

## COMMUNITY CURATION

USING THE COMMUNITY ANNOTATION TOOL (CANTO)

Antonia Lock



## **COMMUNITY CURATION**

USING THE COMMUNITY ANNOTATION TOOL (CANTO)

<del>- Antonia Lock</del> Midori Harris

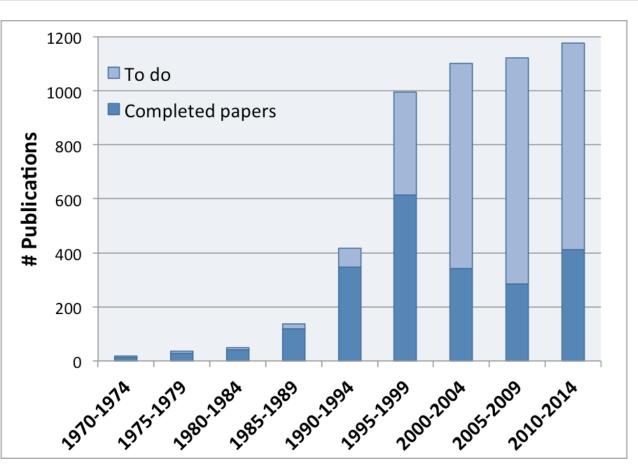
### **COMMUNITY CURATION**

# **PomBase**

- Authors supply draft annotations
- Online community annotation tool: Canto
- Curators review all submissions
- Launched 2012
- 270 submissions to date

## **CURATION STATUS**

# **PomBase**



- 5050 S. pombe publications contain information that we can curate
- We have completed 2200 of these (44%)

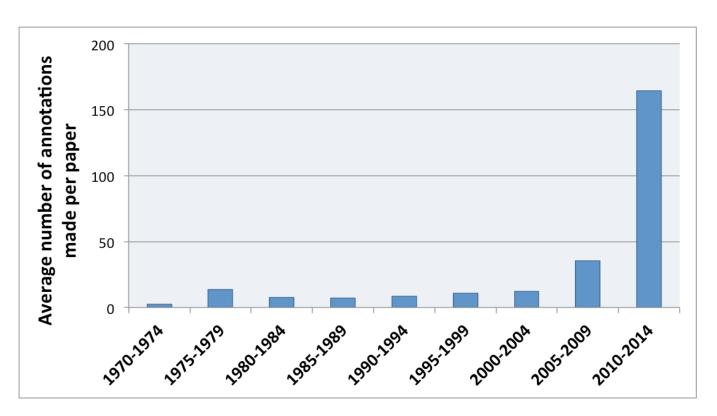
## WHY?

# **PomBase**

 Number of S. pombe papers published each year has reached a plateau

The amount of information contained in each paper

has not!

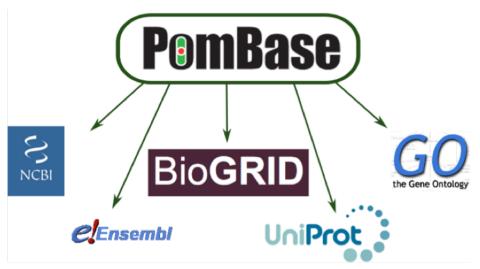


## WHY?

# **PomBase**

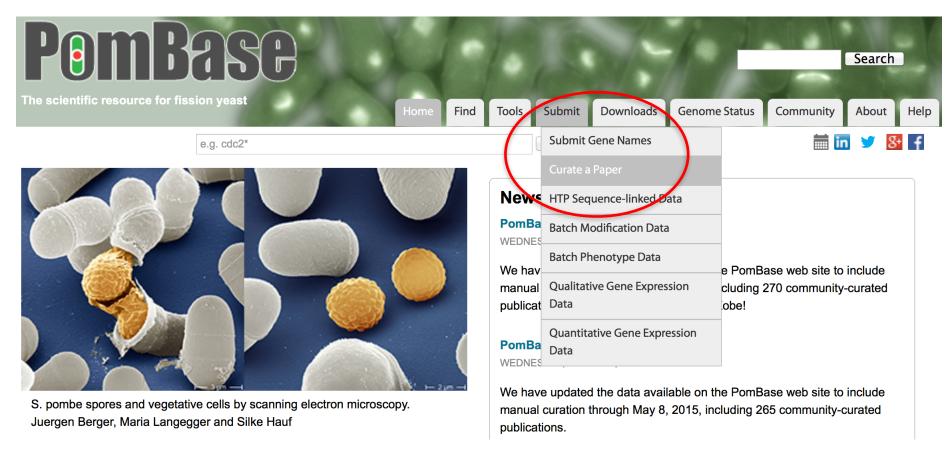
- Database benefits
  - Improved quality of annotations
  - Data assimilated more quickly
- User benefits
  - Improved understanding of formal data representation -> more efficient usage of database resources
  - Improved online visibility of publications due to information

