CACAO training part 2

Jim Hu and Suzi Aleksander For UW Parkside Fall 2014

Outline for today

- Making annotations
- The CACAO scoreboards
 - Session page
 - Team page
 - User page
- Making challenges

Log in



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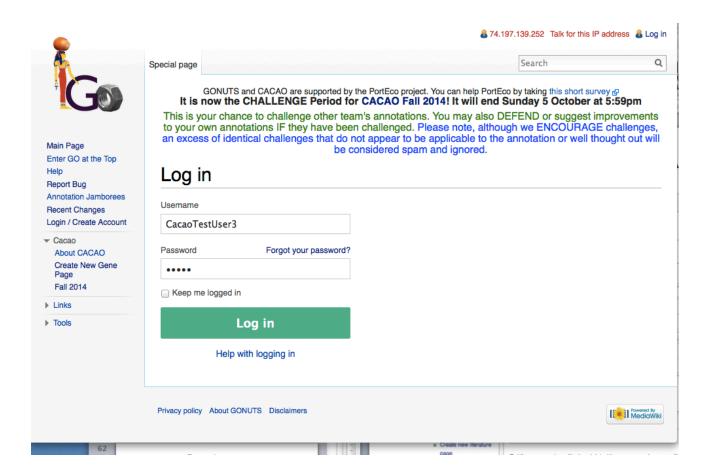
Links

page contributors

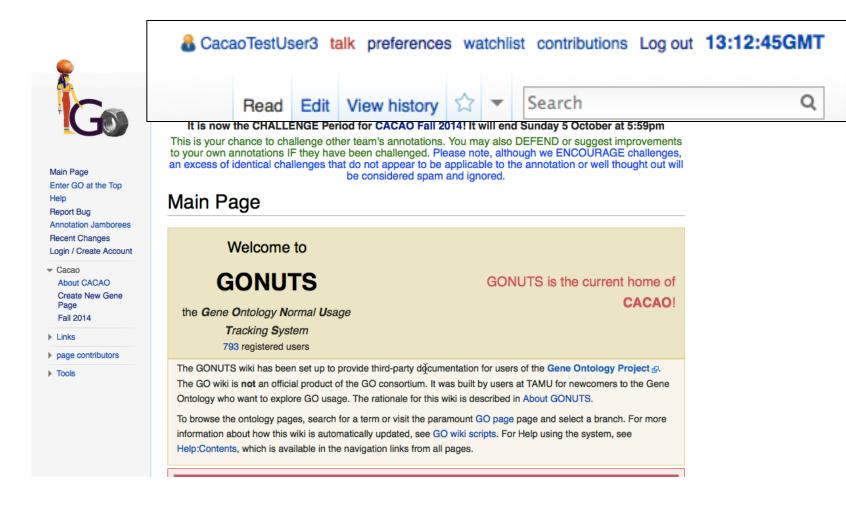
Tools

			8 74.197.13	9.252 Talk for t	this IP address Log	in 13:07:39GMT			
Mai	n Page Discus	Read	View source	View history	Search	Q			
	It is now This is your to your own annotations in they have been chanenged. Heasenole, annotation or well thought out will an excess of identical challenges that do not appear to be applicable to the annotation or well thought out will be considered spam and ignored. Main Page								
-	G the Gene O Tra	/elcome to ONUT Ontology Nor acking Systemer registered us	TS mal Usage em	GON	UTS is the current home of CACAO !				
ſ	The GONUTS wiki has been set up to provide third-party difficumentation for users of the Gene Ontology Project a. The GO wiki is not an official product of the GO consortium. It was built by users at TAMU for newcomers to the Gene Ontology who want to explore GO usage. The rationale for this wiki is described in About GONUTS. To browse the ontology pages, search for a term or visit the paramount GO page page and select a branch. For more information about how this wiki is automatically updated, see GO wiki scripts. For Help using the system, see Help:Contents, which is available in the navigation links from all pages.								





Log in



• Review

- Log in on GONUTS
- Find paper (PMID) and protein (UniProt)
 - Create a reference/PMID page
- Create gene page
- Edit the annotations table: Add a row
 - GO ID
 - Evidence
 - With/from if needed
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 - Note

PMID pages

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Main Page

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k

PMID:24955762

Citation

Abstract

Links

Keywords edit table

Korczynska, M, Xiang, DF, Zhang, Z, Xu, C, Narindoshvili, T, Kamat, SS, Williams, HJ, Chang, SS, Kolb, P, Hillerich, B, Sauder, JM, Burley, SK, Almo, SC, Swaminathan, S, Shoichet, BK and Raushel, FM (2014) Functional annotation and structural characterization of a novel lactonase hydrolyzing Dxylono-1,4-lactone-5-phosphate and L-arabino-1,4-lactone-5-phosphate. *Biochemistry* 53:4727-38

