dictyBase

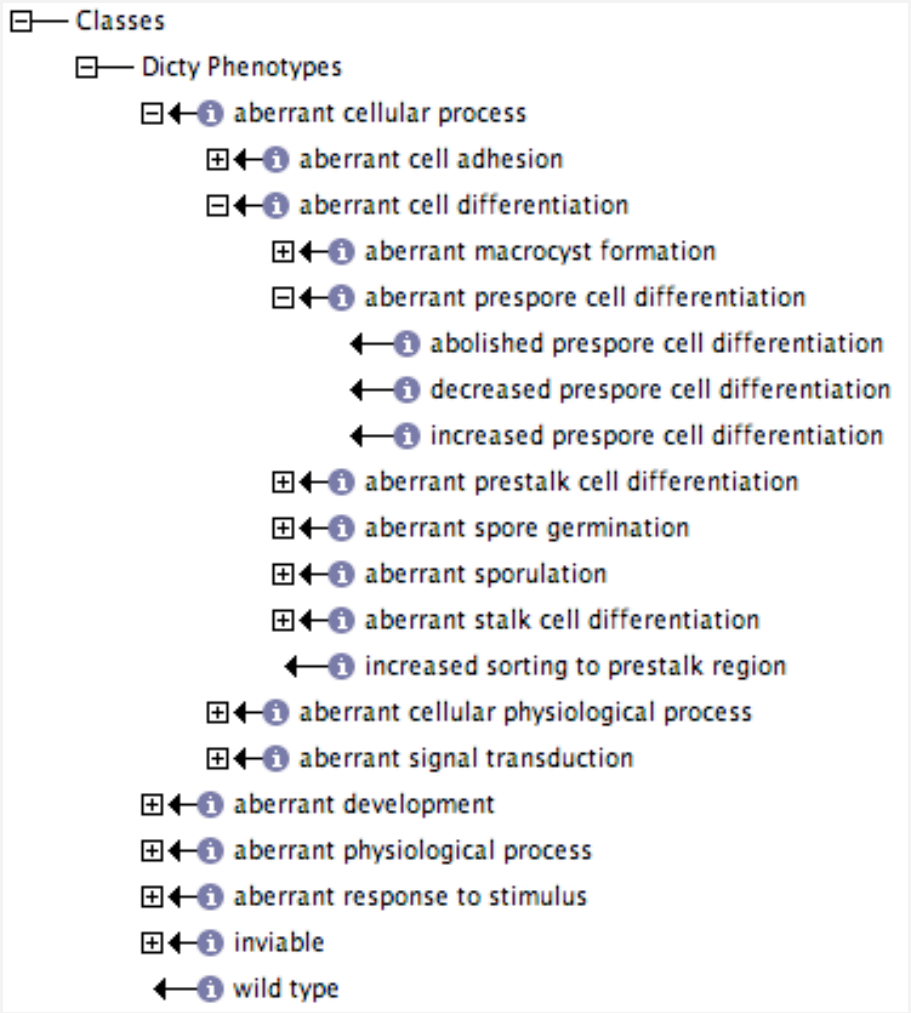
Phenotype Annotation Tool and Ontologies at dictyBase

Phenotype/PATO 2003

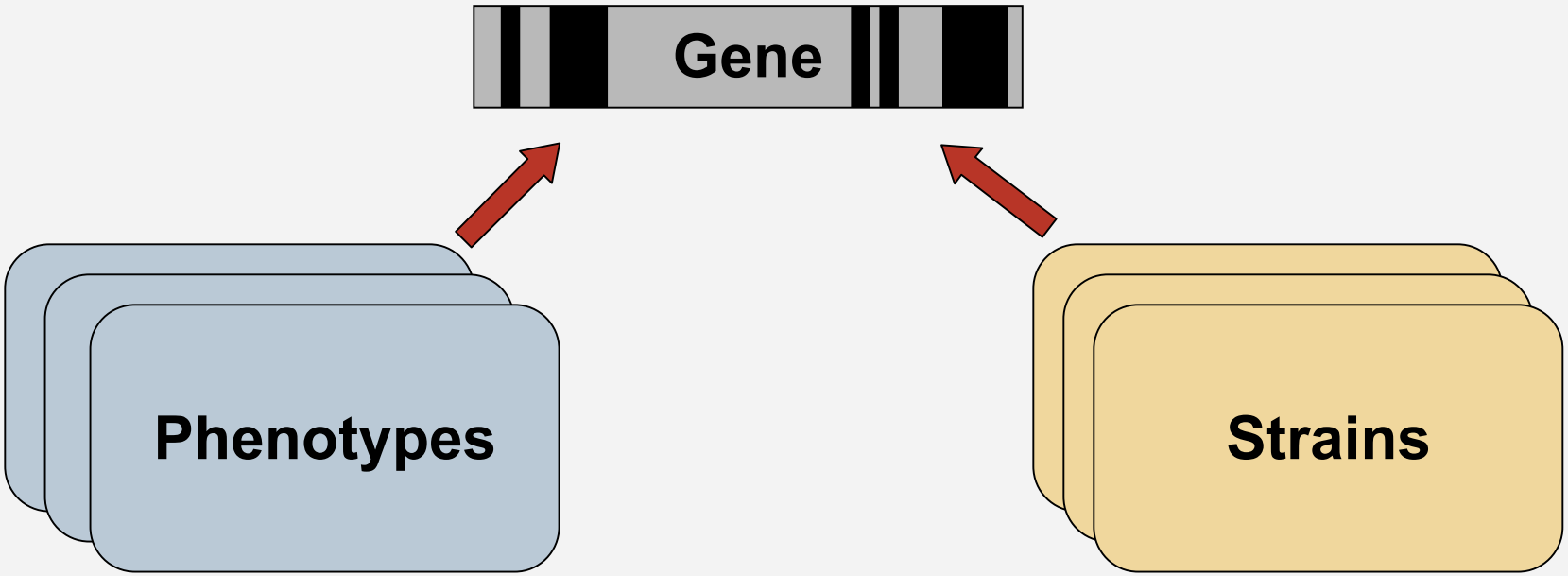
	A	B	C	D	E	F	G	H	I	J	K
1	locus	gen condition/mutan	environm. conditions	observable	attribute	qualifier	assay	values	unit	PMID	extra notes
2	sadA	KO/AX3	petridish HL5	substrate adhesion	ability	abolished/defective	attachment assay	<2	%WT	12499361	
3	sadA	"	petridish HL5	cytokinesis	ability	abolished/defective	DAPI staining	1-12	nuc/cell		52% have a
4	sadA	"	buffer, shaking	phagocytosis	ability	abolished/defective	uptake of latex beads	0	%WT		
5	sadA	"	suspension	vegetative growth	rate	increased	counting of cells	20	%		
6	sadA	"	petridish HL5	actin filament organization	cellular distribution	aberrant	Phalloidin staining				GO:7015
7	sadA	"	vegetative growth	cell motility	rate	increased	speed meas./cell tracking	6.3	um/min		WT 3.2
8	yelA	KO/AX4	solid substratum	mound formation	progression	abolished/defective	observation				
9	yelA	"	solid substratum	spore formation	progression	precocious	observation	6.00	hours	9254905	autonomou
10	yelA	"	bacterial lawn	spore	viability	reduced	plaque formation after def	2	%WT		
11	yelA	"	solid substratum	spore	morphology	aberrant	observation	round	rel WT		WT elongat
12	yelA	"	solid substratum	spore coat	morphology	aberrant	electron microscopy				
13	yelA	"	solid substratum	spore specific expression	timing/progression	precocious	spiA Northern	4	hours		
14	yelA	"	solid substratum	prestalk specific gene expr	level	reduced	ecmA Northern				
15	yelA	db yelA- tacB-or tacC	solid substratum	spore formation	ability	partially rescued	plaque formation after def	15	%	9543721	tagB/C- 0%
16	mlcE	KO/JH10	suspension	cytokinesis	ability	abolished/defective	DAPI staining	>10	nuc./cell	7593282	evtl. lethal
17	mlcE	"	cAMP gradient	chemotaxis	rate	reduced	Zigmond Chamber	5.8	um/min		(by 40-50%
18	mlcE	"	solid substratum	aggregation (loose agg)	progression	delayed	observation	2-3	hours		
19	mlcE	"	solid substratum	stalk formation	size	reduced	observation	short + thick (50%?)			
20	mlcE	"	solid substratum	mound formation	progression	abolished/defective	observation	50.00	%WT		
21	mlcE	"	growth	actin-activated ATPase activ	level	reduced	enzyme activity assay with	<10	%WT		new GO?
22	mlcE	"	high salt	MHC-MLCE binding	ability	increased	myosin solubilization in hi	<30	%		WT >80%
23	mlcE	"	growth	MHC-MLCR binding	ability	reduced	IP whole cells	56	%WT		
24	mlcE	"	growth	MHC-MLCR binding	ability	reduced	IP purified myosin	10	%WT		
25	mlcE	"	development/solid substr	prespore specific gene exp	localization	aberrant	reporter gene assay, pspA				
26	ampA	KO/AX3	starvation in buffer suspe	cell-cell adhesion	ability	increased	agglutination assay	450	%Wt	11884033	
27	ampA	"	growth in suspension	tip formation	progression	delayed	observation	4.5	hours		
28	ampA	"	growth in suspension	fruiting body formation	efficiency	reduced	observation	some	cells		
29	ampA	"	growth on bacteria 2d	mound formation	progression	delayed	observation	7-8	hours		
30	ampA	"	growth on bacteria 2d	mound formation	progression	abolished/defective	observation				
31	ampA	"	growth on bacteria 3d	mound formation	progression	abolished/defective	observation				
32	ampA	"	growth on bacteria 3d	stream formation	progression	abolished/defective	observation				
33	ampA	"	growth in suspension	substrate adhesion	ability	increased	protein retention assay aft	200	%WT		
34	ampA	"	growth in suspension	substrate adhesion	ability	increased	protein retention assay aft	140	%WT		
35	ampA	"	growth on bacteria 3d	substrate adhesion	ability	increased	protein retention assay aft	350	%WT		
36	ampA	"	growth on bacteria 3d	substrate adhesion	ability	increased	protein retention assay aft	260	%WT		
37	ampA	OE/AX3 6x	starvation in buffer suspe	cell-cell adhesion	ability	reduced	size meas. of cell clumps	50	%Wt		
38	ampA	OE/AX3 6x	growth in suspension	mound formation	progression	delayed	observation				
39	ampA	OE/AX3 6x	growth on bacteria 3d	fruiting body formation	progression	abolished/defective	observation				
40	ampA	KO/AX3	LacZ reporter gene	prespore differentiation	preference/efficiency	increased	counting of pspD cells at 1	200	%WT	11973270	

