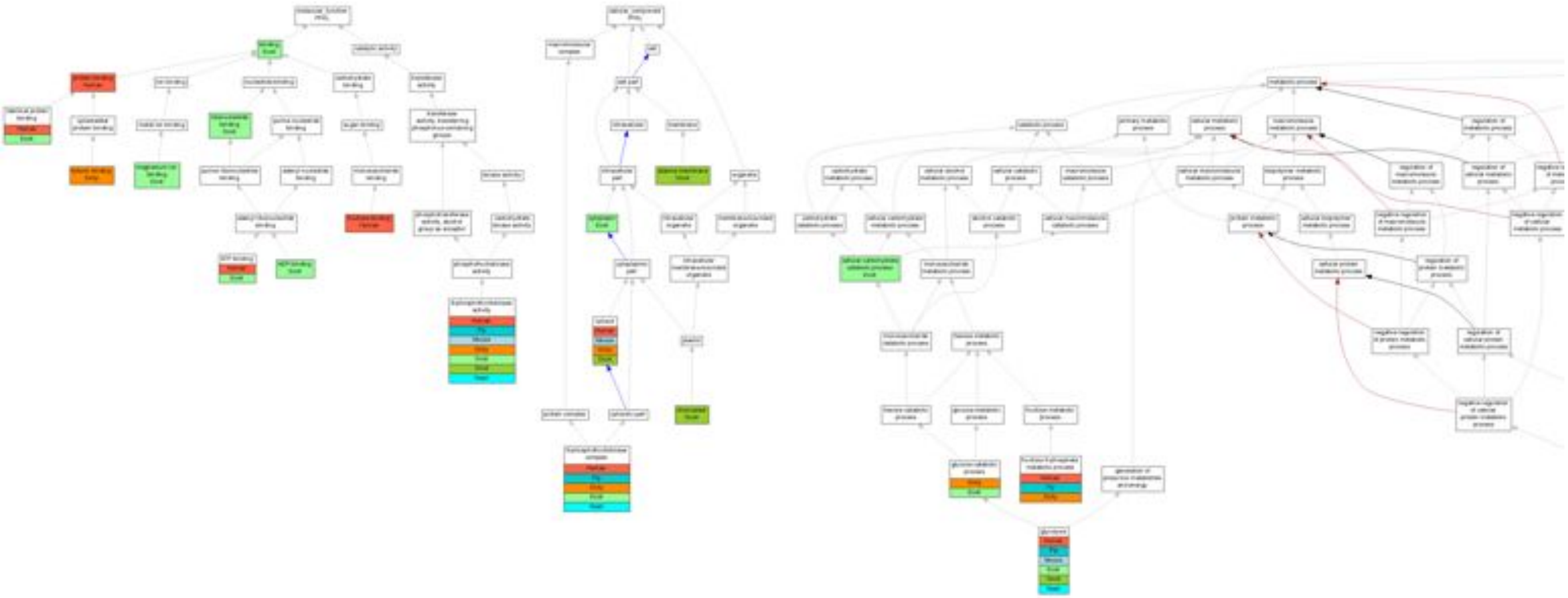
[edit]