A novel lactonase from Mycoplasma synoviae 53 (MS53_0025) and Mycoplasma agalactiae PG2 (MAG_6390) was characterized by protein structure determination, molecular docking, gene context analysis, and library screening. The crystal structure of MS53_0025 was determined to a resolution of 2.06 Å. This protein adopts a typical amidohydrolase (β/a)8-fold and contains a binuclear zinc center located at the C-terminal end of the β -barrel. A phosphate molecule was bound in the active site and hydrogen bonds to Lys217, Lys244, Tyr245, Arg275, and Tyr278. Both docking and gene context analysis were used to narrow the theoretical substrate profile of the enzyme, thus directing empirical screening to identify that MS53_0025 and MAG_6390 catalyze the hydrolysis of d-xylono-1,4-lactone-5-phosphate (2) with kcat/Km values of 4.7 × 10(4) and 5.7 × 10(4) M(-1) s(-1) and I-arabino-1,4-lactone-5-phosphate (7) with kcat/Km values of 1.3 × 10(4) and 2.2 × 10(4) M(-1) s(-1), respectively. The identification of the substrate profile of these two phospho-furanose lactonases emerged only when all methods were integrated and therefore provides a blueprint for future substrate identification of highly related amidohydrolase superfamily members.

Abstract and full text links are automatically created

4 See also

5 References

Significance [edit]

Annotations [edit] Showing 1 to 2 of 2 entries Filter Rows: Evidence: Any/All \$								
Gene product	Qualifier 💧	GO ID 🔶	GO term name	Evidence Code	with/from 🔶	Aspect ≬	Notes	Status 🔶
MYCAP:A5IZ80		GO:0050490 🥵	1,4- lactonase activity	IDA: Inferred from Direct Assay		F	Table 3 shows kinetic parameters for Mag6390 with various substrates	complete

Anywhere the reference is used in an annotation table is shown

PubMed @ PMC4108184 @ Online version:10.1021/bi500595c @

How to create PMID pages

- Search and click the red link
- Make a reference in a table and click the link in a citation
- Edit the URL in the browser
- If you get a message that there is no text, reload the page!

Search r	esults			
PMID:24955762			8 Sear	ch
Content pages	Multimedia	Help and Project pages	Everything	Advanced
There were no res	sults matching	g the query.		
Create the page	" <u>PMID:2495</u>	T62" on this wiki!		
		PMID:24955762 (page does	not exist)	

TITLE 2014 Has HUW CILLED. FICASE DE DA

• Review

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Create a gene page



Create a gene page



Special page

Search

GONUTS and CACAO are supported by the PortEco project. You can help PortEco by taking this short survey It is now the CHALLENGE Period for CACAO Fall 2014! It will end Sunday 5 October at 5:59pm

This is your chance to challenge other team's annotations. You may also DEFEND or suggest improvements to your own annotations IF they have been challenged. Please note, although we ENCOURAGE challenges, an excess of identical challenges that do not appear to be applicable to the annotation or well thought out will be considered spam and ignored.

Create New Gene Page

To create a new gene page, please select a database and enter a unique identifier such as an ID or an accession number. Please be patient, creating a page may take up to 30 seconds.

Create Page

[edit]

Q I

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 corresponding UniProt Accession using in-house tools adapted from the documentation listed here 🗗.

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RHOS4:Q3IVY4

Species (Taxon ID)Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / N 8253 / DSM158). (272943 🔄)						
Gene Name(s) No Information Provided.						
Protein Name(s) Resiniferatoxin-binding, phosphotriesterase-related protein						
External Links						
UniProt Q3IVY4						
EMBL	CP000144					
RefSeq	YP_355201.1					
PDB	3K2G					
PDBsum 3K2G						



