Fungal genomics resources

FungiDB Walk through

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About FungiDB

- FungiDB takes advantage of infrastructure developed by folks at Penn, UGA & elsewhere for the Eukaryotic Pathogen Genome Database (EuPathDB), a national Bioinformatics Resource Center supported by NIAID, The Wellcome Trust, the Gates Foundation, and others.

- The Burroughs Wellcome Fund is supporting a pilot project to determine the utility of a Pan-fungal DB component.

- EuPathDB is a intended for both genome-wide queries and data mining with emphasis on functional and comparative genomics data

- Site launched March 14, 2011 for Asilomar.

- Important to have your feedback, good or bad, about the data and resources in this project, please sign up for an account on the site. Will allow saving and sharing of queries performed on the system too.

Other tools

- Ensembl Fungi - http://fungi.ensembl.org
- JGI Mycocosm - http://jgi.doe.gov/fungi
- Microbes Online (LBL) http://microbesonline.org
- AspGD (Aspergillus), SGD (Saccharomyces), CGD (Candida)
- Comparative Fungal Genomics Platform http://cfgp.riceblast.snu.ac.kr/

This release of FungiDB includes 18 genomes of 17 species of Fungi in Ascomycete, Basidiomycete, and Zygomycota

The following Fungal Genomese are now available via FungiDB:

- Eurotiomycetes; Ascomycota
    - *Aspergillus clavatus*
    - *Aspergillus flavus*
    - *Aspergillus fumigatus* strain Af293
    - *Aspergillus niger*
    - *Aspergillus nidulans (Emericella nidulans)* strain A4
    - *Aspergillus terreus*
    - *Coccidoidies immitis* strain RS
    - *Coccidoidies immitis* strain H538.4
- Sordariomycetes; Ascomyocta
    - *Fusarium oxysporum f. sp. lycopersici*
    - *Gibberella zeae (Fusarium graminearum)*
    - *Gibberella moniliformis (Fusarium verticillioides)*
    - *Magnaporthea oryzae*
    - *Neurospora crassa* strain OR74A
- Saccharomycotina; Ascomyocta
    - *Candida albicans*
    - *Saccharomyces cerevisiae*
- Basidiomycota
    - ***Filobasidiella neoformans*** **(*Cryptococcus neoformans* var. *grubii*) strain H99**
    - *Puccinia graminis*
- Mucormycotina ("Zygomycota")
    - *Rhizopus oryzae (Rhizopus delemar)*

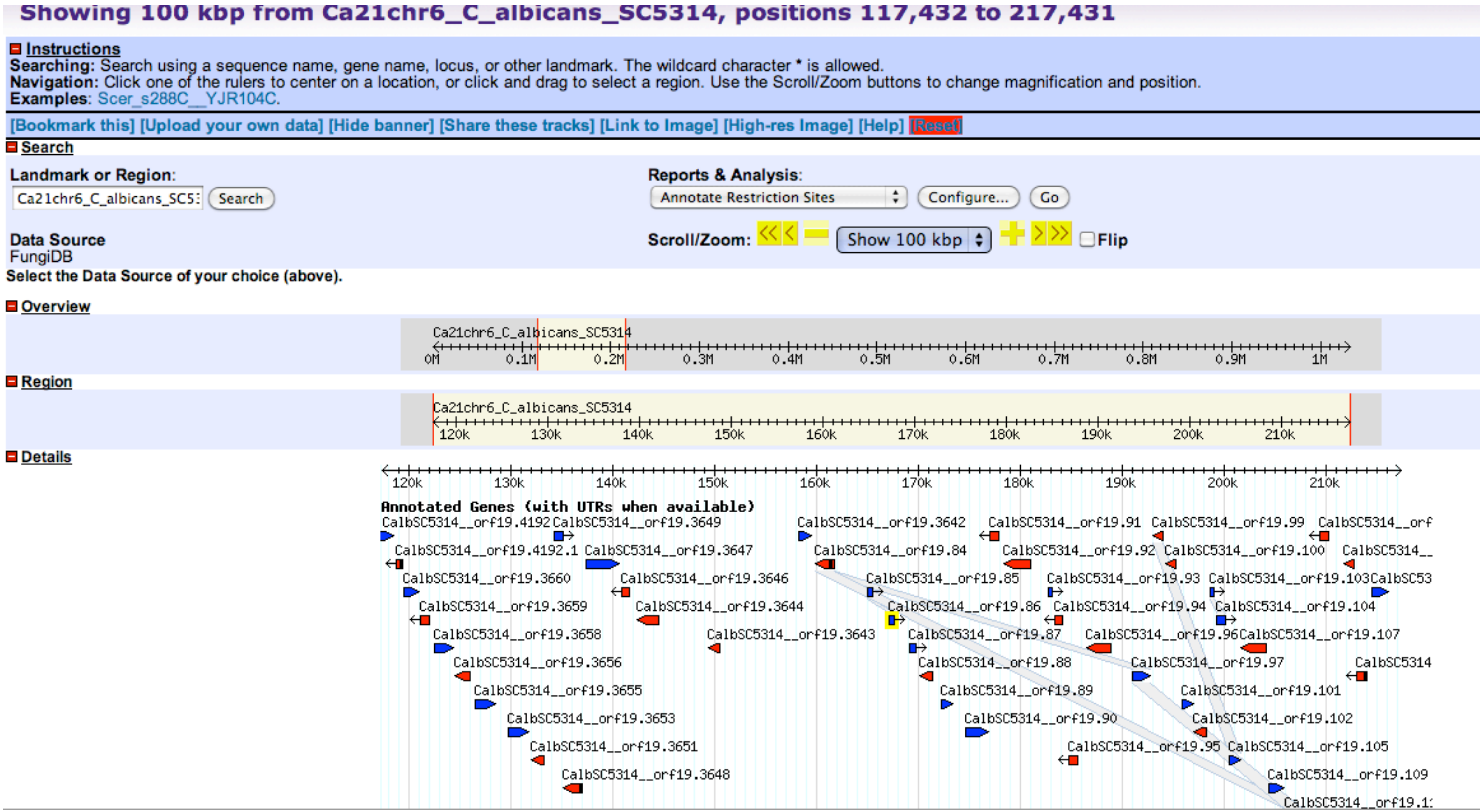
What does the system do?

- Browsing of gene pages (Like SGD)
- Genome browser for seeing genes in genomic context

- Query system for building sophisticated queries allowing for data mining

Genome Browsers

- Usually linear view of DNA coordinates
- Search by feature names, genomic coordinates
- Typically vertical views, though some (NCBI map viewer) draw horizontally



Showing 100 kbp from Ca21chr6_C_albicans_SC5314, positions 117,432 to 217,431

Instructions

Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.
Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.
Examples: Scer_s288C__YJR104C.

[Bookmark this] [Upload your own data] [Hide banner] [Share these tracks] [Link to Image] [High-res Image] [Help] [Reset]

Search

Landmark or Region: Ca21chr6_C_albicans_SC5 [Search]

Reports & Analysis: Annotate Restriction Sites [Configure...] [Go]

Data Source
FungiDB
Select the Data Source of your choice (above).

Scroll/Zoom: Show 100 kbp ☐ Flip

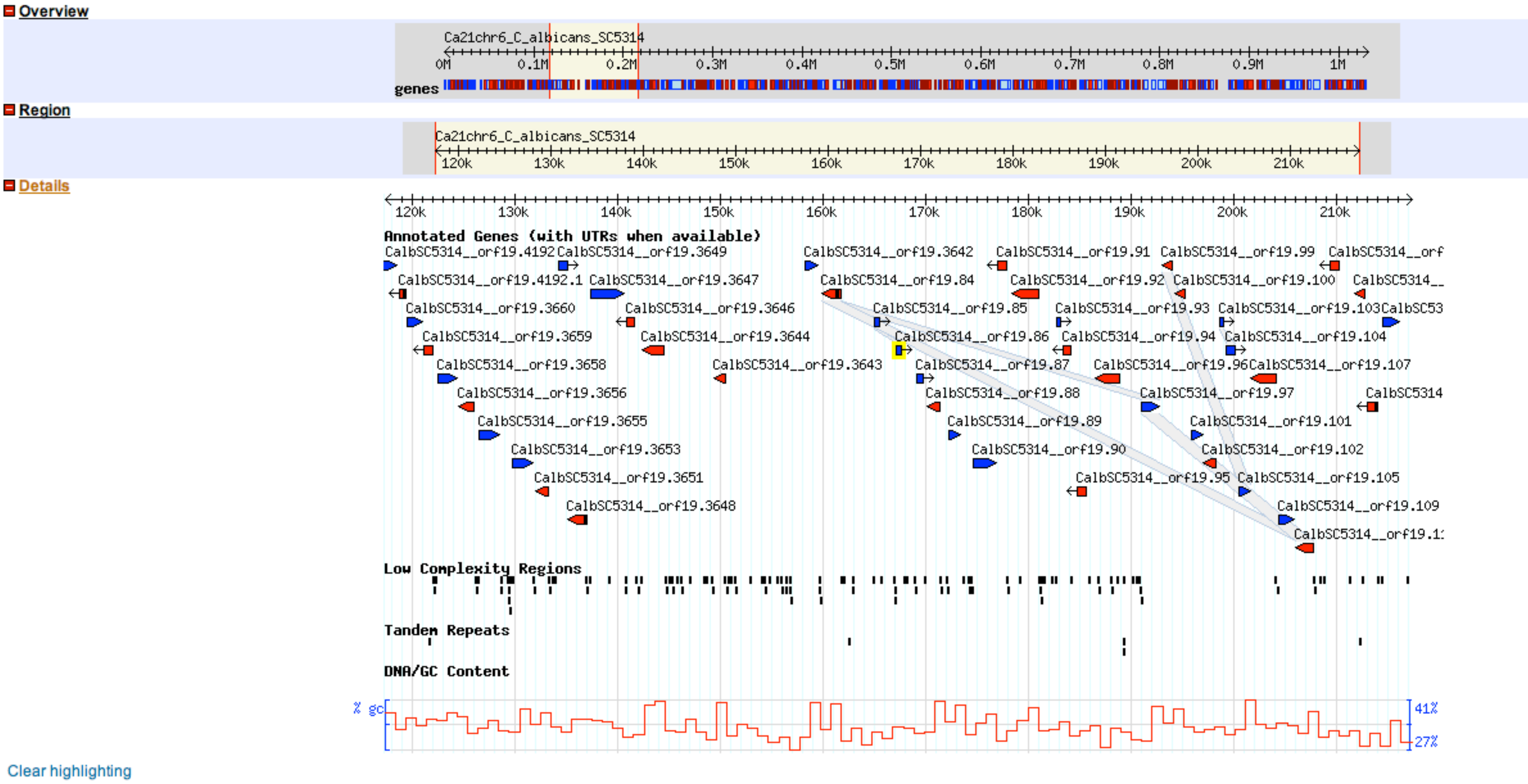
Overview

Region

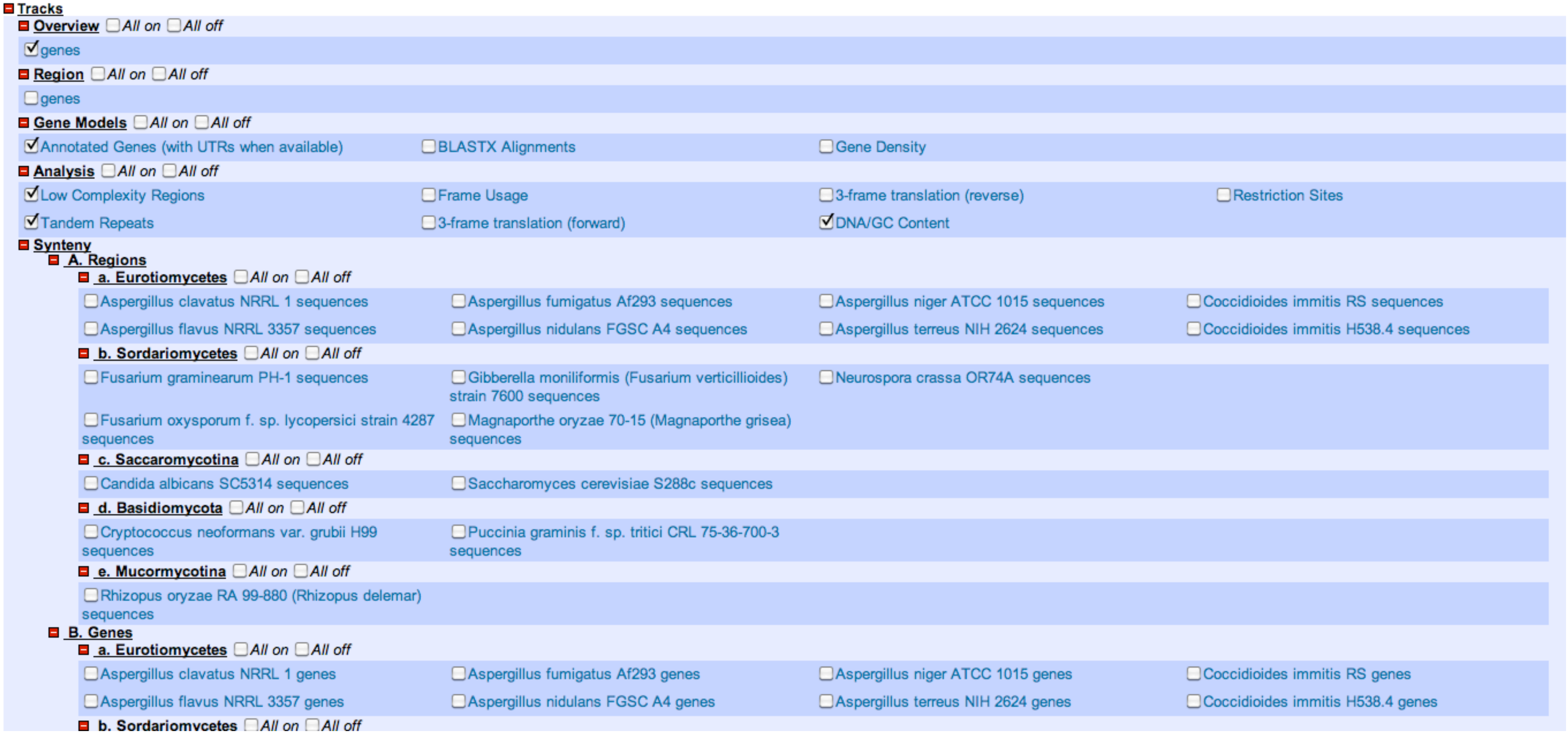
Details

http://beta.fungidb.org/cgi-bin/gbrowse/fungidb/?name=Ca21chr6_C_albicans_SC5314:117432..217431

http://bit.ly/fdb_browser1



http://bit.ly/fdb_browser1



⊟ **Tracks**

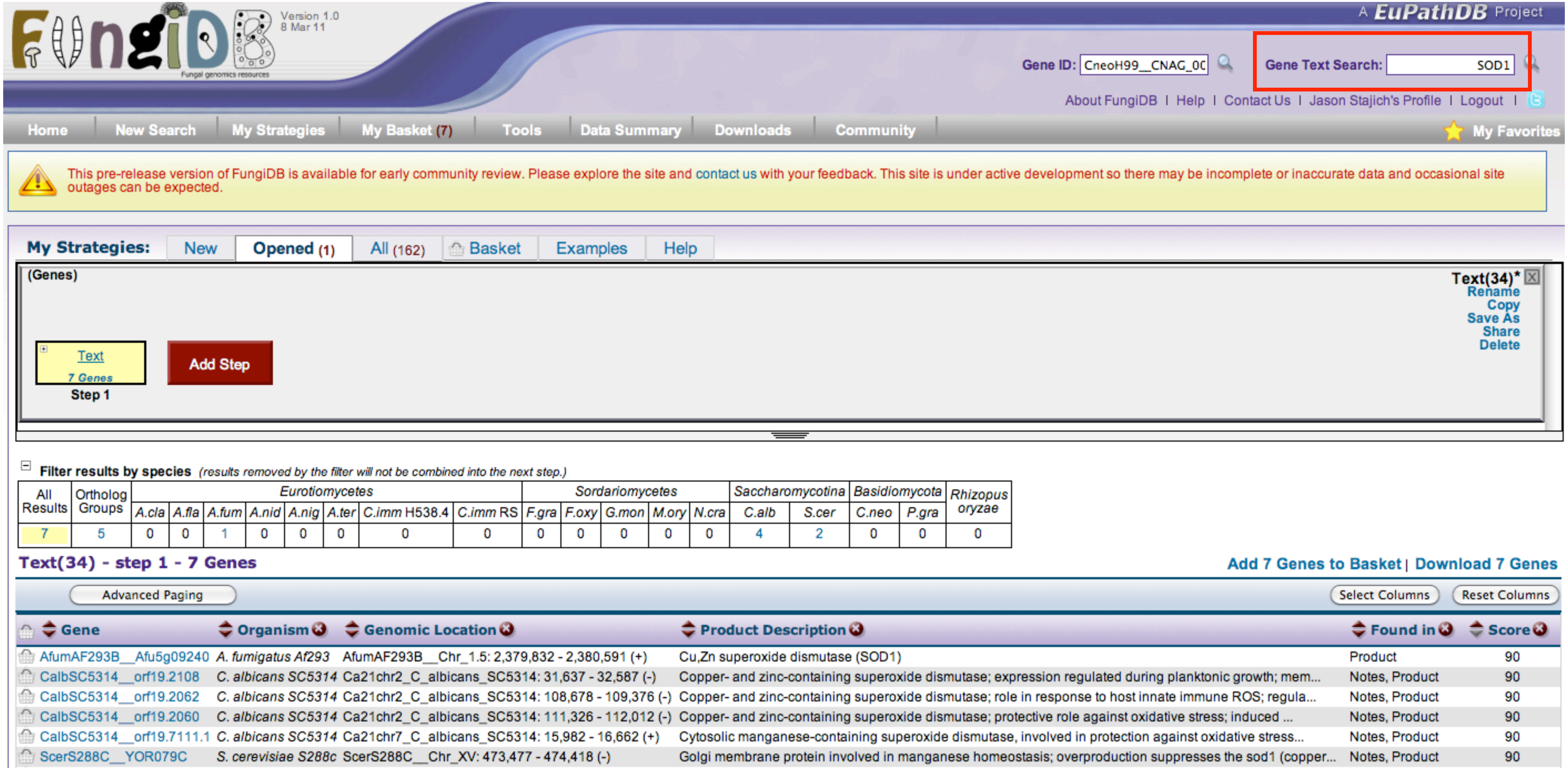
- ⊟ **Overview** ☐*All on* ☐*All off*
  - ☑genes
- ⊟ **Region** ☐*All on* ☐*All off*
  - ☐genes
- ⊟ **Gene Models** ☐*All on* ☐*All off*
  - ☑Annotated Genes (with UTRs when available)
  - ☐BLASTX Alignments
  - ☐Gene Density
- ⊟ **Analysis** ☐*All on* ☐*All off*
  - ☑Low Complexity Regions
  - ☑Tandem Repeats
  - ☐Frame Usage
  - ☐3-frame translation (forward)
  - ☐3-frame translation (reverse)
  - ☑DNA/GC Content
  - ☐Restriction Sites
- ⊟ **Synteny**
  - ⊟ **A. Regions**
    - ⊟ **a. Eurotiomycetes** ☐*All on* ☐*All off*
      - ☐Aspergillus clavatus NRRL 1 sequences
      - ☐Aspergillus flavus NRRL 3357 sequences
      - ☐Aspergillus fumigatus Af293 sequences
      - ☐Aspergillus nidulans FGSC A4 sequences
      - ☐Aspergillus niger ATCC 1015 sequences
      - ☐Aspergillus terreus NIH 2624 sequences
      - ☐Coccidioides immitis RS sequences
      - ☐Coccidioides immitis H538.4 sequences
    - ⊟ **b. Sordariomycetes** ☐*All on* ☐*All off*
      - ☐Fusarium graminearum PH-1 sequences
      - ☐Fusarium oxysporum f. sp. lycopersici strain 4287 sequences
      - ☐Gibberella moniliformis (Fusarium verticillioides) strain 7600 sequences
      - ☐Magnaporthe oryzae 70-15 (Magnaporthe grisea) sequences
      - ☐Neurospora crassa OR74A sequences
    - ⊟ **c. Saccaromycotina** ☐*All on* ☐*All off*
      - ☐Candida albicans SC5314 sequences
      - ☐Saccharomyces cerevisiae S288c sequences
    - ⊟ **d. Basidiomycota** ☐*All on* ☐*All off*
      - ☐Cryptococcus neoformans var. grubii H99 sequences
      - ☐Puccinia graminis f. sp. tritici CRL 75-36-700-3 sequences
    - ⊟ **e. Mucormycotina** ☐*All on* ☐*All off*
      - ☐Rhizopus oryzae RA 99-880 (Rhizopus delemar) sequences
  - ⊟ **B. Genes**
    - ⊟ **a. Eurotiomycetes** ☐*All on* ☐*All off*
      - ☐Aspergillus clavatus NRRL 1 genes
      - ☐Aspergillus flavus NRRL 3357 genes
      - ☐Aspergillus fumigatus Af293 genes
      - ☐Aspergillus nidulans FGSC A4 genes
      - ☐Aspergillus niger ATCC 1015 genes
      - ☐Aspergillus terreus NIH 2624 genes
      - ☐Coccidioides immitis RS genes
      - ☐Coccidioides immitis H538.4 genes
    - ⊟ **b. Sordariomycetes** ☐*All on* ☐*All off*

Gbrowse 2 demo

http://bit.ly/fdb_gb1

Query for Genes by Name

- Gene pages for each gene in the genome
- Have links to other information and external information
- Can be updated to include references to publications, mistakes in annotation, links to other databases



Gene ID: CneoH99__CNAG_0C

Gene Text Search: SOD1

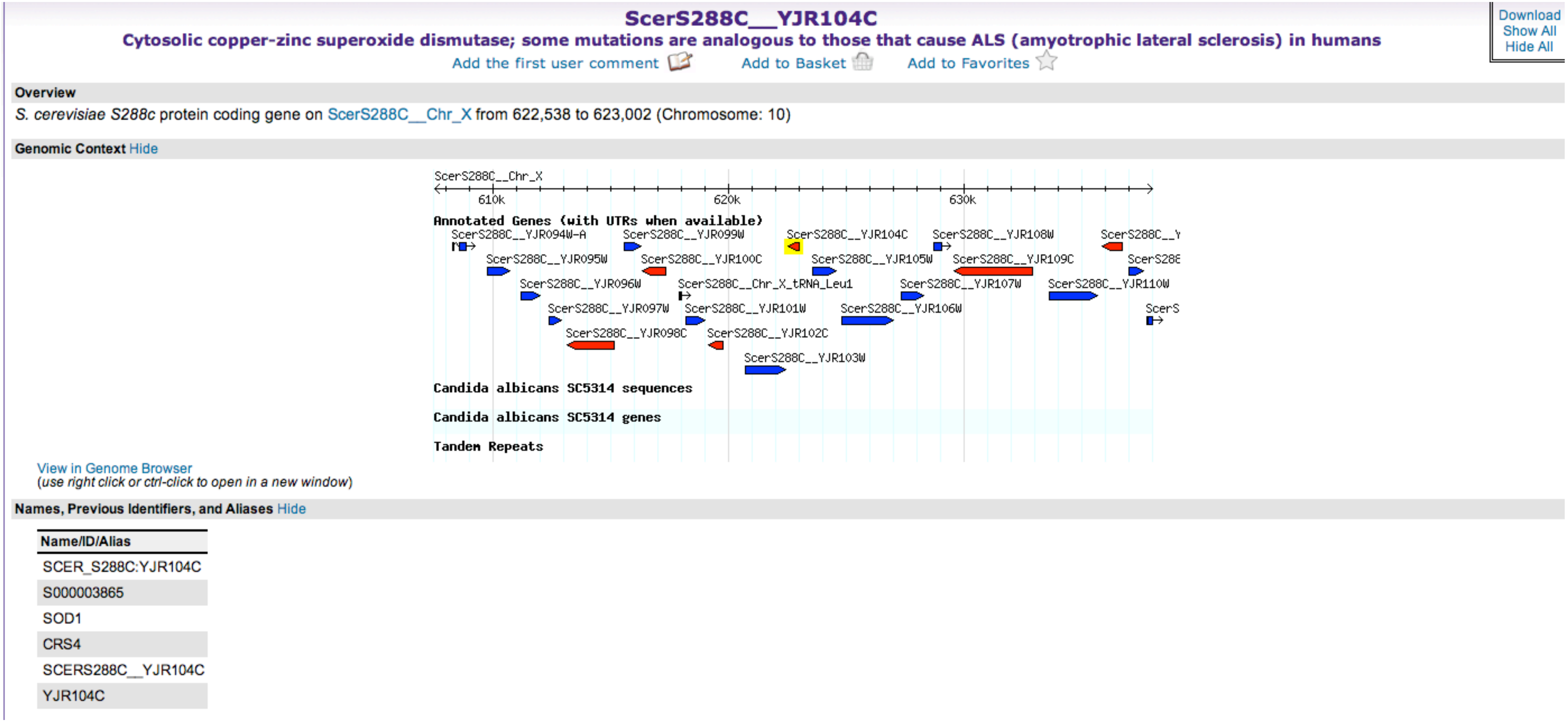
This pre-release version of FungiDB is available for early community review. Please explore the site and contact us with your feedback. This site is under active development so there may be incomplete or inaccurate data and occasional site outages can be expected.

Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
7	5	0	0	1	0	0	0	0	0	0	0	0	0	0	4	2	0	0	0

Text(34) - step 1 - 7 Genes

Gene	Organism	Genomic Location	Product Description	Found in	Score
AfumAF293B__Afu5g09240	*A. fumigatus Af293*	AfumAF293B__Chr_1.5: 2,379,832 - 2,380,591 (+)	Cu,Zn superoxide dismutase (SOD1)	Product	90
CalbSC5314__orf19.2108	*C. albicans SC5314*	Ca21chr2_C_albicans_SC5314: 31,637 - 32,587 (-)	Copper- and zinc-containing superoxide dismutase; expression regulated during planktonic growth; mem...	Notes, Product	90
CalbSC5314__orf19.2062	*C. albicans SC5314*	Ca21chr2_C_albicans_SC5314: 108,678 - 109,376 (-)	Copper- and zinc-containing superoxide dismutase; role in response to host innate immune ROS; regula...	Notes, Product	90
CalbSC5314__orf19.2060	*C. albicans SC5314*	Ca21chr2_C_albicans_SC5314: 111,326 - 112,012 (-)	Copper- and zinc-containing superoxide dismutase; protective role against oxidative stress; induced ...	Notes, Product	90
CalbSC5314__orf19.7111.1	*C. albicans SC5314*	Ca21chr7_C_albicans_SC5314: 15,982 - 16,662 (+)	Cytosolic manganese-containing superoxide dismutase, involved in protection against oxidative stress...	Notes, Product	90
ScerS288C__YOR079C	*S. cerevisiae S288c*	ScerS288C__Chr_XV: 473,477 - 474,418 (-)	Golgi membrane protein involved in manganese homeostasis; overproduction suppresses the sod1 (copper...	Notes, Product	90



ScerS288C__YJR104C

Cytosolic copper-zinc superoxide dismutase; some mutations are analogous to those that cause ALS (amyotrophic lateral sclerosis) in humans

Overview

S. cerevisiae S288c protein coding gene on ScerS288C__Chr_X from 622,538 to 623,002 (Chromosome: 10)

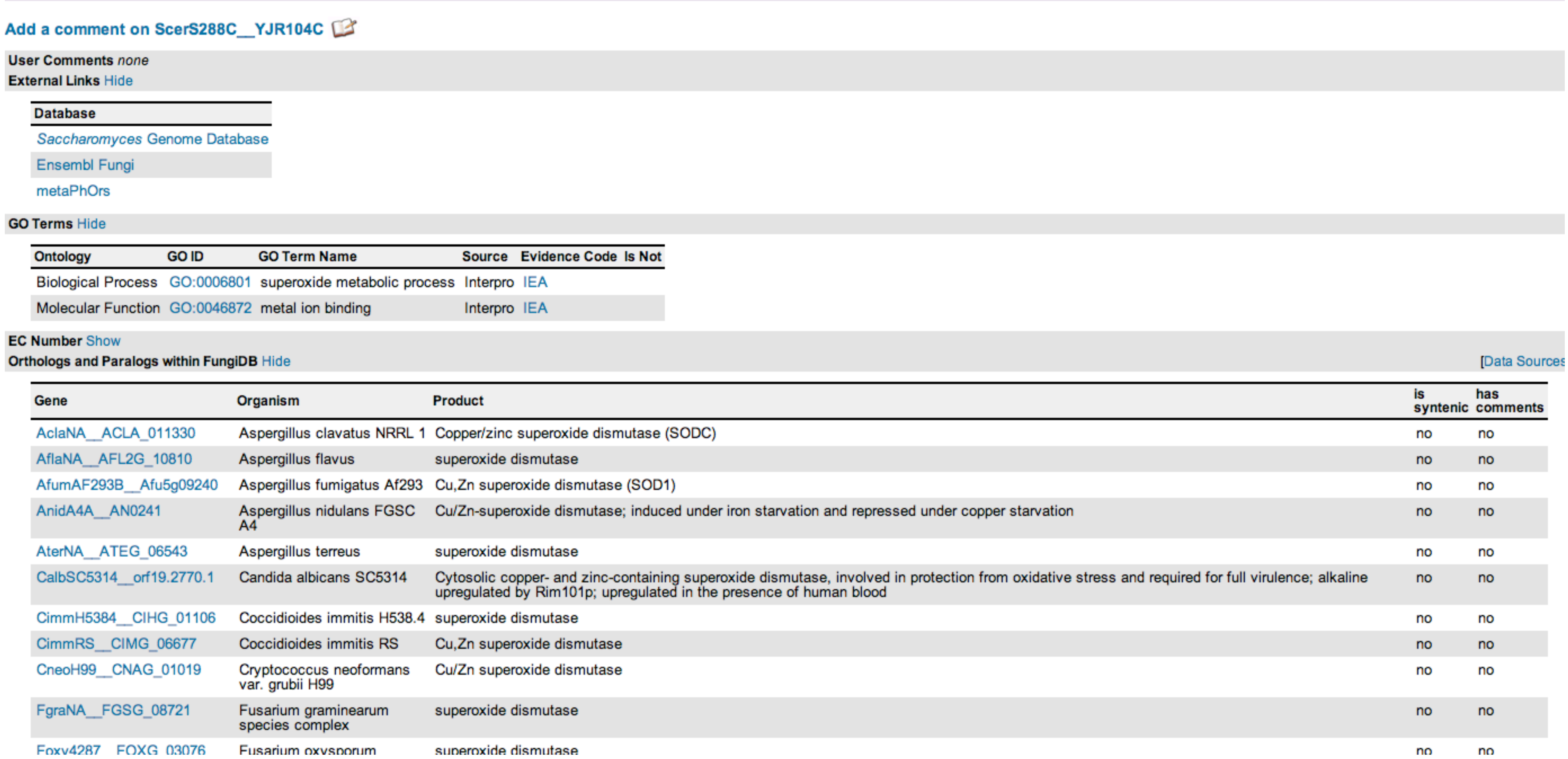
Genomic Context Hide

View in Genome Browser
(*use right click or ctrl-click to open in a new window*)

Names, Previous Identifiers, and Aliases Hide

Name/ID/Alias
SCER_S288C:YJR104C
S000003865
SOD1
CRS4
SCERS288C__YJR104C
YJR104C

http://fungidb.org/gene/ScerS288C__YJR104C



Add a comment on ScerS288C__YJR104C

User Comments *none*

External Links Hide

Database
Saccharomyces Genome Database
Ensembl Fungi
metaPhOrs

GO Terms Hide

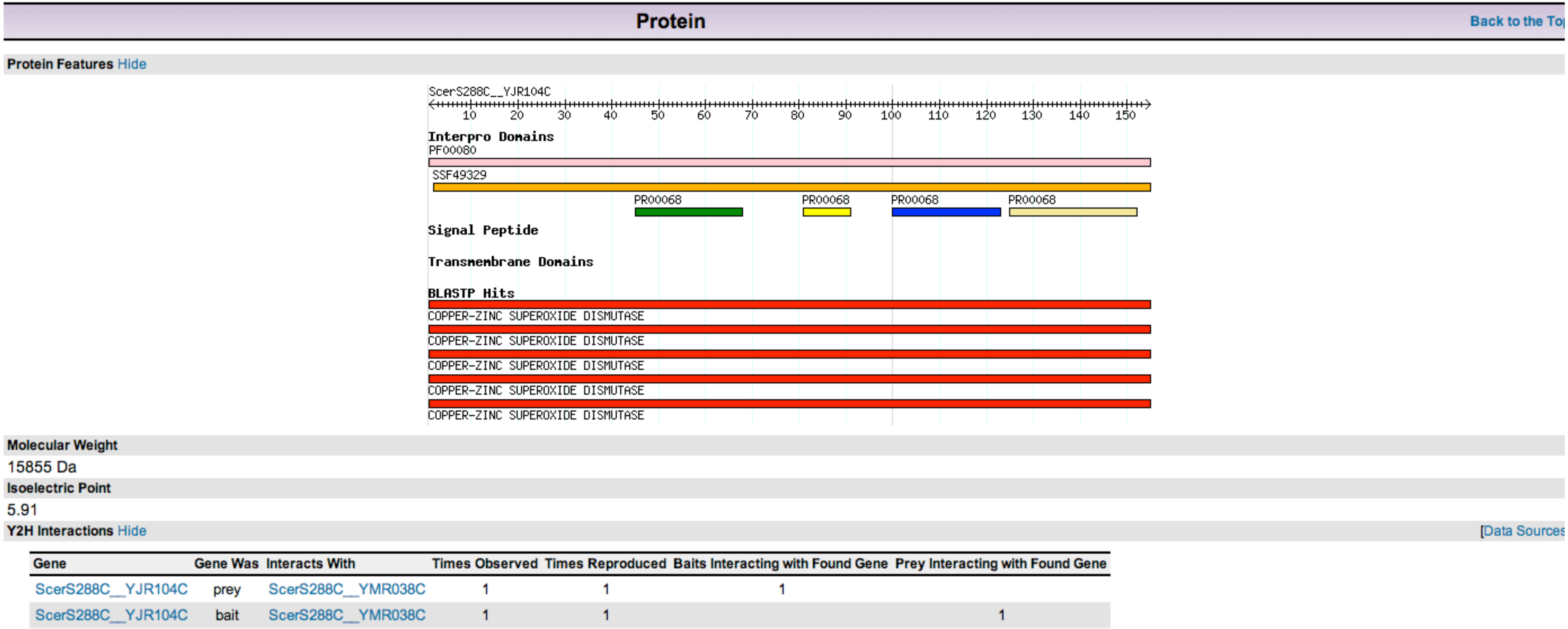
Ontology	GO ID	GO Term Name	Source	Evidence Code	Is Not
Biological Process	GO:0006801	superoxide metabolic process	Interpro	IEA	
Molecular Function	GO:0046872	metal ion binding	Interpro	IEA	