Category	ID	Term	Human	Mouse	Rat	Chicken	Zfish	Fly	Worm	Dicty	Dicot	Yeast	Pombe	Ecoli
Biological Process	GO:0040018	positive regulation of multicellular organism growth	X	X	X	X	X	X	IMP	X	X	X	X	X
Biological Process	GO:0006096	glycolysis	IDA	IDA	X	X	X	IC	X	X	IDA ISS	IMP IDA	X	IDA
Biological Process	GO:0006002	fructose 6-phosphate metabolic process	IDA IMP	X	X	X	X	IMP	X	IDA	X	X	X	X
Biological Process	GO:0031115	negative regulation of microtubule polymerization	X	X	X	X	X	X	X	IDA	X	X	X	X
Biological Process	GO:0006007	glucose catabolic process	X	X	X	X	X	X	X	IGI	X	X	X	IMP
Biological Process	GO:0009792	embryonic development ending in birth or egg hatching	X	X	X	X	X	X	IMP	X	X	X	X	X
Biological Process	GO:0000003	reproduction	X	X	X	X	X	X	IMP	X	X	X	X	X
Biological Process	GO:0044275	cellular carbohydrate catabolic process	X	X	X	X	X	X	X	X	X	X	X	IMP
Biological Process	GO:0016052	carbohydrate catabolic process	X	X	X	X	X	X	X	X	X	X	X	IMP
Biological Process	GO:0046676	negative regulation of insulin secretion	X	IDA	X	X	X	X	X	X	X	X	X	X
Biological Process	GO:0009749	response to glucose stimulus	X	IDA	X	X	X	X	X	X	X	X	X	X
Molecular Function	GO:0003872	6-phosphofructokinase activity	IDA IMP	IDA	X	X	X	IMP	X	IDA IGI	IDA ISS	IMP	X	IMP
Molecular Function	GO:0015631	tubulin binding	X	X	X	X	X	X	X	IPI	X	X	X	X
Molecular Function	GO:0005524	ATP binding	IDA	X	X	X	X	X	X	X	X	X	X	IMP
		identical protein												

EcoliWiki

TEXAS A&M UNIVERSITY

Comparing annotations



Thanks to Mary Dolan @ MGI

Outline

- Using Mediawiki vs. Wikipedia

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  - Background
  - Function
  - Use cases

- Categories
  - As ontologies
  - GONUTS

- Educational Resource
  - Community Assessment of Community Annotation with Ontologies (CACAO)