- 1 Annotations
- 2 Notes

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3 References

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• Review

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 - Reference
 - Note

Showing 1	to 5 of 5 entries						Filter Rows: Evidenc	e: Any/All
ualifier 🏾	GO ID	GO term name	Reference	Evidence Code	with/from	Aspect	Notes	Status
	GO:0008270	zinc ion binding	GO_REF:0000002 අ	IEA: Inferred from Electronic Annotation	InterPro:IPR001559 ଜ InterPro:IPR017947 ଜ	F	Seeded From UniProt	
	GO:0009056	catabolic process	GO_REF:0000002 &	IEA: Inferred from Electronic Annotation	InterPro:IPR001559 ₪ InterPro:IPR017947 ₪	Ρ	Seeded From UniProt	
	GO:0016788	hydrolase activity, acting on ester bonds	GO_REF:0000002 @	IEA: Inferred from Electronic Annotation	InterPro:IPR017947 &	F	Seeded From UniProt	
	GO:0046872	metal ion binding	GO_REF:0000038 &	IEA: Inferred from Electronic Annotation	UniProtKB- KW:KW-0479 &	F	Seeded From UniProt	
	GO:0016788	hydrolase activity, acting on ester bonds	PMID:24832101 ^[1]	IDA: Inferred from Direct Assay		F	Table2 shows kinetic parameters for various substrates. The broad GO term is used as the enzyme acts on carboxylate, phoshphate and phosphonate esters.	complet

Showing 1 to 5 of 5 entries								Filter Rows: Evidence:			
*	Qualifier 💧	GO ID 💧	GO term name	Reference	Evidence Code	with/from	Aspect 💧	Notes 🔶	Status		
Copy protected		GO:0016788	hydrolase activity, acting on ester bonds	GO_REF:0000002	IEA: Inferred from Electronic Annotation	InterPro:IPR017947	F	Seeded From UniProt			
Copy		GO:0046872	metal ion binding	GO_REF:0000038	IEA: Inferred from Electronic Annotation	UniProtKB- KW:KW-0479	F	Seeded From UniProt			
Edit Copy Delete Move Row Dublic		GO:0016788	hydrolase activity, acting on ester bonds	PMID:24832101	IDA: Inferred from Direct Assay		F	Table2 shows kinetic parameters for various substrates. The broad GO term is used as the enzyme acts on carboxylate, phoshphate and phosphonate esters.	complete		
Copy protected		GO:0008270	zinc ion binding	GO_REF:0000002	IEA: Inferred from Electronic Annotation	InterPro:IPR001559 InterPro:IPR017947	F	Seeded From UniProt			
Copy		GO:0009056	catabolic process	GO_REF:0000002	IEA: Inferred from Electronic Annotation	InterPro:IPR001559 InterPro:IPR017947	Р	Seeded From UniProt			

Add row Add multiple

Edit row form

TableEdit

ECOLI:PARC

Qualifier	÷						
GO ID	GO:0003918						
GO term name	DNA topoisomerase type II (ATP-hydrolyzing) activity						
Reference	PMID: + 8227000						
Evidence Code	IDA: Inferred from Direct Assay \$						
with/from							
Aspect	F						
Notes	Topoisomerase assay in Fig 3. ATP dependent decatenation means it is a Type II from Fig 4						
Status	complete						
Public Refresh Save Row Cancel							
1							

GO term warnings

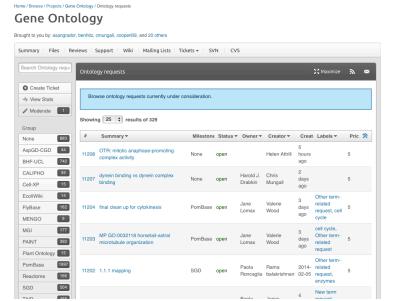
- We don't allow terms that tend to get misused
 - Binding terms
 - Should be used where the binding function by itself is the relevant function
 - Not for substrates and cofactors
 - Response to terms
 - Should be used where the gene product is used to do something in response to the stimulus/stress
 - Not just for changes in gene expression
- Watch out for taxonomy problems
 - Sometimes GO definitions are too specific for eukaryotes or mammals
 - Something that sounds OK isn't
 - Problem can be in the parent terms!

Do you need a new GO term?

- Sometimes things are missing in GO
- BUT, GO is not intended to capture everything.
 - DO: propose new terms for functions, processes, and components that express general concepts
 - DON'T: propose terms that are too specific
 - examples.
 - regulation of expression of a specific gene
 - Phosphorylation of a specific protein (as opposed to a class of proteins)

If you need a new GO term

- http://sourceforge.net
 - Gene Ontology project > Ticket tracker > More > Ontology requests
- New term request
 - "NTR:" in subject
 - Definition
 - Where in the ontology
 - Explanation of why it is needed w/reference(s)



If you need a new GO term

- <u>http://go.termgenie.org</u>
- Use when the new term follows one of the template patterns
 - e.g. regulation
- Gives a temp GO ID
 - This will NOT be in GONUTS right away

TermGenie

TermGenieGO is a tool for creating new terms for the GeneOntology. It uses a pattern-based approach to rapidly generate new te appropriately within the ontology structure. All terms are reviewed by a senior editor before the final commit to the ontology.

For more details on how to use and register for TermGenie, please have a look at the TermGenieGO help pages.