EC Number Show

Orthologs and Paralogs within FungiDB Hide [Data Sources

Gene	Organism	Product	is syntenic	has comments
AclaNA__ACLA_011330	Aspergillus clavatus NRRL 1	Copper/zinc superoxide dismutase (SODC)	no	no
AflaNA__AFL2G_10810	Aspergillus flavus	superoxide dismutase	no	no
AfumAF293B__Afu5g09240	Aspergillus fumigatus Af293	Cu,Zn superoxide dismutase (SOD1)	no	no
AnidA4A__AN0241	Aspergillus nidulans FGSC A4	Cu/Zn-superoxide dismutase; induced under iron starvation and repressed under copper starvation	no	no
AterNA__ATEG_06543	Aspergillus terreus	superoxide dismutase	no	no
CalbSC5314__orf19.2770.1	Candida albicans SC5314	Cytosolic copper- and zinc-containing superoxide dismutase, involved in protection from oxidative stress and required for full virulence; alkaline upregulated by Rim101p; upregulated in the presence of human blood	no	no
CimmH5384__CIHG_01106	Coccidioides immitis H538.4	superoxide dismutase	no	no
CimmRS__CIMG_06677	Coccidioides immitis RS	Cu,Zn superoxide dismutase	no	no
CneoH99__CNAG_01019	Cryptococcus neoformans var. grubii H99	Cu/Zn superoxide dismutase	no	no
FgraNA__FGSG_08721	Fusarium graminearum species complex	superoxide dismutase	no	no
Foxy4287__FOXG_03076	Fusarium oxysporum	superoxide dismutase	no	no

http://fungidb.org/gene/ScerS288C__YJR104C



Protein

Back to the To

Protein Features Hide

Molecular Weight

15855 Da

Isoelectric Point

5.91

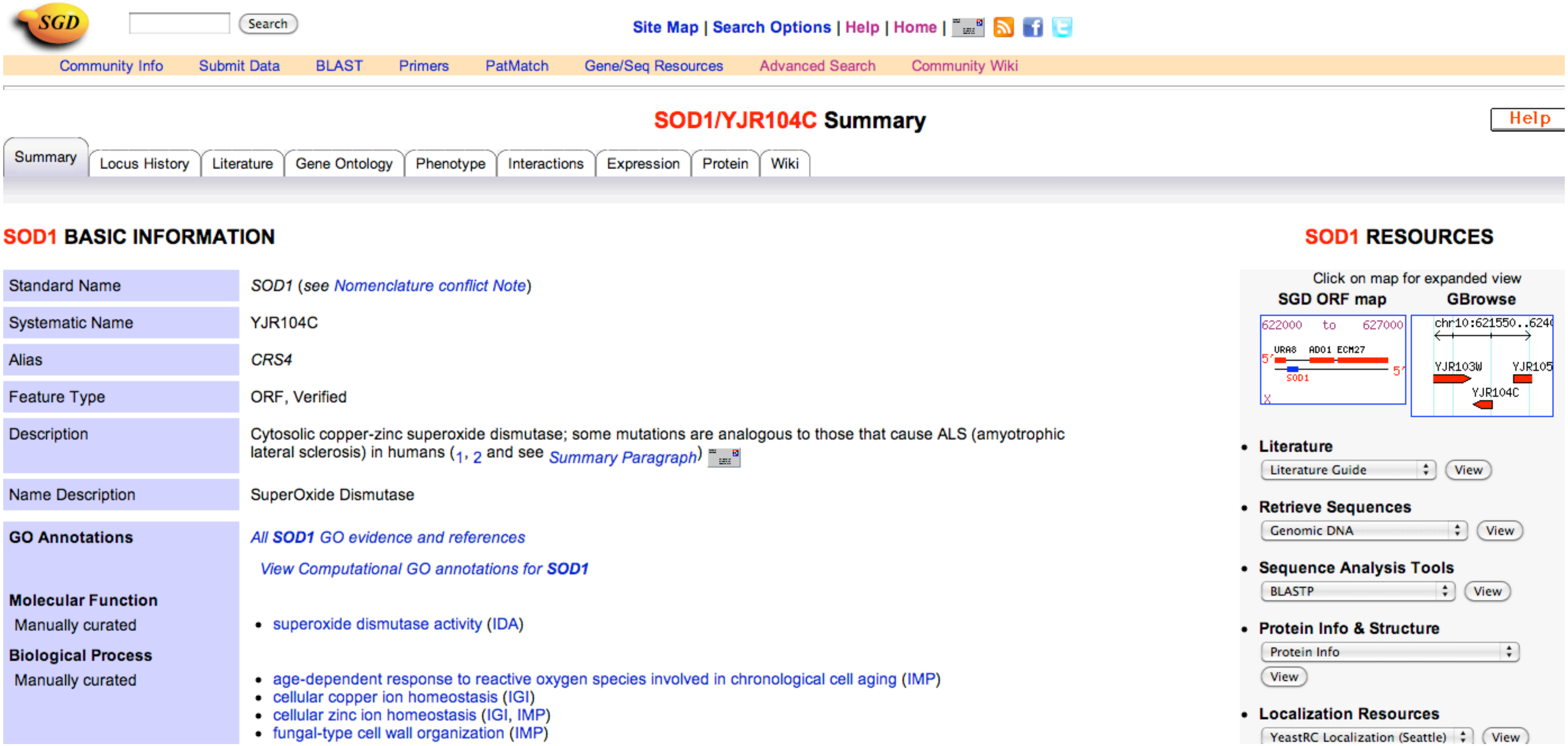
Y2H Interactions Hide

[Data Sources

Gene	Gene Was	Interacts With	Times Observed	Times Reproduced	Baits Interacting with Found Gene	Prey Interacting with Found Gene
ScerS288C__YJR104C	prey	ScerS288C__YMR038C	1	1	1	
ScerS288C__YJR104C	bait	ScerS288C__YMR038C	1	1		1

http://fungidb.org/gene/ScerS288C__YJR104C

Compare to SGD Gene pages



SOD1/YJR104C Summary

SOD1 BASIC INFORMATION

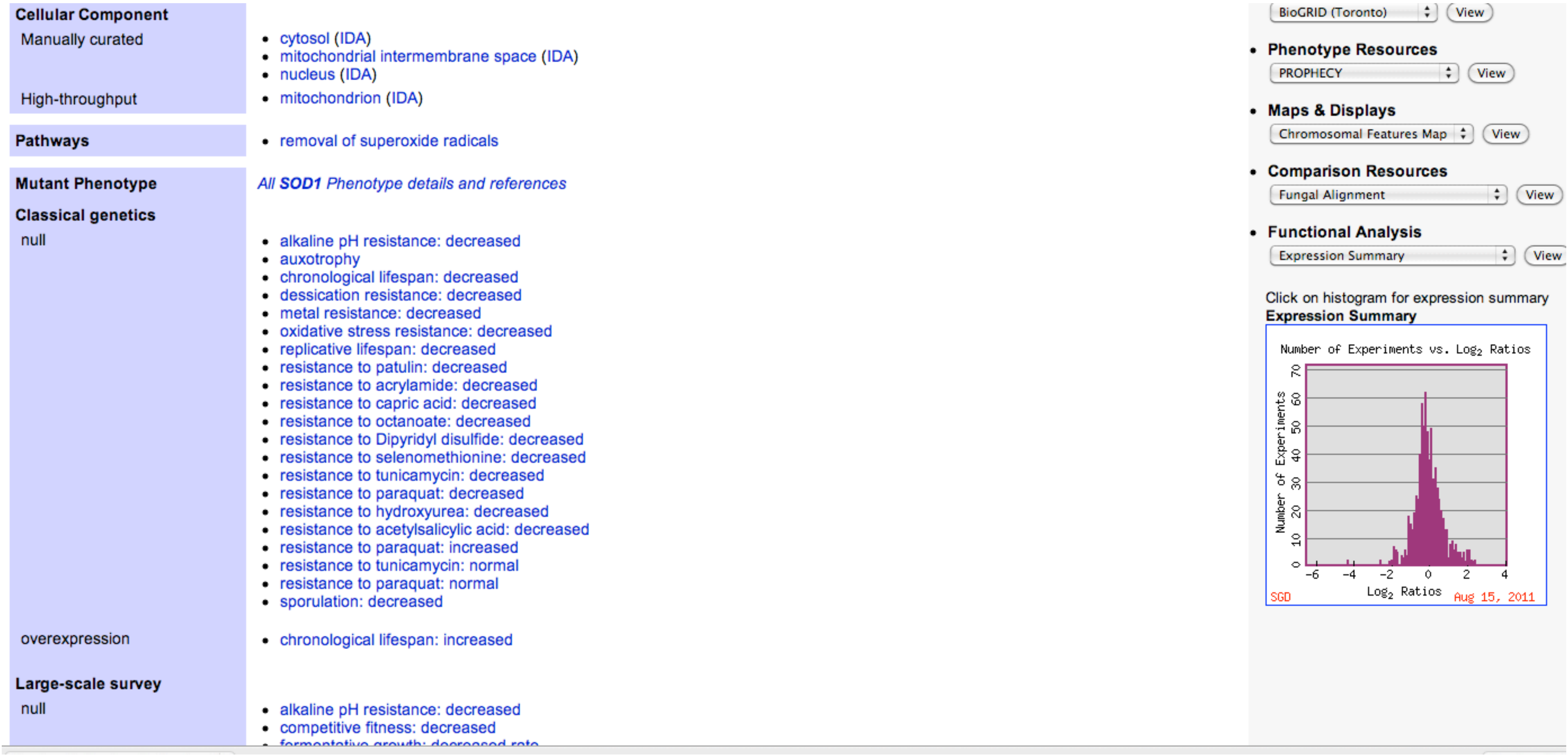
Standard Name	*SOD1* (*see Nomenclature conflict Note*)
Systematic Name	YJR104C
Alias	*CRS4*
Feature Type	ORF, Verified
Description	Cytosolic copper-zinc superoxide dismutase; some mutations are analogous to those that cause ALS (amyotrophic lateral sclerosis) in humans (1, 2 and see *Summary Paragraph*)
Name Description	SuperOxide Dismutase
GO Annotations	*All **SOD1** GO evidence and references* *View Computational GO annotations for **SOD1***
Molecular Function Manually curated	- superoxide dismutase activity (IDA)
Biological Process Manually curated	- age-dependent response to reactive oxygen species involved in chronological cell aging (IMP) - cellular copper ion homeostasis (IGI) - cellular zinc ion homeostasis (IGI, IMP) - fungal-type cell wall organization (IMP)

SOD1 RESOURCES

Click on map for expanded view

- **Literature**
  Literature Guide — View
- **Retrieve Sequences**
  Genomic DNA — View
- **Sequence Analysis Tools**
  BLASTP — View
- **Protein Info & Structure**
  Protein Info — View
- **Localization Resources**
  YeastRC Localization (Seattle) — View

http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SOD1



Cellular Component

Manually curated

- cytosol (IDA)
- mitochondrial intermembrane space (IDA)
- nucleus (IDA)

High-throughput

- mitochondrion (IDA)

Pathways

- removal of superoxide radicals

Mutant Phenotype

*All **SOD1** Phenotype details and references*

Classical genetics

null

- alkaline pH resistance: decreased
- auxotrophy
- chronological lifespan: decreased
- dessication resistance: decreased
- metal resistance: decreased
- oxidative stress resistance: decreased
- replicative lifespan: decreased
- resistance to patulin: decreased
- resistance to acrylamide: decreased
- resistance to capric acid: decreased
- resistance to octanoate: decreased
- resistance to Dipyridyl disulfide: decreased
- resistance to selenomethionine: decreased
- resistance to tunicamycin: decreased
- resistance to paraquat: decreased
- resistance to hydroxyurea: decreased
- resistance to acetylsalicylic acid: decreased
- resistance to paraquat: increased
- resistance to tunicamycin: normal
- resistance to paraquat: normal
- sporulation: decreased

overexpression

- chronological lifespan: increased

Large-scale survey

null

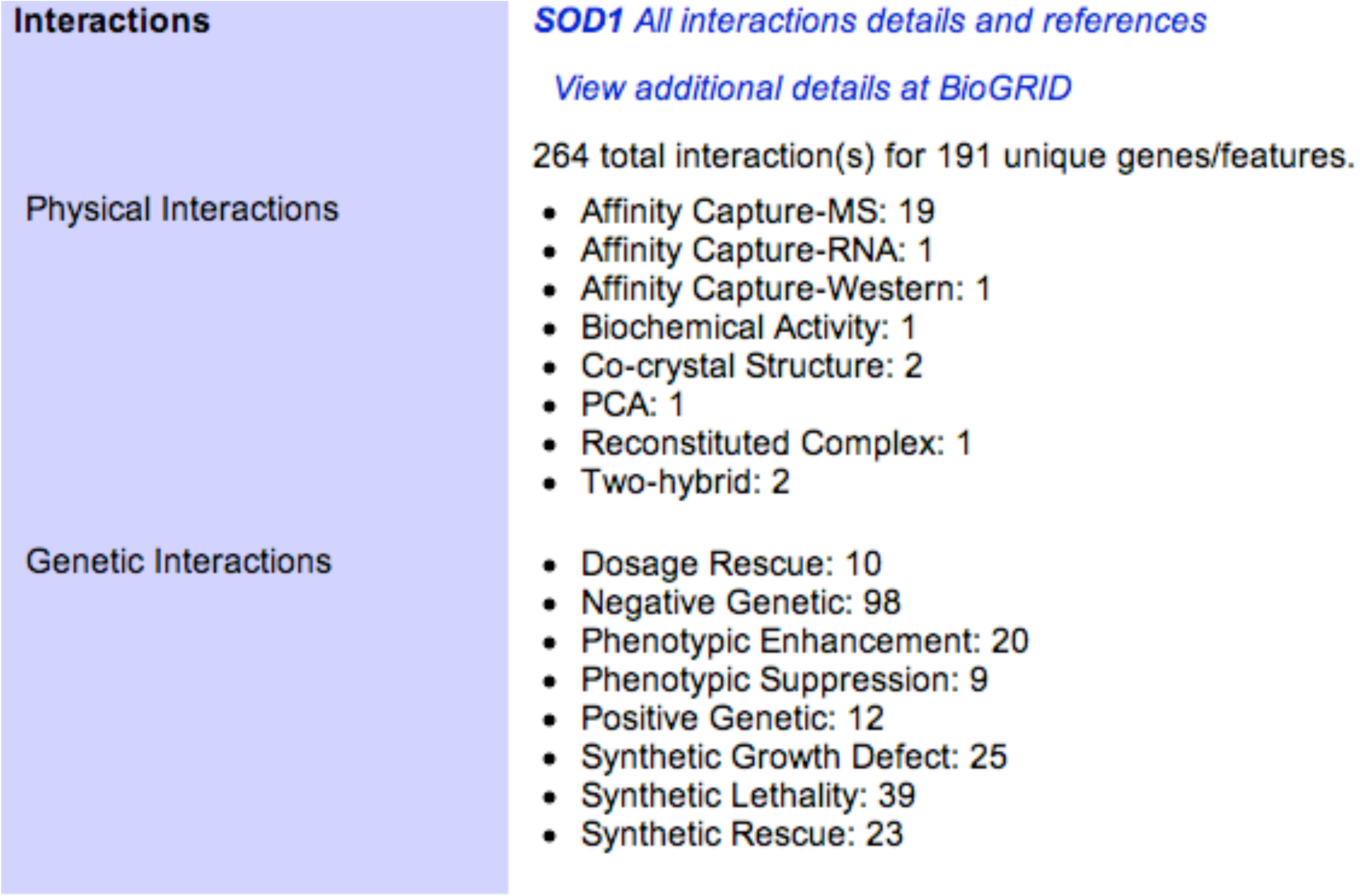
- alkaline pH resistance: decreased
- competitive fitness: decreased
- fermentative growth: decreased rate

- **Phenotype Resources**
- **Maps & Displays**
- **Comparison Resources**
- **Functional Analysis**

Click on histogram for expression summary

Expression Summary

http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SOD1



Interactions

SOD1 All interactions details and references

View additional details at BioGRID

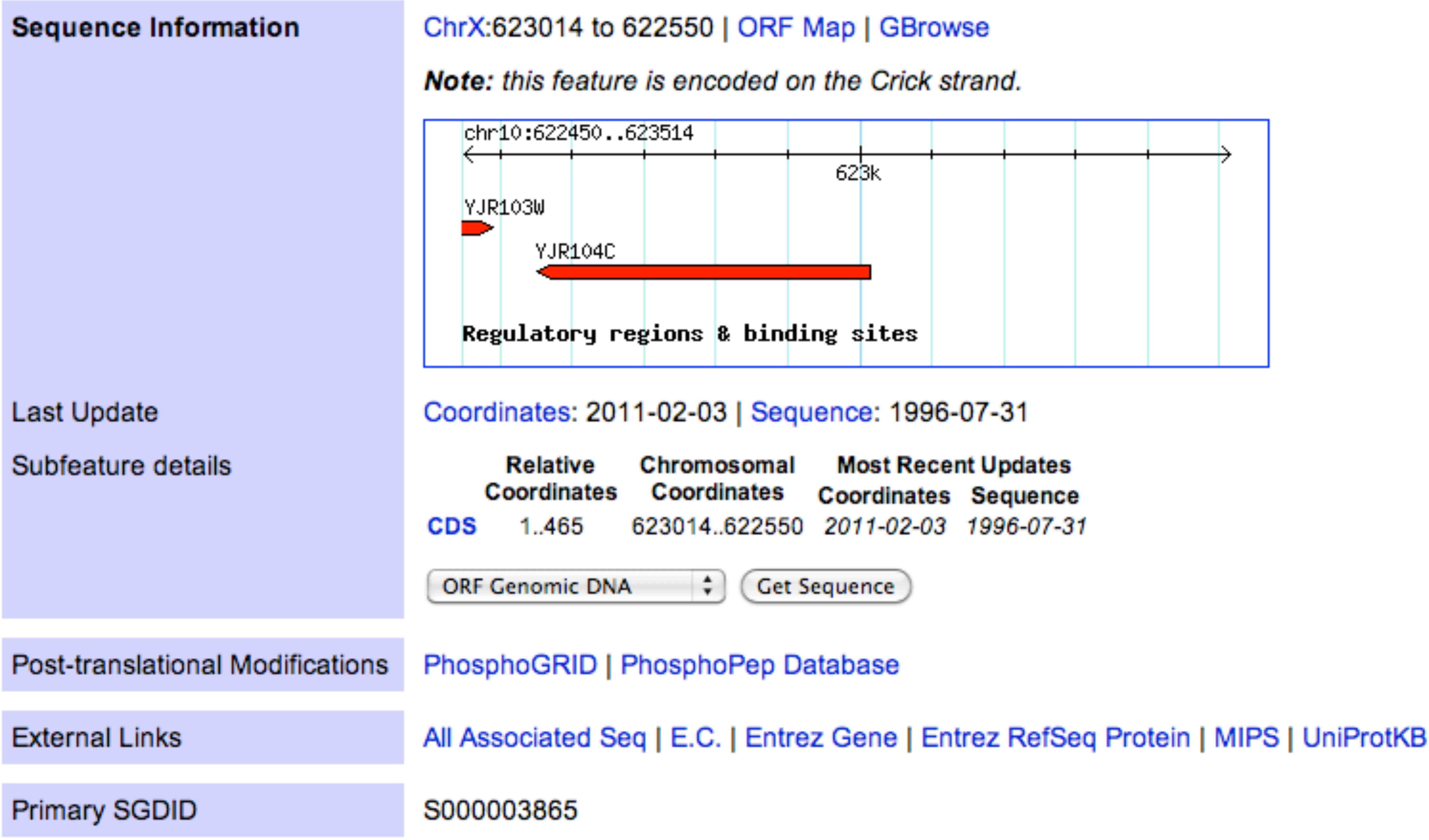
264 total interaction(s) for 191 unique genes/features.

Physical Interactions

- Affinity Capture-MS: 19
- Affinity Capture-RNA: 1
- Affinity Capture-Western: 1
- Biochemical Activity: 1
- Co-crystal Structure: 2
- PCA: 1
- Reconstituted Complex: 1
- Two-hybrid: 2

Genetic Interactions

- Dosage Rescue: 10
- Negative Genetic: 98
- Phenotypic Enhancement: 20
- Phenotypic Suppression: 9
- Positive Genetic: 12
- Synthetic Growth Defect: 25
- Synthetic Lethality: 39
- Synthetic Rescue: 23



Sequence Information

ChrX:623014 to 622550 | ORF Map | GBrowse

***Note:** this feature is encoded on the Crick strand.*

Last Update: Coordinates: 2011-02-03 | Sequence: 1996-07-31

Subfeature details

	Relative Coordinates	Chromosomal Coordinates	Most Recent Updates Coordinates	Sequence
CDS	1..465	623014..622550	*2011-02-03*	*1996-07-31*

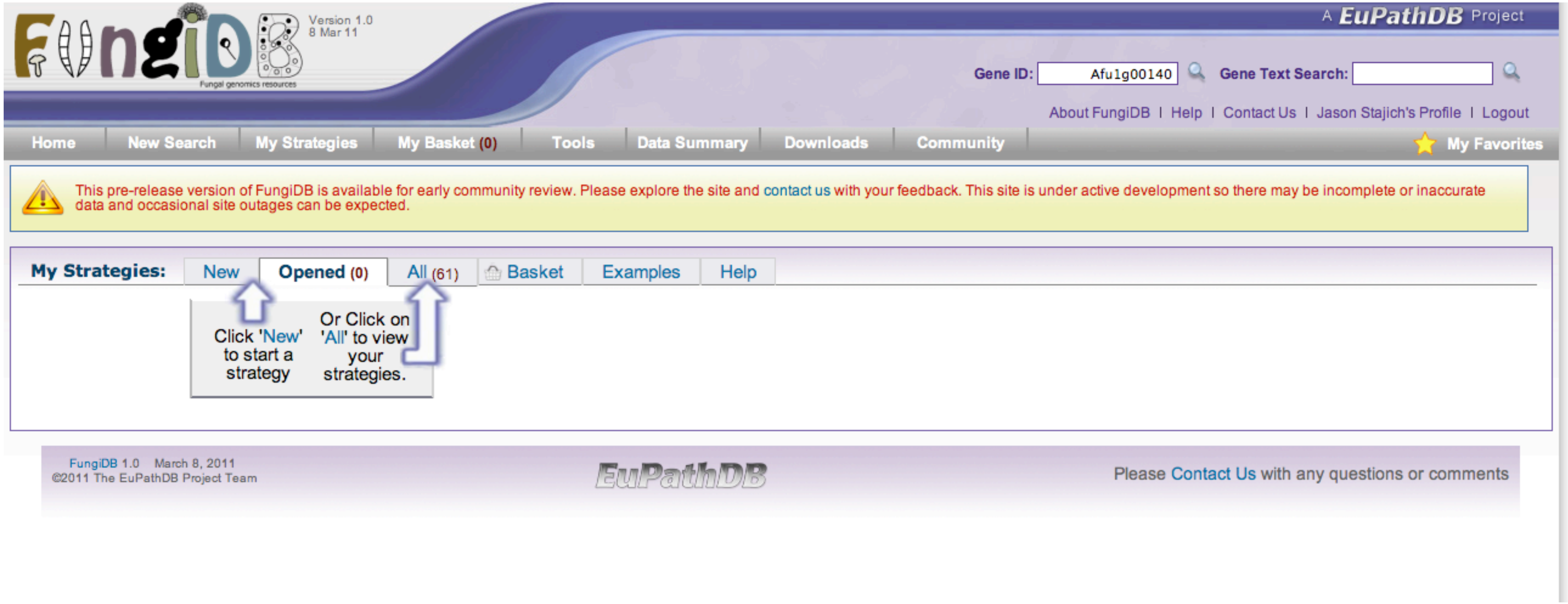
Post-translational Modifications: PhosphoGRID | PhosphoPep Database

External Links: All Associated Seq | E.C. | Entrez Gene | Entrez RefSeq Protein | MIPS | UniProtKB

Primary SGDID: S000003865

http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SOD1

Querying with FungiDB and the Strategies Web Development Kit (WDK)



Gene ID: Afu1g00140

Gene Text Search:

This pre-release version of FungiDB is available for early community review. Please explore the site and contact us with your feedback. This site is under active development so there may be incomplete or inaccurate data and occasional site outages can be expected.

Click 'New' to start a strategy

Or Click on 'All' to view your strategies.

FungiDB 1.0 March 8, 2011
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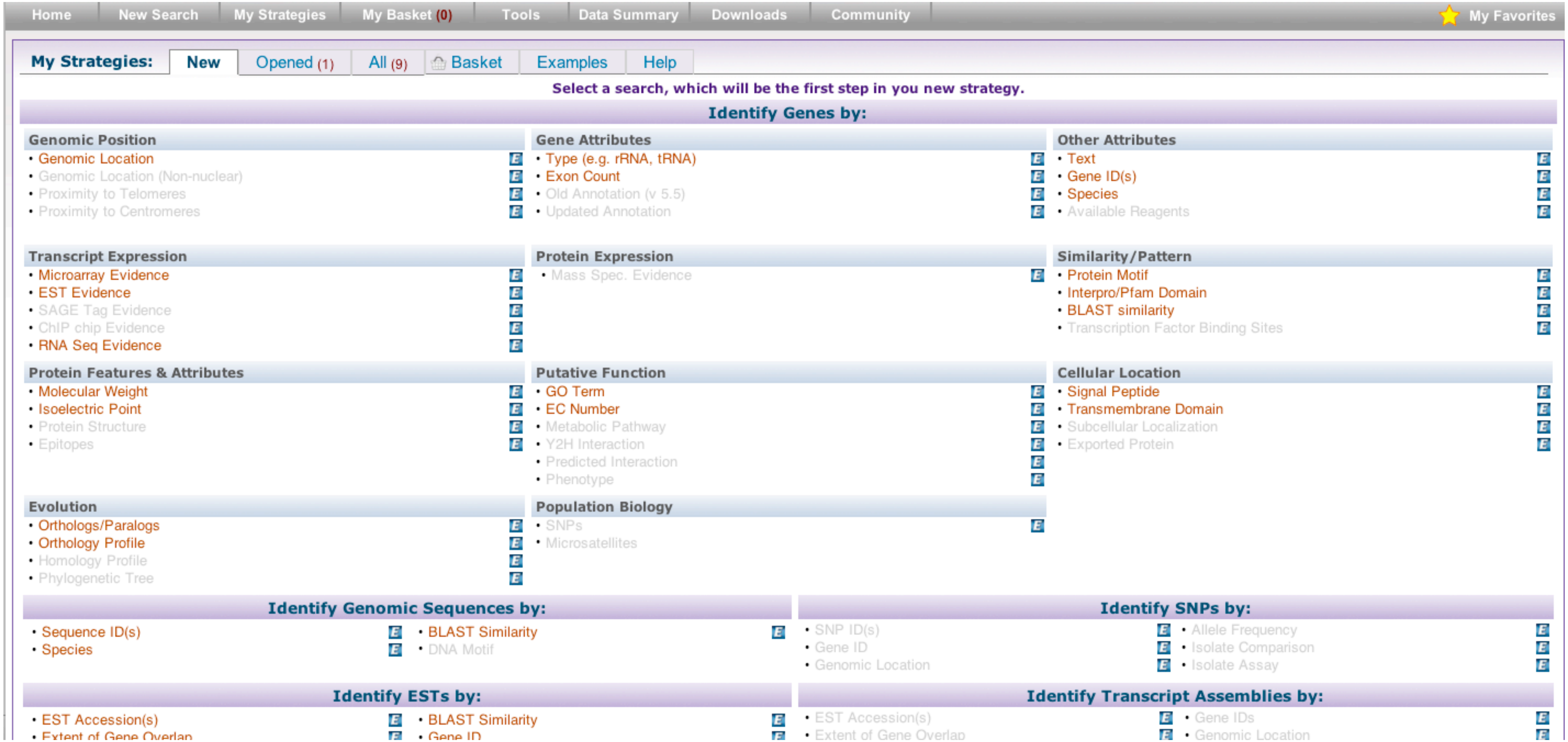
EuPathDB

Please Contact Us with any questions or comments

Query matrix of types of strategies to use for genes



Select a search, which will be the first step in you new strategy.