propagation



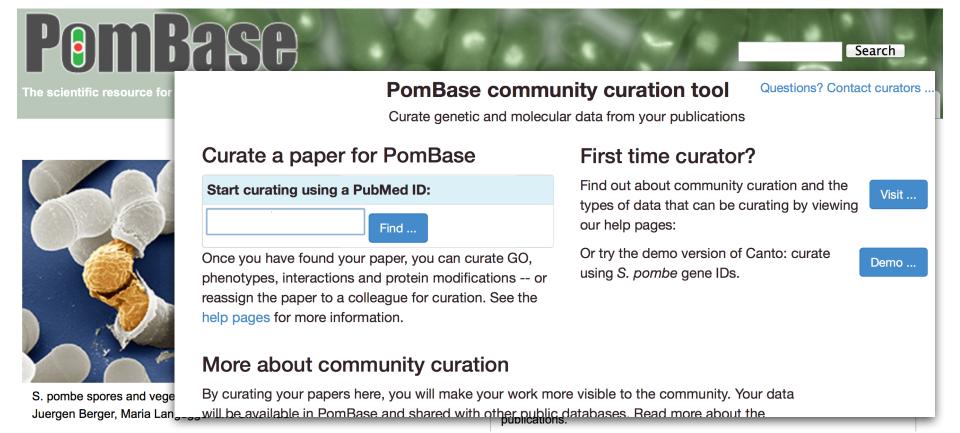
## **PomBase**

- Click the link in the invitation email or
- Go to <u>www.pombase.org</u>



## **PomBase**

- Click the link in the invitation email or
- Go to <u>www.pombase.org</u>





Abstract -

Mol Genet Genomics. 2003 Jul;269(4):437-42. Epub 2003 Apr 2.

A defect in a fatty acyl-CoA synthetase gene, lcf1+, results in a decrease in viability after entry into the stationary phase in fission yeast.

Oshiro T<sup>1</sup>, Aiba H, Mizuno T.

Author information

#### **Abstract**

An intriguing mutant was isolated in Schizosaccharomyces pombe, which is defective in the maintenance of viability after entry into the stationary phase. In the logarithmic growth phase, the mutant cells grow at the same rate as the parental cells. Upon the onset of the stationary phase, however, the mutant cells lose viability very rapidly. It was found that this phenotype was due to a mutational lesion in the lcf1+ gene, which encodes a long-chain fatty acyl-CoA synthetase. The lcf1Deltamutant shows pleiotropic phenotypes, in that they are also sensitive to high temperature (37 degrees C) and to high salt concentrations (0.9 M KCl) in the medium. Based on the fact that Lcf1 is highly homologous to Faa1 and Faa4 of Saccharomyces cerevisiae, both of which have previously been suggested to play roles in the maintenance of endogenous acyl-CoA pools, the possible function of Lcf1 in S. pombe is discussed.

PMID: 12684881 [PubMed - indexed for MEDLINE]

Dampose Send to: - SE

Abstract -

Mol Genet Genomics. 2003 Jul;269(4):437-42. Epub 2003 Apr 2.

## A defect in a fatty acyl-CoA synthetase gene, lcf1+, results in a decrease in viability after entry into the stationary phase in fission yeast.

Oshiro T<sup>1</sup>, Aiba H, Mizuno T.

#### Author information

#### **Abstract**

An intriguing mutant was isolated in Schizosaccharomyces pombe, after entry into the stationary phase. In the logarithmic growth phase parental cells. Upon the onset of the stationary phase, however, the that this phenotype was due to a mutational lesion in the lcf1+ gene synthetase. The lcf1Deltamutant shows pleiotropic phenotypes, in the degrees C) and to high salt concentrations (0.9 M KCl) in the mediu to Faa1 and Faa4 of Saccharomyces cerevisiae, both of which have maintenance of endogenous acyl-CoA pools, the possible function of

PMID: 12684881 [PubMed - indexed for MEDLINE]

#### PomBase community curation

Curate genetic and molecular data from your

#### Curate a paper for PomBase

Start curating using a PubMed ID:

12684881 Find ...

Once you have found your paper, you can curate GO, phenotypes teractions and protein modifications -- or reassign apper to a colleague for curation. See the help pa

#### First time

Find out about types of data our help page

Or try the der using S. pom

#### More about community curation

By curating your papers here, you will make your work more visible to the will be available in PomBase and shared with other public databases. Read

## PamR<sub>4</sub>Se

#### Create gene list for PMID:12684881

Please list the genes studied in this paper using the systematic identifier (eg. SPCC1739.10) or standard name (eg. cdc11) separated by commas, spaces, tabs or one per line.

lcf1 sty1

Back

Continue

■ This paper does not contain any gene-specific information

## **SUMMARY PAGE**

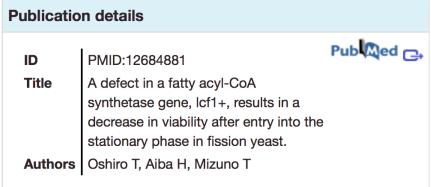
# **PomBase**

PomBase Canto
PMID:12684881 summary

#### **PMID:12684881 summary**

Questions? Contact curators ...