Phenotype Ontology

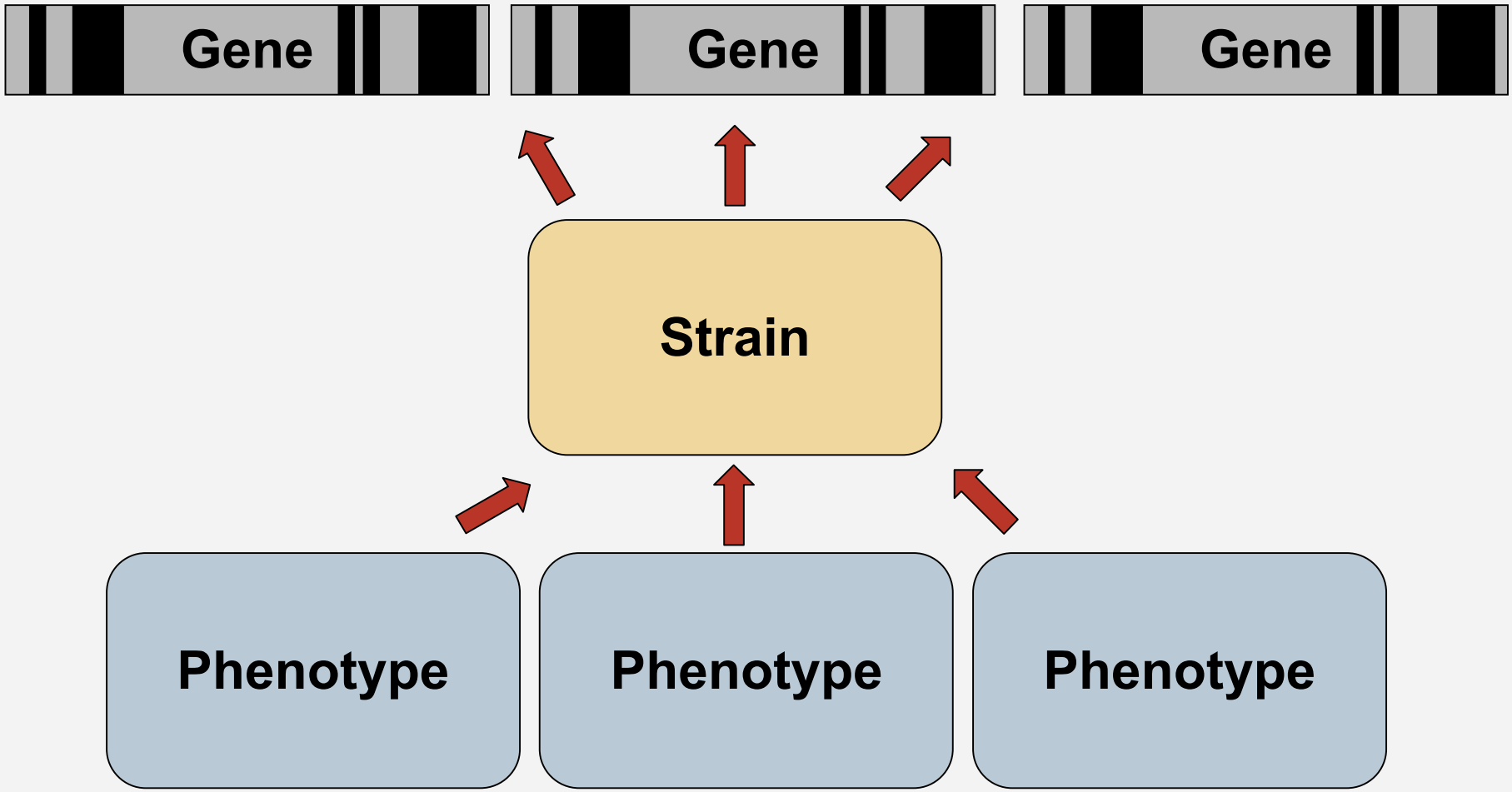
- 420 Phenotype Terms
- 1780 Phenotype Annotations
- 470 Genes with Phenotype Annotation(s)