Identify Genes by:

Genomic Position
- Genomic Location
- Genomic Location (Non-nuclear)
- Proximity to Telomeres
- Proximity to Centromeres

Gene Attributes
- Type (e.g. rRNA, tRNA)
- Exon Count
- Old Annotation (v 5.5)
- Updated Annotation

Other Attributes
- Text
- Gene ID(s)
- Species
- Available Reagents

Transcript Expression
- Microarray Evidence
- EST Evidence
- SAGE Tag Evidence
- ChIP chip Evidence
- RNA Seq Evidence

Protein Expression
- Mass Spec. Evidence

Similarity/Pattern
- Protein Motif
- Interpro/Pfam Domain
- BLAST similarity
- Transcription Factor Binding Sites

Protein Features & Attributes
- Molecular Weight
- Isoelectric Point
- Protein Structure
- Epitopes

Putative Function
- GO Term
- EC Number
- Metabolic Pathway
- Y2H Interaction
- Predicted Interaction
- Phenotype

Cellular Location
- Signal Peptide
- Transmembrane Domain
- Subcellular Localization
- Exported Protein

Evolution
- Orthologs/Paralogs
- Orthology Profile
- Homology Profile
- Phylogenetic Tree

Population Biology
- SNPs
- Microsatellites

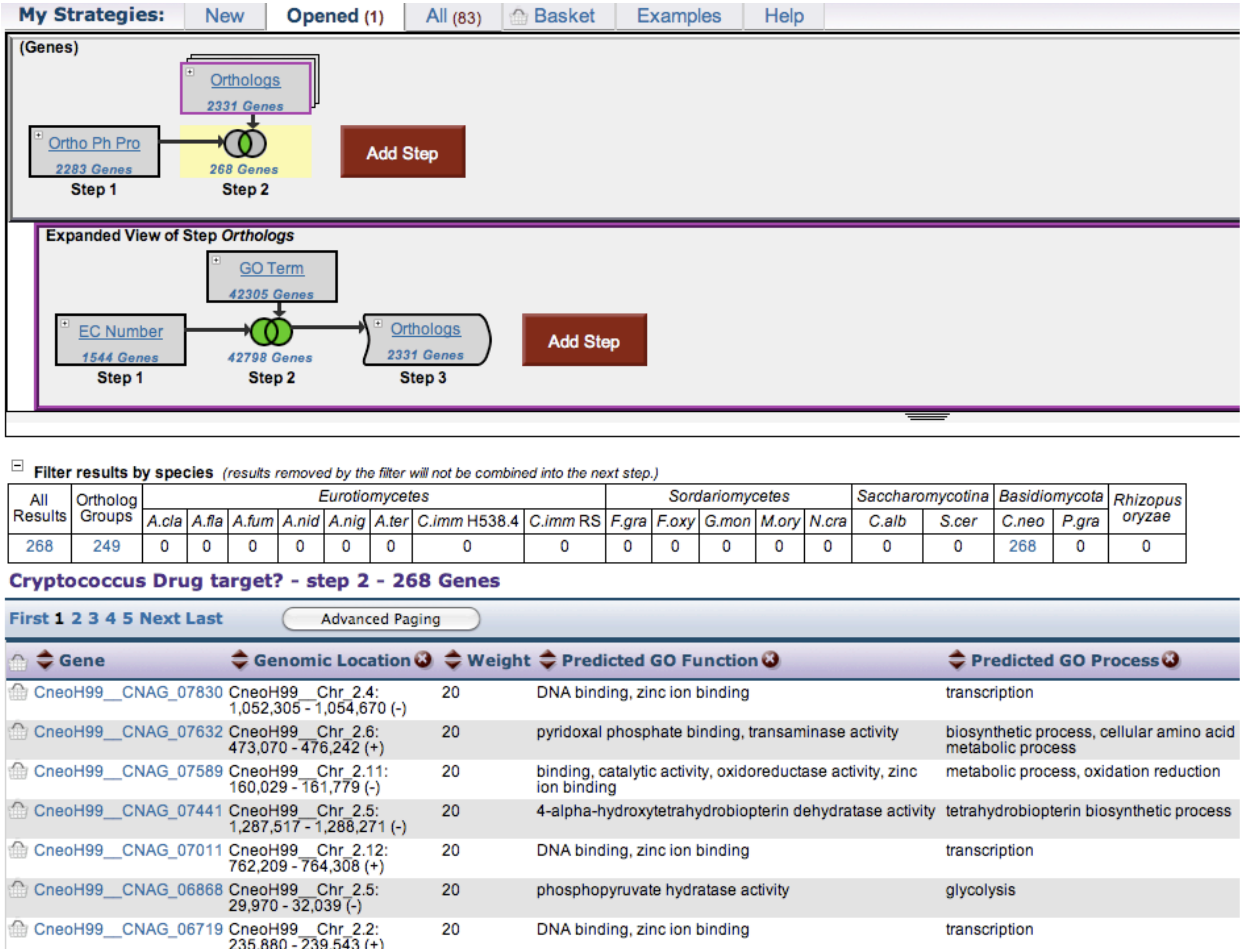
Identify Genomic Sequences by:
- Sequence ID(s)
- Species
- BLAST Similarity
- DNA Motif

Identify SNPs by:
- SNP ID(s)
- Gene ID
- Genomic Location
- Allele Frequency
- Isolate Comparison
- Isolate Assay

Identify ESTs by:
- EST Accession(s)
- Extent of Gene Overlap
- BLAST Similarity
- Gene ID

Identify Transcript Assemblies by:
- EST Accession(s)
- Extent of Gene Overlap
- Gene IDs
- Genomic Location

A strategy for drug targets - http://bit.ly/crypto0



Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
268	249	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	268	0	0

Cryptococcus Drug target? - step 2 - 268 Genes

First 1 2 3 4 5 Next Last Advanced Paging

Gene	Genomic Location	Weight	Predicted GO Function	Predicted GO Process
CneoH99__CNAG_07830	CneoH99__Chr_2.4: 1,052,305 - 1,054,670 (-)	20	DNA binding, zinc ion binding	transcription
CneoH99__CNAG_07632	CneoH99__Chr_2.6: 473,070 - 476,242 (+)	20	pyridoxal phosphate binding, transaminase activity	biosynthetic process, cellular amino acid metabolic process
CneoH99__CNAG_07589	CneoH99__Chr_2.11: 160,029 - 161,779 (-)	20	binding, catalytic activity, oxidoreductase activity, zinc ion binding	metabolic process, oxidation reduction
CneoH99__CNAG_07441	CneoH99__Chr_2.5: 1,287,517 - 1,288,271 (-)	20	4-alpha-hydroxytetrahydrobiopterin dehydratase activity	tetrahydrobiopterin biosynthetic process
CneoH99__CNAG_07011	CneoH99__Chr_2.12: 762,209 - 764,308 (+)	20	DNA binding, zinc ion binding	transcription
CneoH99__CNAG_06868	CneoH99__Chr_2.5: 29,970 - 32,039 (-)	20	phosphopyruvate hydratase activity	glycolysis
CneoH99__CNAG_06719	CneoH99__Chr_2.2: 235,880 - 239,543 (+)	20	DNA binding, zinc ion binding	transcription

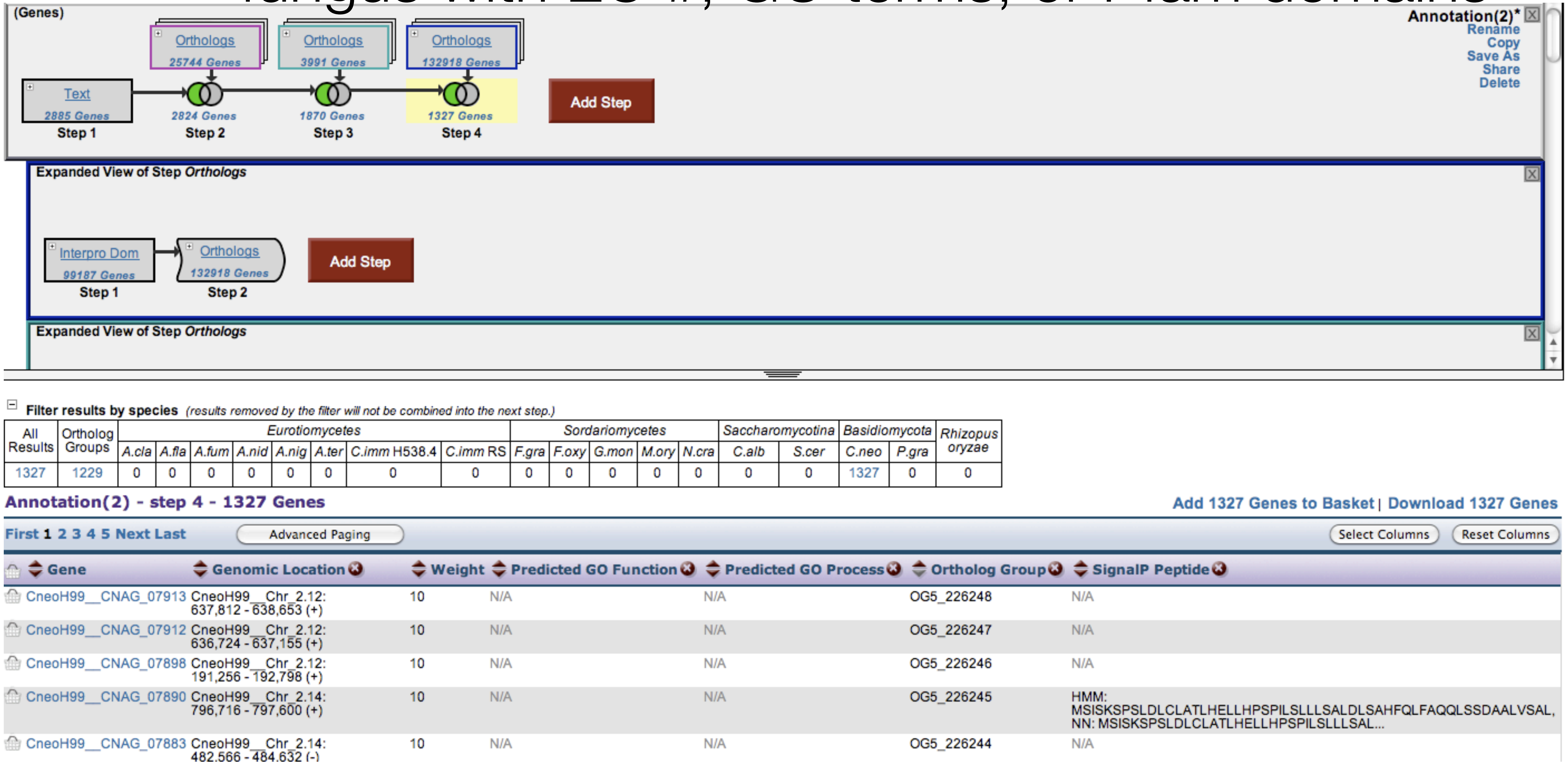
C.neoformans genes with
- no hits in other eukaryotes (excepting fungi), bacteria
- has S.cerevisiae orthologs that have EC terms

OR orthologs in other fungi with GO metabolic terms associated

All C. neoformans genes that do not have orthologs across the phyletic tree with no restriction on orthologs in other fungi. Then it intersects the results with all C. neoformans genes that are c

A strategy for reannotation - http://bit.ly/crypto1

2885 *C.neoformans* genes with desc “"conserved hypothetical protein” but 1327 can be assigned name from ortholog in any fungus with EC #, GO terms, or Pfam domains



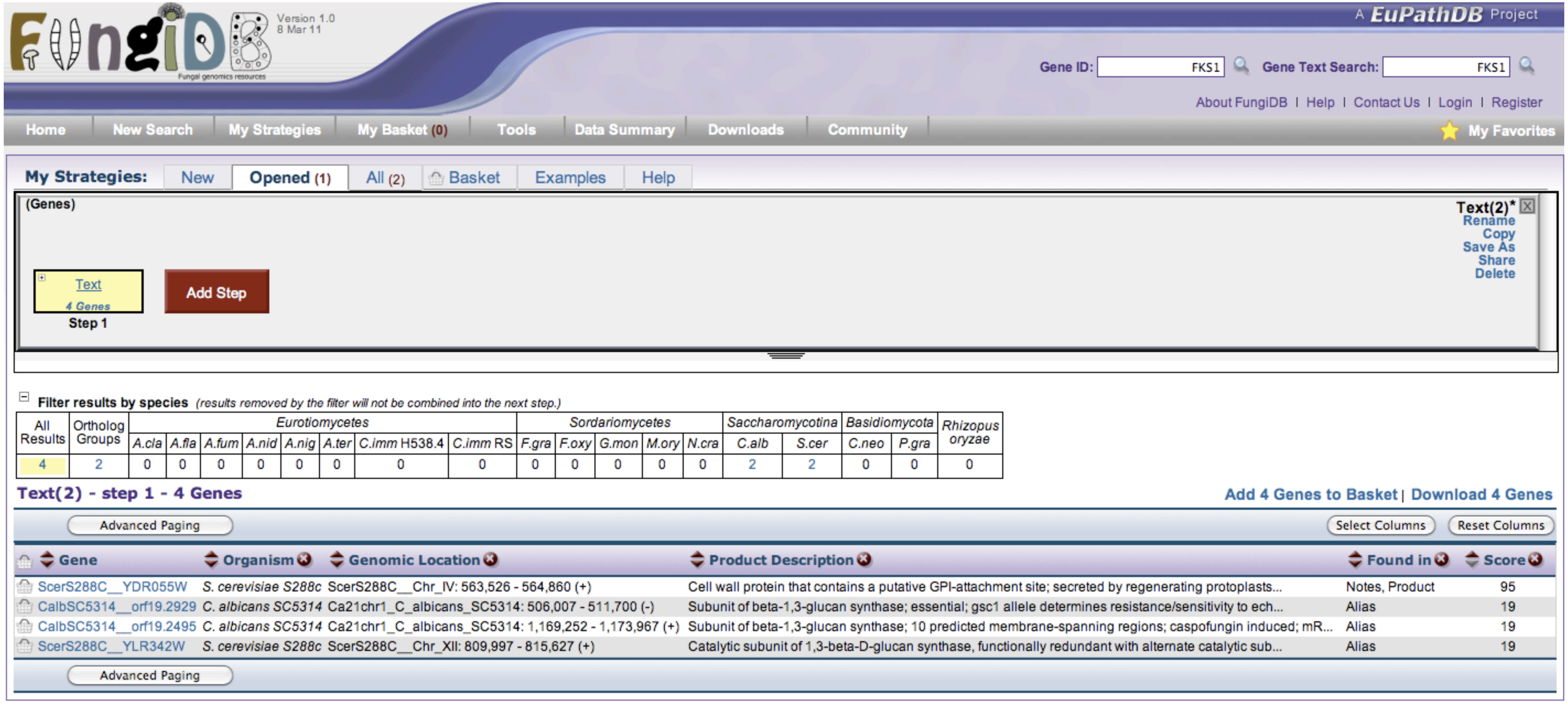
Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
1327	1229	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1327	0	0

Annotation(2) - step 4 - 1327 Genes

Add 1327 Genes to Basket | Download 1327 Genes

Gene	Genomic Location	Weight	Predicted GO Function	Predicted GO Process	Ortholog Group	SignalP Peptide
CneoH99__CNAG_07913	CneoH99__Chr_2.12: 637,812 - 638,653 (+)	10	N/A	N/A	OG5_226248	N/A
CneoH99__CNAG_07912	CneoH99__Chr_2.12: 636,724 - 637,155 (+)	10	N/A	N/A	OG5_226247	N/A
CneoH99__CNAG_07898	CneoH99__Chr_2.12: 191,256 - 192,798 (+)	10	N/A	N/A	OG5_226246	N/A
CneoH99__CNAG_07890	CneoH99__Chr_2.14: 796,716 - 797,600 (+)	10	N/A	N/A	OG5_226245	HMM: MSISKSPSLDLCLATLHELLHPSPILSLLLSALDLSAHFQLFAQQLSSDAALVSAL, NN: MSISKSPSLDLCLATLHELLHPSPILSLLLSAL...
CneoH99__CNAG_07883	CneoH99__Chr_2.14: 482,566 - 484,632 (-)	10	N/A	N/A	OG5_226244	N/A



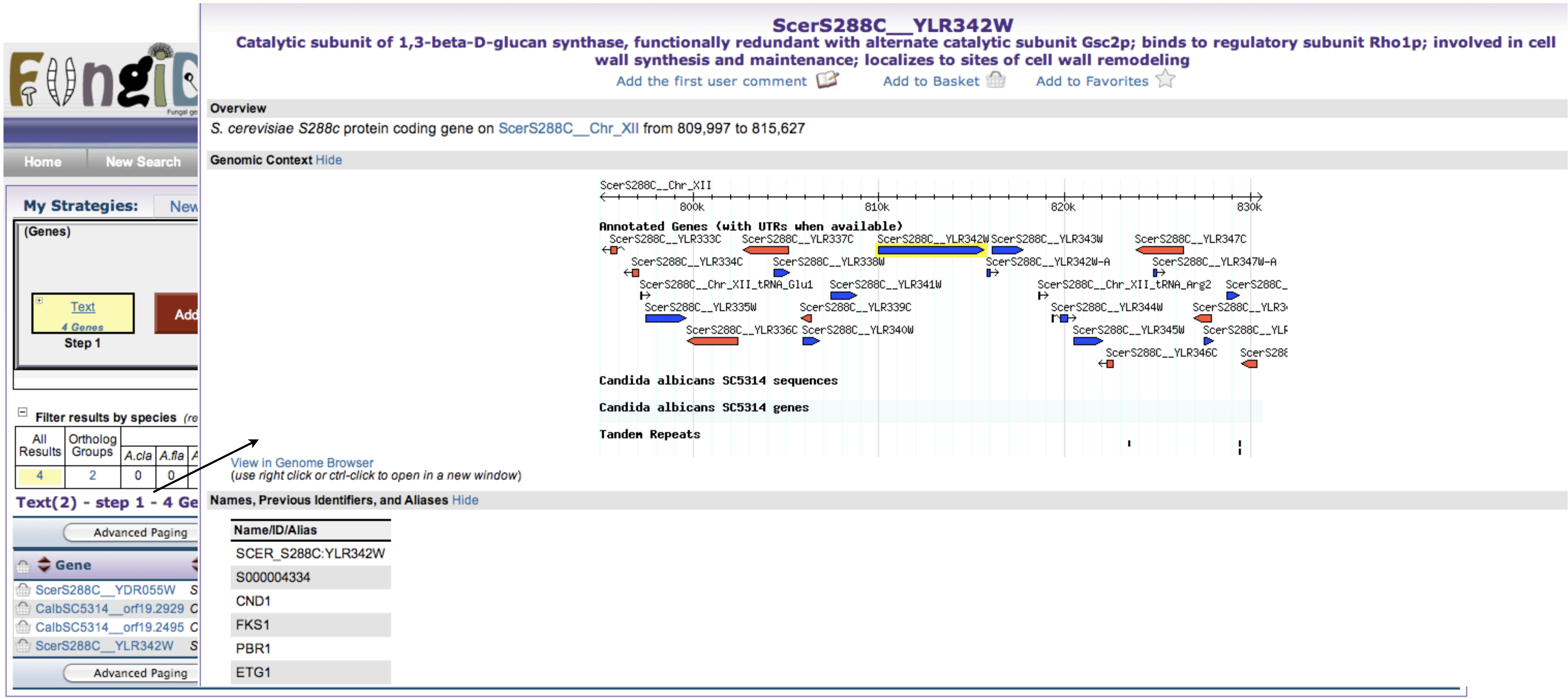
⊟ **Filter results by species** *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0

Text(2) - step 1 - 4 Genes

Add 4 Genes to Basket | **Download 4 Genes**

Gene	Organism	Genomic Location	Product Description	Found in	Score
ScerS288C__YDR055W	*S. cerevisiae S288c*	ScerS288C__Chr_IV: 563,526 - 564,860 (+)	Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts...	Notes, Product	95
CalbSC5314__orf19.2929	*C. albicans SC5314*	Ca21chr1_C_albicans_SC5314: 506,007 - 511,700 (-)	Subunit of beta-1,3-glucan synthase; essential; gsc1 allele determines resistance/sensitivity to ech...	Alias	19
CalbSC5314__orf19.2495	*C. albicans SC5314*	Ca21chr1_C_albicans_SC5314: 1,169,252 - 1,173,967 (+)	Subunit of beta-1,3-glucan synthase; 10 predicted membrane-spanning regions; caspofungin induced; mR...	Alias	19
ScerS288C__YLR342W	*S. cerevisiae S288c*	ScerS288C__Chr_XII: 809,997 - 815,627 (+)	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic sub...	Alias	19



(Genes)

Text
4 Genes
Step 1

Filter results by species

All Results	Ortholog Groups	A.cla	A.fla
4	2	0	0

Text(2) - step 1 - 4 Ge

- ScerS288C__YDR055W
- CalbSC5314__orf19.2929
- CalbSC5314__orf19.2495
- ScerS288C__YLR342W

ScerS288C__YLR342W

Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling

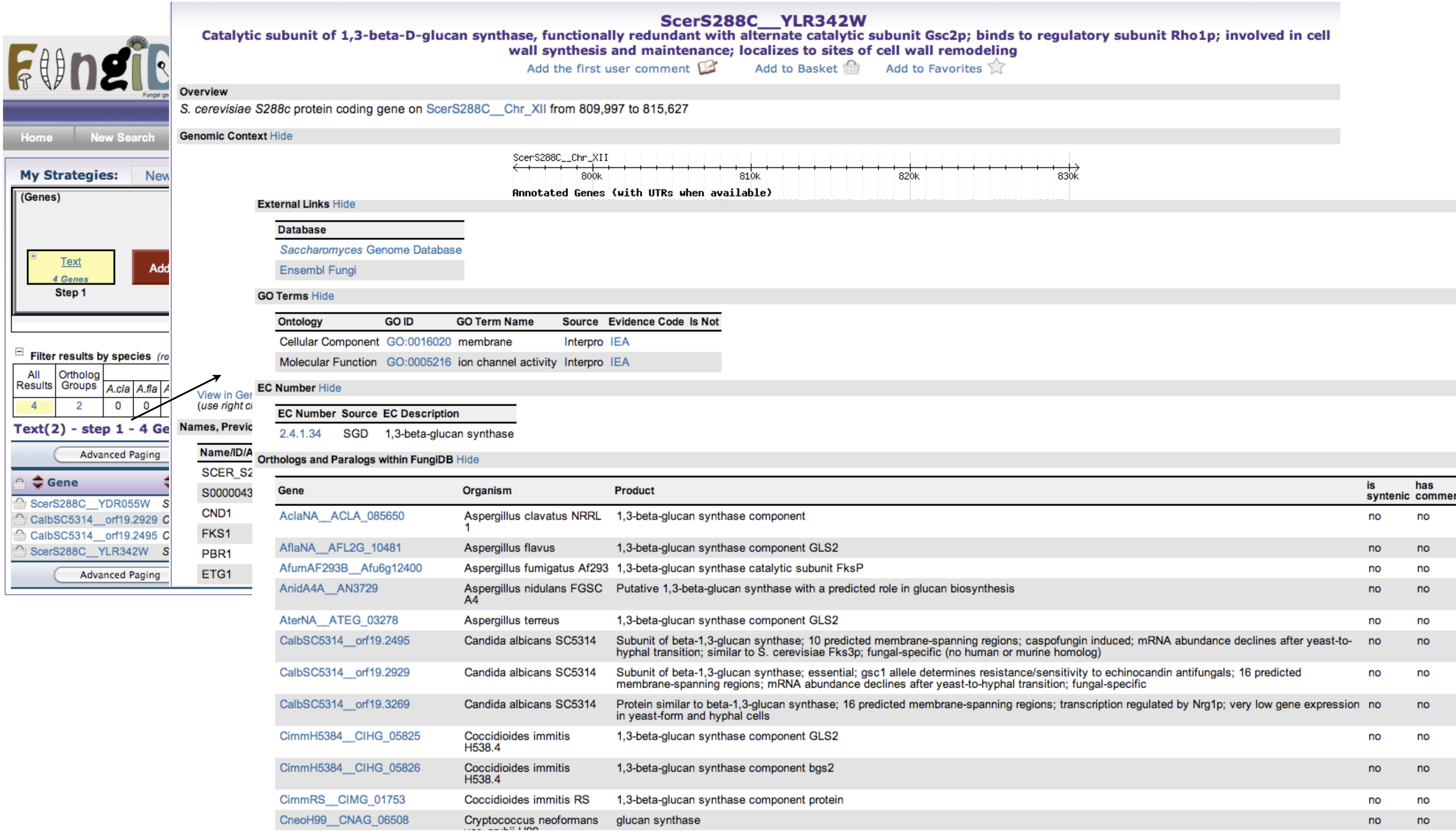
Overview

S. cerevisiae S288c protein coding gene on ScerS288C__Chr_XII from 809,997 to 815,627

Genomic Context

Names, Previous Identifiers, and Aliases

Name/ID/Alias
SCER_S288C:YLR342W
S000004334
CND1
FKS1
PBR1
ETG1



All Results	Ortholog Groups	A.cla	A.fla
4	2	0	0

Text(2) - step 1 - 4 Ge

ScerS288C__YDR055W
CalbSC5314__orf19.2929
CalbSC5314__orf19.2495
ScerS288C__YLR342W

Names, Previo

Name/ID/A
SCER_S2
S0000043
CND1
FKS1
PBR1
ETG1

ScerS288C__YLR342W

Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling

Overview

S. cerevisiae S288c protein coding gene on ScerS288C__Chr_XII from 809,997 to 815,627

Genomic Context Hide

External Links Hide

Database
Saccharomyces Genome Database
Ensembl Fungi

GO Terms Hide

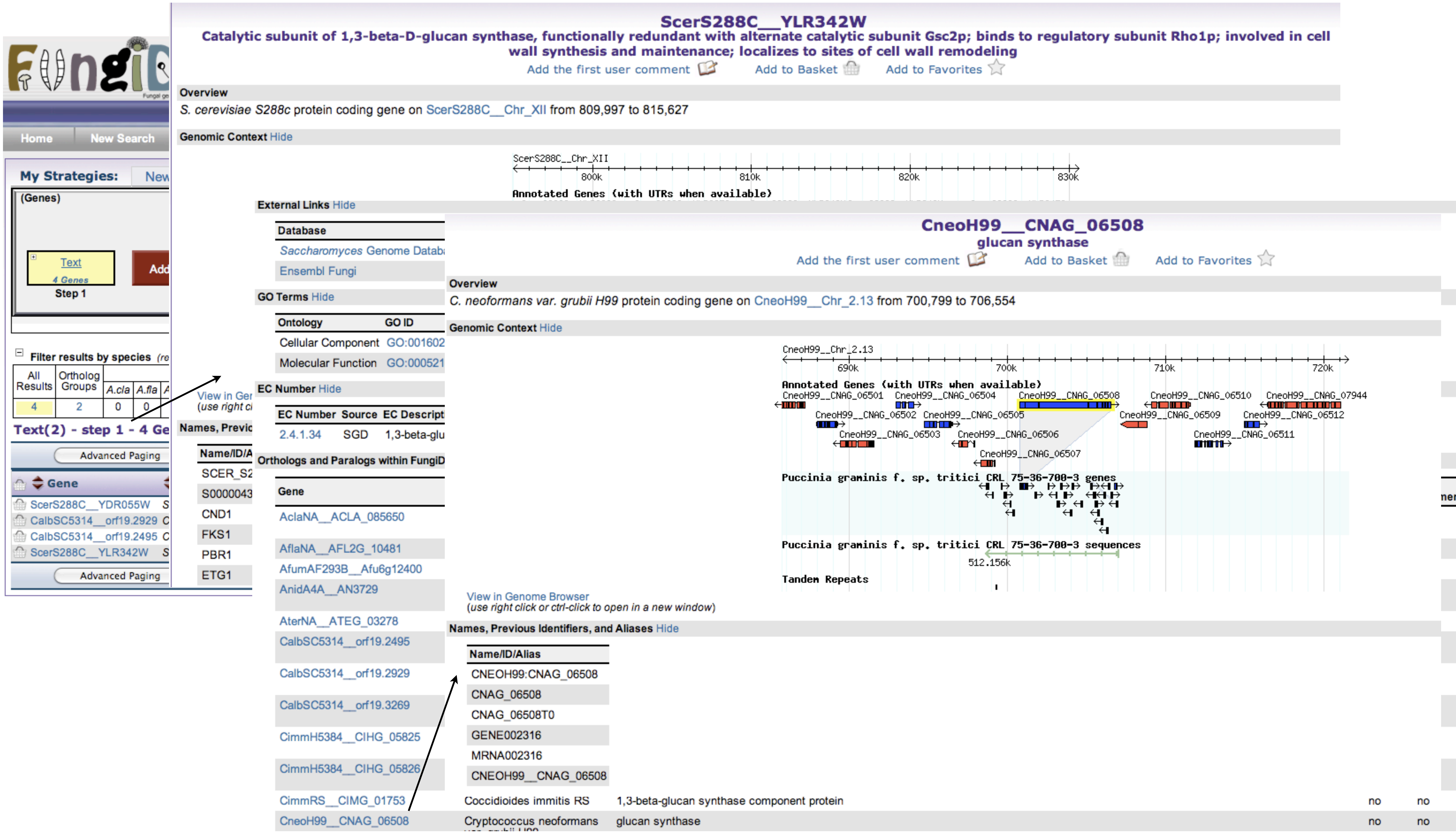
Ontology	GO ID	GO Term Name	Source	Evidence Code	Is Not
Cellular Component	GO:0016020	membrane	Interpro	IEA	
Molecular Function	GO:0005216	ion channel activity	Interpro	IEA	

EC Number Hide

EC Number	Source	EC Description
2.4.1.34	SGD	1,3-beta-glucan synthase

Orthologs and Paralogs within FungiDB Hide

Gene	Organism	Product	is syntenic	has commen
AclaNA__ACLA_085650	Aspergillus clavatus NRRL 1	1,3-beta-glucan synthase component	no	no
AflaNA__AFL2G_10481	Aspergillus flavus	1,3-beta-glucan synthase component GLS2	no	no
AfumAF293B__Afu6g12400	Aspergillus fumigatus Af293	1,3-beta-glucan synthase catalytic subunit FksP	no	no
AnidA4A__AN3729	Aspergillus nidulans FGSC A4	Putative 1,3-beta-glucan synthase with a predicted role in glucan biosynthesis	no	no
AterNA__ATEG_03278	Aspergillus terreus	1,3-beta-glucan synthase component GLS2	no	no
CalbSC5314__orf19.2495	Candida albicans SC5314	Subunit of beta-1,3-glucan synthase; 10 predicted membrane-spanning regions; caspofungin induced; mRNA abundance declines after yeast-to-hyphal transition; similar to S. cerevisiae Fks3p; fungal-specific (no human or murine homolog)	no	no
CalbSC5314__orf19.2929	Candida albicans SC5314	Subunit of beta-1,3-glucan synthase; essential; gsc1 allele determines resistance/sensitivity to echinocandin antifungals; 16 predicted membrane-spanning regions; mRNA abundance declines after yeast-to-hyphal transition; fungal-specific	no	no
CalbSC5314__orf19.3269	Candida albicans SC5314	Protein similar to beta-1,3-glucan synthase; 16 predicted membrane-spanning regions; transcription regulated by Nrg1p; very low gene expression in yeast-form and hyphal cells	no	no
CimmH5384__CIHG_05825	Coccidioides immitis H538.4	1,3-beta-glucan synthase component GLS2	no	no
CimmH5384__CIHG_05826	Coccidioides immitis H538.4	1,3-beta-glucan synthase component bgs2	no	no
CimmRS__CIMG_01753	Coccidioides immitis RS	1,3-beta-glucan synthase component protein	no	no
CneoH99__CNAG_06508	Cryptococcus neoformans	glucan synthase	no	no



Filter results by species (re

All Results	Ortholog Groups	A.cla	A.fla	A
4	2	0	0	

Text(2) - step 1 - 4 Ge

- ScerS288C__YDR055W S
- CalbSC5314__orf19.2929 C
- CalbSC5314__orf19.2495 C
- ScerS288C__YLR342W S

ScerS288C__YLR342W

Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling

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Overview

S. cerevisiae S288c protein coding gene on ScerS288C__Chr_XII from 809,997 to 815,627

Genomic Context Hide

View in Ger
(use right cl

Names, Previo

Name/ID/A
SCER_S2
S0000043
CND1
FKS1
PBR1
ETG1

External Links Hide

Database
Saccharomyces Genome Databa
Ensembl Fungi

GO Terms Hide

Ontology	GO ID
Cellular Component	GO:001602
Molecular Function	GO:000521

EC Number Hide

EC Number	Source	EC Descript
2.4.1.34	SGD	1,3-beta-glu

Orthologs and Paralogs within FungiD

Gene				
AclaNA__ACLA_085650				
AflaNA__AFL2G_10481				
AfumAF293B__Afu6g12400				
AnidA4A__AN3729				
AterNA__ATEG_03278				
CalbSC5314__orf19.2495				
CalbSC5314__orf19.2929				
CalbSC5314__orf19.3269				
CimmH5384__CIHG_05825				
CimmH5384__CIHG_05826				
CimmRS__CIMG_01753	Coccidioides immitis RS	1,3-beta-glucan synthase component protein	no	no
CneoH99__CNAG_06508	Cryptococcus neoformans var. grubii H99	glucan synthase	no	no

CneoH99__CNAG_06508

glucan synthase

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Overview

C. neoformans var. grubii H99 protein coding gene on CneoH99__Chr_2.13 from 700,799 to 706,554

Genomic Context Hide

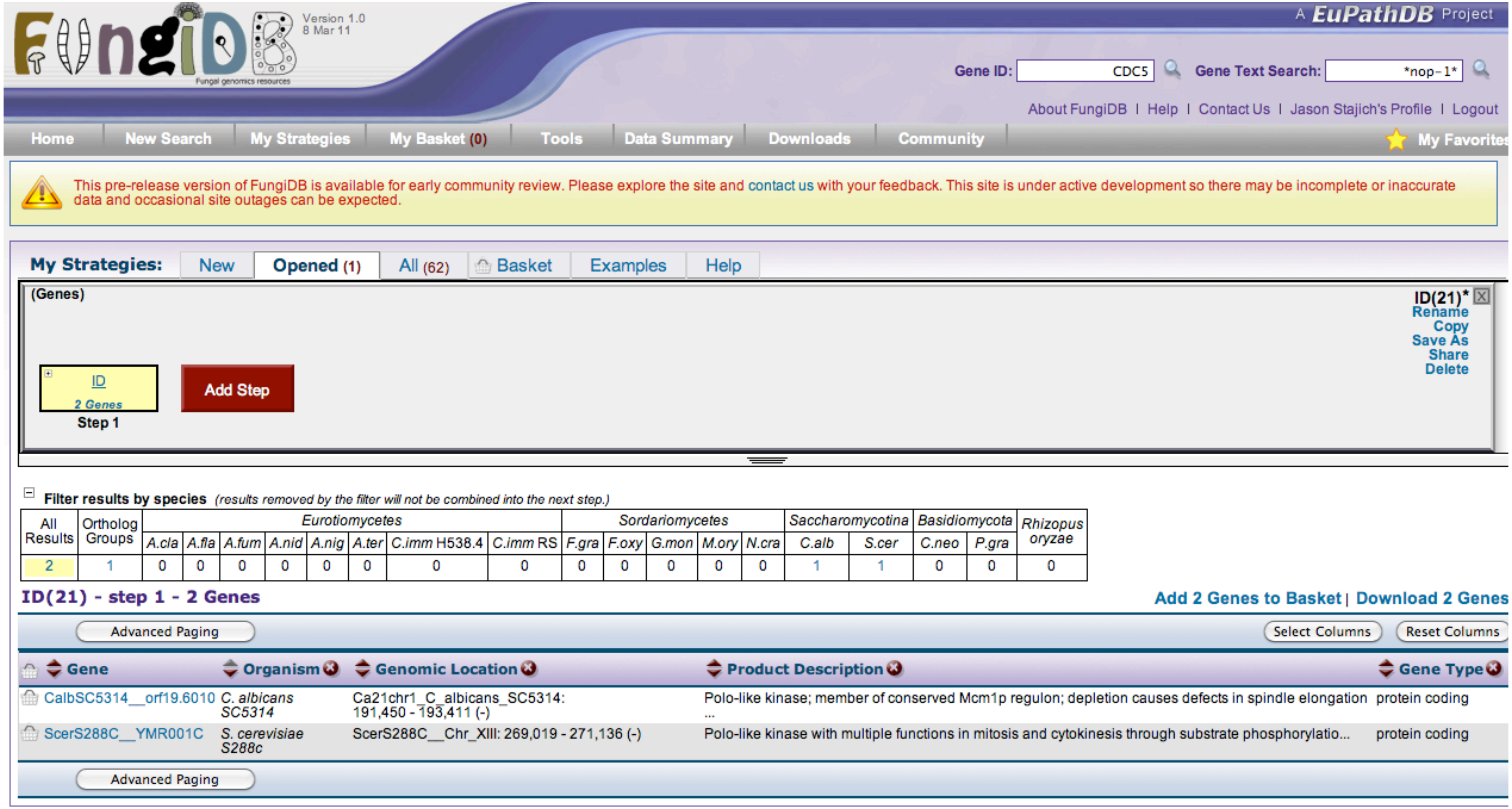
View in Genome Browser
(use right click or ctrl-click to open in a new window)

Names, Previous Identifiers, and Aliases Hide

Name/ID/Alias
CNEOH99:CNAG_06508
CNAG_06508
CNAG_06508T0
GENE002316
MRNA002316
CNEOH99__CNAG_06508

Gene record pages - interface for per-locus view

Result overview - query by text or gene name



Gene ID: CDC5

Gene Text Search: *nop-1*

This pre-release version of FungiDB is available for early community review. Please explore the site and contact us with your feedback. This site is under active development so there may be incomplete or inaccurate data and occasional site outages can be expected.