Pause curation

Submit to curators

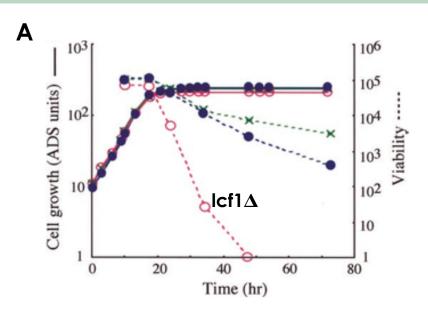
## ADDING ANNOTATIONS



All annotations are based on data from the publication

## PHENOTYPE DATA

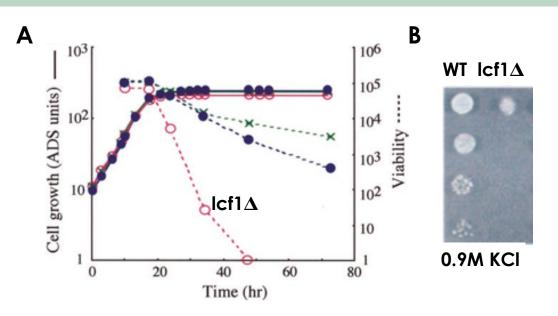
# **PomBase**



A: Loss of viability in stationary phase

## PHENOTYPE DATA

# **PomBase**

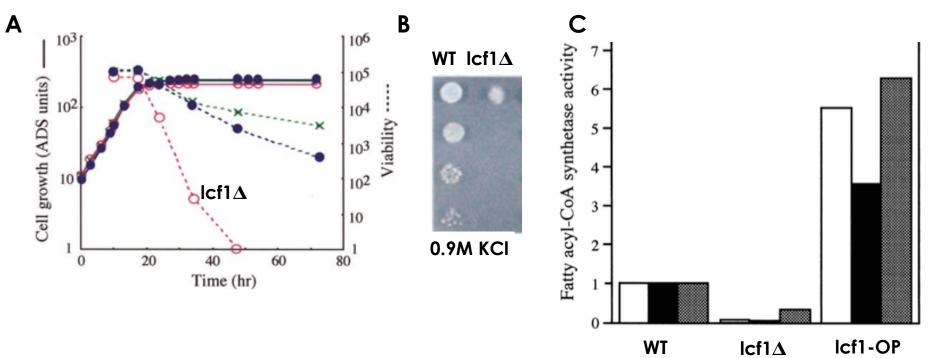


A: Loss of viability in stationary phase

**B:** Sensitive to salt stress

## PHENOTYPE DATA

# **PomBase**



A: Loss of viability in stationary phase

**B:** Sensitive to salt stress

 ${f C:}$  Decreased (lcf1 ${f \Delta}$ ) and increased (lcf1-OP) fatty acyl-CoA synthetase activity in cell extracts

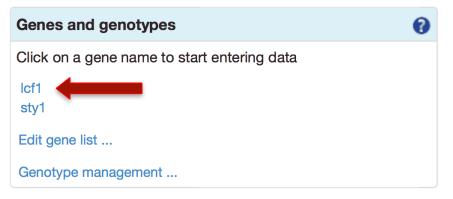
## **SUMMARY PAGE**

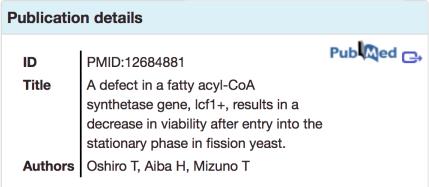
# **PomBase**

PomBase Canto
PMID:12684881 summary

#### PMID:12684881 summary

Questions? Contact curators ...