Previous Phenotype Representation in dictyBase



New Phenotype Representation in dictyBase



Strain and Phenotype Display on the Gene Page

Cellular Component	contractile ring (IDA), cytoplasm (IDA)
Expression	
UCSD Expression Profile | BCM Expression Profile |	
Strains and Phenotypes	
mhkB-	increased myosin II assembly
mhkA-/mhkB-	decreased growth rate, increased myosin II assembly
mhkA-/mhkB-/mhkC-	decreased growth rate, increased myosin II assembly
[act15]:mhkB:FLAG	aberrant cytokinesis
Links	
mhkB Researchers | GeneDB | STKE | Entrez Nucleotide | Entrez Protein | UniProt |	
Community Annotations	
mhkB Community Annotations Page	

Phenotype and Strain Details Page

Phenotype and Strain Details for [act15]:mhkB:FLAG

Phenotype	Notes	Reference
aberrant cytokinesis	mhkB activity disrupts myosin filament formation, thus overexpression mimicks the mhcA null cytokinesis defect **Assay:** nuclei count **Environment:** in suspension	**Rico & Egelhoff (2003)** 'Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.' *J Cell Biochem* 88:521-32 dictyBase paper PubMed Access Full Text

Strain Details			
Strain Descriptor	[act15]:mhkB:FLAG	**Strain ID**	DBS0236665
Synonyms	MHCK-B OE	**Systematic Name**	DBS0236665
Description	FLAG epitope fused at the amino-terminus of mhkB overexpressed in wild type	**Genotype**	axeA2, axeB2, axeC2, mhkB-FLAG [pTX-MKB2], neoR
Mutant Type	overexpression	**Mutagenesis Method**	Extrachromosomal
Strain Type	Axenic, Drug resistant	**Depositor**	
Parental Strain	AX2	**Species**	Dictyostelium discoideum
Plasmid	pTX-MKB2	**Vector**	
References	12532328		
Associated Genes	mhkB		

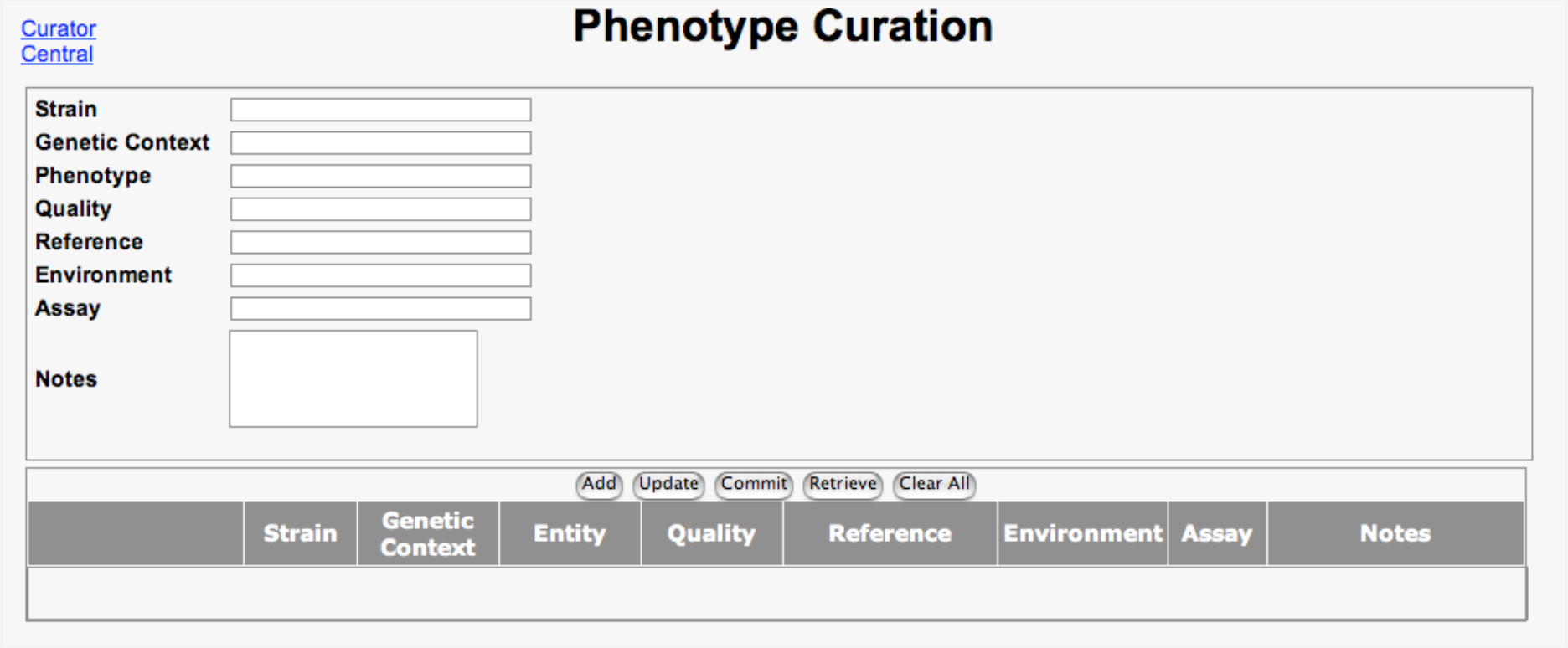
Development of a New Phenotype Annotation Tool

- Developed in collaboration with NCBO
- Similar in functionality to Phenote
- Web-based tool that can be accessed from any computer

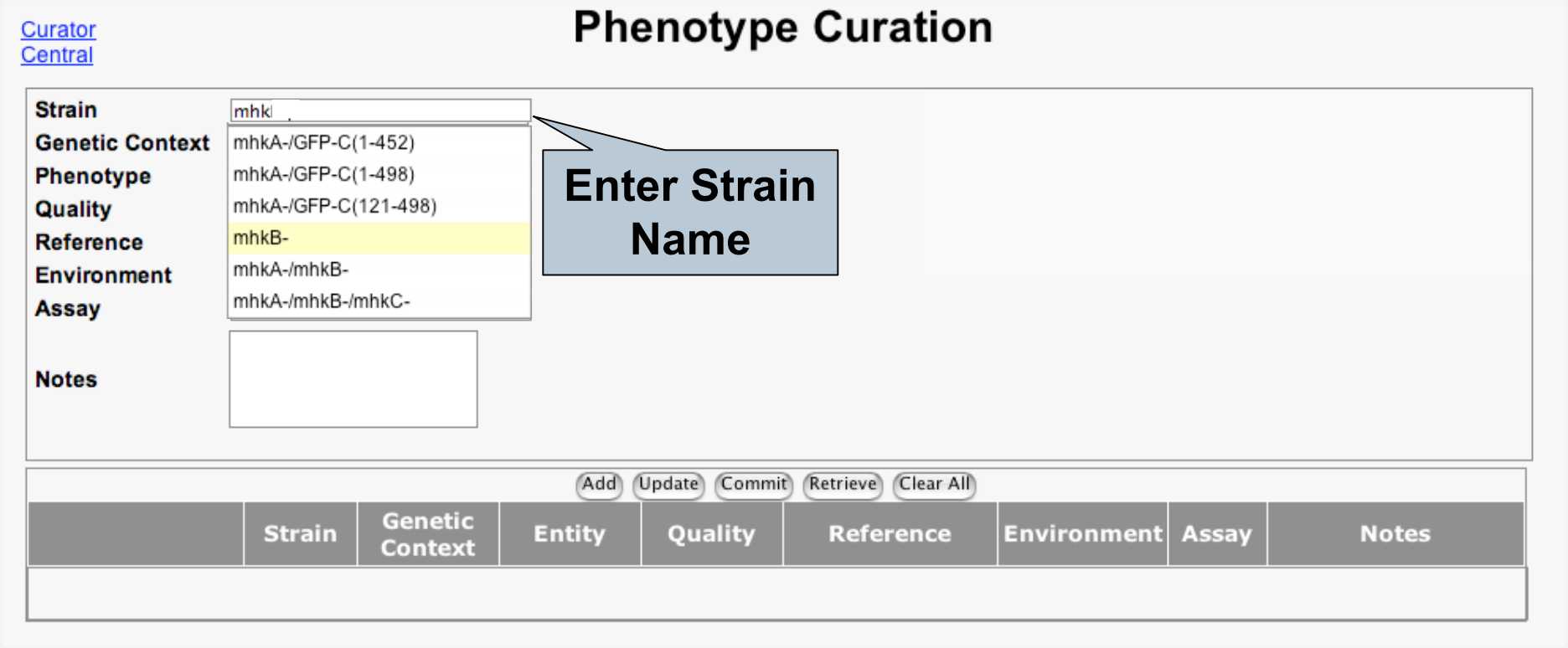
Features of the New Phenotype Annotation Tool