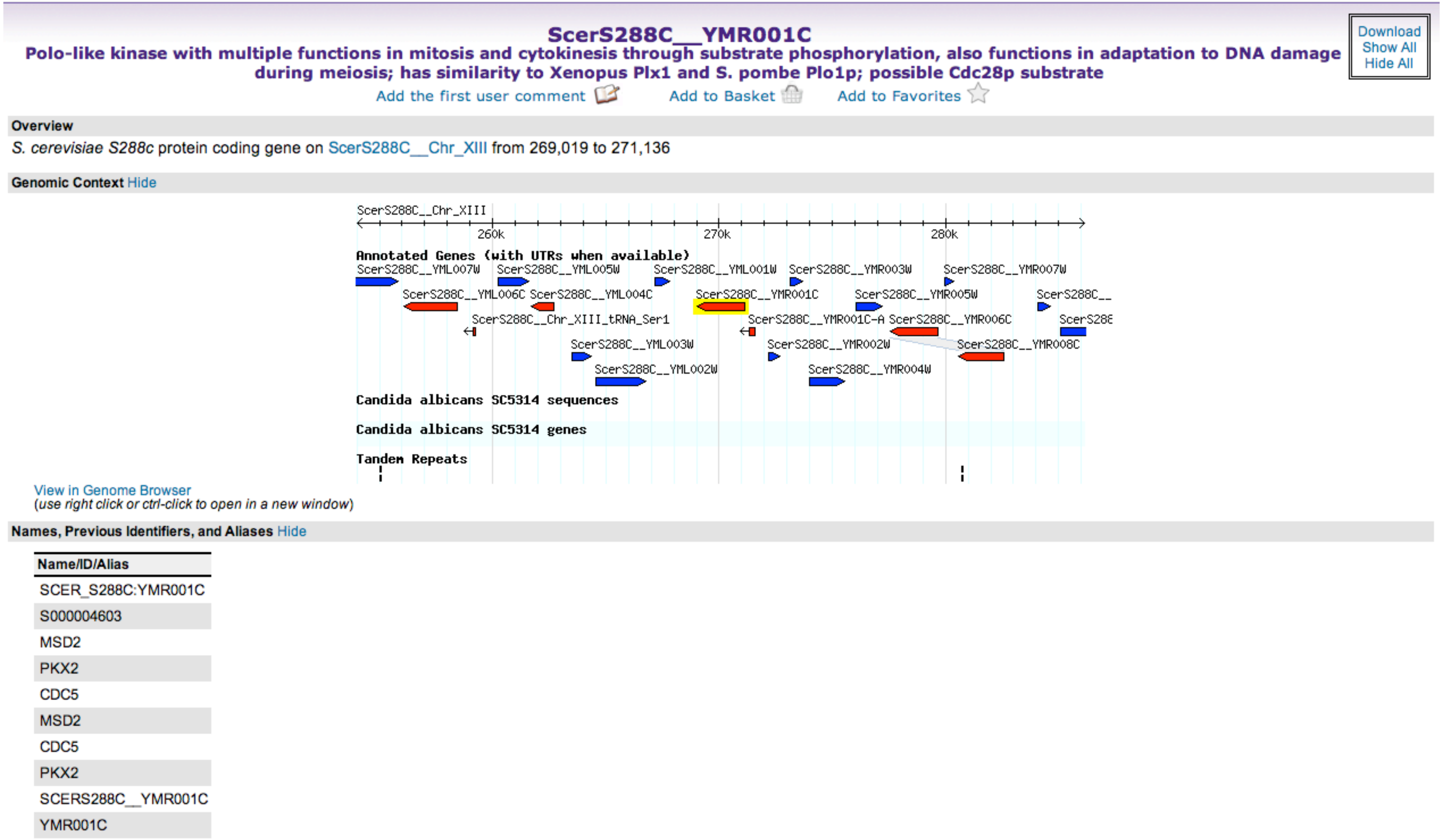
Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0

ID(21) - step 1 - 2 Genes

Gene	Organism	Genomic Location	Product Description	Gene Type
CalbSC5314__orf19.6010	*C. albicans SC5314*	Ca21chr1_C_albicans_SC5314: 191,450 - 193,411 (-)	Polo-like kinase; member of conserved Mcm1p regulon; depletion causes defects in spindle elongation ...	protein coding
ScerS288C__YMR001C	*S. cerevisiae S288c*	ScerS288C__Chr_XIII: 269,019 - 271,136 (-)	Polo-like kinase with multiple functions in mitosis and cytokinesis through substrate phosphorylatio...	protein coding

Gene page overview - has locus view and names/aliases



ScerS288C__YMR001C

Polo-like kinase with multiple functions in mitosis and cytokinesis through substrate phosphorylation, also functions in adaptation to DNA damage during meiosis; has similarity to Xenopus Plx1 and S. pombe Plo1p; possible Cdc28p substrate

Overview

S. cerevisiae S288c protein coding gene on ScerS288C__Chr_XIII from 269,019 to 271,136

Genomic Context

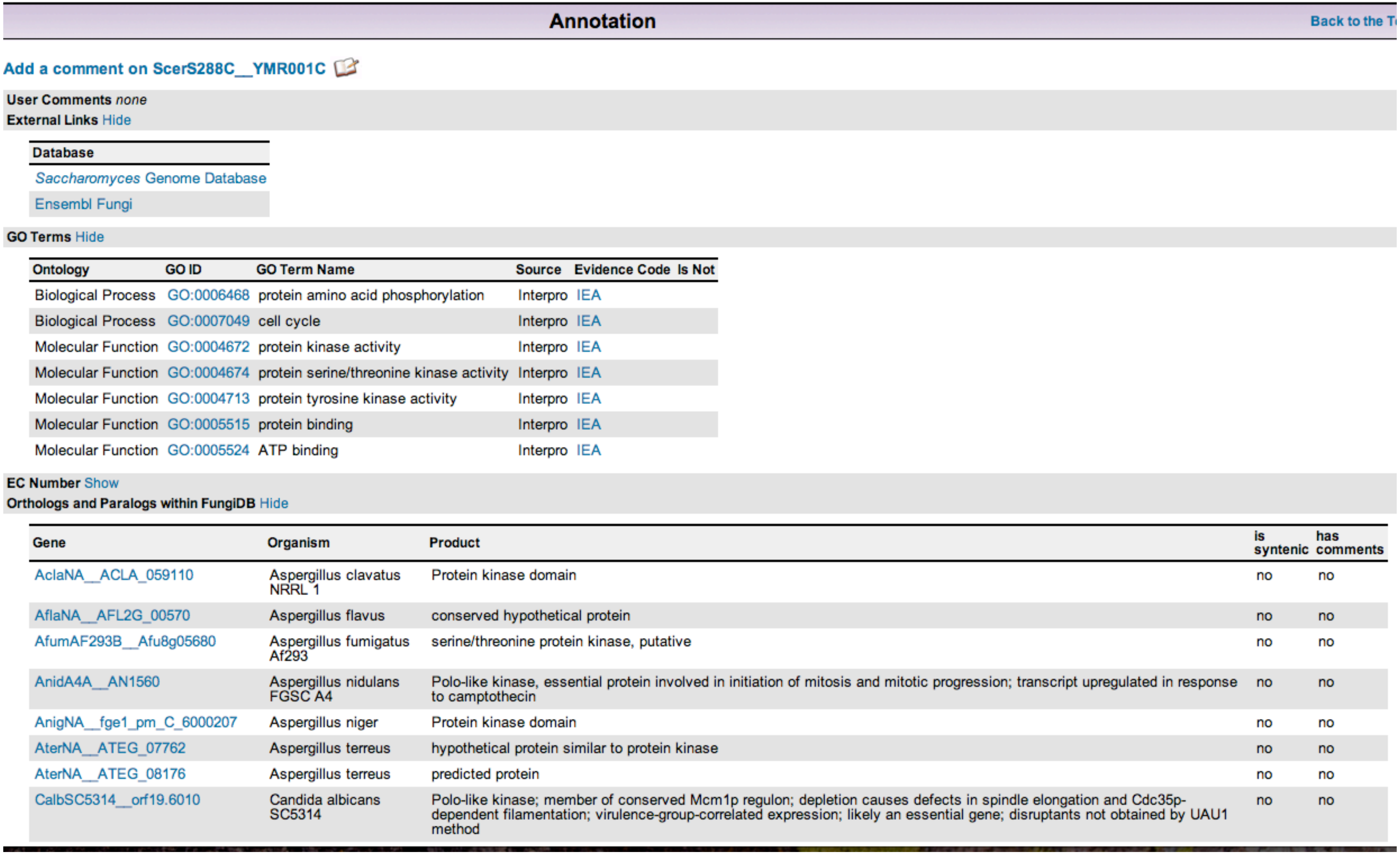
View in Genome Browser
(use right click or ctrl-click to open in a new window)

Names, Previous Identifiers, and Aliases

Name/ID/Alias
SCER_S288C:YMR001C
S000004603
MSD2
PKX2
CDC5
MSD2
CDC5
PKX2
SCERS288C__YMR001C
YMR001C

http://fungidb.org/gene/ScerS288C__YMR001C

Annotation for this gene includes GO terms, links to external DBs, EC numbers (if available), and table of Orthologs



Annotation

Back to the T

Add a comment on ScerS288C__YMR001C

User Comments *none*

External Links Hide

Database
Saccharomyces Genome Database
Ensembl Fungi

GO Terms Hide

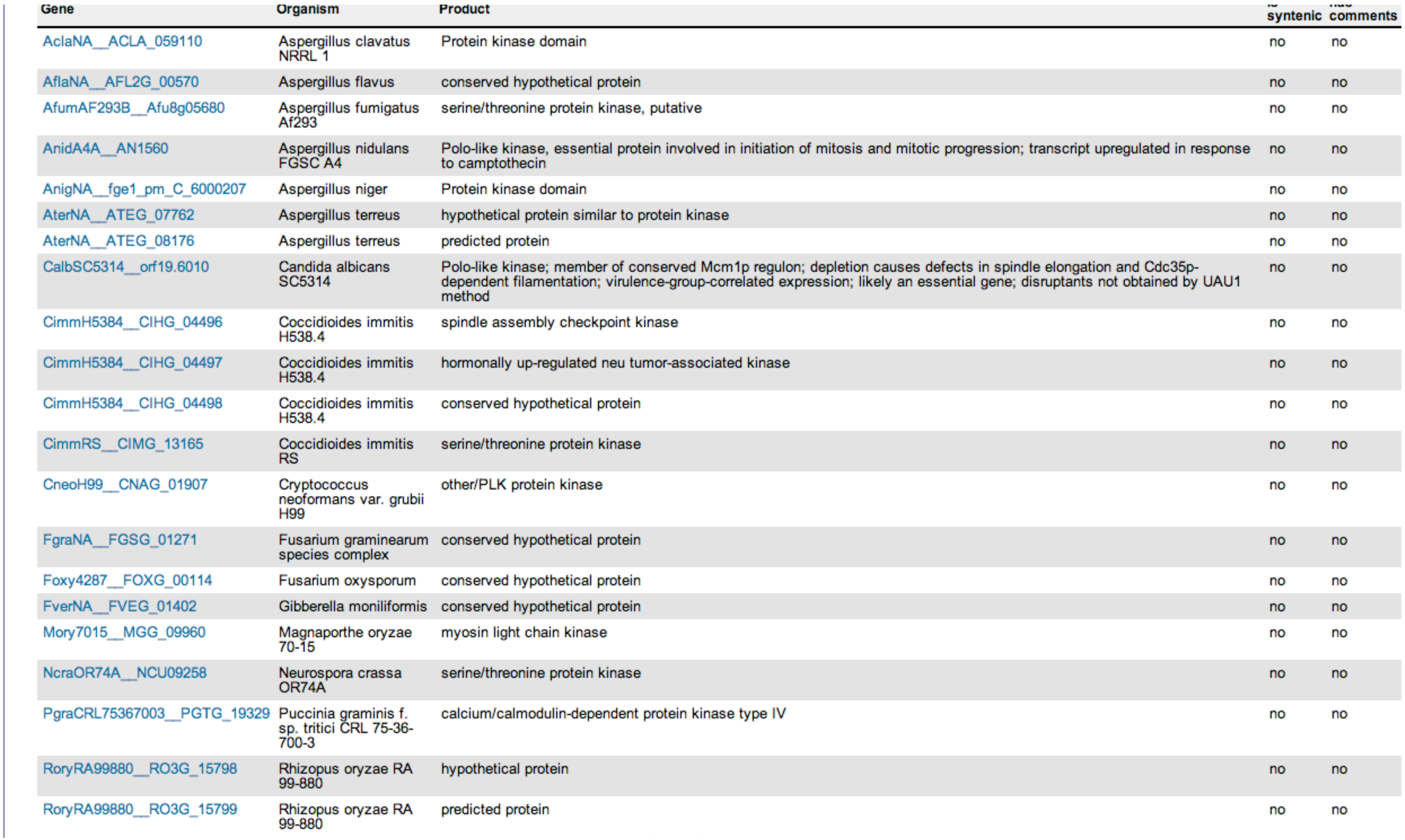
Ontology	GO ID	GO Term Name	Source	Evidence Code	Is Not
Biological Process	GO:0006468	protein amino acid phosphorylation	Interpro	IEA	
Biological Process	GO:0007049	cell cycle	Interpro	IEA	
Molecular Function	GO:0004672	protein kinase activity	Interpro	IEA	
Molecular Function	GO:0004674	protein serine/threonine kinase activity	Interpro	IEA	
Molecular Function	GO:0004713	protein tyrosine kinase activity	Interpro	IEA	
Molecular Function	GO:0005515	protein binding	Interpro	IEA	
Molecular Function	GO:0005524	ATP binding	Interpro	IEA	

EC Number Show

Orthologs and Paralogs within FungiDB Hide

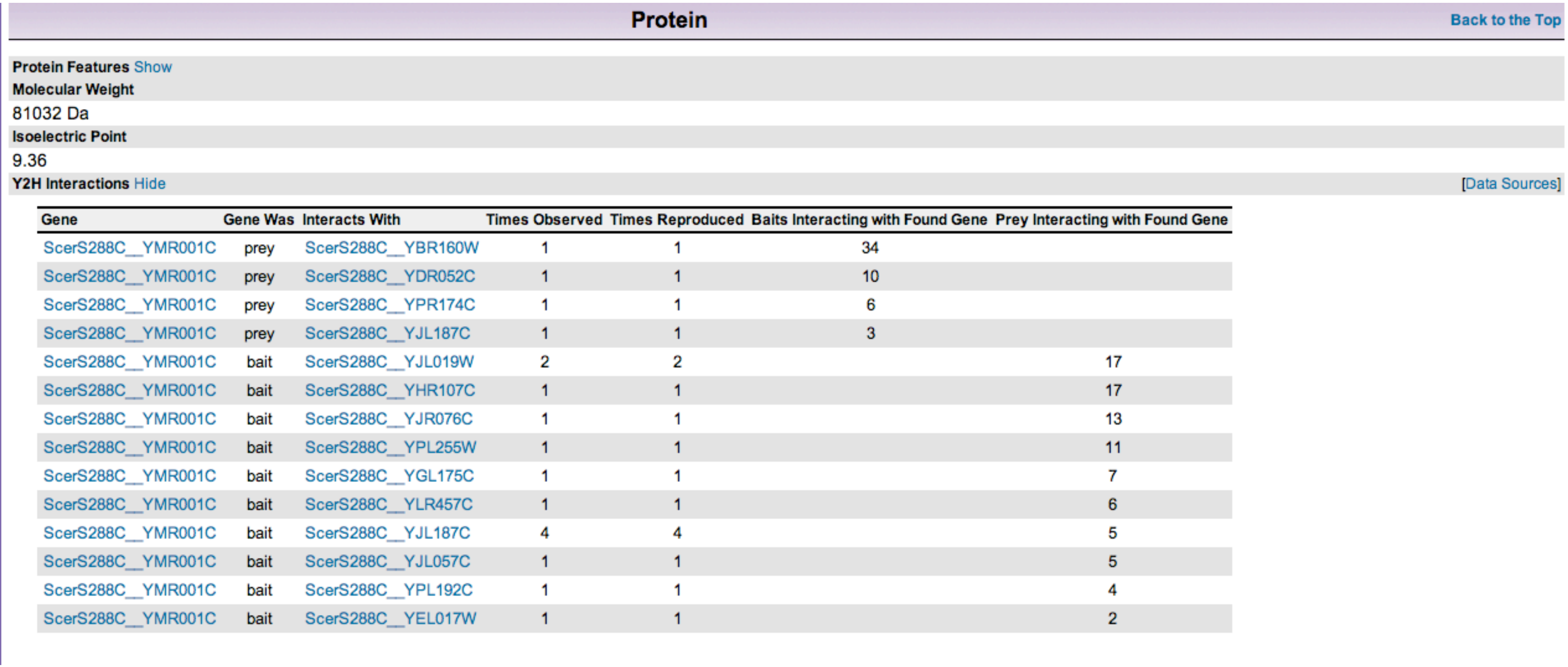
Gene	Organism	Product	is syntenic	has comments
AclaNA__ACLA_059110	Aspergillus clavatus NRRL 1	Protein kinase domain	no	no
AflaNA__AFL2G_00570	Aspergillus flavus	conserved hypothetical protein	no	no
AfumAF293B__Afu8g05680	Aspergillus fumigatus Af293	serine/threonine protein kinase, putative	no	no
AnidA4A__AN1560	Aspergillus nidulans FGSC A4	Polo-like kinase, essential protein involved in initiation of mitosis and mitotic progression; transcript upregulated in response to camptothecin	no	no
AnigNA__fge1_pm_C_6000207	Aspergillus niger	Protein kinase domain	no	no
AterNA__ATEG_07762	Aspergillus terreus	hypothetical protein similar to protein kinase	no	no
AterNA__ATEG_08176	Aspergillus terreus	predicted protein	no	no
CalbSC5314__orf19.6010	Candida albicans SC5314	Polo-like kinase; member of conserved Mcm1p regulon; depletion causes defects in spindle elongation and Cdc35p-dependent filamentation; virulence-group-correlated expression; likely an essential gene; disruptants not obtained by UAU1 method	no	no

Table of Orthologs (cont)



Gene	Organism	Product	syntenic	comments
AclaNA__ACLA_059110	Aspergillus clavatus NRRL 1	Protein kinase domain	no	no
AflaNA__AFL2G_00570	Aspergillus flavus	conserved hypothetical protein	no	no
AfumAF293B__Afu8g05680	Aspergillus fumigatus Af293	serine/threonine protein kinase, putative	no	no
AnidA4A__AN1560	Aspergillus nidulans FGSC A4	Polo-like kinase, essential protein involved in initiation of mitosis and mitotic progression; transcript upregulated in response to camptothecin	no	no
AnigNA__fge1_pm_C_6000207	Aspergillus niger	Protein kinase domain	no	no
AterNA__ATEG_07762	Aspergillus terreus	hypothetical protein similar to protein kinase	no	no
AterNA__ATEG_08176	Aspergillus terreus	predicted protein	no	no
CalbSC5314__orf19.6010	Candida albicans SC5314	Polo-like kinase; member of conserved Mcm1p regulon; depletion causes defects in spindle elongation and Cdc35p-dependent filamentation; virulence-group-correlated expression; likely an essential gene; disruptants not obtained by UAU1 method	no	no
CimmH5384__CIHG_04496	Coccidioides immitis H538.4	spindle assembly checkpoint kinase	no	no
CimmH5384__CIHG_04497	Coccidioides immitis H538.4	hormonally up-regulated neu tumor-associated kinase	no	no
CimmH5384__CIHG_04498	Coccidioides immitis H538.4	conserved hypothetical protein	no	no
CimmRS__CIMG_13165	Coccidioides immitis RS	serine/threonine protein kinase	no	no
CneoH99__CNAG_01907	Cryptococcus neoformans var. grubii H99	other/PLK protein kinase	no	no
FgraNA__FGSG_01271	Fusarium graminearum species complex	conserved hypothetical protein	no	no
Foxy4287__FOXG_00114	Fusarium oxysporum	conserved hypothetical protein	no	no
FverNA__FVEG_01402	Gibberella moniliformis	conserved hypothetical protein	no	no
Mory7015__MGG_09960	Magnaporthe oryzae 70-15	myosin light chain kinase	no	no
NcraOR74A__NCU09258	Neurospora crassa OR74A	serine/threonine protein kinase	no	no
PgraCRL75367003__PGTG_19329	Puccinia graminis f. sp. tritici CRL 75-36-700-3	calcium/calmodulin-dependent protein kinase type IV	no	no
RoryRA99880__RO3G_15798	Rhizopus oryzae RA 99-880	hypothetical protein	no	no
RoryRA99880__RO3G_15799	Rhizopus oryzae RA 99-880	predicted protein	no	no

Protein-Protein interaction table



Protein

Back to the Top

Protein Features Show

Molecular Weight

81032 Da

Isoelectric Point

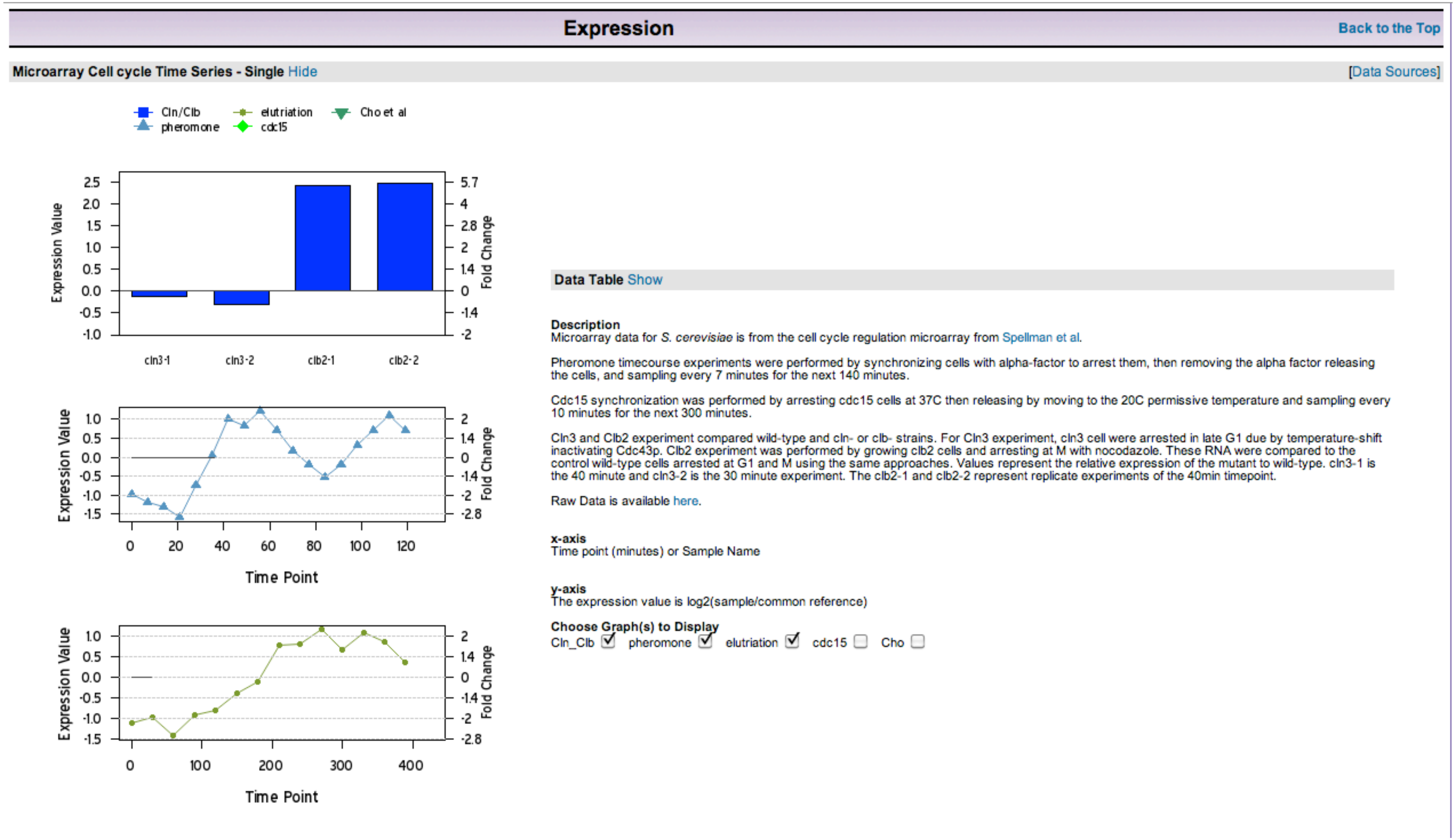
9.36

Y2H Interactions Hide

[Data Sources]

Gene	Gene Was	Interacts With	Times Observed	Times Reproduced	Baits Interacting with Found Gene	Prey Interacting with Found Gene
ScerS288C__YMR001C	prey	ScerS288C__YBR160W	1	1	34	
ScerS288C__YMR001C	prey	ScerS288C__YDR052C	1	1	10	
ScerS288C__YMR001C	prey	ScerS288C__YPR174C	1	1	6	
ScerS288C__YMR001C	prey	ScerS288C__YJL187C	1	1	3	
ScerS288C__YMR001C	bait	ScerS288C__YJL019W	2	2		17
ScerS288C__YMR001C	bait	ScerS288C__YHR107C	1	1		17
ScerS288C__YMR001C	bait	ScerS288C__YJR076C	1	1		13
ScerS288C__YMR001C	bait	ScerS288C__YPL255W	1	1		11
ScerS288C__YMR001C	bait	ScerS288C__YGL175C	1	1		7
ScerS288C__YMR001C	bait	ScerS288C__YLR457C	1	1		6
ScerS288C__YMR001C	bait	ScerS288C__YJL187C	4	4		5
ScerS288C__YMR001C	bait	ScerS288C__YJL057C	1	1		5
ScerS288C__YMR001C	bait	ScerS288C__YPL192C	1	1		4
ScerS288C__YMR001C	bait	ScerS288C__YEL017W	1	1		2

Gene expression section



Expression

Microarray Cell cycle Time Series - Single

Data Table

Description
Microarray data for *S. cerevisiae* is from the cell cycle regulation microarray from Spellman et al.

Pheromone timecourse experiments were performed by synchronizing cells with alpha-factor to arrest them, then removing the alpha factor releasing the cells, and sampling every 7 minutes for the next 140 minutes.

Cdc15 synchronization was performed by arresting cdc15 cells at 37C then releasing by moving to the 20C permissive temperature and sampling every 10 minutes for the next 300 minutes.

Cln3 and Clb2 experiment compared wild-type and cln- or clb- strains. For Cln3 experiment, cln3 cell were arrested in late G1 due by temperature-shift inactivating Cdc43p. Clb2 experiment was performed by growing clb2 cells and arresting at M with nocodazole. These RNA were compared to the control wild-type cells arrested at G1 and M using the same approaches. Values represent the relative expression of the mutant to wild-type. cln3-1 is the 40 minute and cln3-2 is the 30 minute experiment. The clb2-1 and clb2-2 represent replicate experiments of the 40min timepoint.

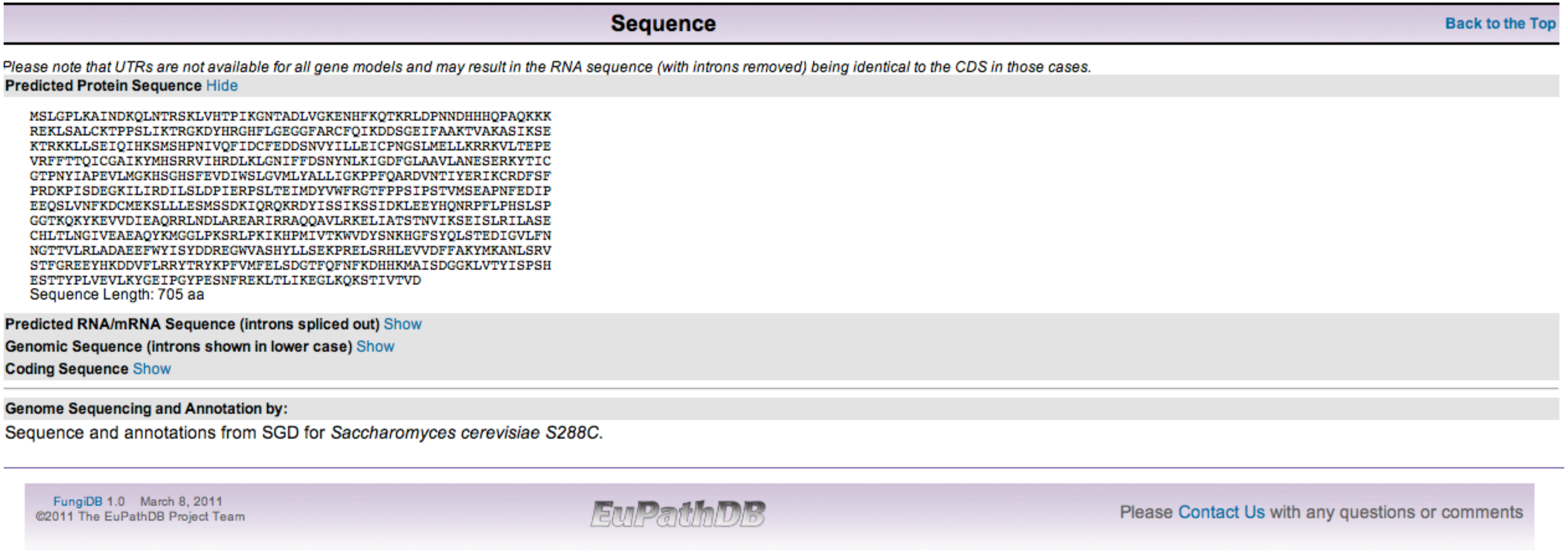
Raw Data is available here.

x-axis
Time point (minutes) or Sample Name

y-axis
The expression value is log2(sample/common reference)

Choose Graph(s) to Display
Cln_Clb ☑ pheromone ☑ elutriation ☑ cdc15 ☐ Cho ☐

Summary of sequence information



Sequence Back to the Top

Please note that UTRs are not available for all gene models and may result in the RNA sequence (with introns removed) being identical to the CDS in those cases.

Predicted Protein Sequence Hide

```
MSLGPLKAINDKQLNTRSKLVHTPIKGNTADLVGKENHFKQTKRLDPNNDHHHQPAQKKK
REKLSALCKTPPSLIKTRGKDYHRGHFLGEGGFARCFQIKDDSGEIFAAKTVAKASIKSE
KTRKKLLSEIQIHKSMSHPNIVQFIDCFEDDSNVYILLEICPNGSLMELLKRRKVLTEPE
VRFFTTQICGAIKYMHSRRVIHRDLKLGNIFFDSNYNLKIGDFGLAAVLANESERKYTIC
GTPNYIAPEVLMGKHSGHSFEVDIWSLGVMLYALLIGKPPFQARDVNTIYERIKCRDFSF
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EEQSLVNFKDCMEKSLLLESMSSDKIQRQKRDYISSIKSSIDKLEEYHQNRPFLPHSLSP
GGTKQKYKEVVDIEAQRRLNDLAREARIRRAQQAVLRKELIATSTNVIKSEISLRILASE
CHLTLNGIVEAEAQYKMGGLPKSRLPKIKHPMIVTKWVDYSNKHGFSYQLSTEDIGVLFN
NGTTVLRLADAEEFWYISYDDREGWVASHYLLSEKPRELSRHLEVVDFFAKYMKANLSRV
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ESTTYPLVEVLKYGEIPGYPESNFREKLTLIKEGLKQKSTIVTVD
```
Sequence Length: 705 aa

Predicted RNA/mRNA Sequence (introns spliced out) Show

Genomic Sequence (introns shown in lower case) Show

Coding Sequence Show

Genome Sequencing and Annotation by:

Sequence and annotations from SGD for *Saccharomyces cerevisiae S288C.*

FungiDB 1.0 March 8, 2011
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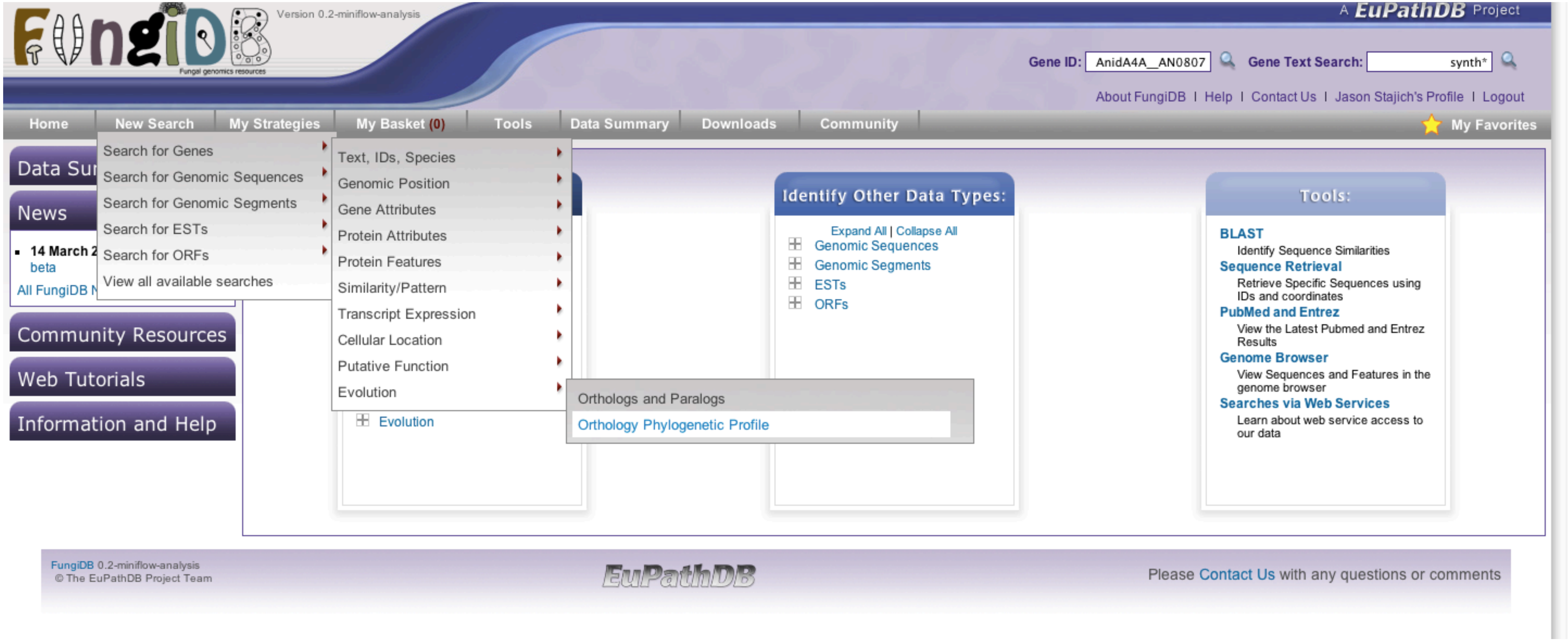
Please Contact Us with any questions or comments

http://fungidb.org/gene/ScerS288C__YMR001C

Querying for phylogenetic profiles

What are *Coccidioides* genes that are Cocci specific and have a signal peptide domain indicating they are likely secreted?