Pause curation

Submit to curators

## **CURATION TYPES**

▶ PomBase Canto

PMID:12684881 summary

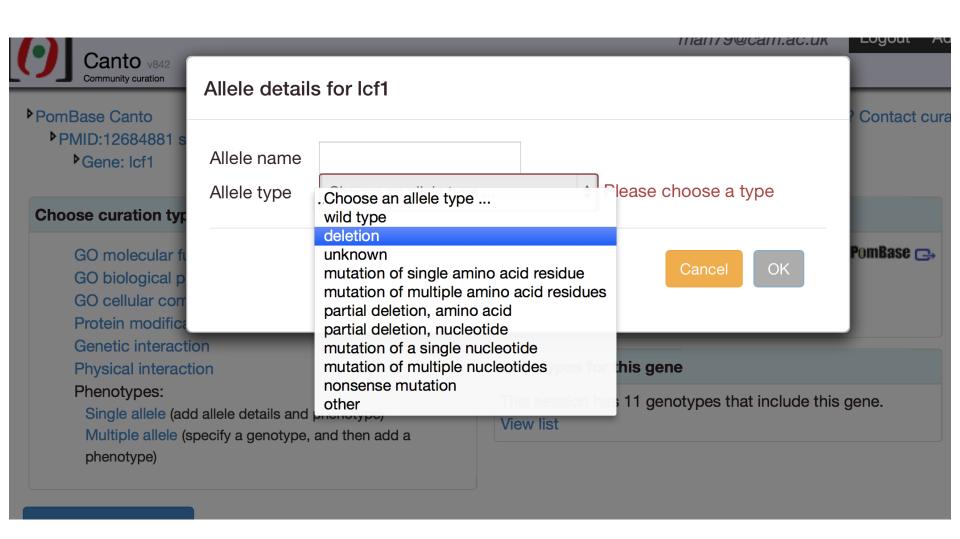
▶Gene: lcf1

# Ge PomBase

## **Choose curation type for lcf1:** GO molecular function GO biological process GO cellular component Protein modification Genetic interaction Physical interaction Phenotypes: Single allele (add allele details and phenotype) Multiple allele (specify a genotype, and then add a phenotype)

## ALLELE DETAILS

# **PomBase**



## ALLELE DETAILS

# PomBase

Canto v842 Community curation	Allele details for	lcf1	? Contact cura
/IID:12684881 s 'Gene: lcf1 se curation typ	Allele name Allele type	Icf1-E4  mutation of single amino acid resid ♦	
GO molecular fu GO biological p	Allele description	E576A eg. K132A	PomBase 🕞
GO cellular com Protein modifica Genetic interact Physical interact Phenotypes: Single allele (ac	Endo Knoc Null (		jene.
Multiple allele ( phenotype)  ck to summary	Not s	specified Cancel OK	

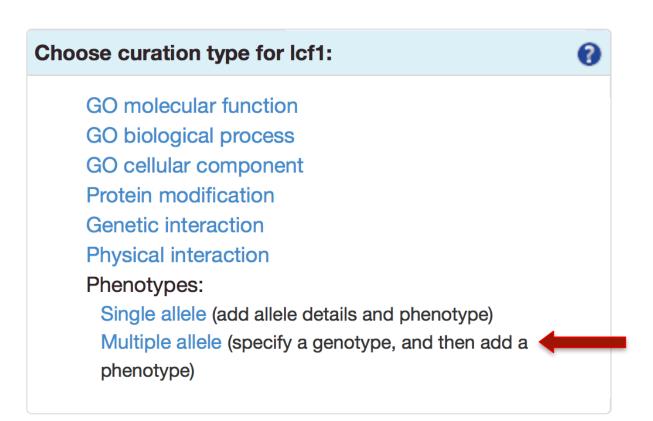
## **GENOTYPES**

PomBase Canto

PMID:12684881 summary

▶Gene: lcf1

# Ger PomBase



## **GENOTYPES**



▶ PomBase Canto

### Add a genotype

PMID:12684881 summary

Add alleles from the genes below until the genotype is fully specified.

#### Name:

short genotype name (optional) ...

#### Background:

genotype background (optional) ...

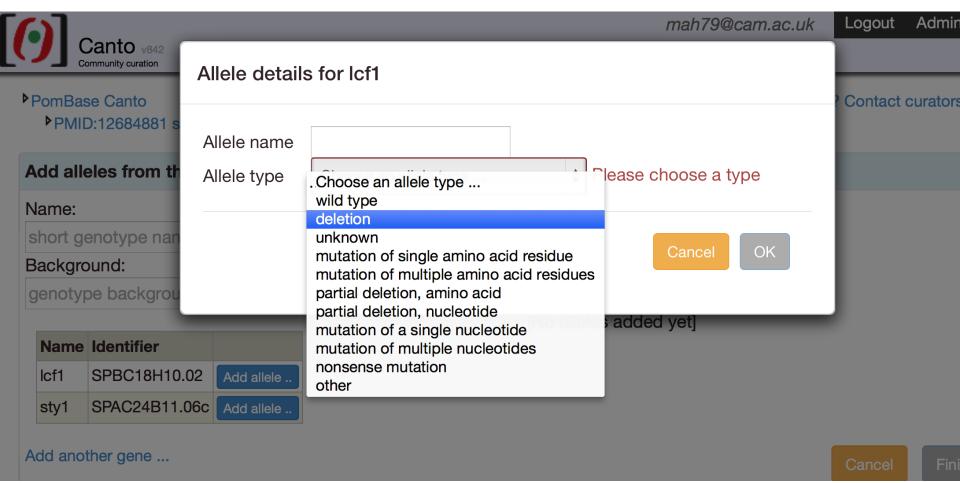
[No alleles added yet]

Name	Identifier	
lcf1	SPBC18H10.02	Add allele
sty1	SPAC24B11.06c	Add allele

Add another gene ...