- Step 1: Ontology Status GeneOntology
- Step 2: Templates

Once you have selected the ontology, the available term generation patterns can be selected from a menu. Select Template regulation: biological_process · Add template View in Tree

After selecting and filling templates, click on the 'Verify Input'-Button below to start the next step.

Step	3:	Review	and	Submit

• Step 4: Final matters

Impressum Error Console

If you need a new GO term

- Annotate to a less specific term
 - Include in your note either
 - Link to sourceforge ticket
 - TermGenie temp ID
- Ask us for help with these!

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<u>ا ا</u>	Step	3:	Review	and	Submit
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 Step	4:	Final	matter

Impressum Error Console

Only during annotation periods



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CACAO Error

Error

Special page

Cacao is currently not in an annotation period. No annotations are allowed by students participating in Cacao. If you feel this message was reached in error, please contact one of your instructors or a system administrator.

Privacy policy About GONUTS Disclaimers



Q

Save the row AND save the table

RHOS4:Q3IVY4	4	
Changes are not saved permanently until you save the table back to the wiki page		
Showing 1 to 6 of 6 entries		Filter Rows:

*	Qualifier 🔶	GO ID 💧 ≬	GO term name	Reference 🔶	Evidence Code	with/from	Aspect	Notes
Copy protected		GO:0016788	hydrolase activity, acting on ester bonds	GO_REF:0000002	IEA: Inferred from Electronic Annotation	InterPro:IPR017947	F	Seed
Copy protected		GO:0046872	metal ion binding	GO_REF:0000038	IEA: Inferred from Electronic Annotation	UniProtKB- KW:KW-0479	F	Seed
Edit Copy Delete		GO:0016788	hydrolase activity,	PMID:24832101	IDA: Inferred from Direct		F	Table parar subst term

Outline for today

- Making annotations
- The CACAO scoreboards
 - Session page
 - Team page
 - User page
- Making challenges

Session Scoreboard

Scoreboard	Round 5 A	nnotations	Round	5 Challenges	Round 5 Need Asses	sment	Round 5
Team		Inning 5 Sta	nding 🔺	Inning 5 Points	Overall Standing	Overall Points	
Team Don't be an	ino-hating	1		93	2	204	
Team Buster McT	hunderstick	2		81	4	121	
Team Go Pro		3		70	1	259	
Team I got Krebs		4		62	3	203	
Team Pitbull Hurr	icanes	5		25	6	75	
Team JAAM		6		22	7	58	
Team Niraali		7		20	5	86	
Team Ecoli		8		15	9	40	
Team Stones Thre	w	9		11	13	32	
Team Loony Toon	s	10		10	14	31	
Team Protein Pus	hers	11		8	12	33	
Team WhiteShyPa	aulCo	11		8	15	30	
Team Hu Ville		12		7	16	23	
Team Bucky Love	rs	13		5	11	34	
Team Diffusion of	Responsibility	13		5	23	5	
Team Despicable	Us	14		0	17	22	
Team Bucky's Bug	gs	14		0	22	10	
Team Bcereus		14		0	19	18	

Session Scoreboard

Scoreb	oard Round	5 Annotations	Round 5 Challenges	Round 5 Need As	ssessment		Round	5 +
Showing	1 to 10 of 202 e	ntries				First Prev	ious 1 2 3 4 5 Next	Last
Status 🍦	Page	User 🍦	Date/Time	GO Term (Aspect)	Reference	Evidence 🍦	Notes	Links
0	PIG:IL6	Drl5141, Team Go Pro	2013-11-04 08:55:36 CST	GO:2000866 - positive regulation of estradiol secretion (P)	PMID:24139936	IDA	Day 15 and 16 of Pregnancy figure 4 show that increased IL-6 leads to increased estradiol 17beta secretion.	challenge
0	PIG:IL1B	Dri5141, Team Go Pro	2013-11-04 08:58:57 CST	GO:2000866 - positive regulation of estradiol secretion (P)	PMID:24139936	IDA	Day 15 and 16 of Figure 4 show that increased IL-1beta resulted in an increase in estradiol 17 beta	challenge
0	PIG:TNFA	Dri5141, Team Go Pro	2013-11-04 09:02:33 CST	GO:2000866 - positive regulation of estradiol secretion (P)	PMID:24139936	IDA	Figure 4.	challenge
8	MYXVL:MT5	Kohli3, Team WhiteShyPaulCo	2013-11-04 09:27:39 CST	GO:0016032 - viral process (P)	PMID:8676463	IMP	Figure 5. Defective growth of M-T5- virus in a CD4+ rabbit T-cell line (RL5).	challenge
0	MYXVL:MT5	Kohli3, Team WhiteShyPaulCo	2013-11-04 09:57:33 CST	GO:0019050 - suppression by virus of host apoptosis (P)	PMID:8676463	ІМР	Figure 7.	challenge