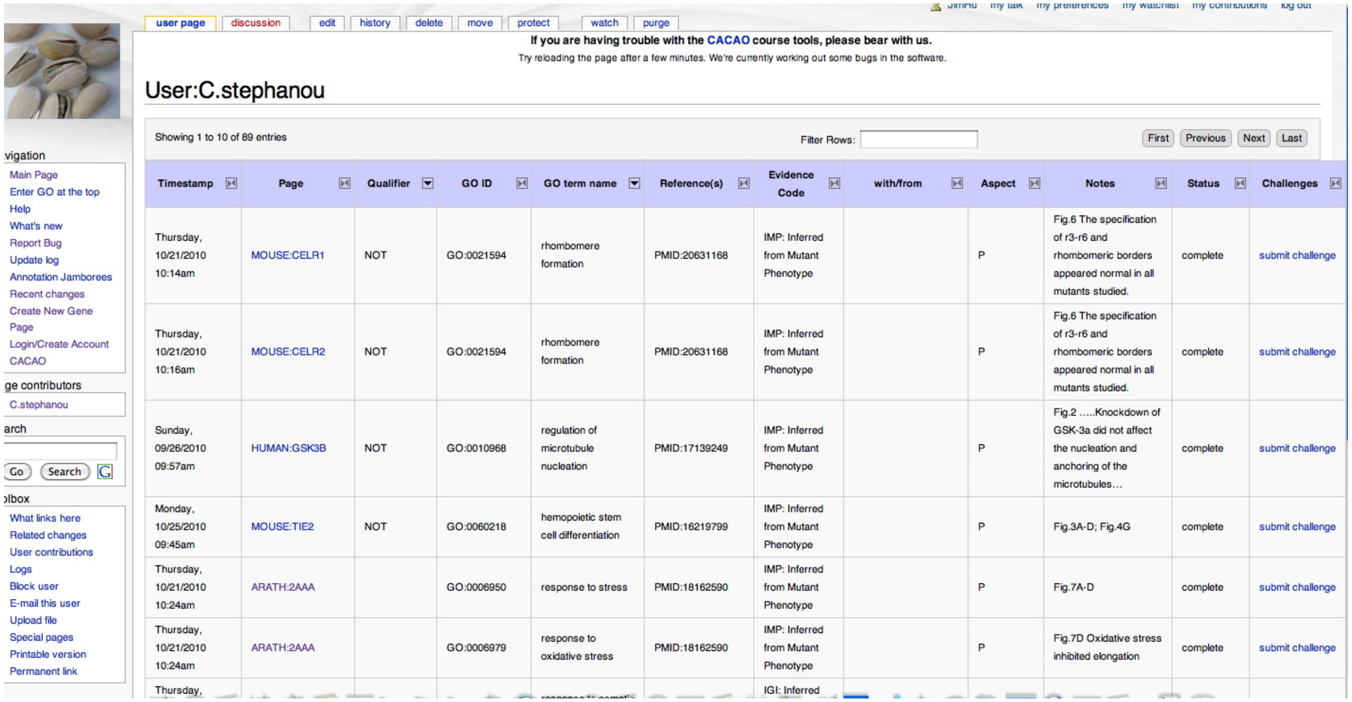
CACAO

coupling annotation to teaching credit

- Teams of students curate
- Faculty supervision
- Support from our team
- Intramural or Intercollegiate competition
- Distributed annotation jamborees
- Assessment via surveys and wiki data-mining

April 2010	(CACAO v0.1)	117 / 153
Fall semester		? / 757

Tracking the players/teams



JimHu my talk my preferences my watchlist my contributions log out

user page | discussion | edit | history | delete | move | protect | watch | purge

If you are having trouble with the CACAO course tools, please bear with us.

Try reloading the page after a few minutes. We're currently working out some bugs in the software.

User:C.stephanou

vigation
- Main Page
- Enter GO at the top
- Help
- What's new
- Report Bug
- Update log
- Annotation Jamborees
- Recent changes
- Create New Gene Page
- Login/Create Account
- CACAO

ge contributors
- C.stephanou

arch

lbox
- What links here
- Related changes
- User contributions
- Logs
- Block user
- E-mail this user
- Upload file
- Special pages
- Printable version
- Permanent link

Showing 1 to 10 of 89 entries

Filter Rows:

Timestamp	Page	Qualifier	GO ID	GO term name	Reference(s)	Evidence Code	with/from	Aspect	Notes	Status	Challenges
Thursday, 10/21/2010 10:14am	MOUSE:CELR1	NOT	GO:0021594	rhombomere formation	PMID:20631168	IMP: Inferred from Mutant Phenotype		P	Fig.6 The specification of r3-r6 and rhombomeric borders appeared normal in all mutants studied.	complete	submit challenge
Thursday, 10/21/2010 10:16am	MOUSE:CELR2	NOT	GO:0021594	rhombomere formation	PMID:20631168	IMP: Inferred from Mutant Phenotype		P	Fig.6 The specification of r3-r6 and rhombomeric borders appeared normal in all mutants studied.	complete	submit challenge
Sunday, 09/26/2010 09:57am	HUMAN:GSK3B	NOT	GO:0010968	regulation of microtubule nucleation	PMID:17139249	IMP: Inferred from Mutant Phenotype		P	Fig.2 .....Knockdown of GSK-3a did not affect the nucleation and anchoring of the microtubules…	complete	submit challenge
Monday, 10/25/2010 09:45am	MOUSE:TIE2	NOT	GO:0060218	hemopoietic stem cell differentiation	PMID:16219799	IMP: Inferred from Mutant Phenotype		P	Fig.3A-D; Fig.4G	complete	submit challenge
Thursday, 10/21/2010 10:24am	ARATH:2AAA		GO:0006950	response to stress	PMID:18162590	IMP: Inferred from Mutant Phenotype		P	Fig.7A-D	complete	submit challenge
Thursday, 10/21/2010 10:24am	ARATH:2AAA		GO:0006979	response to oxidative stress	PMID:18162590	IMP: Inferred from Mutant Phenotype		P	Fig.7D Oxidative stress inhibited elongation	complete	submit challenge
Thursday,						IGI: Inferred					