- Runs on top of the Chado database schema
- Uses terms from ontologies in .obo format for phenotype annotation
- Auto-completes ontology terms similar to Google Suggest
- Built using Web 2.0 technologies such as AJAX

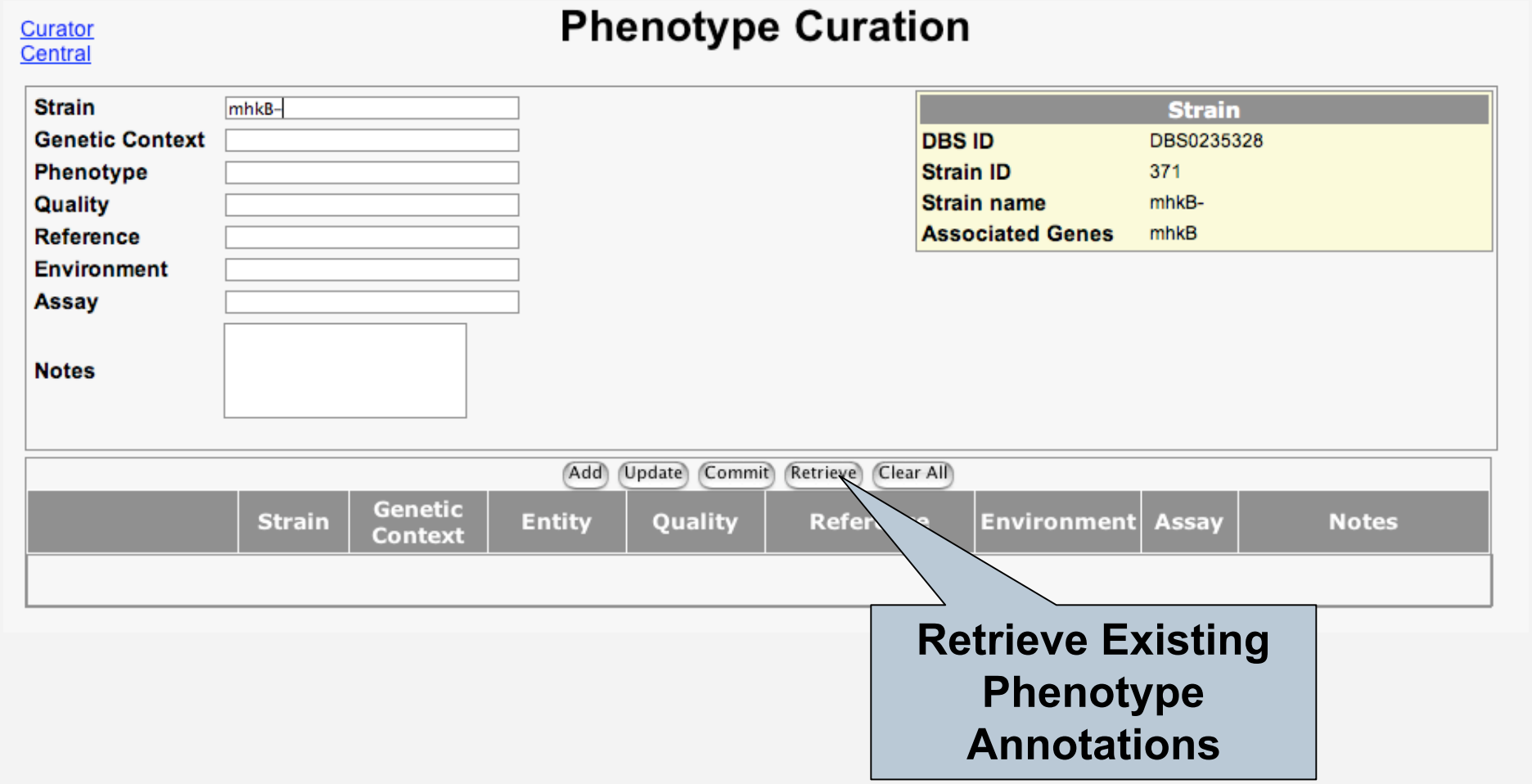
Phenotype Annotation Tool



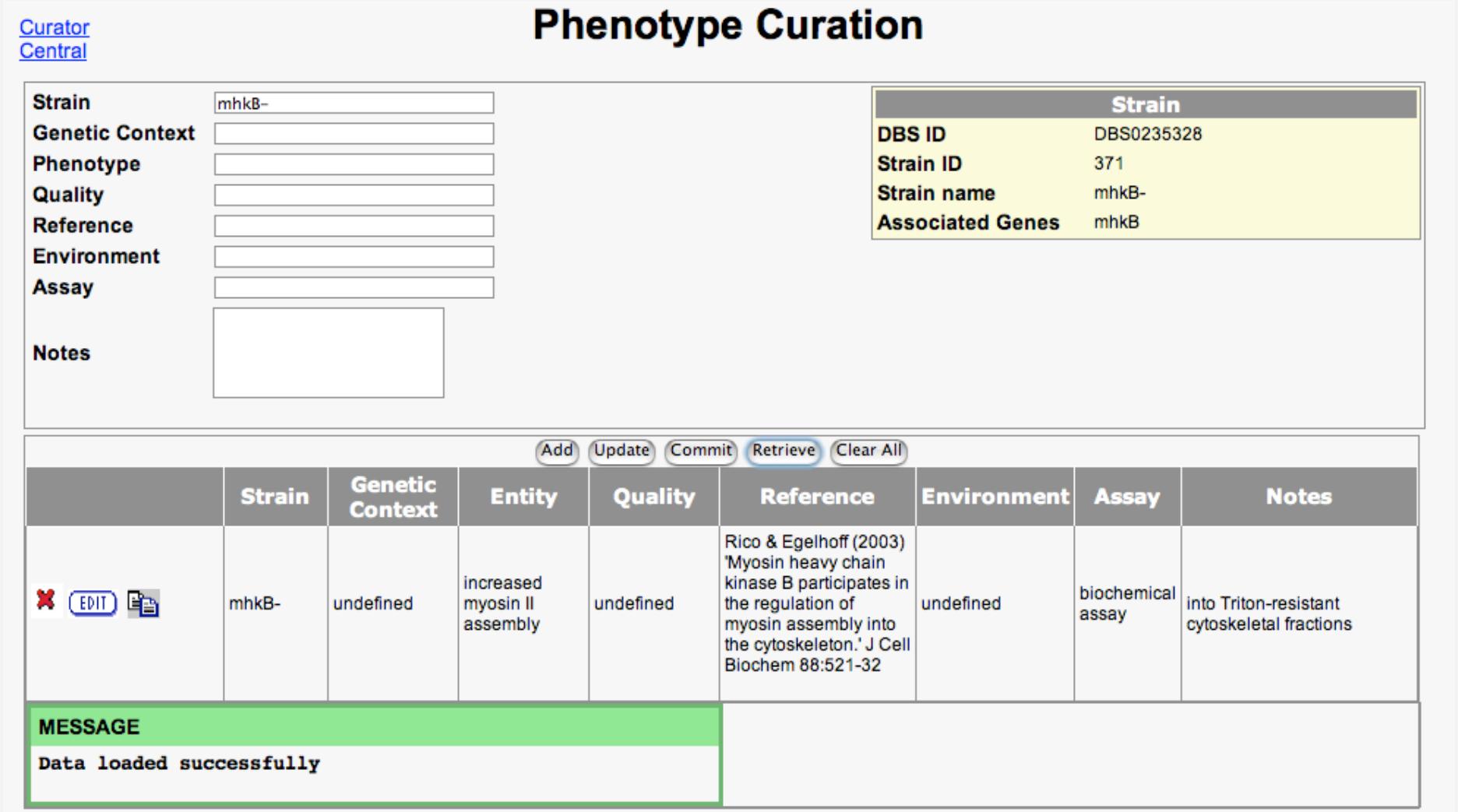
Phenotype Annotation Tool



Phenotype Annotation Tool



Phenotype Annotation Tool



Curator Central

Phenotype Curation

Strain	mhkB-
Genetic Context	
Phenotype	
Quality	
Reference	