Session Scoreboard

Round 5 Annota	ations Round	d 5 Challenges	Round 5 Need	d Assessment			Roun	d 5 ÷
of 5 entries (filtered	l from					First Previous	i Ne	xt Last
Challenging User,Group	Date Last Challenged	Page 🍦	GO Term (Aspect)	Reference	Evidence	Reason for Last Challenge	Links	History
Larichardson, Team WhiteShyPaulCo	2013-11-17 16:45	HUMAN:TRAIP	GO:0034504 - protein localization in nucleus (P)	PMID:19151749	IMP	Shown in Figure 6. The GO TERM is not correct it should be that in TRIP negatively regulates the TNF-mediated activation of NF-kB which is the GO term GO:0050709 which is negative regulation of protein secretion.	challenge or judge	C: 1 A: 3
Roosheel, Team I got Krebs	2013-11-17 16:06	HUMAN:KSYK	GO:0005737 - cytoplasm (C)	PMID:19151749	IDA	I think the qualifier is not needed?	challenge or judge	C: 1 A: 3
Roosheel, Team I got Krebs	2013-11-14 17:06	HUMAN: KSYK	GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P)	PMID:19151749	IMP	Evidence code should be IMP	challenge or judge	C: 1 A: 4
Roosheel, Team I got Krebs	2013-11-14 17:04	HUMAN:NLRC3	GO:0032715 - negative regulation of interleukin-6 production (P)	PMID:22863753	IMP	PMID: 22863753	challenge or judge	C: 2 A: 5
Meganmikkelson, Team Don't be anno-hating	2013-11-12 20:05	PIG:TNFA	GO:2000866 - positive regulation of estradiol secretion (P)	PMID:24139936	IDA	Missing Figure. Notes should include Figure 4	challenge or judge	C: 1 A: 2
	of 5 entries (filtered User,Group Larichardson, Team WhiteShyPaulCo Roosheel, Team I got Krebs Roosheel, Team I got Krebs Roosheel, Team I got Krebs	Challenging User, Group Date Last Challenged Larichardson, Team WhiteShyPaulCo 2013-11-17 16:45 Roosheel, Team I got Krebs 2013-11-14 16:06 Roosheel, Team I got Krebs 2013-11-14 17:06 Roosheel, Team I got Krebs 2013-11-14 17:06 Roosheel, Team I got Krebs 2013-11-14 17:06 Roosheel, Team I got Krebs 2013-11-14 Roosheel, Team I got Krebs 2013-11-14 Roosheel, Team I got Krebs 2013-11-14 Team Don't be 2013-11-12	Challenging User,Group Date Last Challenged Page Larichardson, Team WhiteShyPaulCo 2013-11-17 16:45 HUMAN:TRAIP Roosheel, Team I got Krebs 2013-11-17 16:06 HUMAN:KSYK Roosheel, Team I got Krebs 2013-11-14 17:06 HUMAN:KSYK Roosheel, Team I got Krebs 2013-11-14 17:06 HUMAN:KSYK Roosheel, Team I got Krebs 2013-11-14 17:04 HUMAN:KSYK Roosheel, Team I got Krebs 2013-11-14 17:04 HUMAN:NLRC3 Roosheel, Team I got Krebs 2013-11-12 20:05 PIG:TNFA	Challenging User,Group Date Last Challenged Page GO Term (Aspect) Larichardson, Team WhiteShyPaulCo 2013-11-17 16:45 HUMAN:TRAIP GO:00034504 - protein localization in nucleus (P) Roosheel, Team I got Krebs 2013-11-17 16:06 HUMAN:KSYK GO:0005737 - cytoplasm (C) Roosheel, Team I got Krebs 2013-11-14 17:06 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) Roosheel, Team I got Krebs 2013-11-14 17:06 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) Roosheel, Team I got Krebs 2013-11-14 17:04 HUMAN:NLRC3 HUMAN:NLRC3 GO:0032715 - negative regulation of interleukin-6 production (P) Meganmikkelson, Team Don't be anno-hating 2013-11-12 20:05 PIG:TNFA GO:2000866 - positive regulation	Challenging User,Group Date Last Challenged Page GO Term (Aspect) Reference Larichardson, Team WhiteShyPaulCo 2013-11-17 16:45 HUMAN:TRAIP HUMAN:TRAIP GO:0034504 - protein localization in nucleus (P) PMID:19151749 Roosheel, Team I got Krebs 2013-11-17 16:06 HUMAN:KSYK GO:0005737 - cytoplasm (C) PMID:19151749 Roosheel, Team I got Krebs 2013-11-14 17:06 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) PMID:19151749 Roosheel, Team I got Krebs 2013-11-14 17:04 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) PMID:22863753 Roosheel, Team I got Krebs 2013-11-12 20:05 PIG:TNFA GO:2000866 - positive regulation of estradiol PMID:24139936	Challenging User, Group Date Last Challenged Page GO Term (Aspect) Reference Evidence Larichardson, Team WhiteShyPaulCo 2013-11-17 16:45 HUMAN:TRAIP Distance GO:0034504 - protein localization in nucleus (P) PMID:19151749 IMP Roosheel, Team I got Krebs 2013-11-17 16:06 HUMAN:KSYK GO:0005737 - cytoplasm (C) PMID:19151749 IDA Roosheel, Team I got Krebs 2013-11-14 17:06 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) PMID:19151749 IDA Roosheel, Team I got Krebs 2013-11-14 17:06 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) PMID:19151749 IMP Roosheel, Team I got Krebs 2013-11-14 17:04 HUMAN:NLRC3 GO:0032715 - negative regulation of interleukin-6 production (P) PMID:22863753 IMP Meganmikkelson, anno-hating 2013-11-12 20:05 PIG:TNFA GO:2000866 - positive regulation of estradiol PMID:24139936 IDA	Previous Challenging User,Group Date Last Challenged Page GO Term (Aspect) Reference Evidence Reason for Last Challenge Larichardson, Team WhiteShyPaulCo 2013-11-17 HUMAN:TRAIP GO:0034504 - protein localization in nucleus (P) PMID:19151749 IMP Shown in Figure 6. The GO TERM is not correct it should be that in TRJP negatively regulates the TNF-mediated activation of NF-kB which is the GO term GO:0050709 which is negative regulates the TNF-mediated activation of NF-kB which is negative regulation of protein secretion. Roosheel, Team I got Krebs 2013-11-14 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) PMID:19151749 IMP Evidence code should be IMP Roosheel, Team I got Krebs 2013-11-14 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) PMID:19151749 IMP Evidence code should be IMP Roosheel, Team I got Krebs 2013-11-14 HUMAN:KSYK GO:0010803 - regulation of tumor necrosis factor-mediated signaling pathway (P) PMID:19151749 IMP Evidence code should be IMP Ream I got Krebs 2013-11-14 HUMAN:NLRC3 GO:00132715 - negative regulation of interleukin-6 production (P) PMID:22863753 IMP MID: 22863753 Meganmikkelson, ano-hating 20:05 //ro	Instruction Instruction