Query for Phylogenetic profile

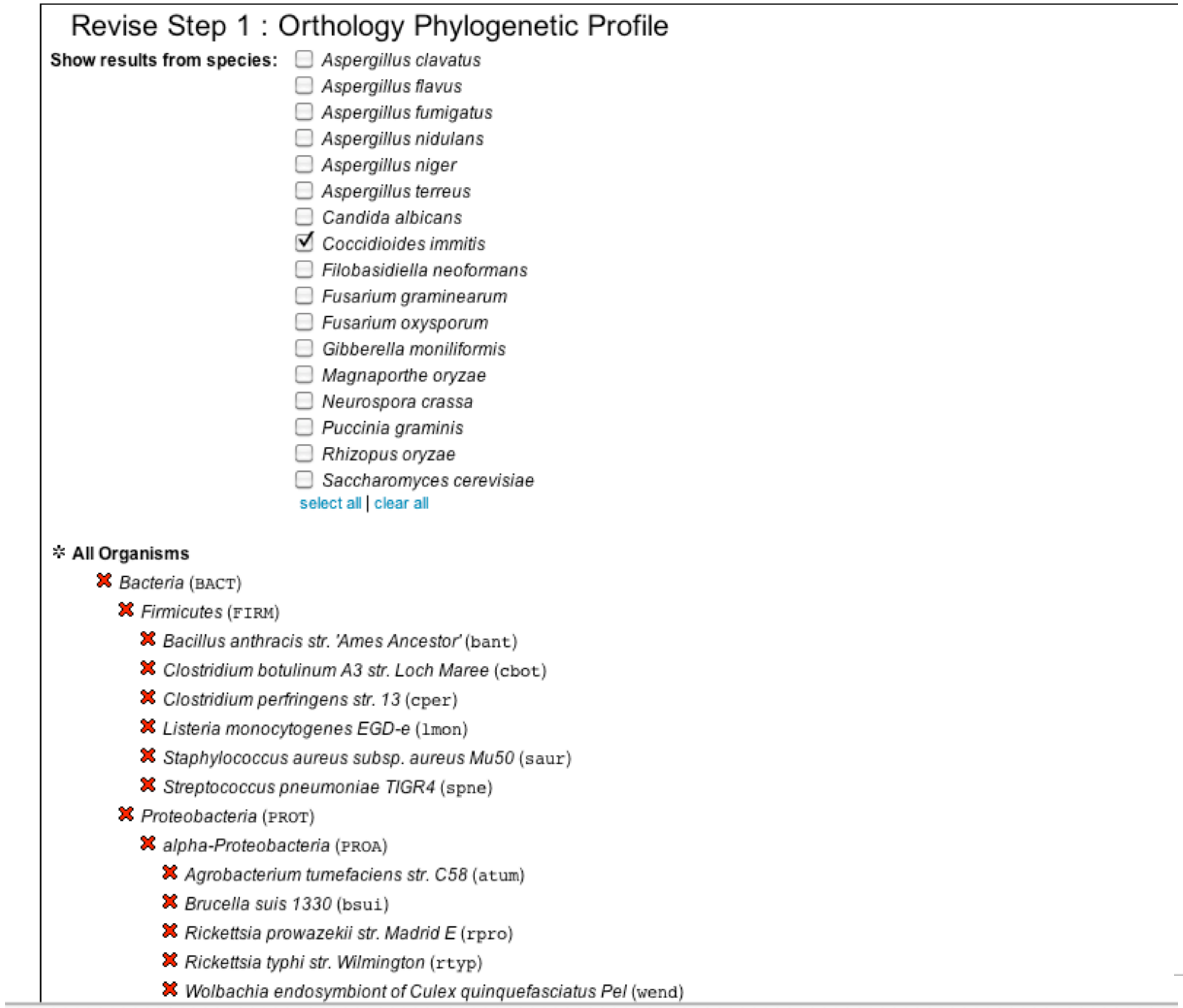


Gene ID: AnidA4A__AN0807

Gene Text Search: synth*

Please Contact Us with any questions or comments

Choose only *Coccidioides* orthologs, not found in Bacteria, Animals, etc



Revise Step 1 : Orthology Phylogenetic Profile

Show results from species:

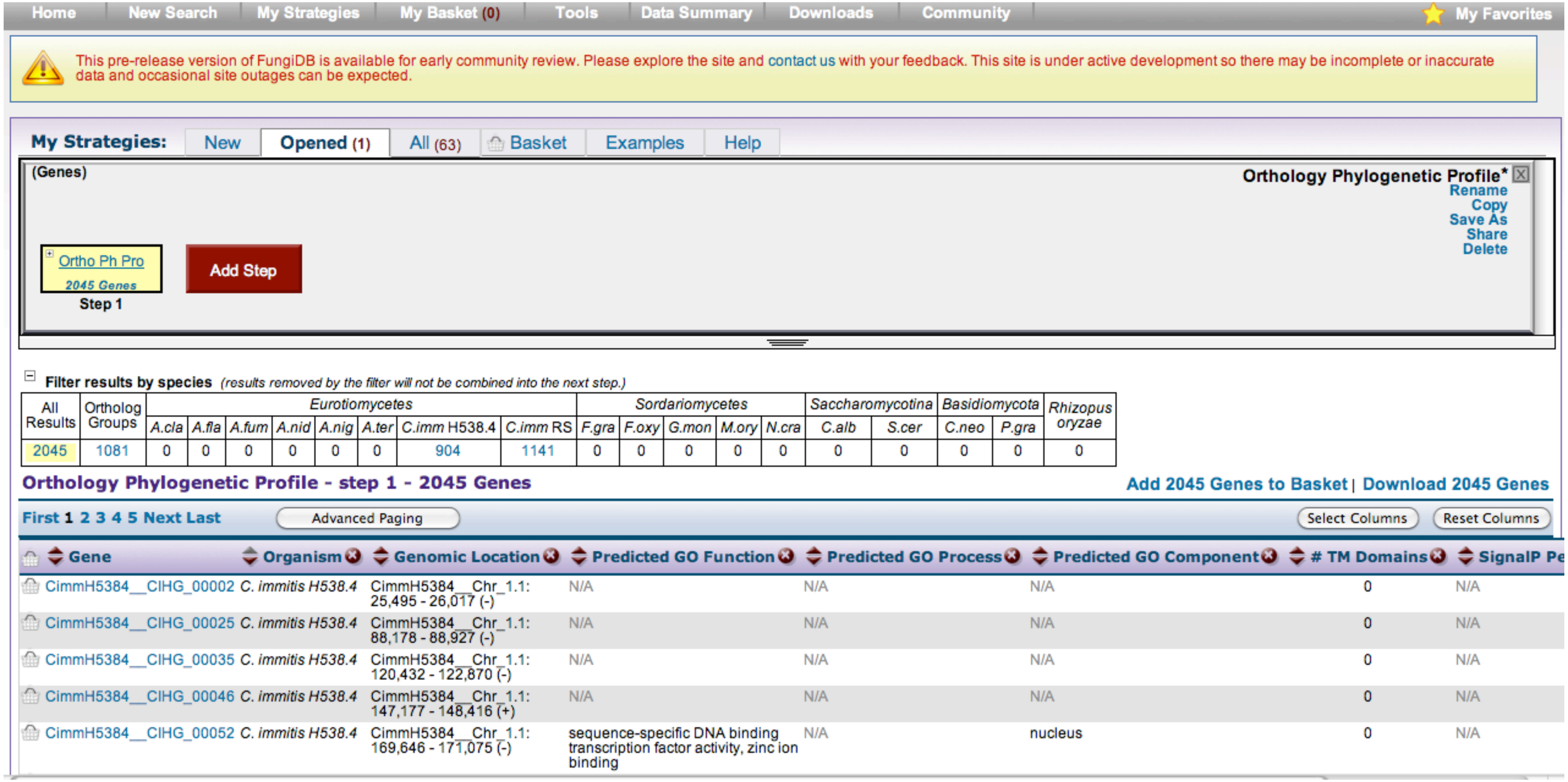
- ☐ *Aspergillus clavatus*
- ☐ *Aspergillus flavus*
- ☐ *Aspergillus fumigatus*
- ☐ *Aspergillus nidulans*
- ☐ *Aspergillus niger*
- ☐ *Aspergillus terreus*
- ☐ *Candida albicans*
- ☑ *Coccidioides immitis*
- ☐ *Filobasidiella neoformans*
- ☐ *Fusarium graminearum*
- ☐ *Fusarium oxysporum*
- ☐ *Gibberella moniliformis*
- ☐ *Magnaporthe oryzae*
- ☐ *Neurospora crassa*
- ☐ *Puccinia graminis*
- ☐ *Rhizopus oryzae*
- ☐ *Saccharomyces cerevisiae*

select all | clear all

✲ **All Organisms**
- ✗ *Bacteria* (BACT)
  - ✗ *Firmicutes* (FIRM)
    - ✗ *Bacillus anthracis str. 'Ames Ancestor'* (bant)
    - ✗ *Clostridium botulinum A3 str. Loch Maree* (cbot)
    - ✗ *Clostridium perfringens str. 13* (cper)
    - ✗ *Listeria monocytogenes EGD-e* (lmon)
    - ✗ *Staphylococcus aureus subsp. aureus Mu50* (saur)
    - ✗ *Streptococcus pneumoniae TIGR4* (spne)
  - ✗ *Proteobacteria* (PROT)
    - ✗ *alpha-Proteobacteria* (PROA)
      - ✗ *Agrobacterium tumefaciens str. C58* (atum)
      - ✗ *Brucella suis 1330* (bsui)
      - ✗ *Rickettsia prowazekii str. Madrid E* (rpro)
      - ✗ *Rickettsia typhi str. Wilmington* (rtyp)
      - ✗ *Wolbachia endosymbiont of Culex quinquefasciatus Pel* (wend)

- ● *Puccinia graminis f. sp. tritici CRL 75-36-700-3* (pgra)
- ✲ *Ascomycota* (ASCO)
  - ✗ *Aspergillus clavatus NRRL 1* (acla)
  - ✗ *Aspergillus flavus* (afla)
  - ✗ *Aspergillus fumigatus Af293* (afum)
  - ✗ *Aspergillus nidulans FGSC A4* (ania)
  - ✗ *Aspergillus niger* (anig)
  - ✗ *Aspergillus oryzae RIB40* (aory)
  - ✗ *Aspergillus terreus* (ater)
  - ✗ *Candida albicans SC5314* (cals)
  - ✗ *Candida glabrata CBS 138* (cgla)
  - ✓ *Coccidioides immitis RS* (cimm)
  - ✓ *Coccidioides immitis H538.4* (cimn)
  - ✓ *Coccidioides posadasii RMSCC 3488* (cpos)
  - ✗ *Debaryomyces hansenii CBS767* (dhan)
  - ✗ *Eremothecium gossypii* (egos)
  - ✗ *Fusarium graminearum species complex* (fgra)
  - ✗ *Fusarium oxysporum f. sp. lycopersici 4286* (foxy)
  - ✗ *Gibberella moniliformis* (fver)
  - ✗ *Gibberella zeae PH-1* (gzea)
  - ✗ *Kluyveromyces lactis NRRL Y-1140* (klac)
  - ✗ *Magnaporthe oryzae 70-15* (mory)
  - ✗ *Neurospora crassa OR74A* (ncra)
  - ✗ *Scheffersomyces stipitis CBS 6054* (psti)
  - ✗ *Saccharomyces cerevisiae S288c* (scer)
  - ✗ *Schizosaccharomyces pombe* (spom)
  - ✗ *Yarrowia lipolytica CLIB122* (ylip)
- ● *Zygomycota* (ZYGO)

Find those Cocci genes which are only found in *Coccidioides*



This pre-release version of FungiDB is available for early community review. Please explore the site and contact us with your feedback. This site is under active development so there may be incomplete or inaccurate data and occasional site outages can be expected.

(Genes)

Orthology Phylogenetic Profile*

Ortho Ph Pro
2045 Genes
Step 1

Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
2045	1081	0	0	0	0	0	0	904	1141	0	0	0	0	0	0	0	0	0	0

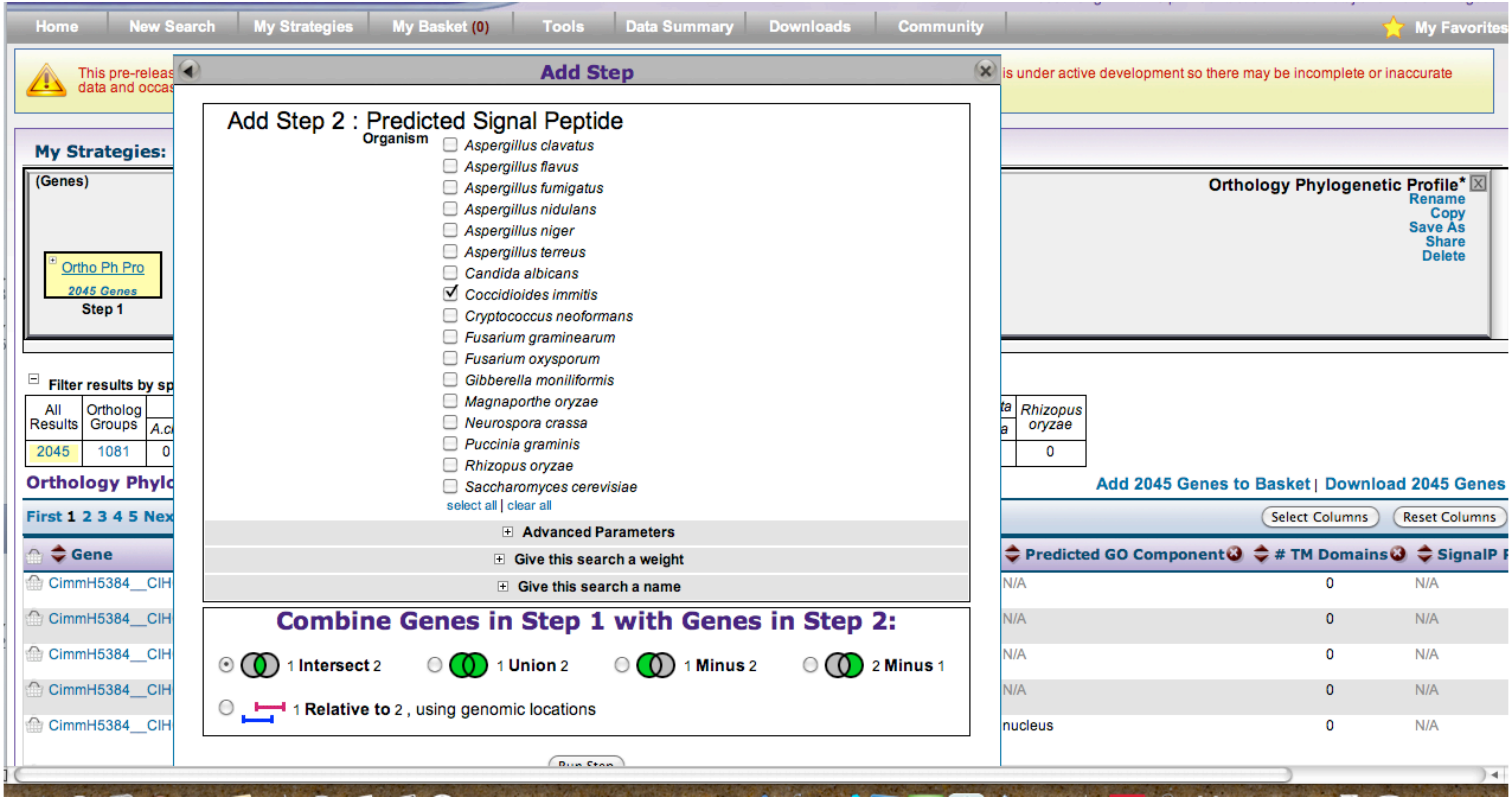
Orthology Phylogenetic Profile - step 1 - 2045 Genes

Add 2045 Genes to Basket | **Download 2045 Genes**

First 1 2 3 4 5 Next Last

Gene	Organism	Genomic Location	Predicted GO Function	Predicted GO Process	Predicted GO Component	# TM Domains	SignalP Pe
CimmH5384__CIHG_00002	*C. immitis H538.4*	CimmH5384__Chr_1.1: 25,495 - 26,017 (-)	N/A	N/A	N/A	0	N/A
CimmH5384__CIHG_00025	*C. immitis H538.4*	CimmH5384__Chr_1.1: 88,178 - 88,927 (-)	N/A	N/A	N/A	0	N/A
CimmH5384__CIHG_00035	*C. immitis H538.4*	CimmH5384__Chr_1.1: 120,432 - 122,870 (-)	N/A	N/A	N/A	0	N/A
CimmH5384__CIHG_00046	*C. immitis H538.4*	CimmH5384__Chr_1.1: 147,177 - 148,416 (+)	N/A	N/A	N/A	0	N/A
CimmH5384__CIHG_00052	*C. immitis H538.4*	CimmH5384__Chr_1.1: 169,646 - 171,075 (-)	sequence-specific DNA binding transcription factor activity, zinc ion binding	N/A	nucleus	0	N/A

Add constraint that they must also have Signal Peptide domain



This pre-releas… data and occas… is under active development so there may be incomplete or inaccurate

Add Step 2 : Predicted Signal Peptide

Organism

- ☐ *Aspergillus clavatus*
- ☐ *Aspergillus flavus*
- ☐ *Aspergillus fumigatus*
- ☐ *Aspergillus nidulans*
- ☐ *Aspergillus niger*
- ☐ *Aspergillus terreus*
- ☐ *Candida albicans*
- ☑ *Coccidioides immitis*
- ☐ *Cryptococcus neoformans*
- ☐ *Fusarium graminearum*
- ☐ *Fusarium oxysporum*
- ☐ *Gibberella moniliformis*
- ☐ *Magnaporthe oryzae*
- ☐ *Neurospora crassa*
- ☐ *Puccinia graminis*
- ☐ *Rhizopus oryzae*
- ☐ *Saccharomyces cerevisiae*

select all | clear all

⊞ **Advanced Parameters**

⊞ **Give this search a weight**

⊞ **Give this search a name**

Combine Genes in Step 1 with Genes in Step 2:

● 1 **Intersect** 2 ○ 1 **Union** 2 ○ 1 **Minus** 2 ○ 2 **Minus** 1

○ 1 **Relative to** 2 , using genomic locations

Filter results by sp…

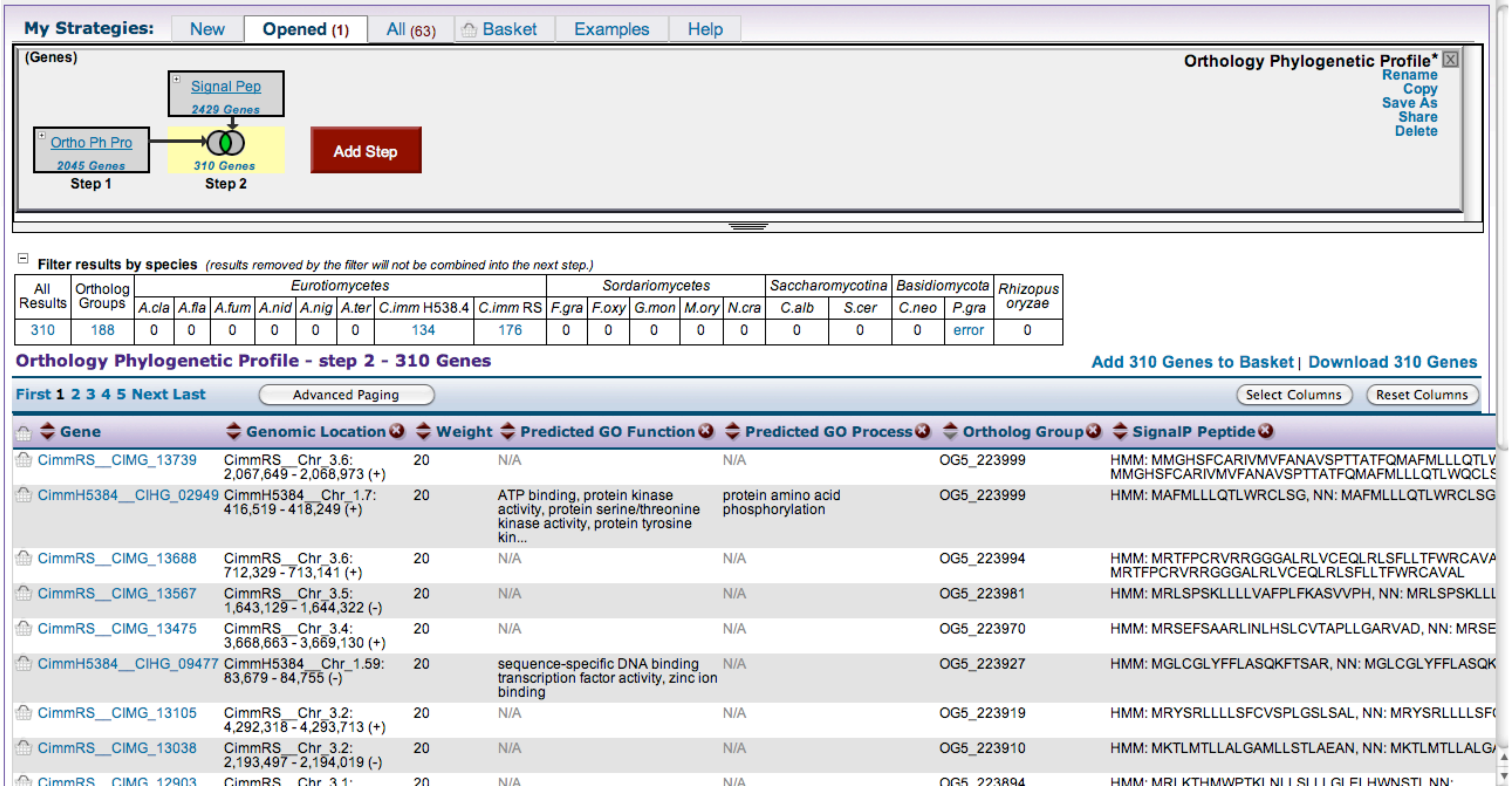
All Results	Ortholog Groups	A.c…	…	Rhizopus oryzae
2045	1081	0		0

Orthology Phyl…

First 1 2 3 4 5 Nex…

Gene	…	Predicted GO Component	# TM Domains	SignalP …
CimmH5384__CIH…		N/A	0	N/A
CimmH5384__CIH…		N/A	0	N/A
CimmH5384__CIH…		N/A	0	N/A
CimmH5384__CIH…		N/A	0	N/A
CimmH5384__CIH…		nucleus	0	N/A

The complete list, can scroll to see what are their functions



Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm H538.4*	*C.imm RS*	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
310	188	0	0	0	0	0	0	134	176	0	0	0	0	0	0	0	0	error	0

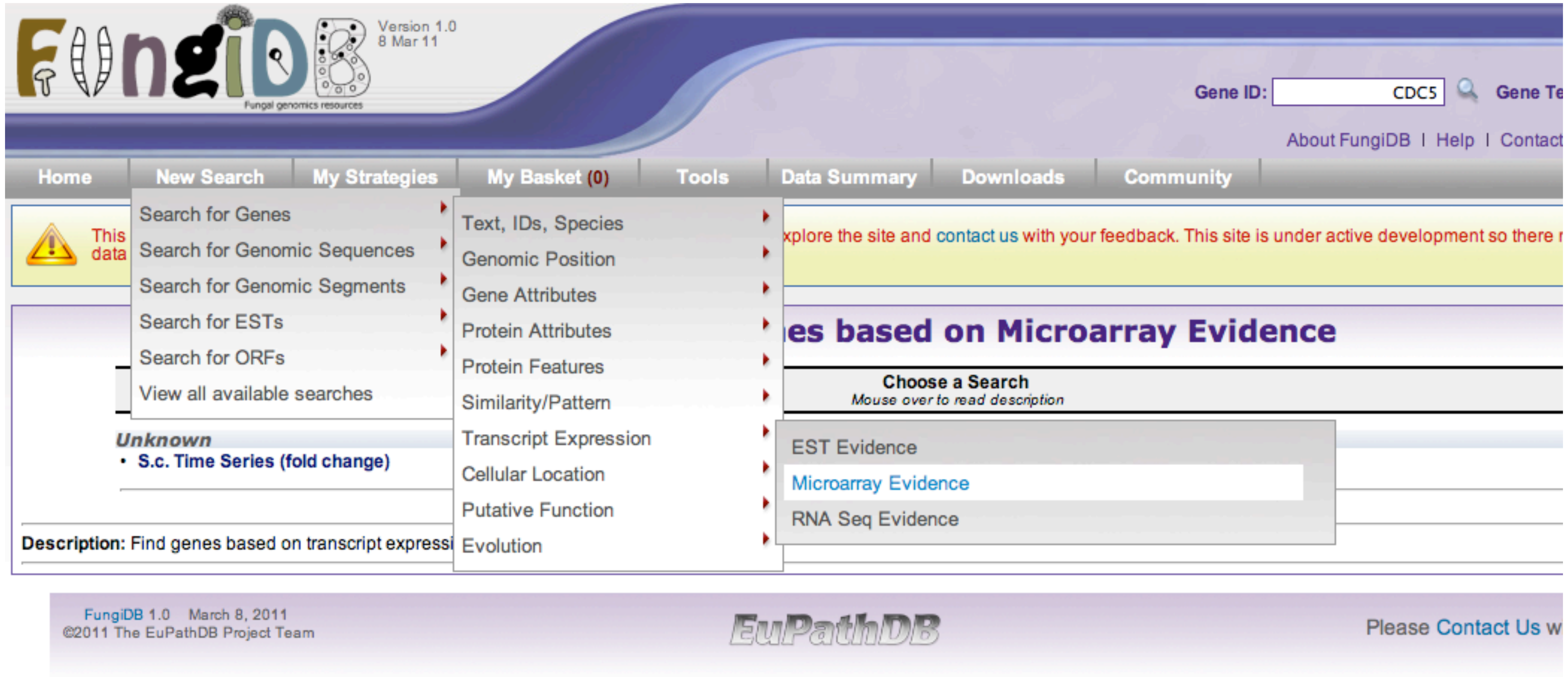
Orthology Phylogenetic Profile - step 2 - 310 Genes

Gene	Genomic Location	Weight	Predicted GO Function	Predicted GO Process	Ortholog Group	SignalP Peptide
CimmRS__CIMG_13739	CimmRS__Chr_3.6: 2,067,649 - 2,068,973 (+)	20	N/A	N/A	OG5_223999	HMM: MMGHSFCARIVMVFANAVSPTTATFQMAFMLLLQTLV MMGHSFCARIVMVFANAVSPTTATFQMAFMLLLQTLWQCLS
CimmH5384__CIHG_02949	CimmH5384__Chr_1.7: 416,519 - 418,249 (+)	20	ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kin...	protein amino acid phosphorylation	OG5_223999	HMM: MAFMLLLQTLWRCLSG, NN: MAFMLLLQTLWRCLSG
CimmRS__CIMG_13688	CimmRS__Chr_3.6: 712,329 - 713,141 (+)	20	N/A	N/A	OG5_223994	HMM: MRTFPCRVRRGGGALRLVCEQLRLSFLLTFWRCAVA MRTFPCRVRRGGGALRLVCEQLRLSFLLTFWRCAVAL
CimmRS__CIMG_13567	CimmRS__Chr_3.5: 1,643,129 - 1,644,322 (-)	20	N/A	N/A	OG5_223981	HMM: MRLSPSKLLLLVAFPLFKASVVPH, NN: MRLSPSKLLL
CimmRS__CIMG_13475	CimmRS__Chr_3.4: 3,668,663 - 3,669,130 (+)	20	N/A	N/A	OG5_223970	HMM: MRSEFSAARLINLHSLCVTAPLLGARVAD, NN: MRSE
CimmH5384__CIHG_09477	CimmH5384__Chr_1.59: 83,679 - 84,755 (-)	20	sequence-specific DNA binding transcription factor activity, zinc ion binding	N/A	OG5_223927	HMM: MGLCGLYFFLASQKFTSAR, NN: MGLCGLYFFLASQK
CimmRS__CIMG_13105	CimmRS__Chr_3.2: 4,292,318 - 4,293,713 (+)	20	N/A	N/A	OG5_223919	HMM: MRYSRLLLLSFCVSPLGSLSAL, NN: MRYSRLLLLSF
CimmRS__CIMG_13038	CimmRS__Chr_3.2: 2,193,497 - 2,194,019 (-)	20	N/A	N/A	OG5_223910	HMM: MKTLMTLLALGAMLLSTLAEAN, NN: MKTLMTLLALG
CimmRS__CIMG_12903	CimmRS__Chr_3.1:	20	N/A	N/A	OG5_223894	HMM: MRLKTHMWPTKLNLLSLLLGLFLHWNSTL, NN:

http://bit.ly/fdb_cocciSecreted

Query by expression patterns or values

Using cell-cycle gene microarray results in *S. cerevisiae*, what are C.albicans genes that peak in G2 (of yeast)



This data xplore the site and contact us with your feedback. This site is under active development so there r

es based on Microarray Evidence

Choose a Search
Mouse over to read description

Unknown
- **S.c. Time Series (fold change)**

Description: Find genes based on transcript expressi

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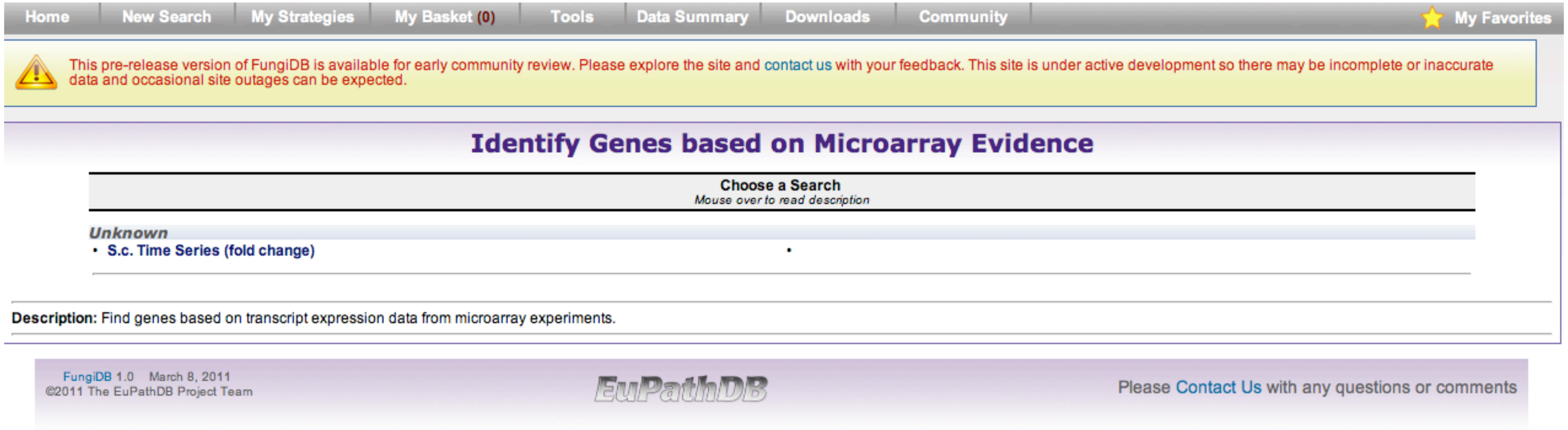
Please Contact Us w



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Identify Genes based on Microarray Evidence

Choose a Search
Mouse over to read description

Unknown
- **S.c. Time Series (fold change)**

Description: Find genes based on transcript expression data from microarray experiments.