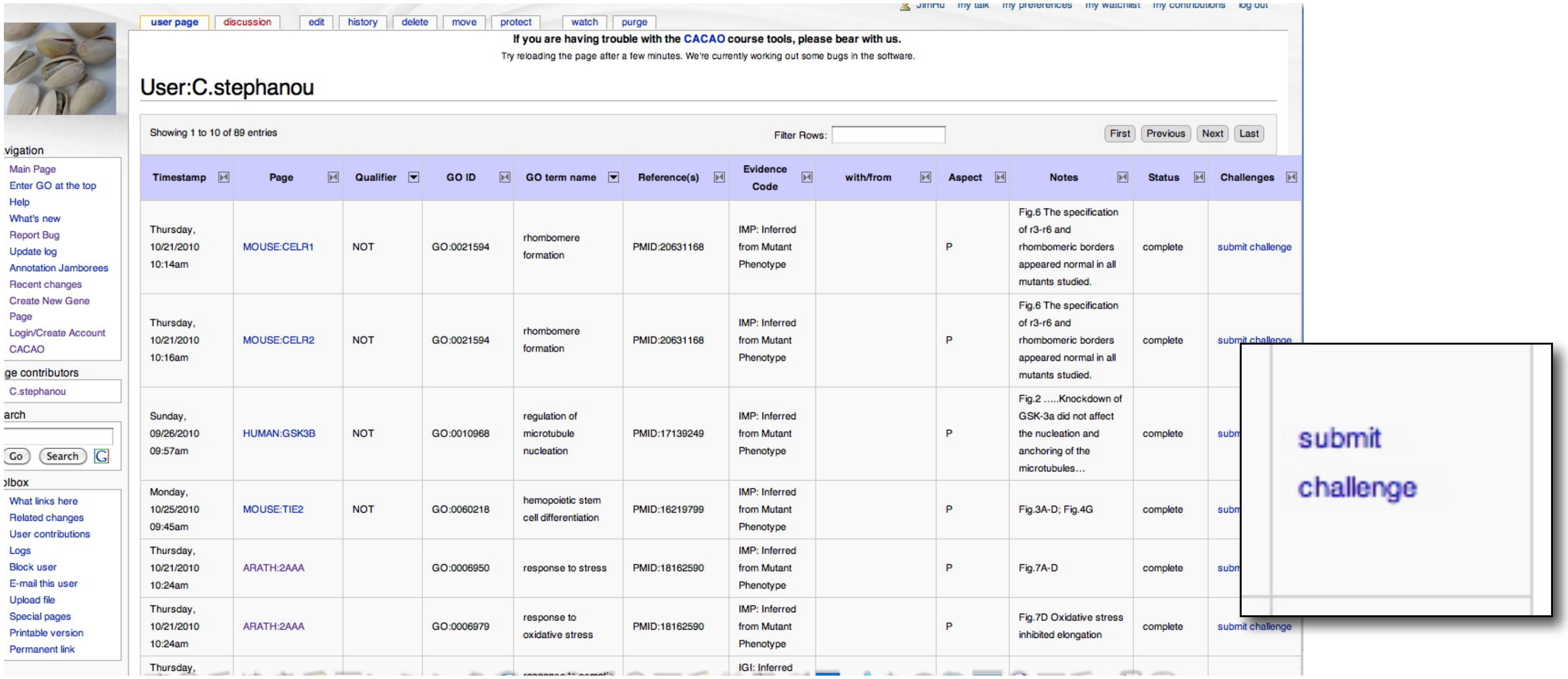
- An extension tag added to a user page identifies all the annotations made by that user