Environment	
Assay	
Notes	

Strain	
DBS ID	DBS0235328
Strain ID	371
Strain name	mhkB-
Associated Genes	mhkB

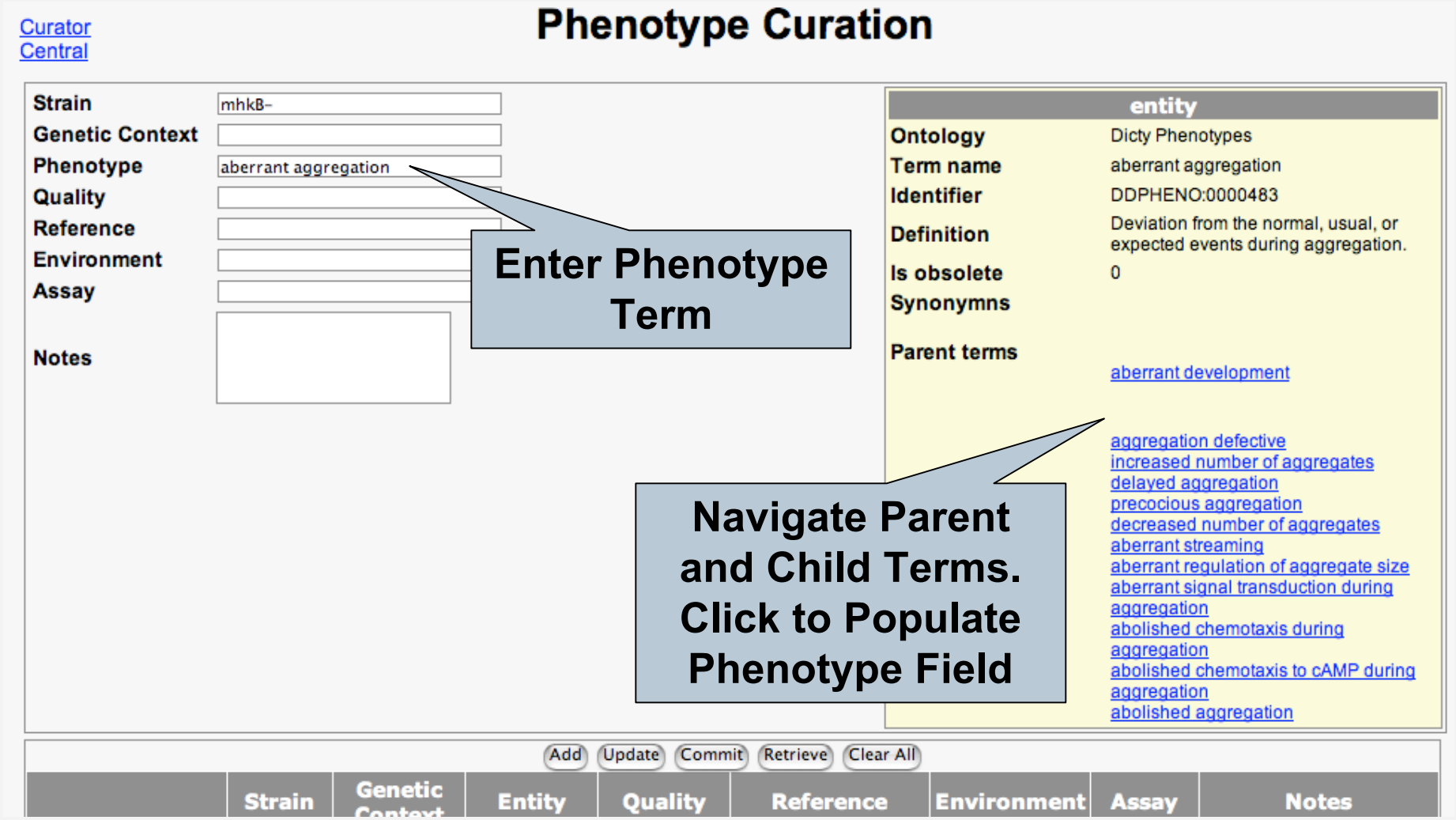
Add | Update | Commit | Retrieve | Clear All

	Strain	Genetic Context	Entity	Quality	Reference	Environment	Assay	Notes
EDIT	mhkB-	undefined	increased myosin II assembly	undefined	Rico & Egelhoff (2003) 'Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.' J Cell Biochem 88:521-32	undefined	biochemical assay	into Triton-resistant cytoskeletal fractions