Team scoreboards

Status 🍦	Page	User	Date/Time	GO Term (Aspect)	Reference	Evidence	Notes	Links
0	CAEEL:APN1	Jlensmire, Team Protein Pushers	2013-09-14 21:18:52 CDT	GO:0006284 - base-excision repair (P)	PMID:22819077	ISA with/from UniProtKB:P22936	Figure 1 shows C.elegans APN-1 shows homology to Yeast Apn1, which is involved in DNA repair	challeng
0	EBOZM:VP40	Lleopold, Team Protein Pushers	2013-09-14 22:23:23 CDT	GO:0046788 - egress of virus within host cell (P)	PMID:23297401	IMP	Figure 8	challeng
0	CAEEL:APN1	Jlensmire, Team Protein Pushers	2013-09-15 11:59:26 CDT	GO:0017005 - 3'-tyrosyl-DNA phosphodiesterase activity (F)	PMID:22819077	IDA	Figure 10C shows that APN-1 exhibits a 3' repair diesterase activity	challeng
0	CAEEL:APN1	Jlensmire, Team Protein Pushers	2013-09-15 12:17:10 CDT	GO:0006284 - base-excision repair (P)	PMID:22819077	IDA	Figure 10 shows that APN-1 has the ability to repair various DNA lesions	challeng
Ô	BOMMO:Q5CCJ5	Jlensmire, Team Protein Pushers	2013-09-15 12:36:31 CDT	GO:0008284 - positive regulation of cell proliferation (P)	PMID:23781494	IDA	Figure 6	challeng
0	SALTI:MGTC	Jlensmire, Team Protein Pushers	2013-09-15 13:21:17 CDT	GO:0009405 - pathogenesis (P)	PMID:19436747	IMP	Figure 2. MgtC mutants showed decreased survival in human cells as compared to the WT	challeng
•	EBOZM:VP40	Lleopold, Team Protein Pushers	2013-09-25 16:53:47 CDT	GO:0019076 - release of virus from host (P)	PMID:23297401	IMP	Figure 2B, 2C show that when certain key amino acids are mutated (L213A, L295A, V298A) they do not induce the same amount of surface pressure into the plasma membrane as compared to WT	challeng