<myAnnotations />

EcoliWiki

TEXAS A&M UNIVERSITY

Tracking the players/teams



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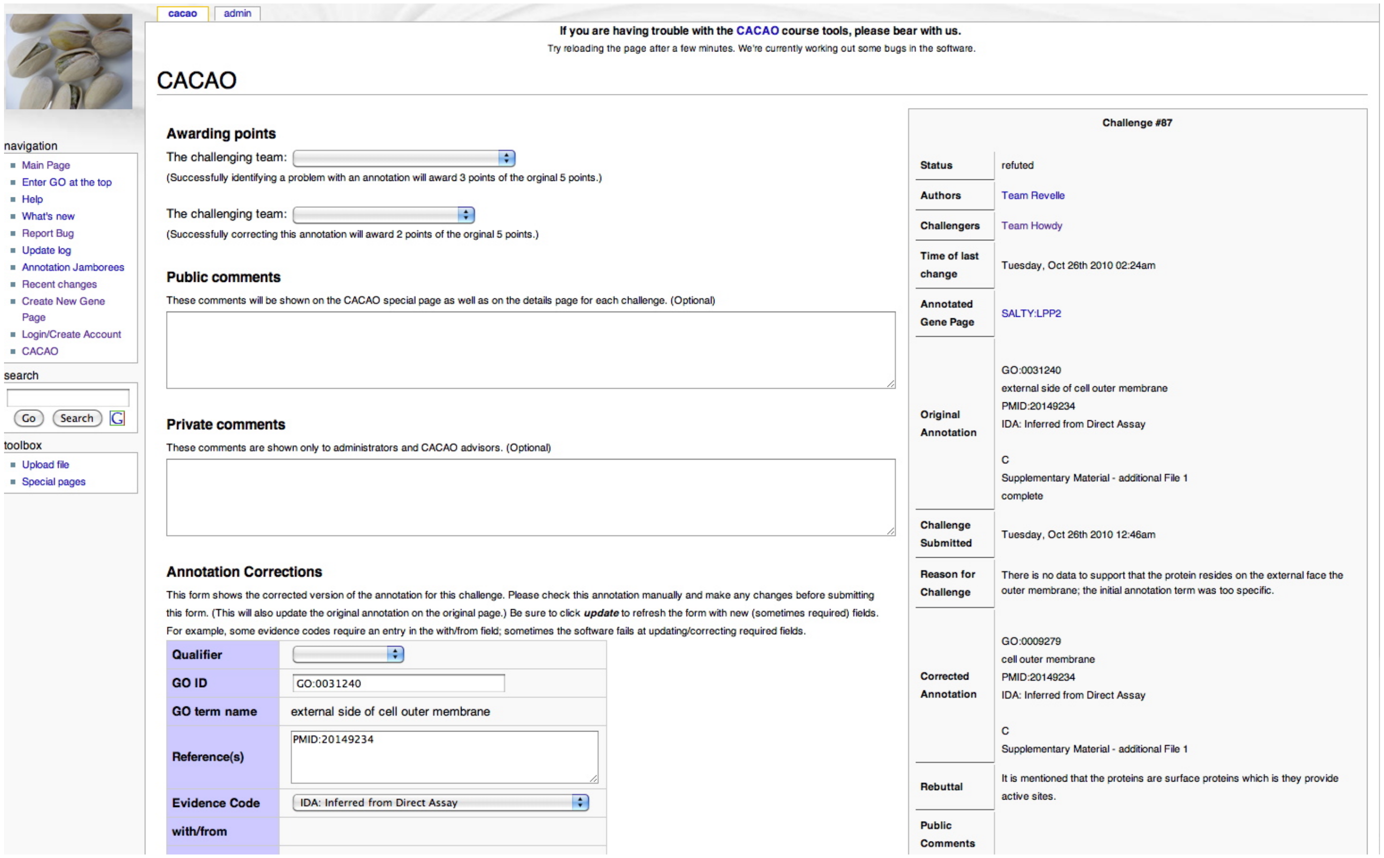
Judgement



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CACAO

Awarding points

The challenging team:

(Successfully identifying a problem with an annotation will award 3 points of the orginal 5 points.)

The challenging team:

(Successfully correcting this annotation will award 2 points of the orginal 5 points.)

Public comments

These comments will be shown on the CACAO special page as well as on the details page for each challenge. (Optional)

Private comments

These comments are shown only to administrators and CACAO advisors. (Optional)

Annotation Corrections

This form shows the corrected version of the annotation for this challenge. Please check this annotation manually and make any changes before submitting this form. (This will also update the original annotation on the original page.) Be sure to click ***update*** to refresh the form with new (sometimes required) fields. For example, some evidence codes require an entry in the with/from field; sometimes the software fails at updating/correcting required fields.