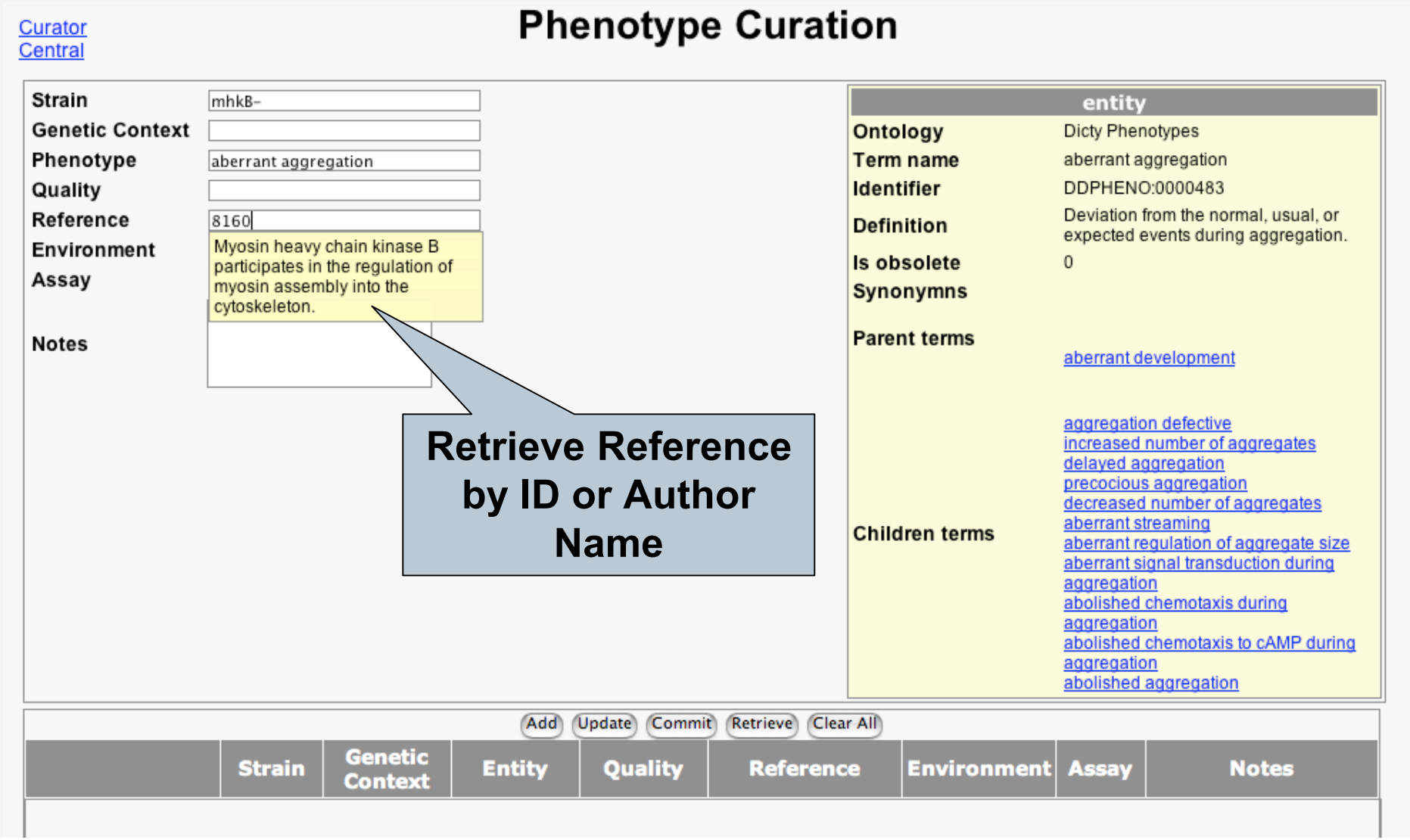
MESSAGE

Data loaded successfully

Phenotype Annotation Tool



Phenotype Annotation Tool



Phenotype Annotation Tool

Curator Central

Phenotype Curation

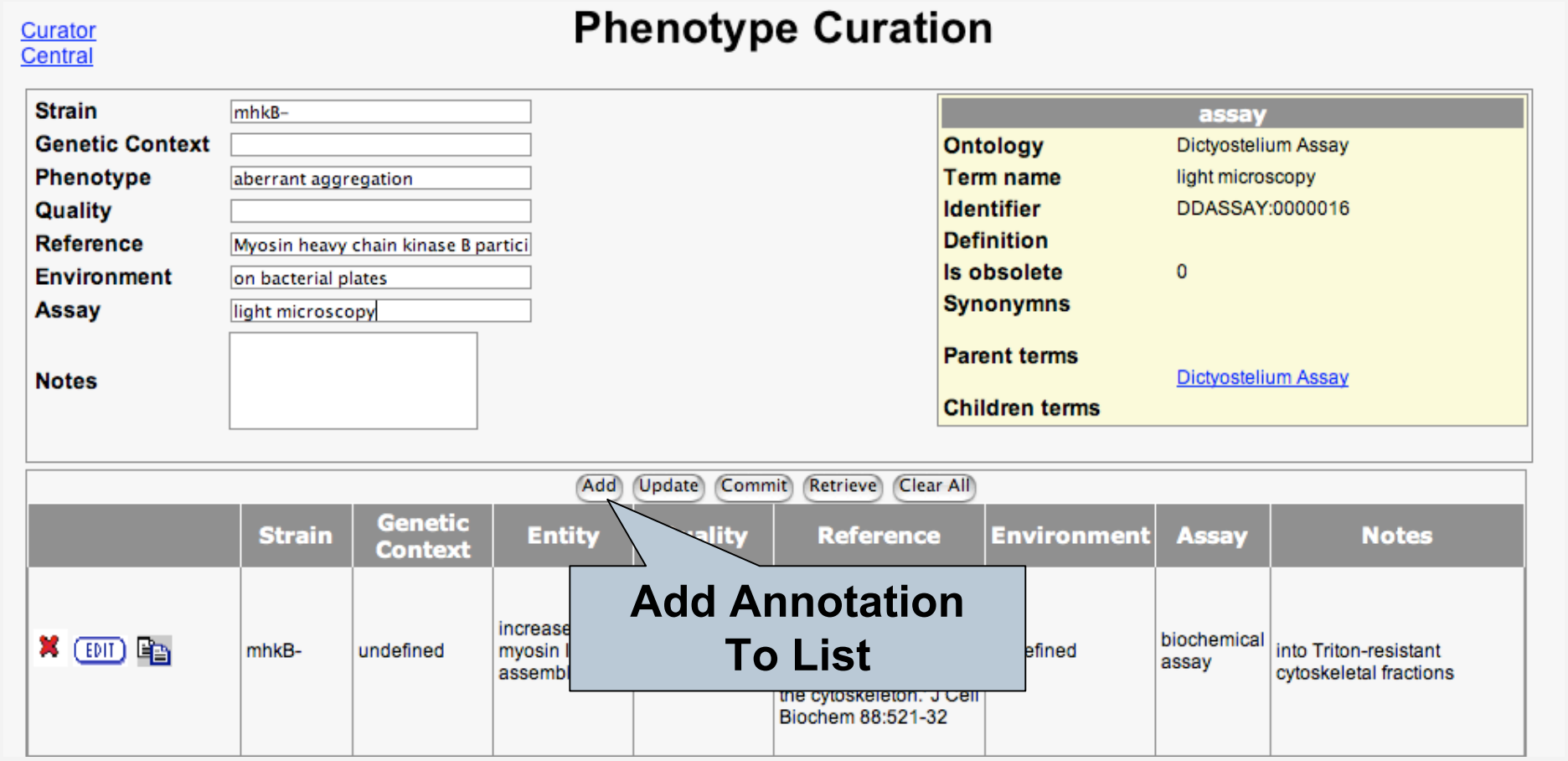
Strain	mhkB-
Genetic Context	
Phenotype	aberrant aggregation
Quality	
Reference	Myosin heavy chain kinase B partici
Environment	
Assay	
Notes	

Reference	
Reference no	8160
Pubmed ID	12532328
Citation	**Rico & Egelhoff (2003)** 'Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.' *J Cell Biochem* 88:521-32 dictyBase paper PubMed Access Full Text