## **GENOTYPES**

# **PomBase**



▶ PomBase Canto

PMID:12684881 summary

Genotype: lcf1delta

## Ques

#### Search for phenotype term



Annotate normal or abnormal phenotypes, and the associated alleles. A phenotype is any observable characteristic or trait of an organism; examples include multinucleate, abnormal spindle, inviable. more ...

Start typing a phenotype in the search box. If you do not find the term you are looking for with your initial search, begin with a broad term (cell phenotype, multinucleate, abnormal spindle, inviable) more ...



A: Loss of viability in stationary phase

▶ PomBase Canto

PMID:12684881 summary

▶Genotype: lcf1delta

## Ques

#### Search for phenotype term



Annotate normal or abnormal phenotypes, and the associated alleles. A phenotype is any observable characteristic or trait of an organism; examples include multinucleate, abnormal spindle, inviable. more ...

Start typing a phenotype in the search box. If you do not find the term you are looking for with your initial search, begin with a broad term (cell phenotype, multinucleate, abnormal spindle, inviable) more ...

<- Back

A: Loss of viability in stationary phase

B: Sensitive to salt stress

C: Decreased ( $lcf1\Delta$ ) and increased (lcf1-OP) fatty acyl-CoA synthetase activity in cell extracts

PomBase Canto

▶PMID:12684881 summary

Genotype: lcf1delta

# Dam Das B

#### Search for phenotype term



Annotate normal or abnormal phenotypes, and the associated alleles. A phenotype is any observable characteristic or trait of an organism; examples include multinucleate, abnormal spindle, inviable. more ...

Start typing a phenotype in the search box. If you do not find the term you are looking for with your initial search, begin with a broad term (cell phenotype, multinucleate, abnormal spindle, inviable) more ...

loss of viability in stationary

#### loss of viability in stationary phase (FYPO:0000245)

loss of viability at low temperature (FYPO:0003903)

loss of viability at high temperature (FYPO:0001387)

normal viability in stationary phase (FYPO:0001310)

increased viability in stationary phase (FYPO:0001309)

loss of viability upon nutrient depletion (FYPO:0000244)

loss of viability upon glucose starvation (FYPO:0004162)

#### Term name

loss of viability in stationary phase

#### **Definition**

A cell population phenotype in which a smaller than normal proportion of the population remains viable after entering stationary phase.

Dom Doguestions

▶ PomBase Canto

PMID:12684881 summary

▶ Genotype: lcf1delta

#### Search for phenotype term



Annotate normal or abnormal phenotypes, and the associated alleles. A phenotype is any observable characteristic or trait of an organism; examples include multinucleate, abnormal spindle, inviable. more ...

Start typing a phenotype in the search box. If you do not find the term you are looking for with your initial search, begin with a broad term (cell phenotype, multinucleate, abnormal spindle, inviable) more ...

sensitive to salt

#### sensitive to salt stress (FYPO:0000271)

sensitive to tacrolimus during salt stress (FYPO:0001749)

sensitive to arsenic (FYPO:0000093)

sensitive to benomyl (FYPO:0000094)

sensitive to bismuth (FYPO:0000758)

sensitive to cadmium (FYPO:0000096)

concitive to calcium (EVDO:000000)

#### Term name

sensitive to salt stress

### **Definition**

A cell phenotype observed in the vegetative growth phase of the life cycle in which cells show increased sensitivity to a salt stress.

## **EVIDENCE & CONDITIONS**

# **PomBase**

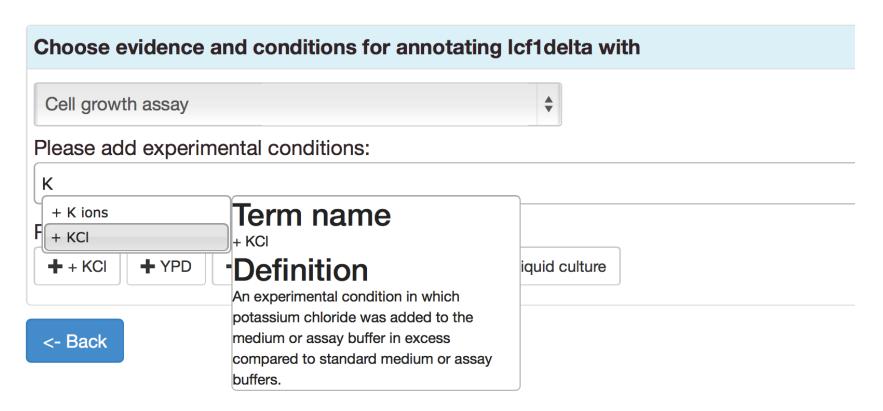
▶ PomBase Canto

PMID:12684881 summary

Genotype: lcf1delta

Search: "sensitive to salt stress"

sensitive to salt stress



## DUPLICATE (1)

# **PomBase**

#### phenotype

New single allele annotations for lcf1delta for PMID:12684881 Add ...