FungiDB 1.0 March 8, 2011
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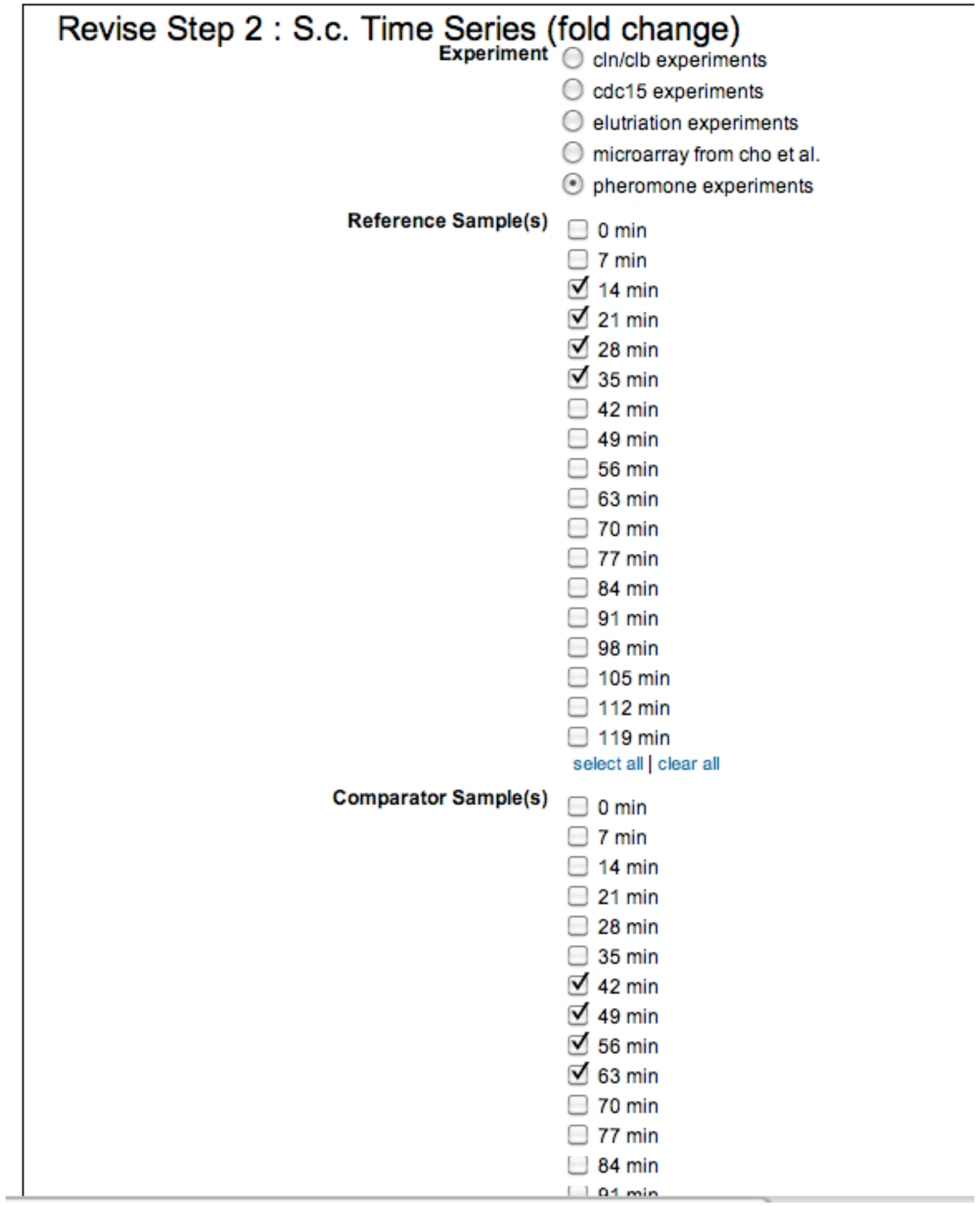
EuPathDB
Please Contact Us with any questions or comments

Identify those that have peak in G2

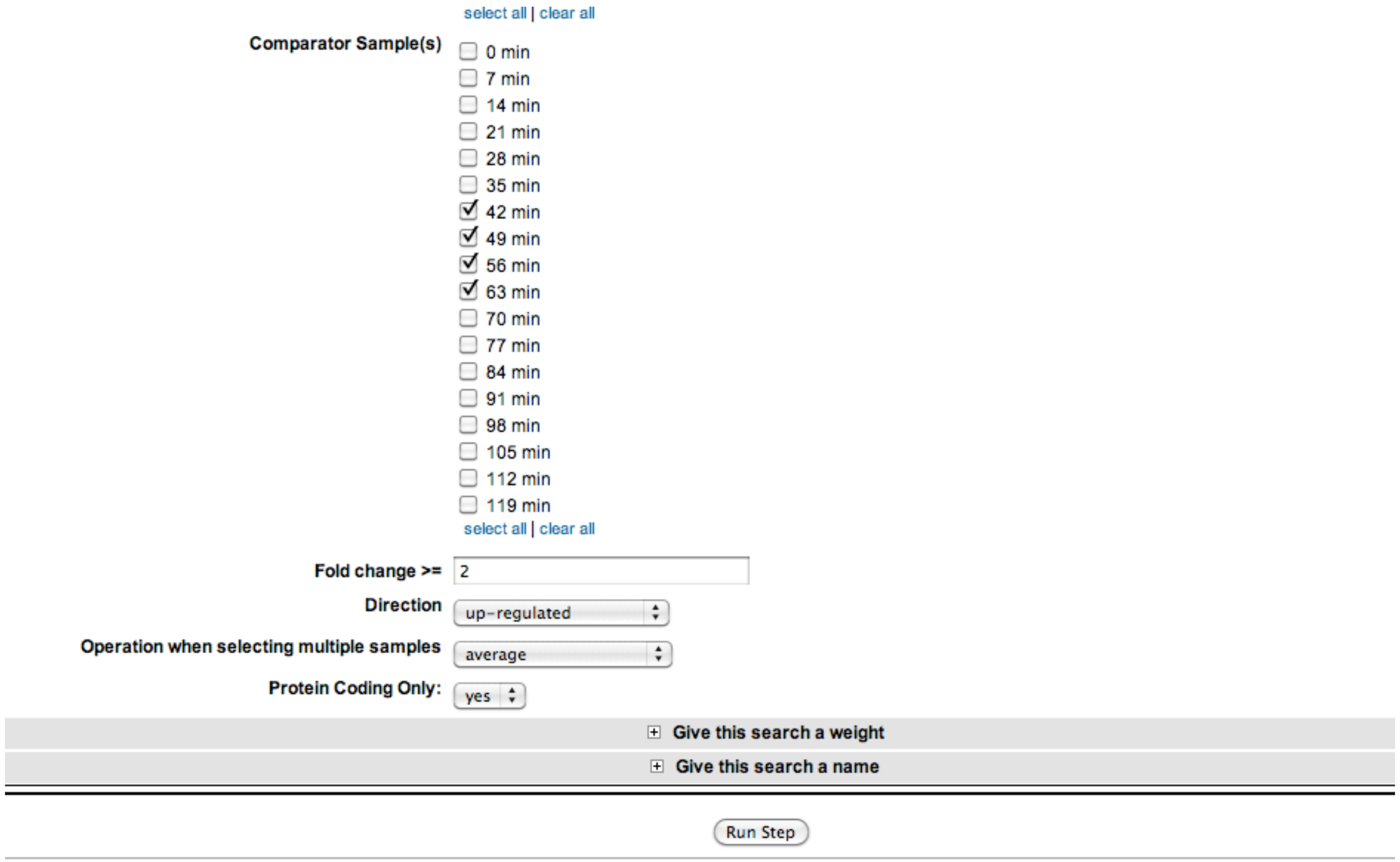


Revise Step 2 : S.c. Time Series (fold change)

Experiment
○ cln/clb experiments
○ cdc15 experiments
○ elutriation experiments
○ microarray from cho et al.
● pheromone experiments

Reference Sample(s)
☐ 0 min
☐ 7 min
☑ 14 min
☑ 21 min
☑ 28 min
☑ 35 min
☐ 42 min
☐ 49 min
☐ 56 min
☐ 63 min
☐ 70 min
☐ 77 min
☐ 84 min
☐ 91 min
☐ 98 min
☐ 105 min
☐ 112 min
☐ 119 min
select all | clear all

Comparator Sample(s)
☐ 0 min
☐ 7 min
☐ 14 min
☐ 21 min
☐ 28 min
☐ 35 min
☑ 42 min
☑ 49 min
☑ 56 min
☑ 63 min
☐ 70 min
☐ 77 min
☐ 84 min
☐ 91 min

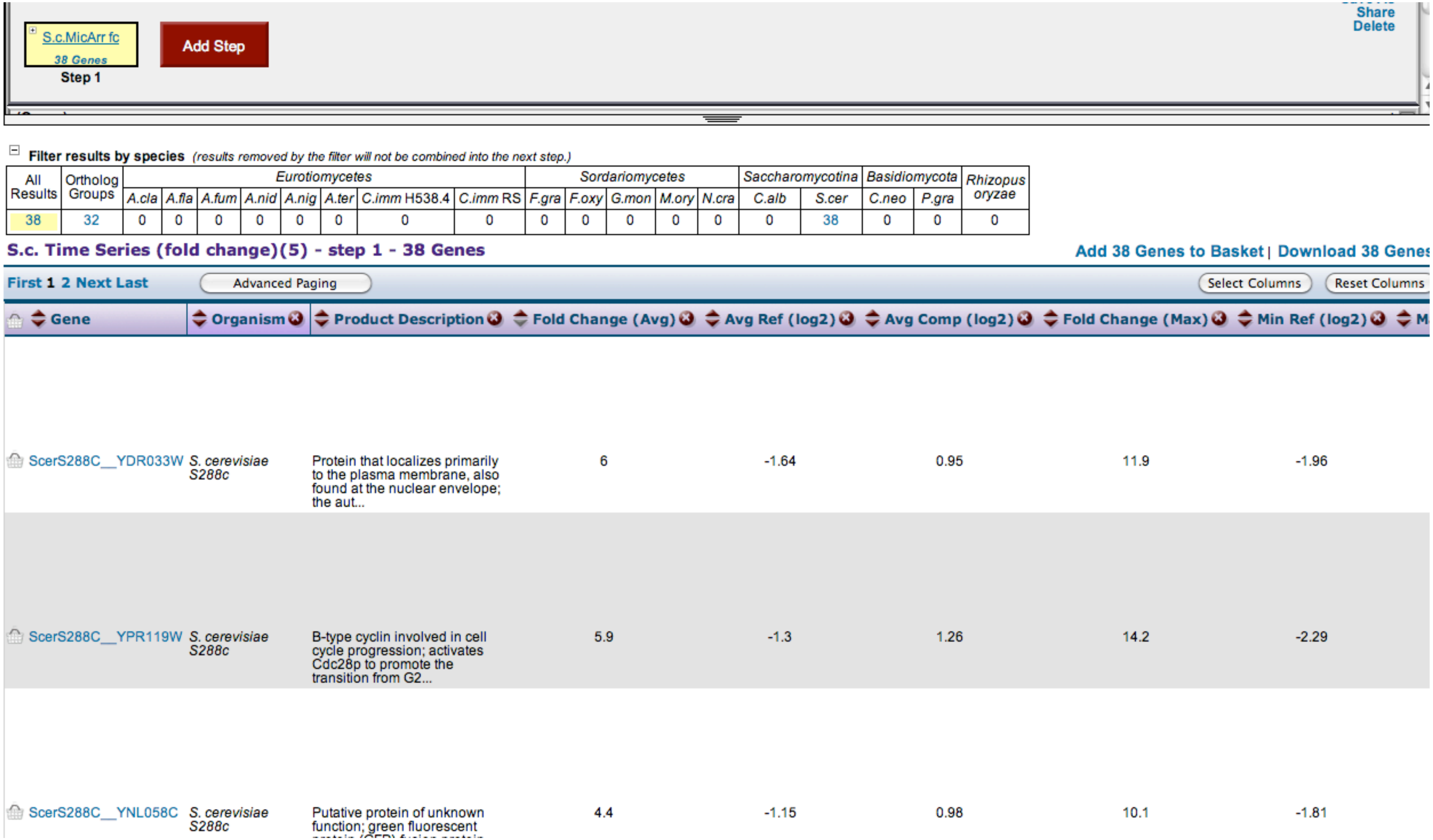


select all | clear all

Comparator Sample(s)
☐ 0 min
☐ 7 min
☐ 14 min
☐ 21 min
☐ 28 min
☐ 35 min
☑ 42 min
☑ 49 min
☑ 56 min
☑ 63 min
☐ 70 min
☐ 77 min
☐ 84 min
☐ 91 min
☐ 98 min
☐ 105 min
☐ 112 min
☐ 119 min
select all | clear all

Fold change >= 2
Direction up-regulated
Operation when selecting multiple samples average
Protein Coding Only: yes

List of results for S. cerevisiae



Filter results by species *(results removed by the filter will not be combined into the next step.)*

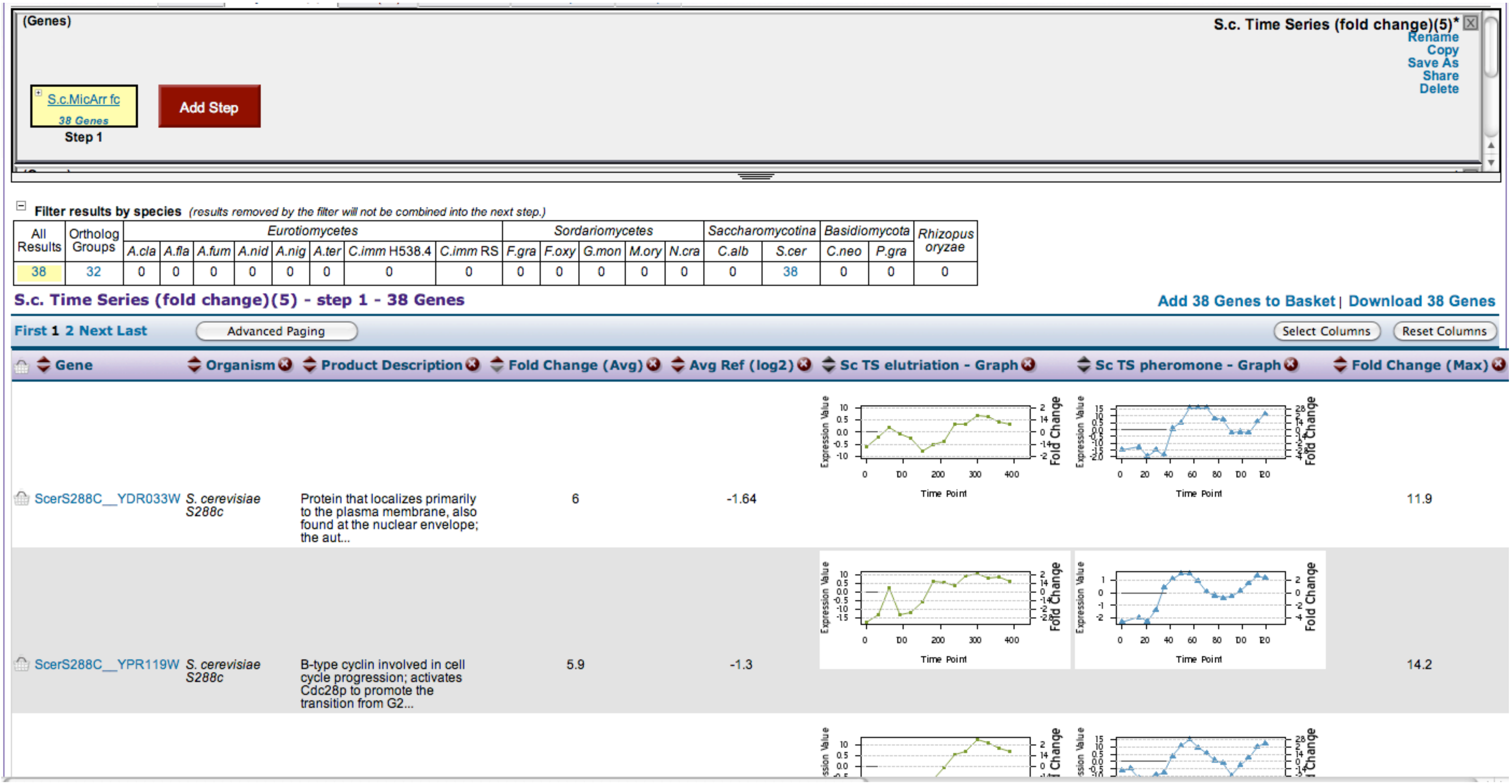
All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
38	32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	38	0	0	0

S.c. Time Series (fold change)(5) - step 1 - 38 Genes

Add 38 Genes to Basket | Download 38 Genes

Gene	Organism	Product Description	Fold Change (Avg)	Avg Ref (log2)	Avg Comp (log2)	Fold Change (Max)	Min Ref (log2)	M
ScerS288C__YDR033W	*S. cerevisiae S288c*	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; the aut...	6	-1.64	0.95	11.9	-1.96	
ScerS288C__YPR119W	*S. cerevisiae S288c*	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2...	5.9	-1.3	1.26	14.2	-2.29	
ScerS288C__YNL058C	*S. cerevisiae S288c*	Putative protein of unknown function; green fluorescent	4.4	-1.15	0.98	10.1	-1.81	

Can add columns which show you summary of expression pattern



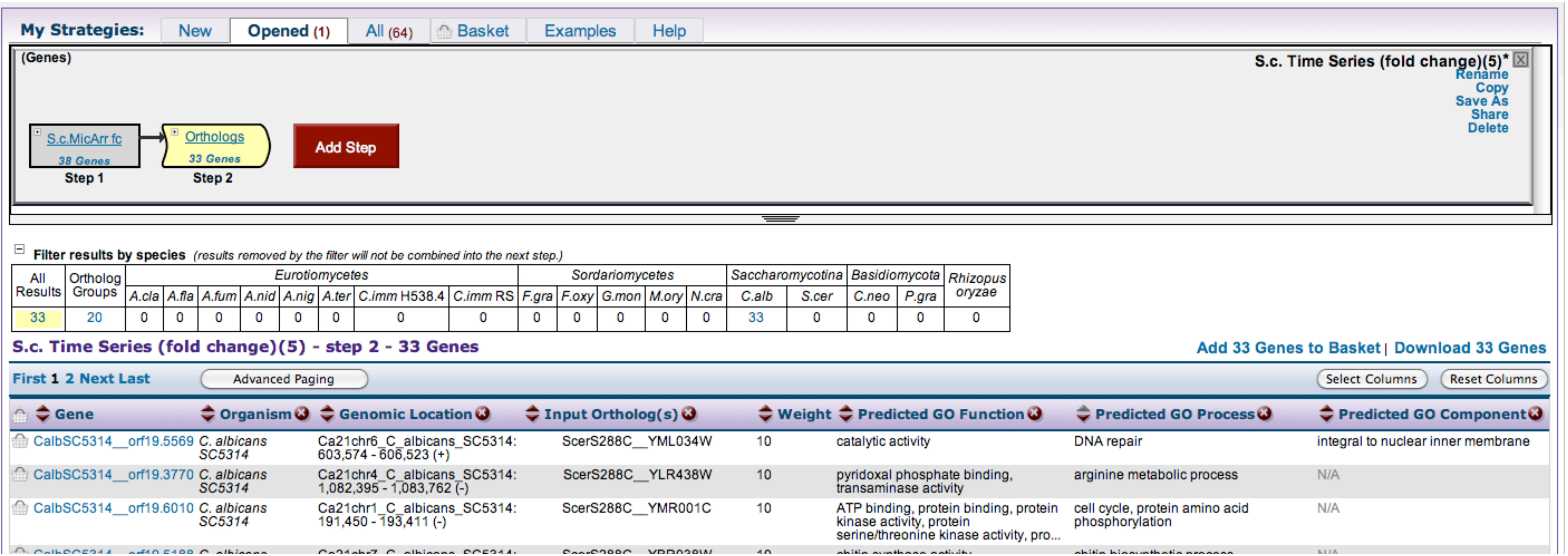
Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm H538.4*	*C.imm RS*	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
38	32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	38	0	0	0

S.c. Time Series (fold change)(5) - step 1 - 38 Genes

Gene	Organism	Product Description	Fold Change (Avg)	Avg Ref (log2)	Sc TS elutriation - Graph	Sc TS pheromone - Graph	Fold Change (Max)
ScerS288C__YDR033W	*S. cerevisiae S288c*	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; the aut...	6	-1.64			11.9
ScerS288C__YPR119W	*S. cerevisiae S288c*	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2...	5.9	-1.3			14.2

Orthology Transform to *C.albicans*



Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm H538.4*	*C.imm RS*	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
33	20	0	0	0	0	0	0	0	0	0	0	0	0	0	33	0	0	0	0

S.c. Time Series (fold change)(5) - step 2 - 33 Genes

Add 33 Genes to Basket | Download 33 Genes

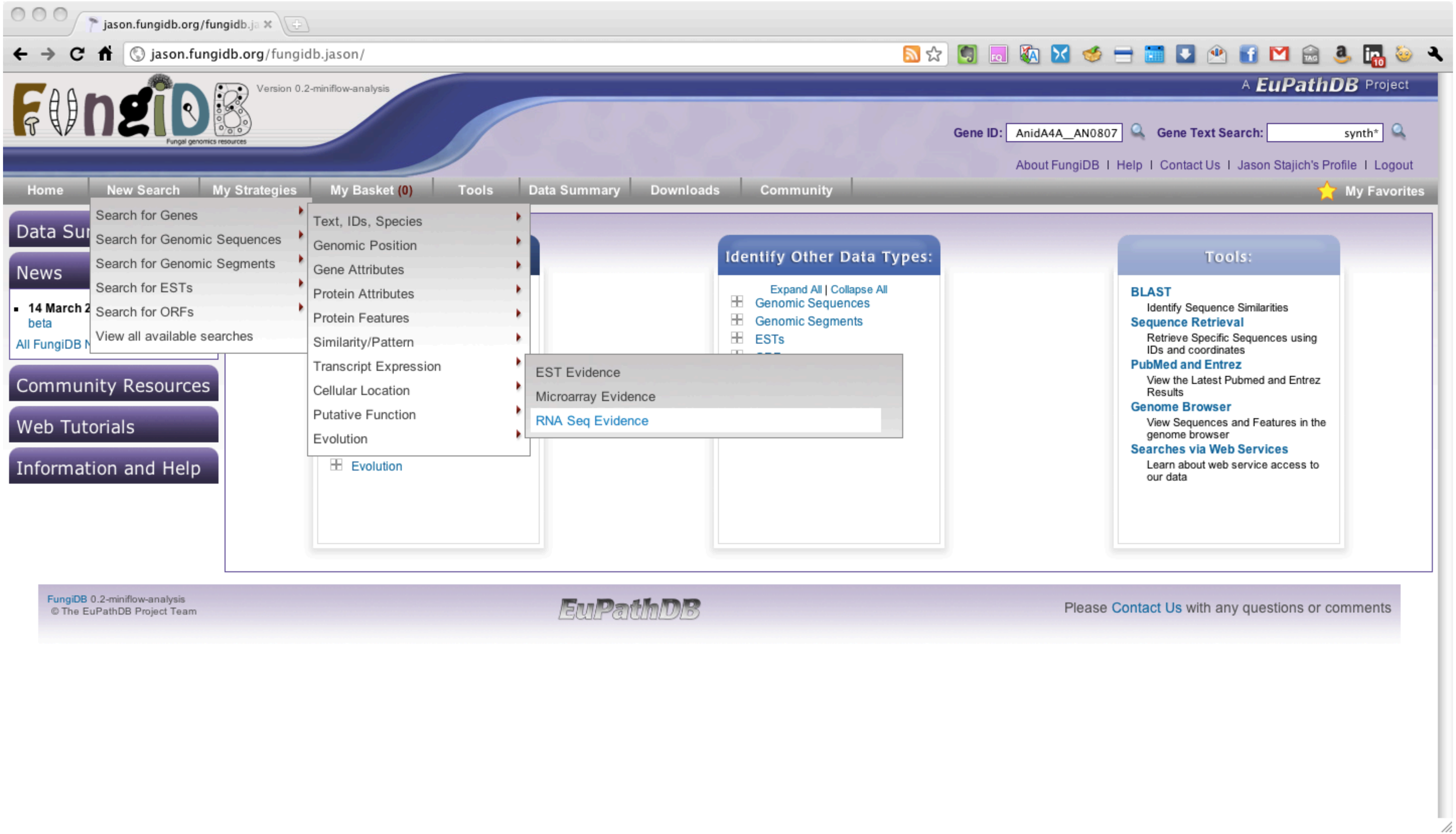
First 1 2 Next Last

Gene	Organism	Genomic Location	Input Ortholog(s)	Weight	Predicted GO Function	Predicted GO Process	Predicted GO Component
CalbSC5314__orf19.5569	*C. albicans SC5314*	Ca21chr6_C_albicans_SC5314: 603,574 - 606,523 (+)	ScerS288C__YML034W	10	catalytic activity	DNA repair	integral to nuclear inner membrane
CalbSC5314__orf19.3770	*C. albicans SC5314*	Ca21chr4_C_albicans_SC5314: 1,082,395 - 1,083,762 (-)	ScerS288C__YLR438W	10	pyridoxal phosphate binding, transaminase activity	arginine metabolic process	N/A
CalbSC5314__orf19.6010	*C. albicans SC5314*	Ca21chr1_C_albicans_SC5314: 191,450 - 193,411 (-)	ScerS288C__YMR001C	10	ATP binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, pro...	cell cycle, protein amino acid phosphorylation	N/A

http://bit.ly/fdb_cellcycle1

RNA-Seq - querying across experiments and visualizing expressed regions

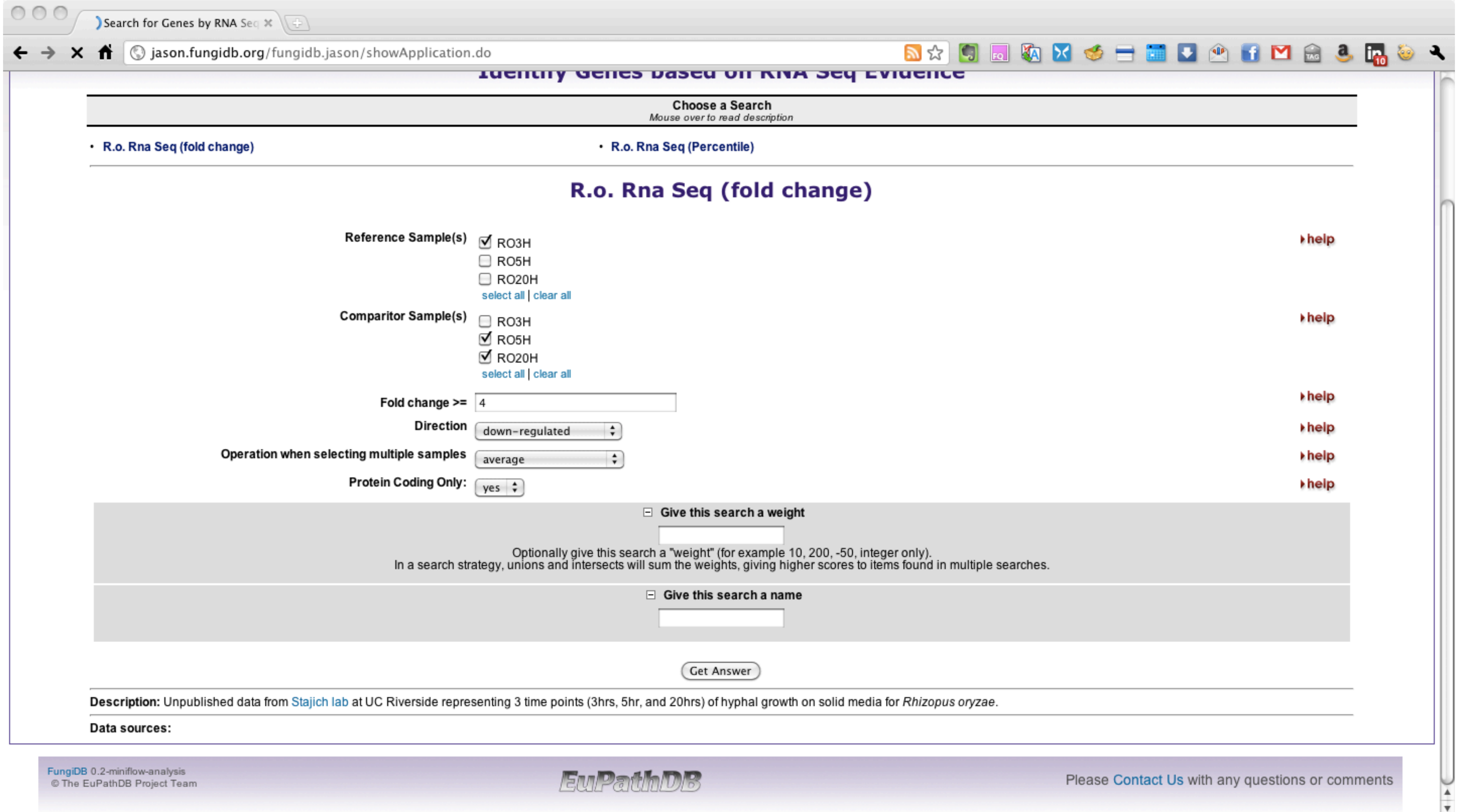
Construct a RNA-Seq query



Gene ID: AnidA4A_AN0807

Gene Text Search: synth*

Query for genes that are >= 4 fold downregulated comparing time points R03H (3hrs) and the average of R05H and RO20H



Identify Genes based on RNA Seq Evidence

Choose a Search
Mouse over to read description

- R.o. Rna Seq (fold change)
- R.o. Rna Seq (Percentile)

R.o. Rna Seq (fold change)

Reference Sample(s)
☑ RO3H
☐ RO5H
☐ RO20H
select all | clear all

Comparitor Sample(s)
☐ RO3H
☑ RO5H
☑ RO20H
select all | clear all

Fold change >= 4
Direction down-regulated
Operation when selecting multiple samples average
Protein Coding Only: yes

Give this search a weight

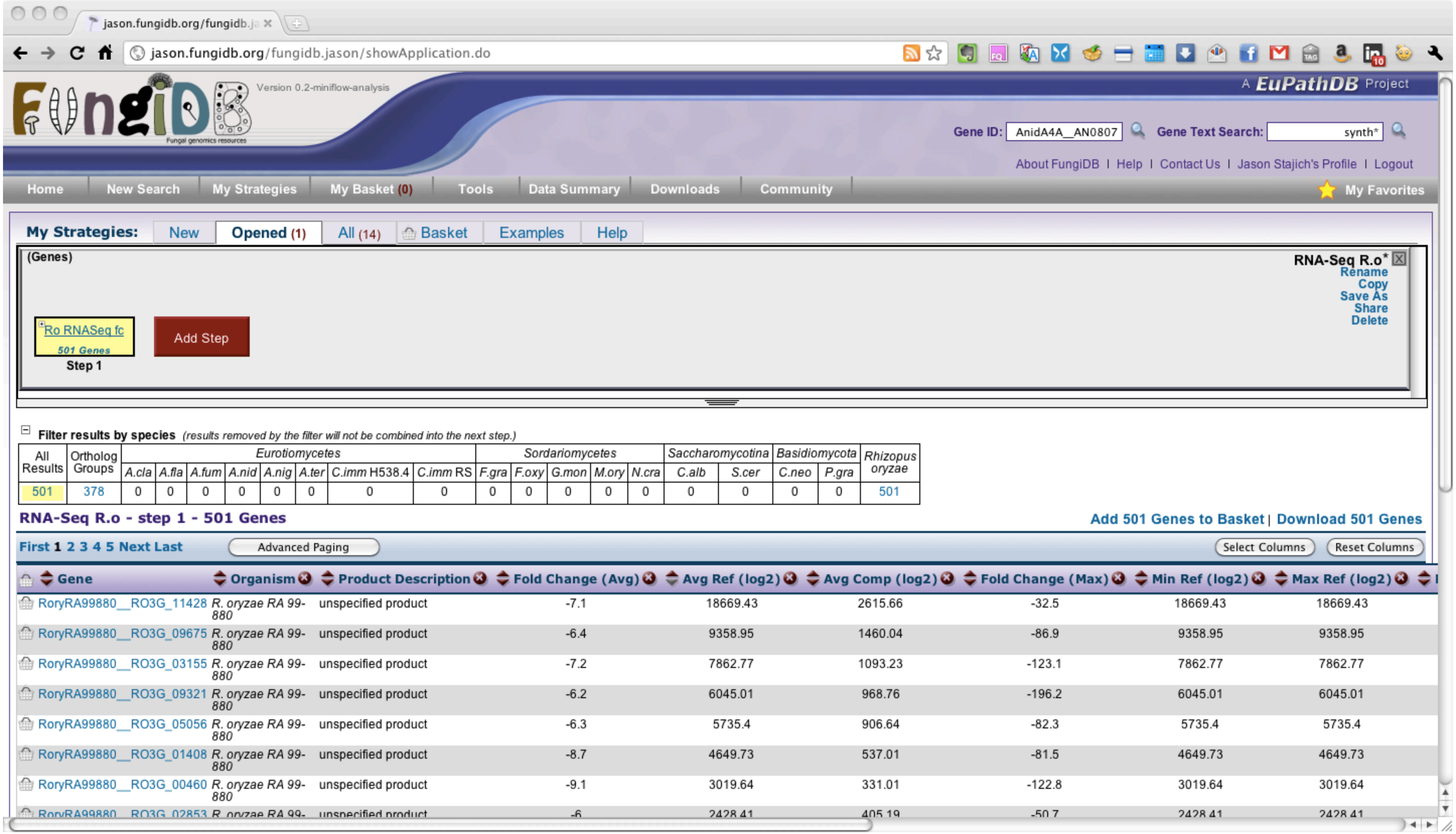
Optionally give this search a "weight" (for example 10, 200, -50, integer only).
In a search strategy, unions and intersects will sum the weights, giving higher scores to items found in multiple searches.

Give this search a name

Description: Unpublished data from Stajich lab at UC Riverside representing 3 time points (3hrs, 5hr, and 20hrs) of hyphal growth on solid media for *Rhizopus oryzae*.