User scoreboards

User:Lleopold

My Annotations

tatus 🍦	Page	Date/Time	GO Term (Aspect)	Reference	Evidence	Notes	Links
0	HPV16:VE5	2013-10-13 10:09:56 CDT	GO:0005886 - plasma membrane (C)	PMID:19712955	IDA	Figure 3 shows localization to the plasma membrane via immunofluorescence data	challenge
0	HPV16:VE5	2013-10-13 10:32:31 CDT	GO:0019048 - modulation by virus of host morphology or physiology (P)	PMID:20686024	IDA	Figure 8 depicts the inhibition of endoscme vesicle fusion by HP16 E5 protein	challenge
0	EBOZM:VP40	2013-09-25 16:53:47 CDT	GO:0019076 - release of virus from host (P)	PMID:23297401	IMP	Figure 2B, 2C show that when cortain key amino acids are mutated (L213A, L295A, V298A) they do not induce the same amount of surface pressure into the plasma membrane as compared to WT	challenge
0	EBOZM:VP40	2013-11-10 15:34:32 CST	GO:0020002 - host cell plasma membrane (C)	PMID:23297401	IMP	Figure 8: Western blots of cells transfected with WT VP40 and several hydrophobic mutants demonstrate that C-terminal domain plasma membrane penetration is critical for viral egress.	challenge
0	EBOZM:VP40	2013-09-25 17:11:46 CDT	GO:0031235 - intrinsic component of the cytoplasmic side of the plasma membrane (C)	PMID:23297401	IMP	Figure 3	challenge
0	EBOZM:VP40	2013-09-14 22:23:23 CDT	GO:0046788 - egress of virus within host cell (P)	PMID:23297401	IMP	Figure 8	challenge
0	HPV16:VE5	2013-11-10 14:52:22 CST	GO:0072657 - protein localization in membrane (P)	PMID:19712955	IDA	Figure 3 shows protein localization to the plasma membrane via immunofluresence assay	challenge

Annotations challenged by Lleopold

Showin	ig 1 to 3 of 3 entries					First	Previous	s 1 Next	L
Status	Author, Group	Page 🔻	GO Term (Aspect)	Reference	Evide	nce	Links	Page history	
0	Smahoney2, Team Pitbull Hurricanes		GO:0043190 - ATP-binding cassette (ABC) transporter complex (C)	PMID:24169575	IMP		challenge	C: 1	

Outline for today

- Making annotations
- The CACAO scoreboards
 - Session page
 - Team page
 - User page
- Making challenges

« Previo	us Annotatio	in								Next Annotation
Qualifier	GO ID	GO	term name	Reference	Evidence Code	with	Aspect	Notes	Status	
	GO:0000155 p	hosphorela	ty sensor kinase activity	PMID:15916958	IMP: Inferred from Mutant Phenotype		Molecular Function	Fig. 1 & Fig. 6.	complete	
	n made on page roup Team Rubb		E6Z3 n 2014-03-02 13:56:03	CST.						
History	Points	s Ne	ew Challenge							
Entry Type	Challeng		Time/Date 🔻		Challenge	e Reaso	n			Points/Assessmen
Private Assessment	Suzialeksa	inder	2014-05-22 16:34:16 CDT	You need to be a	an instructor to view these notes.					Requires Changes x Protein
Private Assessment	Suzialeksa	inder	2014-04-16 16:22:31 CDT	You need to be a	an instructor to view these notes.					Corrected Through Challenges > Protein > Publication > Qualifier - Go term > Evidence + With/From > Notes - Unique/Original
Challenge	Jonathanc, Team Rubi		2014-04-12 17:14:35 CDT	Notes are insuffi	cient.					0
Public Assessment	Briddle24		2014-04-01 19:51:44 CDT	Megans earns cr	edit for the annotation.					Corrected Through Challenges > Protein > Publication > Qualifier - Go term > Evidence - With/From > Notes - Unique/Original
Challenge	Megans, Team Rubb	by ducky			re 2A - Shows that when LuxP is r ry low levels of bioluminescence e					4

- There are many ways to get to the challenge view
- You will see a history of the challenges and assessments
- If the judges have already looked at it, there will be clues about what we think is good and bad about this annotation

Cacao

« Previous Annotation

Next Annotation »