Genes	Genotype	Term ID	Term name	Evidence code	Conditions	Curator
lcf1	lcf1∆	FYPO:0000271	sensitive to salt stress	Cell growth assay	+ KCI	Antonia Lock <a.lock@ucl.ac.uk></a.lock@ucl.ac.uk>
lcf1	lcf1∆	FYPO:0000245	loss of viability in stationary phase	Cell growth assay		Antonia Lock <a.lock@ucl.ac.uk></a.lock@ucl.ac.uk>

### Edit fields to create a new phenotype annotation for lcf1delta

Genotype	lcf1delta						
Term name	sensitive to salt stress						
Evidence code	Cell growth assay						
	Please add experimental conditions:						
	+ KCI *						
	Type a condition						
	Previously used conditions (click to add to list):						
	+ + KCI + YPD + agar plates + glucose MM						
	+ liquid culture						
Term suggestion	Name						
	Definition						
Comment							
Annotation extension							
Curator	Antonia Lock <a.lock@ucl.ac.uk></a.lock@ucl.ac.uk>						

## RETURN TO SUMMARY

# Pom Base

▶ PomBase Canto

PMID:12684881 summary

Genotype: lcf1delta

Genotype: lcf1delta

Questio

Actions ...

Add a new phenotype for this genotype ...

**Genotype details** 

Name

**Background** 

**Description** | lcf1∆

[none]

lcf1Δ - lcf1

Edit ...

<- Back to summary

#### phenotype

New single allele annotations for lcf1delta for PMID:12684881 Add ...

Genes	Genotype	Term ID	Term name	Evidence code	Conditions	Curator	
lcf1	lcf1∆	FYPO:0000271	sensitive to salt stress	Cell growth assay	+ KCI	Antonia Lock <a.lock@ucl.ac.uk></a.lock@ucl.ac.uk>	Edit Duplicate
							Delete
lcf1	lcf1∆	FYPO:0000271	sensitive to salt stress	Cell growth assay	+ NaCl	Antonia Lock <a.lock@ucl.ac.uk></a.lock@ucl.ac.uk>	Edit

## DUPLICATE (2)

▶PomBase Canto ▶PMID:12684881 summary

### **PMID:12684881 summary**



Genes and genotypes

Click on a gene name to start entering data

Icf1
sty1

Edit gene list ...

Genotype management ...

Publication details							
ID	PMID:12684881	Pub Med 🕞					
Title	A defect in a fatty acyl-CoA synthetase gene, lcf1+, results in a decrease in viability after entry into the stationary phase in fission yeast.						
Authors	Oshiro T, Aiba H, Mizuno T						

Pause curation

Submit to curators

# New single allele annotations for PMID:12684881 Add ...

Genes	Genotype	Term ID	Term name	Evidence code	Conditions	Curator	
lcf1	lcf1∆	FYPO:0000245	loss of	Cell growth		Antonia Lock	Edit
			viability in	assay		<a.lock@ucl.ac.uk></a.lock@ucl.ac.uk>	Duplica
			stationary			`	Delete
			phase				

#### Edit fields to create a new phenotype annotation for lcf1delta

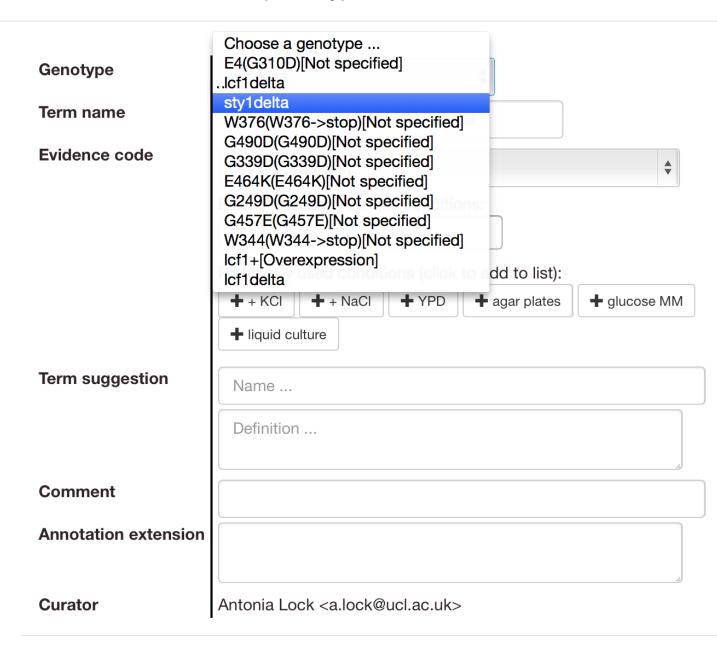
0:

ar

101

ot

е





# **PomBase**

- Can be based on direct observations
  - e.g. enzyme assays using purified proteins
- Can be based on phenotypes
  - Knock out an enzyme with a predicted function and see the activity decrease
  - Overexpress an enzyme with a predicted function and see the activity increase