Data sources:

501 genes meet the criteria



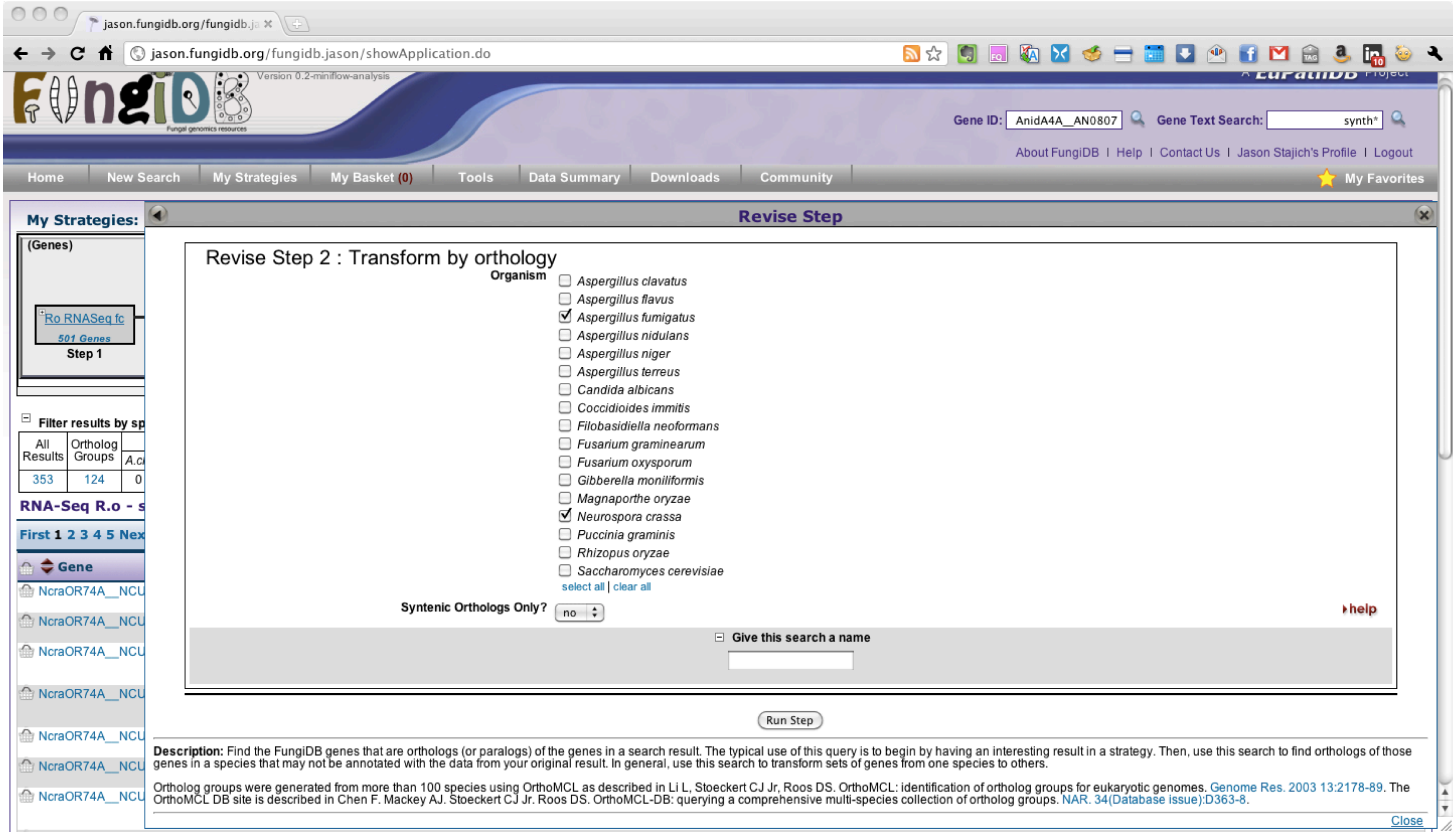
Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm H538.4*	*C.imm RS*	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
501	378	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	501

RNA-Seq R.o - step 1 - 501 Genes

Gene	Organism	Product Description	Fold Change (Avg)	Avg Ref (log2)	Avg Comp (log2)	Fold Change (Max)	Min Ref (log2)	Max Ref (log2)
RoryRA99880__RO3G_11428	*R. oryzae RA 99-880*	unspecified product	-7.1	18669.43	2615.66	-32.5	18669.43	18669.43
RoryRA99880__RO3G_09675	*R. oryzae RA 99-880*	unspecified product	-6.4	9358.95	1460.04	-86.9	9358.95	9358.95
RoryRA99880__RO3G_03155	*R. oryzae RA 99-880*	unspecified product	-7.2	7862.77	1093.23	-123.1	7862.77	7862.77
RoryRA99880__RO3G_09321	*R. oryzae RA 99-880*	unspecified product	-6.2	6045.01	968.76	-196.2	6045.01	6045.01
RoryRA99880__RO3G_05056	*R. oryzae RA 99-880*	unspecified product	-6.3	5735.4	906.64	-82.3	5735.4	5735.4
RoryRA99880__RO3G_01408	*R. oryzae RA 99-880*	unspecified product	-8.7	4649.73	537.01	-81.5	4649.73	4649.73
RoryRA99880__RO3G_00460	*R. oryzae RA 99-880*	unspecified product	-9.1	3019.64	331.01	-122.8	3019.64	3019.64
RoryRA99880__RO3G_02853	*R. oryzae RA 99-*	unspecified product	-6	2428.41	405.19	-50.7	2428.41	2428.41

Which of these are in Aspergillus or Neurospora?



Gene ID: AnidA4A__AN0807

Gene Text Search: synth*

All Results	Ortholog Groups	A.c
353	124	0

Revise Step 2 : Transform by orthology

Organism

- ☐ *Aspergillus clavatus*
- ☐ *Aspergillus flavus*
- ☑ *Aspergillus fumigatus*
- ☐ *Aspergillus nidulans*
- ☐ *Aspergillus niger*
- ☐ *Aspergillus terreus*
- ☐ *Candida albicans*
- ☐ *Coccidioides immitis*
- ☐ *Filobasidiella neoformans*
- ☐ *Fusarium graminearum*
- ☐ *Fusarium oxysporum*
- ☐ *Gibberella moniliformis*
- ☐ *Magnaporthe oryzae*
- ☑ *Neurospora crassa*
- ☐ *Puccinia graminis*
- ☐ *Rhizopus oryzae*
- ☐ *Saccharomyces cerevisiae*

select all | clear all

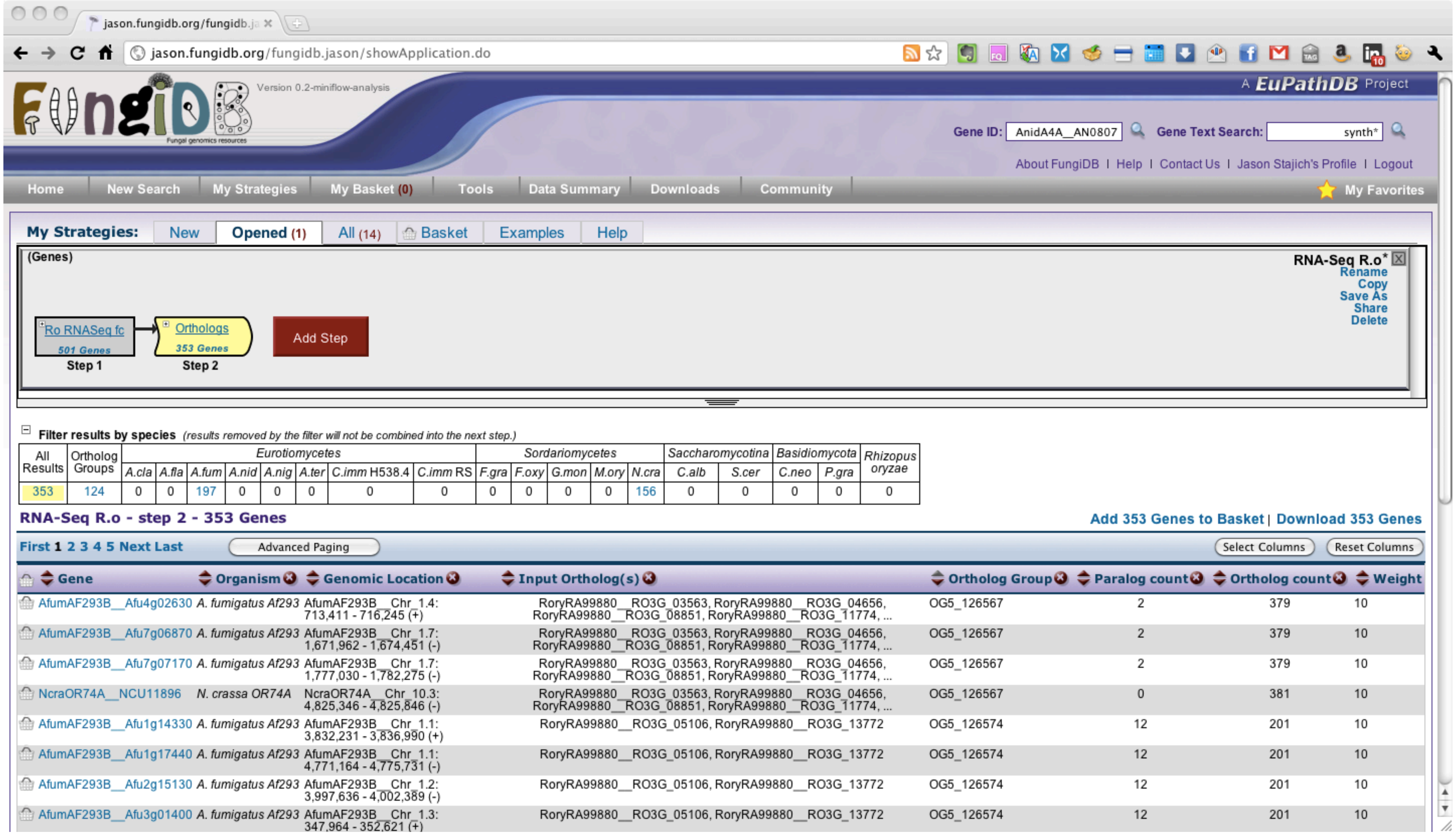
Syntenic Orthologs Only? no

Give this search a name

Description: Find the FungiDB genes that are orthologs (or paralogs) of the genes in a search result. The typical use of this query is to begin by having an interesting result in a strategy. Then, use this search to find orthologs of those genes in a species that may not be annotated with the data from your original result. In general, use this search to transform sets of genes from one species to others.

Ortholog groups were generated from more than 100 species using OrthoMCL as described in Li L, Stoeckert CJ Jr, Roos DS. OrthoMCL: identification of ortholog groups for eukaryotic genomes. Genome Res. 2003 13:2178-89. The OrthoMCL DB site is described in Chen F. Mackey AJ. Stoeckert CJ Jr. Roos DS. OrthoMCL-DB: querying a comprehensive multi-species collection of ortholog groups. NAR. 34(Database issue):D363-8.

197 in *A.fumigatus*, 156 in *N.crassa*
can see info of the orthology (1:1 or 1:many)



Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
353	124	0	0	197	0	0	0	0	0	0	0	0	0	156	0	0	0	0	0

RNA-Seq R.o - step 2 - 353 Genes

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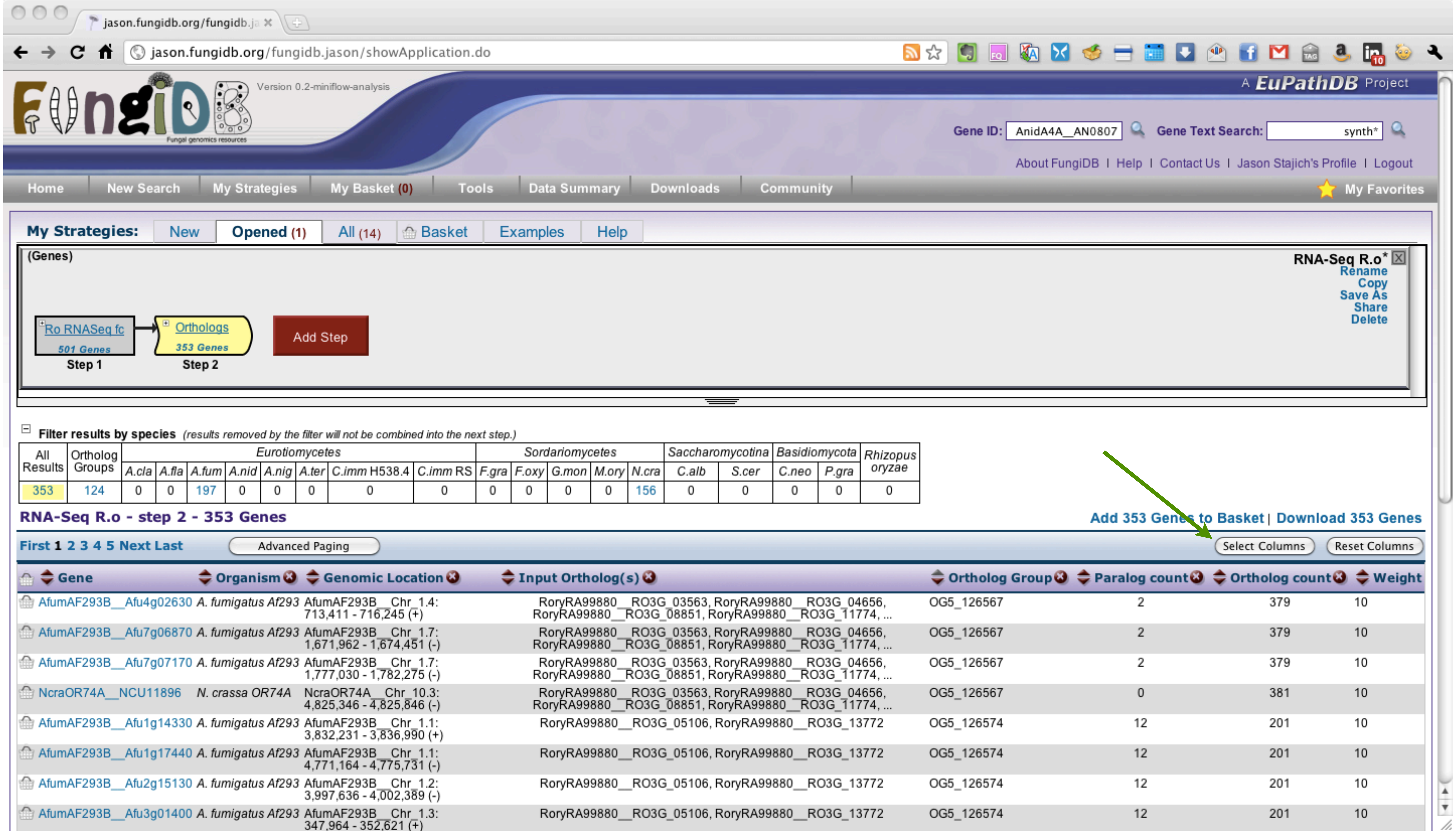
First 1 2 3 4 5 Next Last

Gene	Organism	Genomic Location	Input Ortholog(s)	Ortholog Group	Paralog count	Ortholog count	Weight
AfumAF293B__Afu4g02630	*A. fumigatus Af293*	AfumAF293B__Chr_1.4: 713,411 - 716,245 (+)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
AfumAF293B__Afu7g06870	*A. fumigatus Af293*	AfumAF293B__Chr_1.7: 1,671,962 - 1,674,451 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
AfumAF293B__Afu7g07170	*A. fumigatus Af293*	AfumAF293B__Chr_1.7: 1,777,030 - 1,782,275 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
NcraOR74A__NCU11896	*N. crassa OR74A*	NcraOR74A__Chr_10.3: 4,825,346 - 4,825,846 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	0	381	10
AfumAF293B__Afu1g14330	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 3,832,231 - 3,836,990 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu1g17440	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 4,771,164 - 4,775,731 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu2g15130	*A. fumigatus Af293*	AfumAF293B__Chr_1.2: 3,997,636 - 4,002,389 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu3g01400	*A. fumigatus Af293*	AfumAF293B__Chr_1.3: 347,964 - 352,621 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10

197 in *A.fumigatus*, 156 in *N.crassa*
can see info of the orthology (1:1 or 1:many)



Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm H538.4*	*C.imm RS*	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
353	124	0	0	197	0	0	0	0	0	0	0	0	0	156	0	0	0	0	0

RNA-Seq R.o - step 2 - 353 Genes

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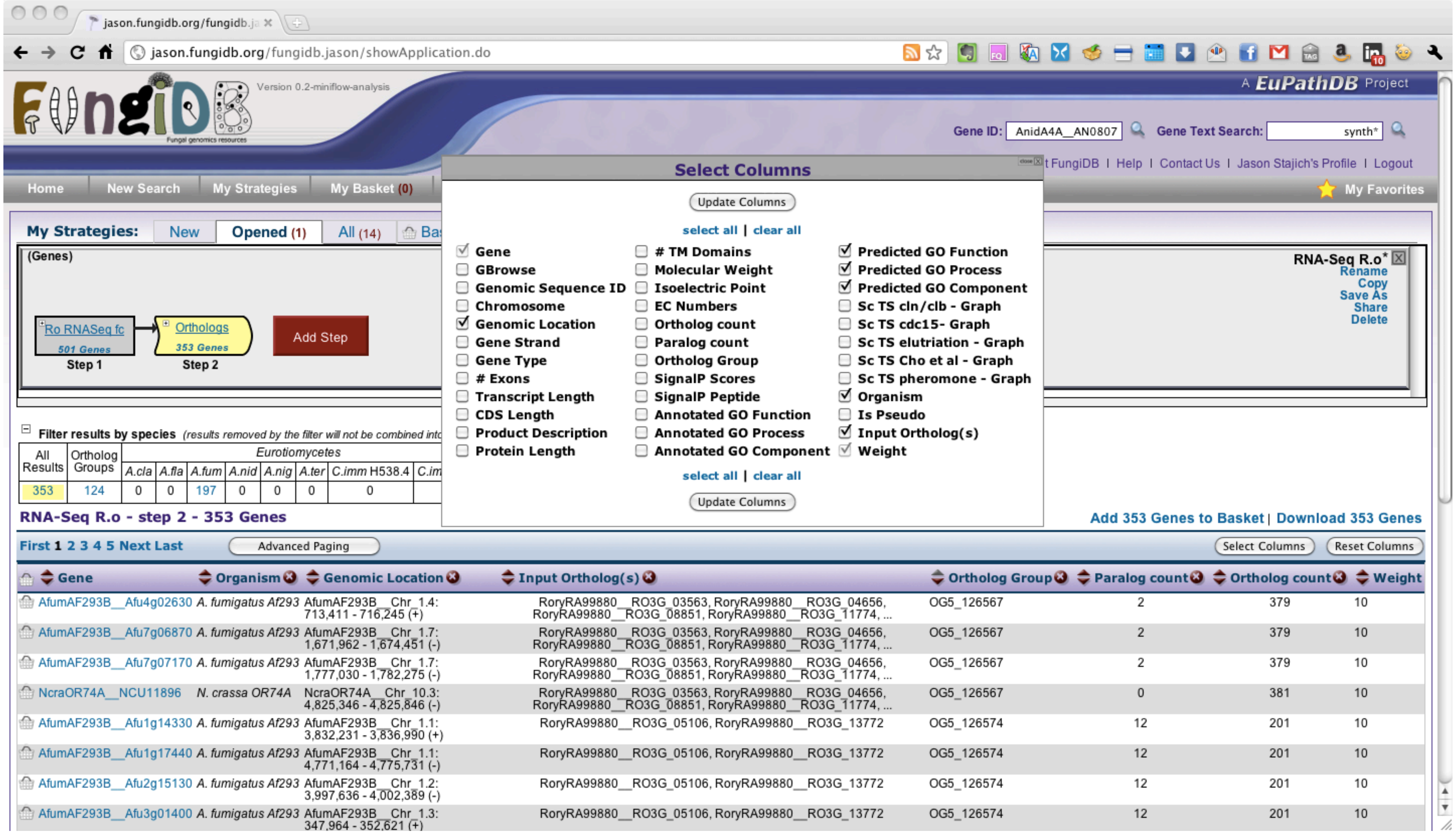
Gene	Organism	Genomic Location	Input Ortholog(s)	Ortholog Group	Paralog count	Ortholog count	Weight
AfumAF293B__Afu4g02630	*A. fumigatus Af293*	AfumAF293B__Chr_1.4: 713,411 - 716,245 (+)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
AfumAF293B__Afu7g06870	*A. fumigatus Af293*	AfumAF293B__Chr_1.7: 1,671,962 - 1,674,451 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
AfumAF293B__Afu7g07170	*A. fumigatus Af293*	AfumAF293B__Chr_1.7: 1,777,030 - 1,782,275 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
NcraOR74A__NCU11896	*N. crassa OR74A*	NcraOR74A__Chr_10.3: 4,825,346 - 4,825,846 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	0	381	10
AfumAF293B__Afu1g14330	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 3,832,231 - 3,836,990 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu1g17440	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 4,771,164 - 4,775,731 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu2g15130	*A. fumigatus Af293*	AfumAF293B__Chr_1.2: 3,997,636 - 4,002,389 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu3g01400	*A. fumigatus Af293*	AfumAF293B__Chr_1.3: 347,964 - 352,621 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10

Turn on some more columns to see GO info



Select Columns

Update Columns

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☑ Gene	☐ # TM Domains	☑ Predicted GO Function
☐ GBrowse	☐ Molecular Weight	☑ Predicted GO Process
☐ Genomic Sequence ID	☐ Isoelectric Point	☑ Predicted GO Component
☐ Chromosome	☐ EC Numbers	☐ Sc TS cln/clb - Graph
☑ Genomic Location	☐ Ortholog count	☐ Sc TS cdc15- Graph
☐ Gene Strand	☐ Paralog count	☐ Sc TS elutriation - Graph
☐ Gene Type	☐ Ortholog Group	☐ Sc TS Cho et al - Graph
☐ # Exons	☐ SignalP Scores	☐ Sc TS pheromone - Graph
☐ Transcript Length	☐ SignalP Peptide	☑ Organism
☐ CDS Length	☐ Annotated GO Function	☐ Is Pseudo
☐ Product Description	☐ Annotated GO Process	☑ Input Ortholog(s)
☐ Protein Length	☐ Annotated GO Component	☑ Weight

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Update Columns

My Strategies: New | Opened (1) | All (14) | Ba

(Genes)

Ro RNASeq fc
501 Genes
Step 1

Orthologs
353 Genes
Step 2

Add Step

RNA-Seq R.o*
Rename
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Filter results by species (results removed by the filter will not be combined into

All Results	Ortholog Groups	Eurotiomycetes							
		A.cla	A.fla	A.fum	A.nid	A.nig	A.ter	C.imm H538.4	C.im
353	124	0	0	197	0	0	0	0	

RNA-Seq R.o - step 2 - 353 Genes

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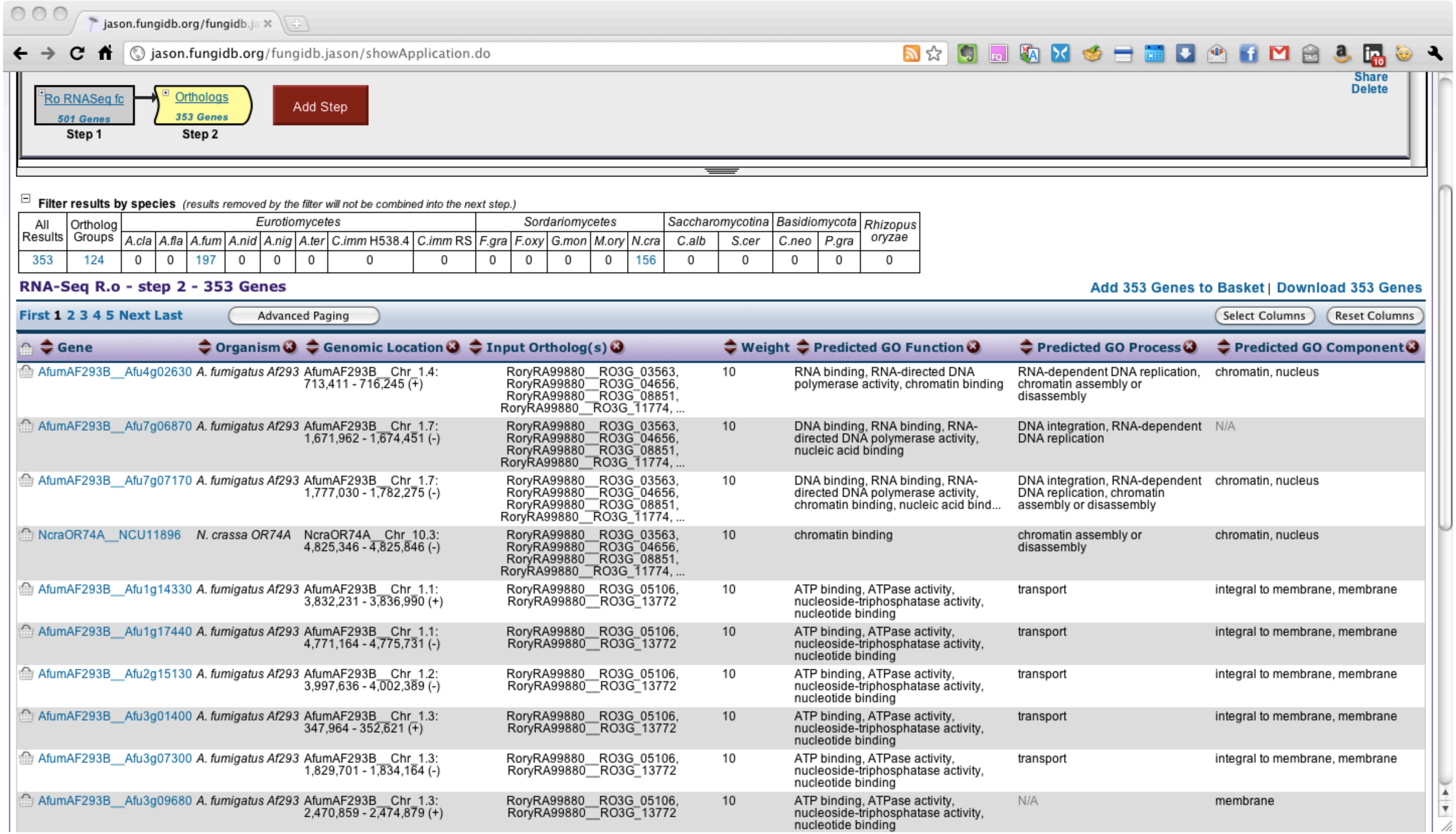
Gene	Organism	Genomic Location	Input Ortholog(s)	Ortholog Group	Paralog count	Ortholog count	Weight
AfumAF293B__Afu4g02630	*A. fumigatus Af293*	AfumAF293B__Chr_1.4: 713,411 - 716,245 (+)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
AfumAF293B__Afu7g06870	*A. fumigatus Af293*	AfumAF293B__Chr_1.7: 1,671,962 - 1,674,451 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
AfumAF293B__Afu7g07170	*A. fumigatus Af293*	AfumAF293B__Chr_1.7: 1,777,030 - 1,782,275 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	2	379	10
NcraOR74A__NCU11896	*N. crassa OR74A*	NcraOR74A__Chr_10.3: 4,825,346 - 4,825,846 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	OG5_126567	0	381	10
AfumAF293B__Afu1g14330	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 3,832,231 - 3,836,990 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu1g17440	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 4,771,164 - 4,775,731 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu2g15130	*A. fumigatus Af293*	AfumAF293B__Chr_1.2: 3,997,636 - 4,002,389 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10
AfumAF293B__Afu3g01400	*A. fumigatus Af293*	AfumAF293B__Chr_1.3: 347,964 - 352,621 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	OG5_126574	12	201	10

See the GO information for the orthologs in *A.fumigatus*



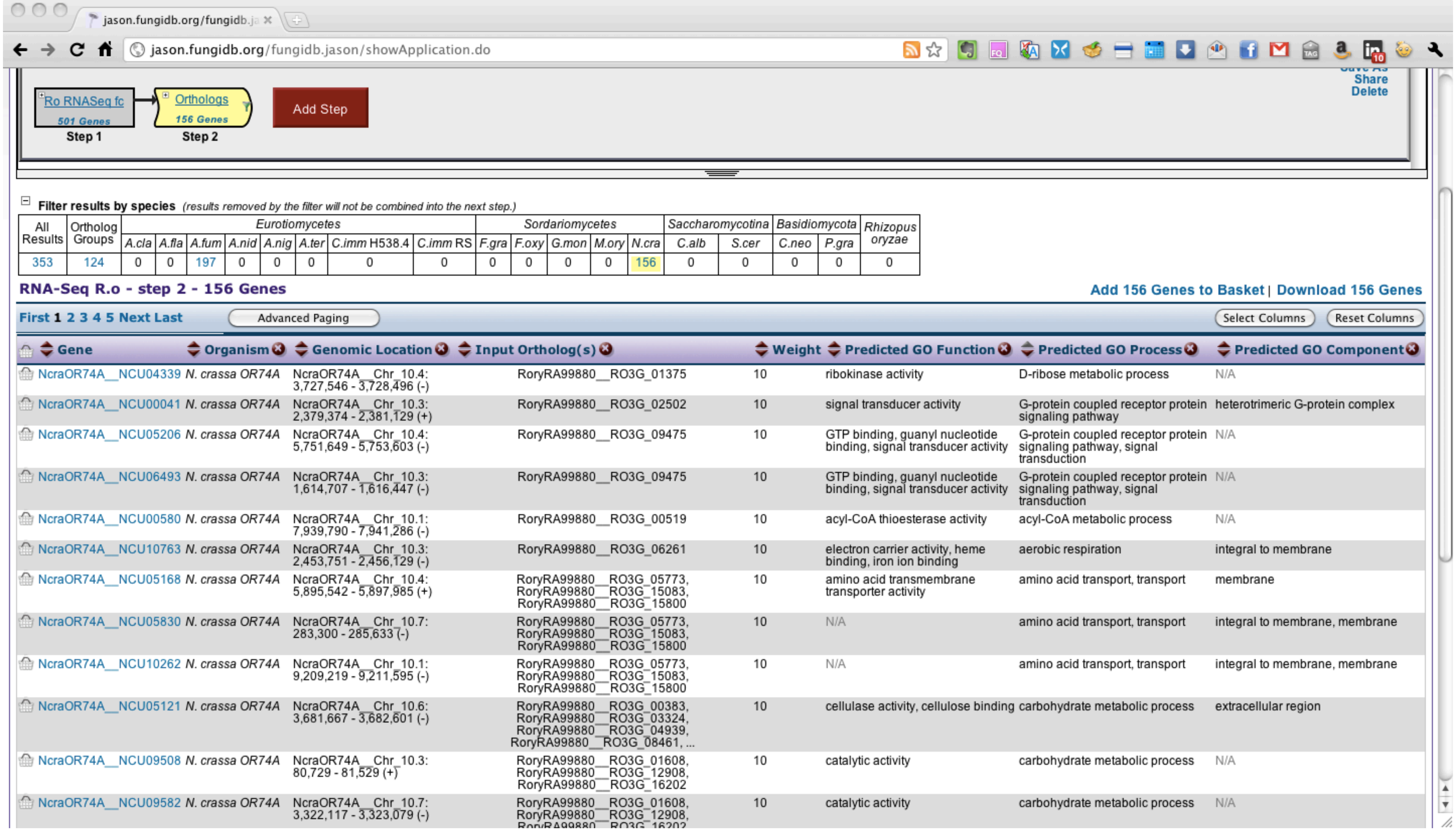
Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
353	124	0	0	197	0	0	0	0	0	0	0	0	0	156	0	0	0	0	0

RNA-Seq R.o - step 2 - 353 Genes

Gene	Organism	Genomic Location	Input Ortholog(s)	Weight	Predicted GO Function	Predicted GO Process	Predicted GO Component
AfumAF293B__Afu4g02630	*A. fumigatus Af293*	AfumAF293B__Chr_1.4: 713,411 - 716,245 (+)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	10	RNA binding, RNA-directed DNA polymerase activity, chromatin binding	RNA-dependent DNA replication, chromatin assembly or disassembly	chromatin, nucleus
AfumAF293B__Afu7g06870	*A. fumigatus Af293*	AfumAF293B__Chr_1.7: 1,671,962 - 1,674,451 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	10	DNA binding, RNA binding, RNA-directed DNA polymerase activity, nucleic acid binding	DNA integration, RNA-dependent DNA replication	N/A
AfumAF293B__Afu7g07170	*A. fumigatus Af293*	AfumAF293B__Chr_1.7: 1,777,030 - 1,782,275 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	10	DNA binding, RNA binding, RNA-directed DNA polymerase activity, chromatin binding, nucleic acid bind...	DNA integration, RNA-dependent DNA replication, chromatin assembly or disassembly	chromatin, nucleus
NcraOR74A__NCU11896	*N. crassa OR74A*	NcraOR74A__Chr_10.3: 4,825,346 - 4,825,846 (-)	RoryRA99880__RO3G_03563, RoryRA99880__RO3G_04656, RoryRA99880__RO3G_08851, RoryRA99880__RO3G_11774, ...	10	chromatin binding	chromatin assembly or disassembly	chromatin, nucleus
AfumAF293B__Afu1g14330	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 3,832,231 - 3,836,990 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	10	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	transport	integral to membrane, membrane
AfumAF293B__Afu1g17440	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 4,771,164 - 4,775,731 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	10	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	transport	integral to membrane, membrane
AfumAF293B__Afu2g15130	*A. fumigatus Af293*	AfumAF293B__Chr_1.2: 3,997,636 - 4,002,389 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	10	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	transport	integral to membrane, membrane
AfumAF293B__Afu3g01400	*A. fumigatus Af293*	AfumAF293B__Chr_1.3: 347,964 - 352,621 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	10	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	transport	integral to membrane, membrane
AfumAF293B__Afu3g07300	*A. fumigatus Af293*	AfumAF293B__Chr_1.3: 1,829,701 - 1,834,164 (-)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	10	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	transport	integral to membrane, membrane
AfumAF293B__Afu3g09680	*A. fumigatus Af293*	AfumAF293B__Chr_1.3: 2,470,859 - 2,474,879 (+)	RoryRA99880__RO3G_05106, RoryRA99880__RO3G_13772	10	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	N/A	membrane

See the GO information for the orthologs in *N.crassa*



Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
353	124	0	0	197	0	0	0	0	0	0	0	0	0	156	0	0	0	0	0