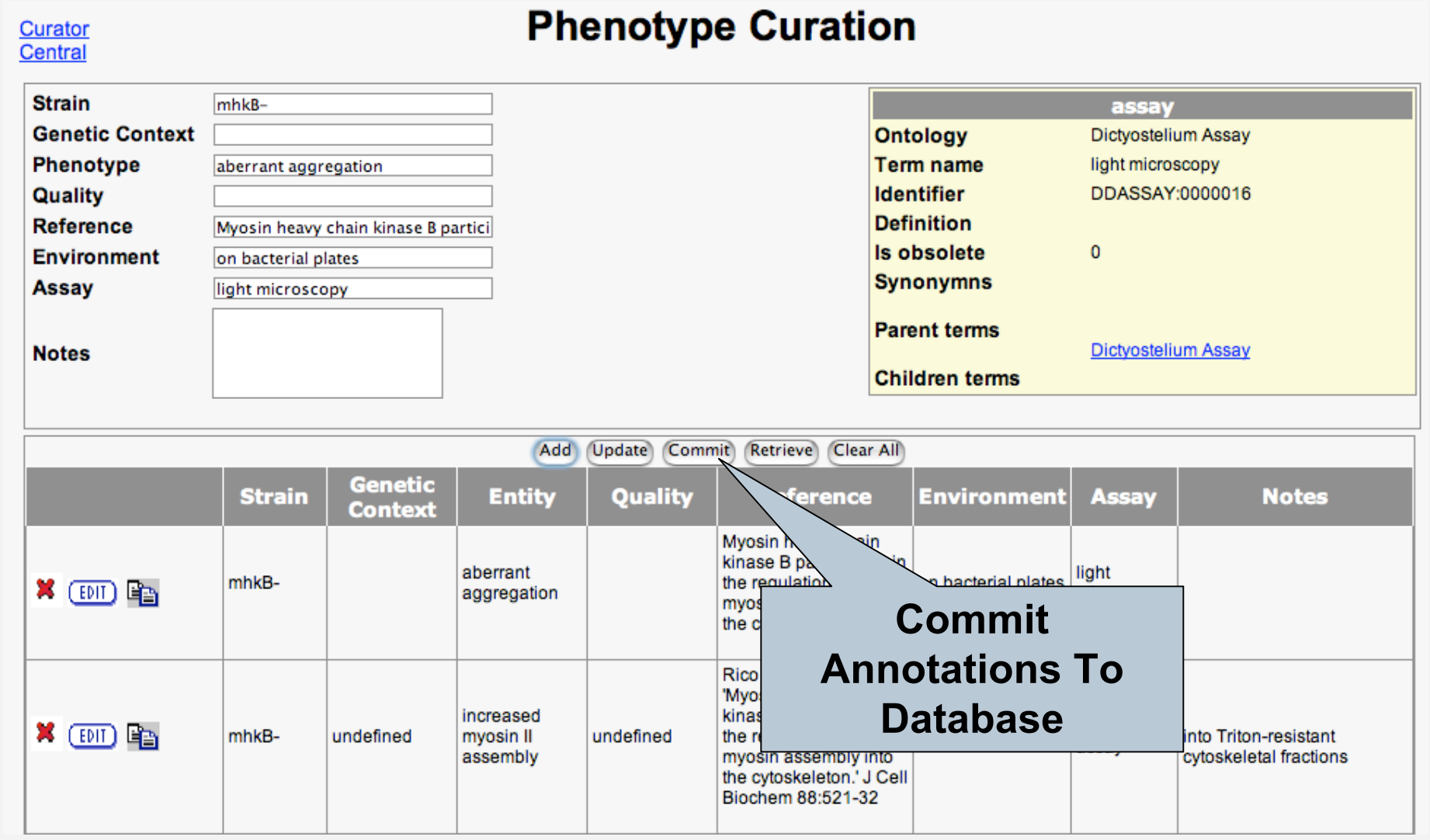
Add Update Commit Retrieve Clear All

	Strain	Genetic Context	Entity	Quality	Reference	Environment	Assay	Notes
EDIT	mhkB-	undefined	increased myosin II assembly	undefined	Rico & Egelhoff (2003) 'Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.' J Cell Biochem 88:521-32	undefined	biochemical assay	into Triton-resistant cytoskeletal fractions

Phenotype Annotation Tool



Phenotype Annotation Tool



Phenotype Annotation Tool

Curator Central

Phenotype Curation

Strain	mhkB-
Genetic Context	
Phenotype	aberrant aggregation
Quality	
Reference	Myosin heavy chain kinase B partici
Environment	on bacterial plates
Assay	light microscopy
Notes	

assay	
Ontology	Dictyostelium Assay
Term name	light microscopy
Identifier	DDASSAY:0000016
Definition	
Is obsolete	0
Synonymns	
Parent terms	Dictyostelium Assay
Children terms	

Add Update Commit Retrieve Clear All

	Strain	Genetic Context	Entity	Quality	Reference	Environment	Assay	Notes
EDIT	mhkB-		aberrant aggregation		Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.	on bacterial plates	light microscopy	
EDIT	mhkB-	undefined	increased myosin II assembly	undefined	Rico & Egelhoff (2003) 'Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.' J Cell Biochem 88:521-32	undefined	biochemical assay	into Triton-resistant cytoskeletal fractions