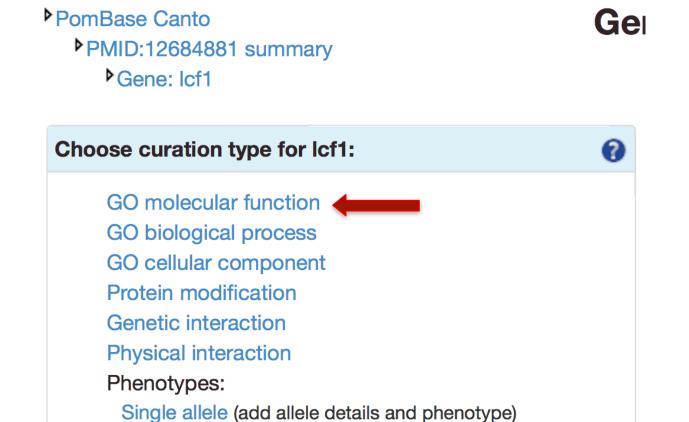
# **PomBase**

- Can be based on direct observations
  - e.g. enzyme assays using purified proteins
- Can be based on phenotypes
  - Knock out an enzyme with a predicted function and see the activity decrease
    - Icf1∆- decreased fatty acyl-CoA synthetase activity
  - Overexpress an enzyme with a predicted function and see the activity increase
    - Icf1-OP increased fatty acyl-CoA synthetase activity
  - Also infer involvement in process: fatty acyl-CoA metabolism

## MOLECULAR FUNCTION

# **PomBase**

- Lcf1 contains a synthetase/ligase protein domain
- Infer that Lcf1 itself performs this function



Multiple allele (specify a genotype, and then add a

Q

PMID:12684881 summary

▶Gene: Icf1

#### Search for GO molecular function term



A molecular function is a catalytic (e.g. protein serine/threonine kinase activity, pyruvate carboxylase activity) or binding activity, or any other activity that occurs at the molecular level. more ...

Start typing a molecular function in the search box. If you do not find the term you are looking for with your initial search, begin with a broad term (transporter, transferase activity) more ...

fatty acyl synthase

fatty-acyl-CoA synthase activity (GO:0004321)

fatty-acyl-ethyl-ester synthase activity (GO:0030339)

acyl-[acyl-carrier-protein] hydrolase activity (GO:0016297)

methylene-fatty-acyl-phospholipid synthase activity (GO:0004481)

cyclopropane-fatty-acyl-phospholipid synthase activity (GO:0008825)

fatty-acyl-CoA binding (GO:0000062)

fatty-acyl group transporter activity (GO:0015246)

### Term name

fatty-acyl-CoA synthase activity

### Definition

Catalysis of the reaction: acetyl-CoA + n malonyl-CoA + 2n NADH + 2n NADPH + 4n H+ = a long-chain acyl-CoA + n CoA + n CO2 + 2n NAD+ + 2n NADP+.

## **BIOLOGICAL PROCESS**

PomBase Canto

PMID:12684881 summary

Gene: lcf1

#### Search for GO biological process term



A biological process is series of events accomplished by one or more ordered assemblies of molecular functions, such as cell cycle, transport, or signal transduction. more ...

Start typing a biological process in the search box. If you do not find the term you are looking for with your initial search, begin with a broad term (cell cycle, transport) more ...

fatty acyl

fatty-acyl group transport (GO:0015915)

fatty-acyl-CoA transport (GO:0015916)

fatty-acyl-CoA catabolic process (GO:0036115)

fatty-acyl-CoA metabolic process (GO:0035337)

fatty-acyl-CoA biosynthetic process (GO:0046949)

long-chain fatty-acyl-CoA catabolic process (GO:0036116)

long-chain fatty-acyl-CoA metabolic process (GO:0035336)

### Term name

fatty-acyl-CoA metabolic process

### **Definition**

The chemical reactions and pathways involving a fatty-acyl-CoA, any derivative of coenzyme A in which the sulfhydryl group is in thiolester linkage with a fatty-acyl group.