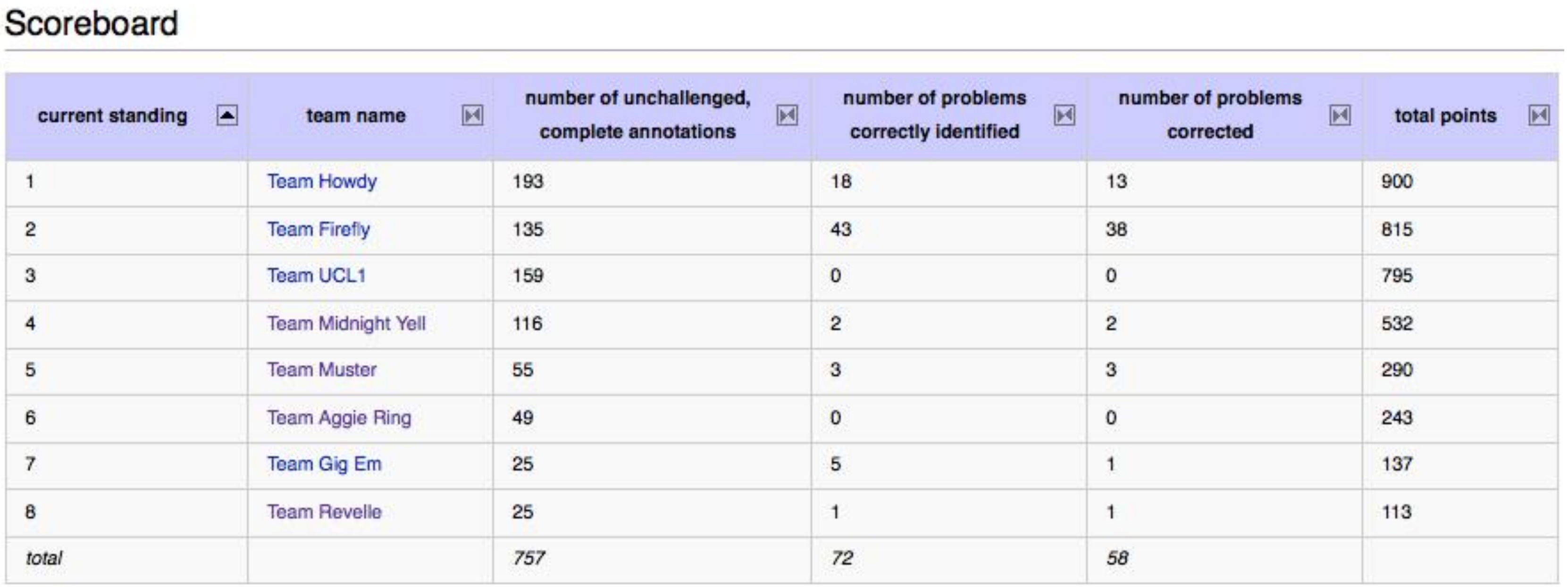
Qualifier	
GO ID	GO:0031240
GO term name	external side of cell outer membrane
Reference(s)	PMID:20149234
Evidence Code	IDA: Inferred from Direct Assay
with/from	

Challenge #87

Status	refuted
Authors	Team Revelle
Challengers	Team Howdy
Time of last change	Tuesday, Oct 26th 2010 02:24am
Annotated Gene Page	SALTY:LPP2
Original Annotation	GO:0031240 external side of cell outer membrane PMID:20149234 IDA: Inferred from Direct Assay C Supplementary Material - additional File 1 complete
Challenge Submitted	Tuesday, Oct 26th 2010 12:46am
Reason for Challenge	There is no data to support that the protein resides on the external face the outer membrane; the initial annotation term was too specific.
Corrected Annotation	GO:0009279 cell outer membrane PMID:20149234 IDA: Inferred from Direct Assay C Supplementary Material - additional File 1
Rebuttal	It is mentioned that the proteins are surface proteins which is they provide active sites.
Public Comments	