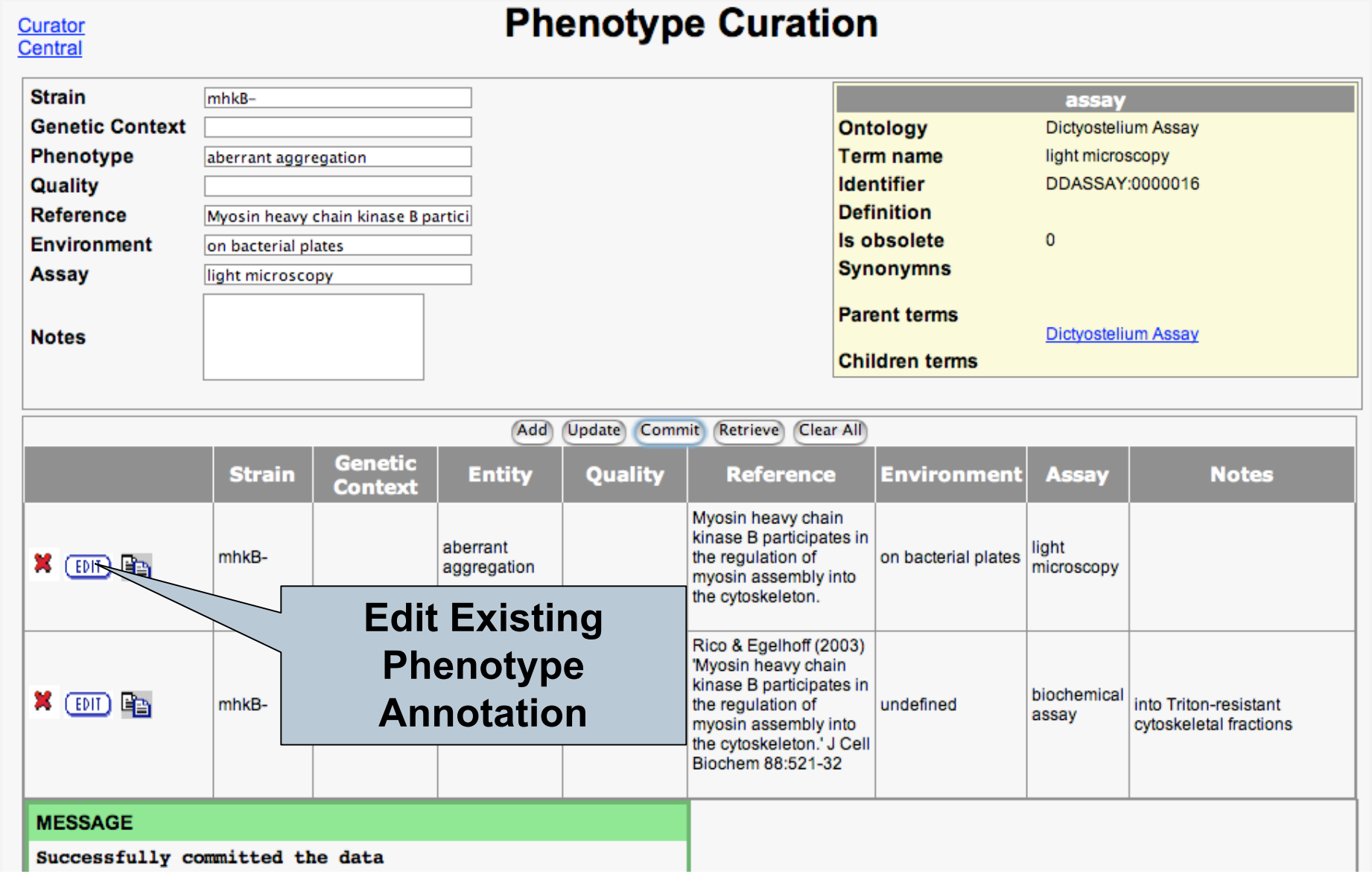
MESSAGE

Successfully committed the data

Resulting Phenotype Display on the Gene Page

Cellular Component	contractile ring (IDA), cytoplasm (IDA)
Expression	
UCSD Expression Profile | BCM Expression Profile |	
Strains and Phenotypes	
mhkB-	increased myosin II assembly, aberrant aggregation
mhkA-/mhkB-	decreased growth rate, increased myosin II assembly
mhkA-/mhkB-/mhkC-	decreased growth rate, increased myosin II assembly
[act15]:mhkB:FLAG	aberrant cytokinesis
Links	
mhkB Researchers | GeneDB | STKE | Entrez Nucleotide | Entrez Protein | UniProt |	
Community Annotations	
mhkB Community Annotations Page	

Phenotype Annotation Tool



Phenotype Annotation Tool

Curator Central

Phenotype Curation

Strain	mhkB-
Genetic Context	
Phenotype	aberrant aggregation
Quality	
Reference	Myosin heavy chain kinase B partici
Environment	on bacterial plates
Assay	light microscopy
Notes	

assay	
Ontology	Dictyostelium Assay
Term name	light microscopy
Identifier	DDASSAY:0000016
Definition	
Is obsolete	0
Synonymns	
Parent terms	Dictyostelium Assay
Children terms	

Add Update Commit Retrieve Clear All

	Strain	Genetic Context	Entity	Quality	Reference	Environment	Assay	Notes
EDIT	mhkB-		aberrant aggregation		Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.	on bacterial plates	light microscopy	
EDIT	mhkB-	undefined	increased myosin II assembly	undefined	Rico & Egelhoff (2003) 'Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.' J Cell Biochem 88:521-32	undefined	biochemical assay	into Triton-resistant cytoskeletal fractions

Phenotype Annotation Tool

Curator Central

Phenotype Curation

Strain	mhkB-
Genetic Context	
Phenotype	aberrant aggregation
Quality	
Reference	Myosin heavy chain kinase B partici
Environment	on solid surfaces
Assay	light microscopy
Notes	

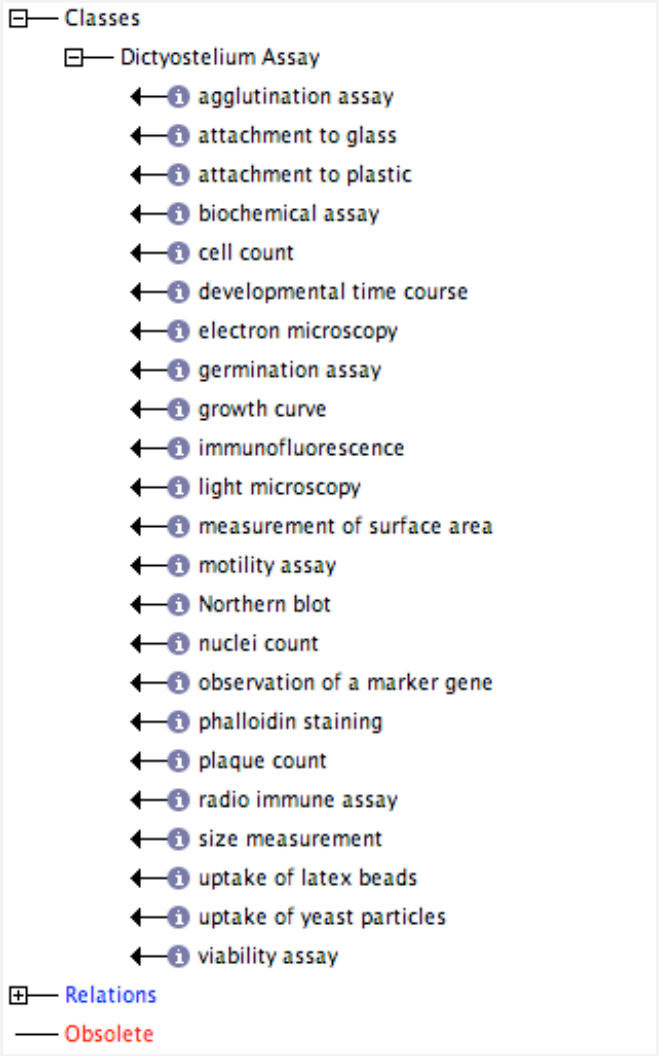
environment	
Ontology	environment
Term name	on solid surfaces
Identifier	DDENVIR:0000008
Definition	
Is obsolete	0
Synonymns	
Parent terms	environmental condition
Children terms	

Add | Update | Commit | Retrieve | Clear All

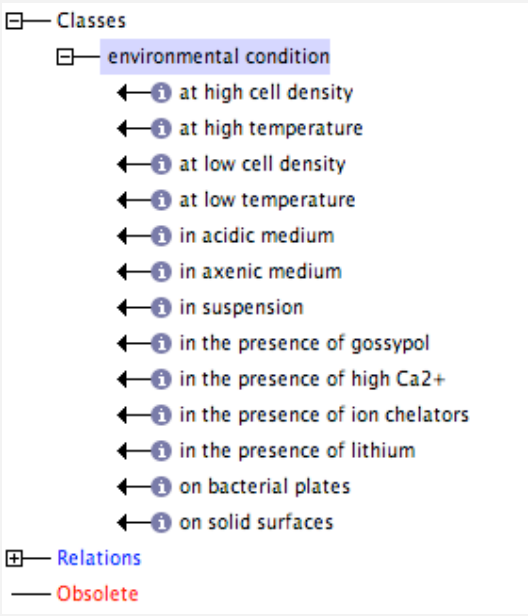
	Strain	Genetic Context	Entity	Quality	Reference	Environment	Assay	Notes
EDIT	mhkB-		aberrant aggregation		Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.	on solid surfaces	light microscopy	
EDIT	mhkB-	undefined	increased myosin II assembly	undefined	Rico & Egelhoff (2003) 'Myosin heavy chain kinase B participates in the regulation of myosin assembly into the cytoskeleton.' J Cell Biochem 88:521-32	undefined	biochemical assay	into Triton-resistant cytoskeletal fractions

Additional Ontologies

Assay



Environment



Future Directions

- Dissection of Dicty phenotype ontology terms to fit PATO Entity-Quality model
- Collaboration with other groups on PATO and phenotype-related ontologies (e.g., genetic context, environmental conditions)
- Provide phenotype annotation tool to GMOD as open-source software

Acknowledgements

Principal Investigators

- Rex Chisholm
- Warren Kibbe

Curators

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- Karen Pilcher

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- Sohel Merchant

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