## TERM DETAILS

▶ PomBase Canto

**Questions? Conta** 

▶PMID:12684881 summary

▶Gene: lcf1

Search: "fatty-acyl-CoA metabolic process"

▶ fatty-acyl-CoA metabolic process

#### Please read the definition of the currently selected term to ensure that it accurately describes your gene:

ID GO:0035337
 Ontology biological\_process
 Term name fatty-acyl-CoA metabolic process
 Definition The chemical reactions and pathways involving a fatty-acyl-CoA, any derivative of coenzyme A in which the sulfhydryl group is in thiolester linkage with a fatty-acyl group.
 Synonyms fatty acyl CoA metabolic process fatty-acyl-CoA metabolism

View term ancestry in:



If possible, please refine your term selection. Clicking on a child term from the list below selects it and shows its definition (and children, if any):

2-methylbut-2-enoyl-CoA(4-) metabolic process
2-methylbutanoyl-CoA(4-) metabolic process
3-methylbut-2-enoyl-CoA(4-) metabolic process
L-methylmalonyl-CoA metabolic process
fatty-acyl-CoA biosynthetic process
fatty-acyl-CoA catabolic process
isovaleryl-CoA(4-) metabolic process
long-chain fatty-acyl-CoA metabolic process
malonyl-CoA metabolic process
malonyl-CoA metabolic process

## TERM DETAILS

▶ PomBase Canto

**Questions? Conta** 

View term ancestry in:

AmiGO□→

▶PMID:12684881 summary

▶Gene: lcf1

Search: "fatty-acyl-CoA metabolic process"

▶ fatty-acyl-CoA metabolic process

#### Please read the definition of the currently selected term to ensure that it accurately describes your gene:

GO:0035337 ID

Ontology

biological\_process

Term name

fatty-acyl-CoA metabolic process

**Definition** 

The chemical reactions and pathways involving a fatty-acyl-CoA, any derivative of coenzyme A in which the sulfhydryl group is in thiolester linkage with a fatty-acyl group.

**Synonyms** | fatty acyl CoA metabolic process

If you need a more specific term to describe the experiment you are annotating, and if none of terms above is appropriate, you can suggest a new term:

Suggest a new child term for GO:0035337 ...

<- Back

Otherwise, use the currently selected term:

Proceed ->

L-methylmalonyl-CoA metabolic process fatty-acyl-CoA biosynthetic process fatty-acyl-CoA catabolic process isovaleryl-CoA(4-) metabolic process long-chain fatty-acyl-CoA metabolic process malonyl-CoA metabolic process

## **GO EVIDENCE**

## **PomBase**

```
▶ PomBase Canto
```

PMID:12684881 summary

▶Gene: lcf1

Search: "fatty-acyl-CoA metabolic process"

fatty-acyl-CoA metabolic process

blong-chain fatty-acyl-CoA metabolic process

### Choose evidence for annotating lcf1 with

..Choose an evidence code ...

**IMP** 

**IDA** 

IGI

IPI

**EXP** 

## **FINISHING**

▶PomBase Canto

▶PMID:12684881 summary

Gene: lcf1

Optional comment:

Questions? Contact curators ...



#### You have made the following annotation:

Systematic identifier	Gene name	Term ID	Term name	Evidence code	With
SPBC18H10.02	lcf1	GO:0035336	long-chain fatty-acyl-CoA metabolic process	IMP	

Please provide any additional details you have about this process, such as:

- i) Direct or indirect targets of the process, such as gene targets of transcriptional or translational regulation, protein targets of a localisation process, etc.
- ii) The period or phase (e.g. during S phase; during sporulation) when the gene product acts in the process The curators will record this additional information in PomBase.

Optional annotati	on extension:		

You can annotate other genes from your list with the same term and evidence by selecting genes below:

sty1 (SPAC24B11.06c)

Finish

## **FINISHING**

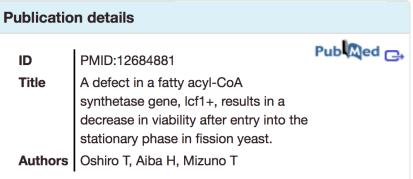
# **PomBase**

PomBase Canto
PMID:12684881 summary

#### **PMID:12684881 summary**

Questions? Contact curators ...





Pause curation

Submit to curators

## **ACKNOWLEDGEMENTS**

# **PomBase**

Curators: Valerie Wood (Cambridge), Midori Harris (Cambridge), Antonia Lock (UCL)

**Programmers:** Kim Rutherford (Cambridge), Mark McDowall (EBI), Dan Staines (EBI), Ensembl Genomes Team (EBI)

**Additional Pls:** Steve Oliver (Cambridge), Paul Kersey (EBI), Jürg Bähler (UCL)

**You:** S. pombe researchers, especially all community curators, past and future!

PomBase is funded by the Wellcome Trust and run by a consortium comprising the University of Cambridge, the European Bioinformatics Institute, and University College London.