Qualifier	GO ID	GO term name	Reference	Evidence Code	with	Aspect	Notes	Status
	GO:0050490	1,4-lactonase activity	PMID:24955762	IDA: Inferred from Direct Assay		Molecular Function	Table 3 shows kinetic parameters for Ms0025 with various substrates	complete
		ge: MYCS5:Q4A724 noth) on 2014-09-21 1						

History	Points	New Challenge	New Assessment	Fix Annotation	
Please prov	ide the reas	son for this challenge	and any supporting evid	dence. Please enter p	laintext or wikitext, no HTML.
(ĥ
Submit a ne	w challenge				

- Explain what is wrong
 - As with annotations, the default is that your challenge is wrong unless you can convince us clearly
- You can use wikitext markup in your challenge
 - Useful for links:
 - Internal link [[page_name]]
 - Internal link with link text [[page_name|link text]]
 - Category page links need a ':' prefix
 - External link [[URL link text]]
 - Examples:
 - link to a GO term [[:Category:GO:0050490_!_1,4-lactonase_activity] Category:GO:0050490_!_1,4-lactonase_activity]]
 - Link to a UniProt page [http://www.uniprot.org/uniprot/Q4A724 Q4A724]
 - Links and wikitext are not required (but they make life easier)

- You cannot lose points for making bad challenges
 - But you will annoy the judges if you are not thoughtful
- Look at the other challenges
 - Whoever challenges a particular aspect of the annotation first gets credit, UNLESS
 - The later challenge does a better job of correcting the whole annotation
- Try to figure out if the annotation is fixable
 - If you can't salvage part of the annotation, the "fix" should be a new annotation.

What the judges do

GONUTS		Cacao - (GONUTS		Table	Edit – G	ONUTS dev 1.21	J	tetramer.tamu.edu / tetramer mysql A /	.]	+	
Qualifier	GO ID	GO term name	Reference	Evide	nce Code	with	Aspect		Notes	Statu	s	
	GO:0050490	1,4-lactonase activity	PMID:24955762	IDA: Inferr Assay	ed from Direct		Molecular Function	Table 3 sho substrates	ws kinetic parameters for Ms0025 with various	compl	ete	
		ge: MYCS5:Q4A724 noth) on 2014-09-21 1										

Did not check	Incorrect	Correct							
•	\bigcirc	\bigcirc	Protein						
•	\bigcirc	\bigcirc	Publication						
•	\bigcirc	\bigcirc	Qualifier						
	\bigcirc	\bigcirc	Go term						
•	\bigcirc	\bigcirc	Evidence						
	\bigcirc	\bigcirc	With/From						
$\overline{\bullet}$	\bigcirc	\bigcirc	Notes						
			Notes						
Please select the	t.		Unique/Original after checking each part	of the annotation. It	s not requir	ed that you	ı mark eac	h part of	the annotation
correct/incorrect	e appropriate t.	Assessme	Unique/Original after checking each part ent			-		h part of	the annotation
Please select the correct/incorrect Acceptable Unacceptable	e appropriate t.	Assessme	Unique/Original after checking each part			-		h part of	the annotation
Please select the correct/incorrect Acceptable Unacceptable Requires Changes	e appropriate t.	Assessme	Unique/Original after checking each part ent			-		h part of	the annotation
Please select the correct/incorrect Acceptable Unacceptable	e appropriate t.	Assessme	Unique/Original after checking each part ent which describes the curre	ent state of this annot	ation. This fi	ield is requi	red.		
Please select the correct/incorrect Acceptable Unacceptable Requires Changes Flagged	e appropriate t. s	Assessme om the list w	Unique/Original after checking each part ent	ent state of this annot	ation. This fi	ield is requi	red.		
Please select the correct/incorrect Acceptable Unacceptable Requires Changes Flagged Corrected Throug	e appropriate t. s	Assessme om the list w	Unique/Original after checking each part ent which describes the curre assessment, please sele	ent state of this annot	ation. This fi	ield is requi	red.		
Please select the correct/incorrect Acceptable Unacceptable Requires Changes Flagged Corrected Throug	e appropriate t. s	Assessme om the list w	Unique/Original after checking each part ent which describes the curre assessment, please sele	ent state of this annot	ation. This fi	ield is requi	red.		
Please select the correct/incorrect Acceptable Unacceptable Requires Changes Flagged Corrected Throug	e appropriate t. s	Assessme om the list w	Unique/Original after checking each part ent which describes the curre assessment, please sele	ent state of this annot	ation. This fi	ield is requi	red.		

Remember

- Asking for help is not cheating in CACAO
- Contact us: <u>ecoliwiki@gmail.com</u> is read by both Jim and Suzi