- Mentors with curator experience judge the challenges/rebuttals

Overall scoreboard

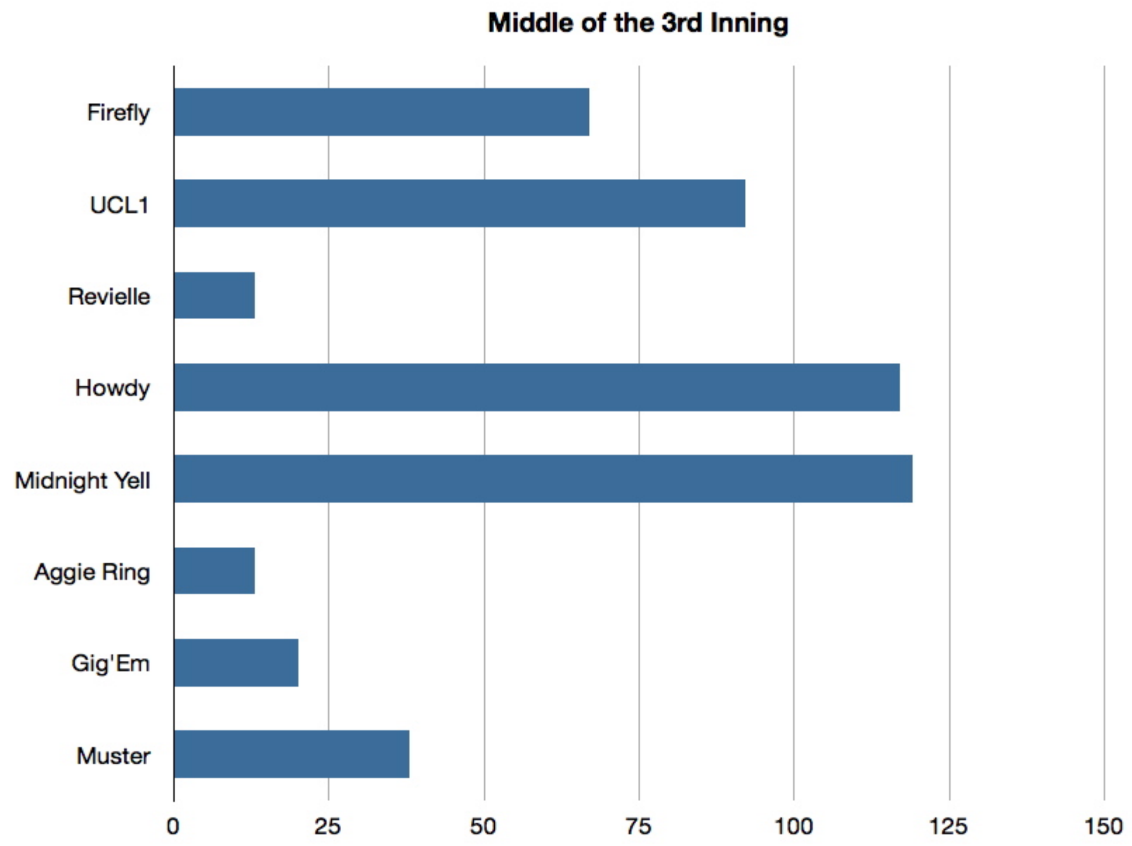


Scoreboard

current standing	team name	number of unchallenged, complete annotations	number of problems correctly identified	number of problems corrected	total points
1	Team Howdy	193	18	13	900
2	Team Firefly	135	43	38	815
3	Team UCL1	159	0	0	795
4	Team Midnight Yell	116	2	2	532
5	Team Muster	55	3	3	290
6	Team Aggie Ring	49	0	0	243
7	Team Gig Em	25	5	1	137
8	Team Revelle	25	1	1	113
total		*757*	*72*	*58*	

- A scoreboard page gathers information about all teams and challenges

Students want to win



- The lead has been changing hands every inning

Acknowledgements

- EcoliWiki/GONUTS Team
  - Jim Hu, P.I.
  - Debby Siegele, co-P.I.
  - Brenley McIntosh
  - Adrienne Zweifel
  - Dave Clements
  - Nathan Liles
  - Amanda Supak
  - Chanchala Lairikyengbam
  - Joy Wang
- CACAO
  - Mentors at University College London
  - undergrads / grad students