RNA-Seq R.o - step 2 - 156 Genes

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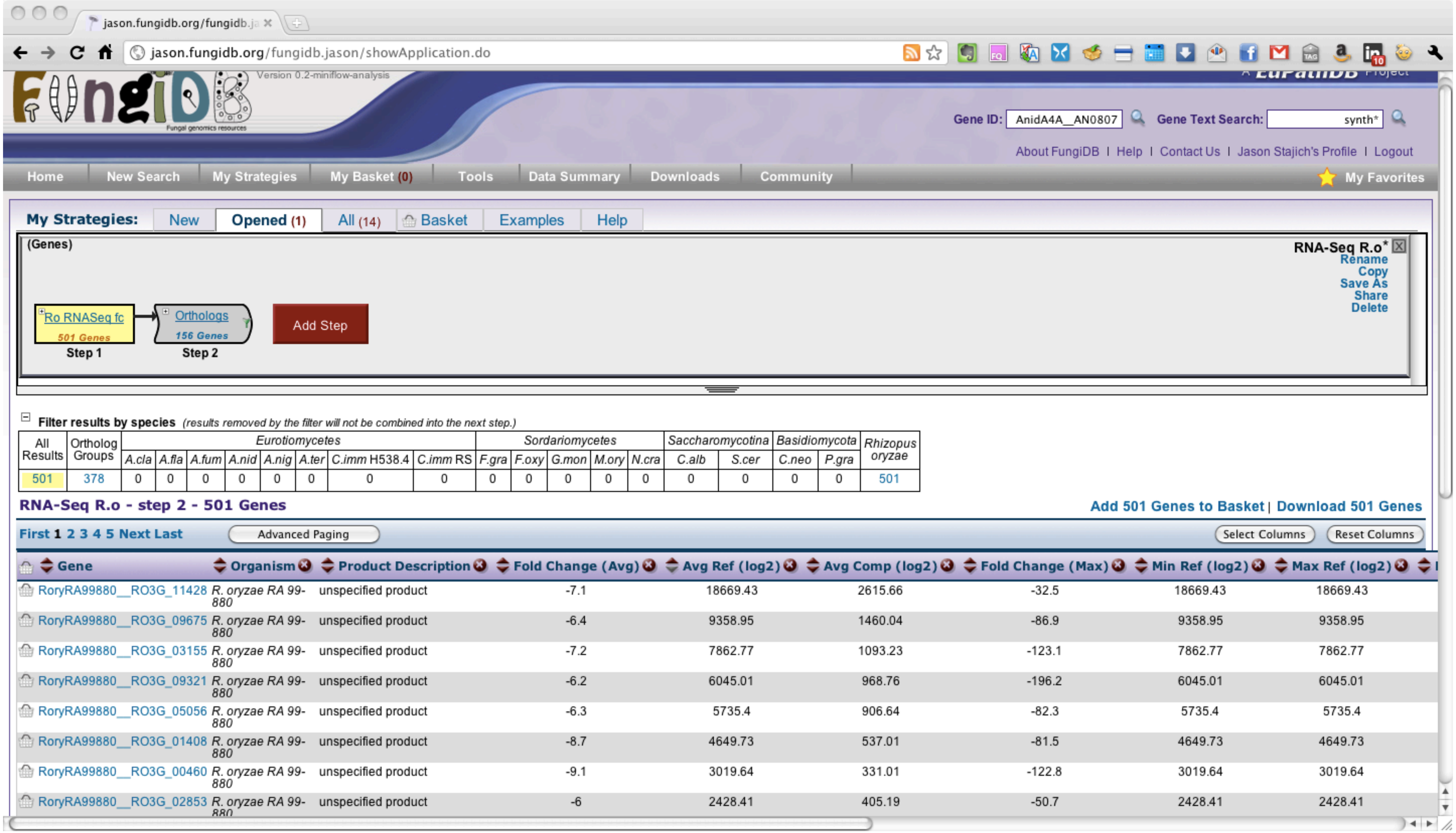
Gene	Organism	Genomic Location	Input Ortholog(s)	Weight	Predicted GO Function	Predicted GO Process	Predicted GO Component
NcraOR74A__NCU04339	*N. crassa OR74A*	NcraOR74A__Chr_10.4: 3,727,546 - 3,728,496 (-)	RoryRA99880__RO3G_01375	10	ribokinase activity	D-ribose metabolic process	N/A
NcraOR74A__NCU00041	*N. crassa OR74A*	NcraOR74A__Chr_10.3: 2,379,374 - 2,381,129 (+)	RoryRA99880__RO3G_02502	10	signal transducer activity	G-protein coupled receptor protein signaling pathway	heterotrimeric G-protein complex
NcraOR74A__NCU05206	*N. crassa OR74A*	NcraOR74A__Chr_10.4: 5,751,649 - 5,753,603 (-)	RoryRA99880__RO3G_09475	10	GTP binding, guanyl nucleotide binding, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction	N/A
NcraOR74A__NCU06493	*N. crassa OR74A*	NcraOR74A__Chr_10.3: 1,614,707 - 1,616,447 (-)	RoryRA99880__RO3G_09475	10	GTP binding, guanyl nucleotide binding, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction	N/A
NcraOR74A__NCU00580	*N. crassa OR74A*	NcraOR74A__Chr_10.1: 7,939,790 - 7,941,286 (-)	RoryRA99880__RO3G_00519	10	acyl-CoA thioesterase activity	acyl-CoA metabolic process	N/A
NcraOR74A__NCU10763	*N. crassa OR74A*	NcraOR74A__Chr_10.3: 2,453,751 - 2,456,129 (-)	RoryRA99880__RO3G_06261	10	electron carrier activity, heme binding, iron ion binding	aerobic respiration	integral to membrane
NcraOR74A__NCU05168	*N. crassa OR74A*	NcraOR74A__Chr_10.4: 5,895,542 - 5,897,985 (+)	RoryRA99880__RO3G_05773, RoryRA99880__RO3G_15083, RoryRA99880__RO3G_15800	10	amino acid transmembrane transporter activity	amino acid transport, transport	membrane
NcraOR74A__NCU05830	*N. crassa OR74A*	NcraOR74A__Chr_10.7: 283,300 - 285,633 (-)	RoryRA99880__RO3G_05773, RoryRA99880__RO3G_15083, RoryRA99880__RO3G_15800	10	N/A	amino acid transport, transport	integral to membrane, membrane
NcraOR74A__NCU10262	*N. crassa OR74A*	NcraOR74A__Chr_10.1: 9,209,219 - 9,211,595 (-)	RoryRA99880__RO3G_05773, RoryRA99880__RO3G_15083, RoryRA99880__RO3G_15800	10	N/A	amino acid transport, transport	integral to membrane, membrane
NcraOR74A__NCU05121	*N. crassa OR74A*	NcraOR74A__Chr_10.6: 3,681,667 - 3,682,601 (-)	RoryRA99880__RO3G_00383, RoryRA99880__RO3G_03324, RoryRA99880__RO3G_04939, RoryRA99880__RO3G_08461, ...	10	cellulase activity, cellulose binding	carbohydrate metabolic process	extracellular region
NcraOR74A__NCU09508	*N. crassa OR74A*	NcraOR74A__Chr_10.3: 80,729 - 81,529 (+)	RoryRA99880__RO3G_01608, RoryRA99880__RO3G_12908, RoryRA99880__RO3G_16202	10	catalytic activity	carbohydrate metabolic process	N/A
NcraOR74A__NCU09582	*N. crassa OR74A*	NcraOR74A__Chr_10.7: 3,322,117 - 3,323,079 (-)	RoryRA99880__RO3G_01608, RoryRA99880__RO3G_12908, RoryRA99880__RO3G_16202	10	catalytic activity	carbohydrate metabolic process	N/A

Re-Select the Rhizopus gene set, can sort by expression level



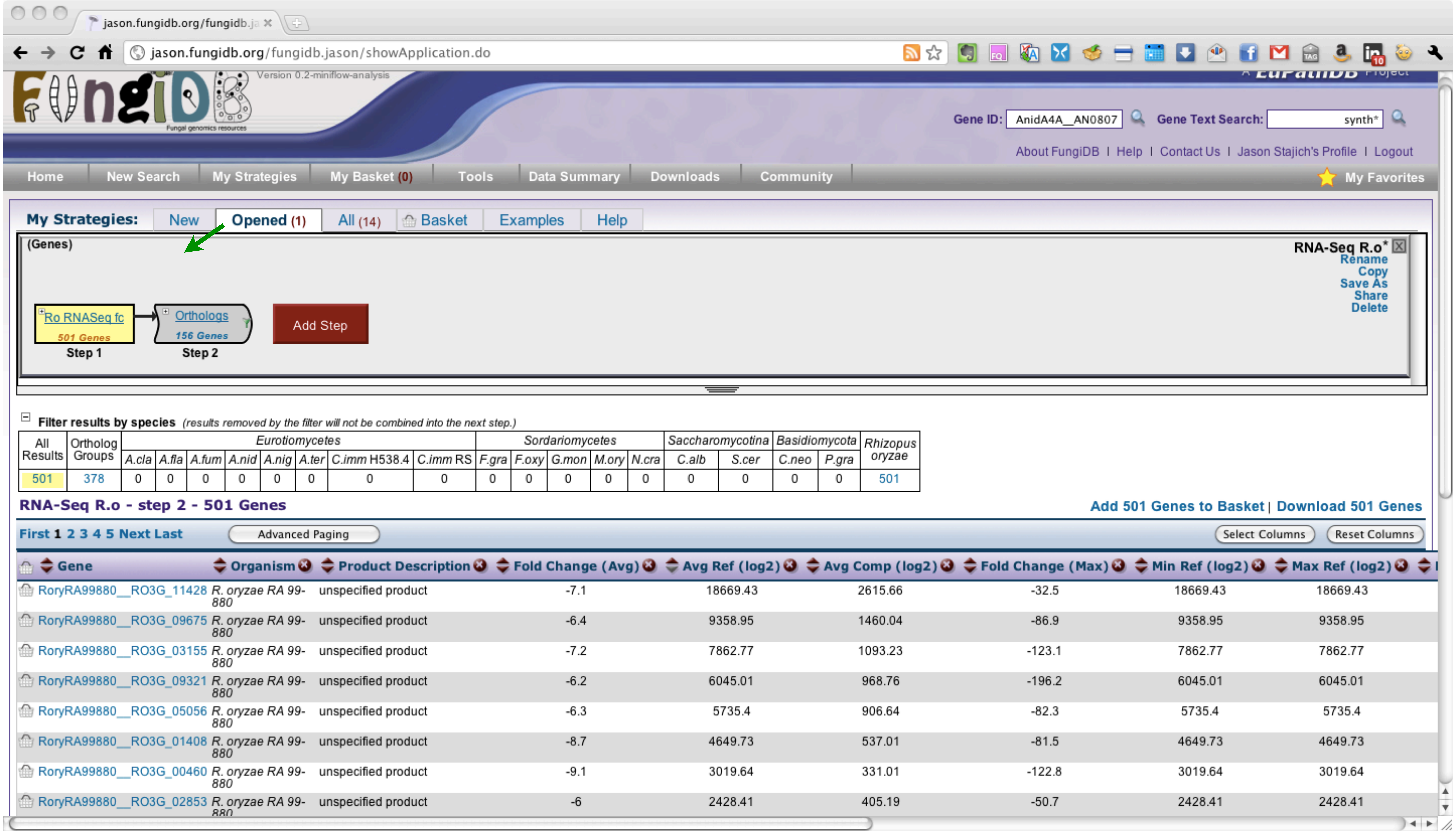
Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
501	378	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	501

RNA-Seq R.o - step 2 - 501 Genes

Gene	Organism	Product Description	Fold Change (Avg)	Avg Ref (log2)	Avg Comp (log2)	Fold Change (Max)	Min Ref (log2)	Max Ref (log2)
RoryRA99880__RO3G_11428	*R. oryzae RA 99-880*	unspecified product	-7.1	18669.43	2615.66	-32.5	18669.43	18669.43
RoryRA99880__RO3G_09675	*R. oryzae RA 99-880*	unspecified product	-6.4	9358.95	1460.04	-86.9	9358.95	9358.95
RoryRA99880__RO3G_03155	*R. oryzae RA 99-880*	unspecified product	-7.2	7862.77	1093.23	-123.1	7862.77	7862.77
RoryRA99880__RO3G_09321	*R. oryzae RA 99-880*	unspecified product	-6.2	6045.01	968.76	-196.2	6045.01	6045.01
RoryRA99880__RO3G_05056	*R. oryzae RA 99-880*	unspecified product	-6.3	5735.4	906.64	-82.3	5735.4	5735.4
RoryRA99880__RO3G_01408	*R. oryzae RA 99-880*	unspecified product	-8.7	4649.73	537.01	-81.5	4649.73	4649.73
RoryRA99880__RO3G_00460	*R. oryzae RA 99-880*	unspecified product	-9.1	3019.64	331.01	-122.8	3019.64	3019.64
RoryRA99880__RO3G_02853	*R. oryzae RA 99-880*	unspecified product	-6	2428.41	405.19	-50.7	2428.41	2428.41

Re-Select the Rhizopus gene set, can sort by expression level



Gene ID: AnidA4A__AN0807

Gene Text Search: synth*

(Genes)

RNA-Seq R.o*

Ro RNASeq fc — 501 Genes — Step 1

Orthologs — 156 Genes — Step 2

Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm H538.4*	*C.imm RS*	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
501	378	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	501

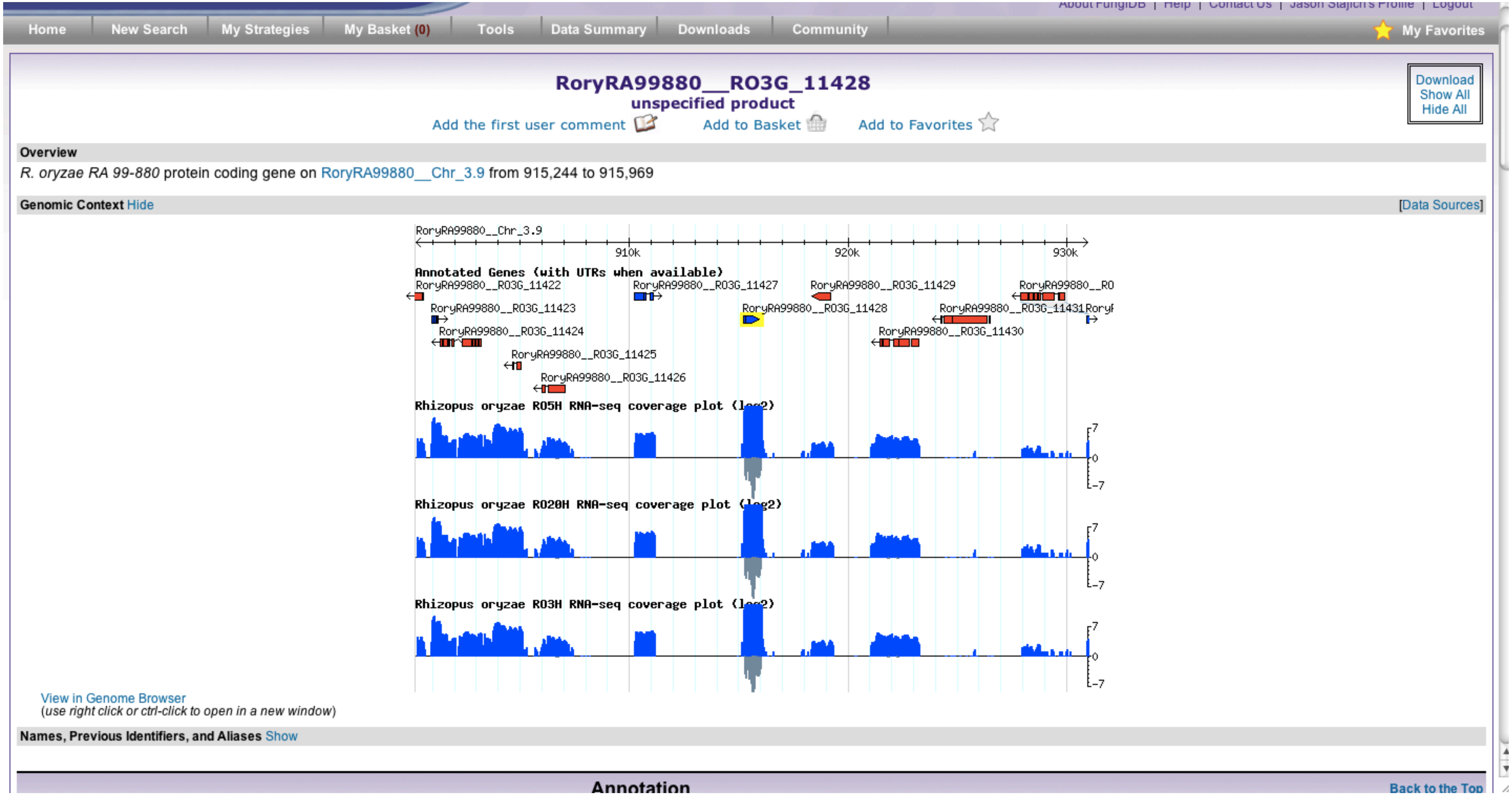
RNA-Seq R.o - step 2 - 501 Genes

Add 501 Genes to Basket | Download 501 Genes

First 1 2 3 4 5 Next Last

Gene	Organism	Product Description	Fold Change (Avg)	Avg Ref (log2)	Avg Comp (log2)	Fold Change (Max)	Min Ref (log2)	Max Ref (log2)
RoryRA99880__RO3G_11428	*R. oryzae RA 99-880*	unspecified product	-7.1	18669.43	2615.66	-32.5	18669.43	18669.43
RoryRA99880__RO3G_09675	*R. oryzae RA 99-880*	unspecified product	-6.4	9358.95	1460.04	-86.9	9358.95	9358.95
RoryRA99880__RO3G_03155	*R. oryzae RA 99-880*	unspecified product	-7.2	7862.77	1093.23	-123.1	7862.77	7862.77
RoryRA99880__RO3G_09321	*R. oryzae RA 99-880*	unspecified product	-6.2	6045.01	968.76	-196.2	6045.01	6045.01
RoryRA99880__RO3G_05056	*R. oryzae RA 99-880*	unspecified product	-6.3	5735.4	906.64	-82.3	5735.4	5735.4
RoryRA99880__RO3G_01408	*R. oryzae RA 99-880*	unspecified product	-8.7	4649.73	537.01	-81.5	4649.73	4649.73
RoryRA99880__RO3G_00460	*R. oryzae RA 99-880*	unspecified product	-9.1	3019.64	331.01	-122.8	3019.64	3019.64
RoryRA99880__RO3G_02853	*R. oryzae RA 99-880*	unspecified product	-6	2428.41	405.19	-50.7	2428.41	2428.41

Look an individual genes, here is one of the most highly expressed



RoryRA99880__RO3G_11428

unspecified product

Overview

R. oryzae RA 99-880 protein coding gene on RoryRA99880__Chr_3.9 from 915,244 to 915,969

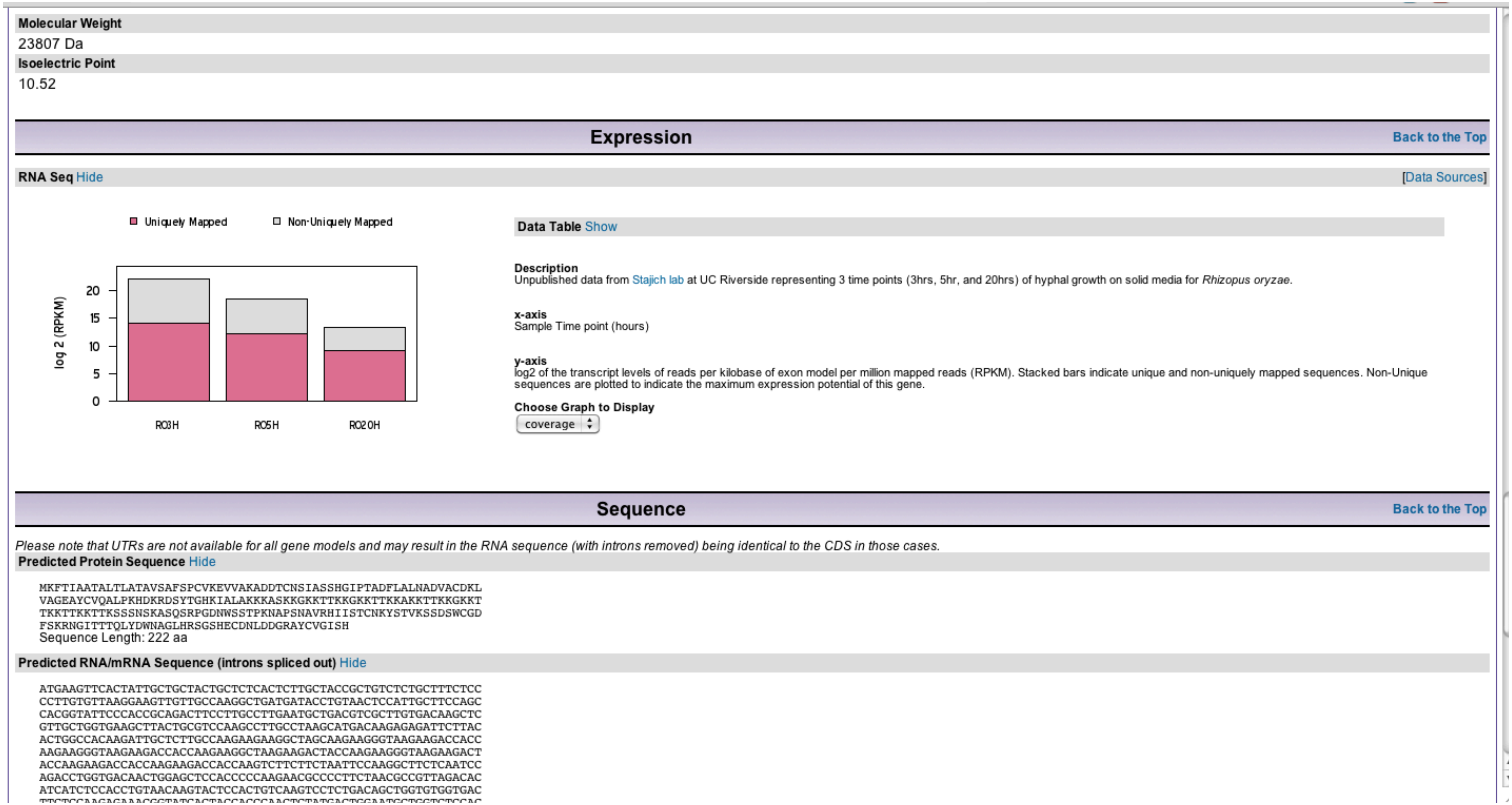
Genomic Context Hide [Data Sources]

Names, Previous Identifiers, and Aliases Show

Annotation

http://fungidb.org/gene/RoryRA99880__RO3G_11428

Summary of expression values



Molecular Weight

23807 Da

Isoelectric Point

10.52

Expression

RNA Seq Hide

[Data Sources]

Data Table Show

Description
Unpublished data from Stajich lab at UC Riverside representing 3 time points (3hrs, 5hr, and 20hrs) of hyphal growth on solid media for *Rhizopus oryzae*.

x-axis
Sample Time point (hours)

y-axis
log2 of the transcript levels of reads per kilobase of exon model per million mapped reads (RPKM). Stacked bars indicate unique and non-uniquely mapped sequences. Non-Unique sequences are plotted to indicate the maximum expression potential of this gene.

Choose Graph to Display
coverage

Sequence

Please note that UTRs are not available for all gene models and may result in the RNA sequence (with introns removed) being identical to the CDS in those cases.

Predicted Protein Sequence Hide

```
MKFTIAATALTLATAVSAFSPCVKEVVAKADDTCNSIASSHGIPTADFLALNADVACDKL
VAGEAYCVQALPKHDKRDSYTGHKIALAKKKASKKGKKTTKKGKKTTKKAKKTTKKGKKT
TKKTTKKTTKSSSNSKASQSRPGDNWSSTPKNAPSNAVRHIISTCNKYSTVKSSDSWCGD
FSKRNGITTTQLYDWNAGLHRSGSHECDNLDDGRAYCVGISH
```

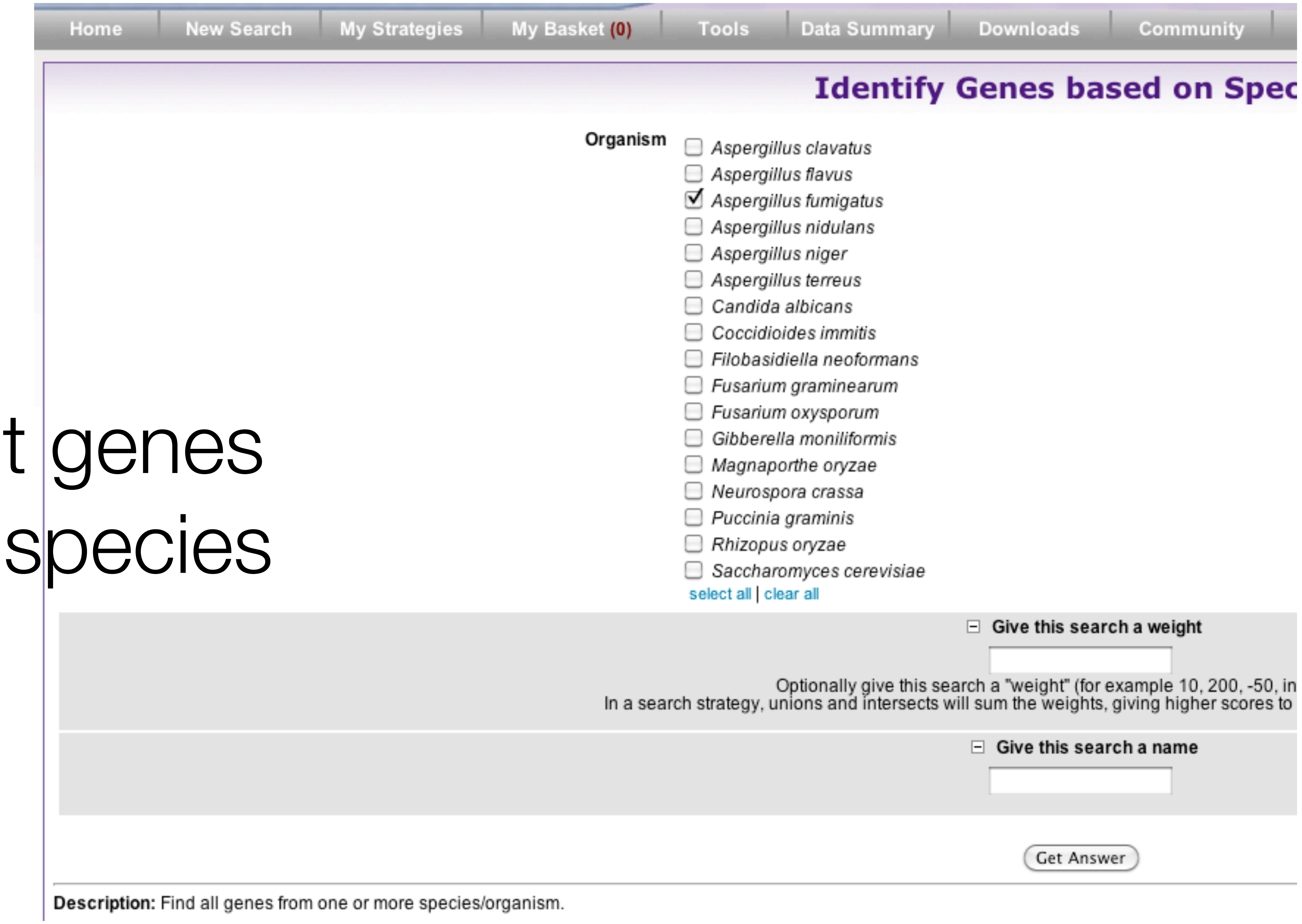
Sequence Length: 222 aa

Predicted RNA/mRNA Sequence (introns spliced out) Hide

```
ATGAAGTTCACTATTGCTGCTACTGCTCTCACTCTTGCTACCGCTGTCTCTGCTTTCTCC
CCTTGTGTTAAGGAAGTTGTTGCCAAGGCTGATGATACCTGTAACTCCATTGCTTCCAGC
CACGGTATTCCCACCGCAGACTTCCTTGCCTTGAATGCTGACGTCGCTTGTGACAAGCTC
GTTGCTGGTGAAGCTTACTGCGTCCAAGCCTTGCCTAAGCATGACAAGAGAGATTCTTAC
ACTGGCCACAAGATTGCTCTTGCCAAGAAGAAGGCTAGCAAGAAGGGTAAGAAGACCACC
AAGAAGGGTAAGAAGACCACCAAGAAGGCTAAGAAGACTACCAAGAAGGGTAAGAAGACT
ACCAAGAAGACCACCAAGAAGACCACCAAGTCTTCTTCTAATTCCAAGGCTTCTCAATCC
AGACCTGGTGACAACTGGAGCTCCACCCCCAAGAACGCCCCTTCTAACGCCGTTAGACAC
ATCATCTCCACCTGTAACAAGTACTCCACTGTCAAGTCCTCTGACAGCTGGTGTGGTGAC
```

Can also get to a strategy with the top menu bar

List genes by species



Identify Genes based on Spec

Organism

- ☐ *Aspergillus clavatus*
- ☐ *Aspergillus flavus*
- ☑ *Aspergillus fumigatus*
- ☐ *Aspergillus nidulans*
- ☐ *Aspergillus niger*
- ☐ *Aspergillus terreus*
- ☐ *Candida albicans*
- ☐ *Coccidioides immitis*
- ☐ *Filobasidiella neoformans*
- ☐ *Fusarium graminearum*
- ☐ *Fusarium oxysporum*
- ☐ *Gibberella moniliformis*
- ☐ *Magnaporthe oryzae*
- ☐ *Neurospora crassa*
- ☐ *Puccinia graminis*
- ☐ *Rhizopus oryzae*
- ☐ *Saccharomyces cerevisiae*

select all | clear all

⊟ **Give this search a weight**

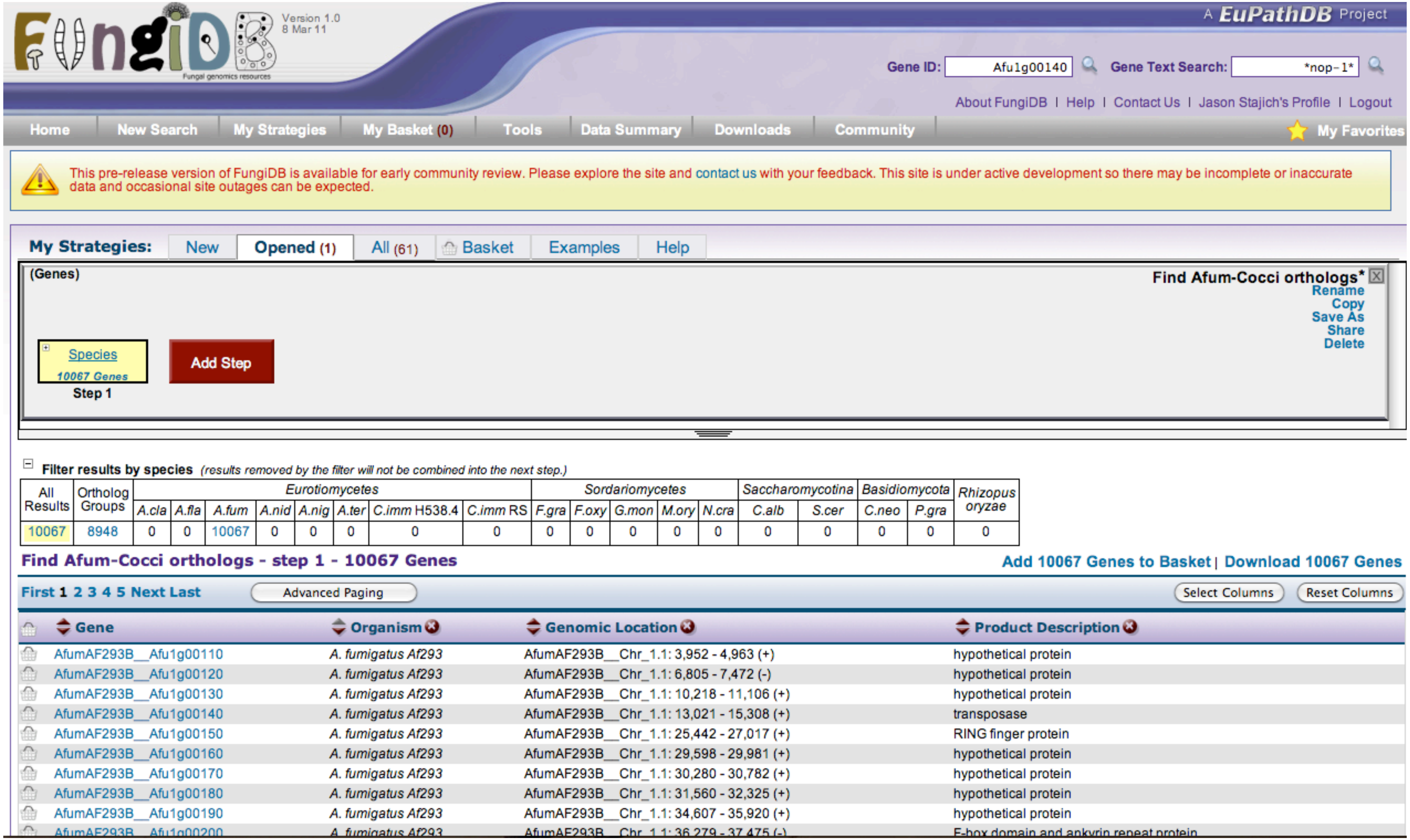
Optionally give this search a "weight" (for example 10, 200, -50, in
In a search strategy, unions and intersects will sum the weights, giving higher scores to

⊟ **Give this search a name**

Get Answer

Description: Find all genes from one or more species/organism.

10,067 *A.fumigatus* genes



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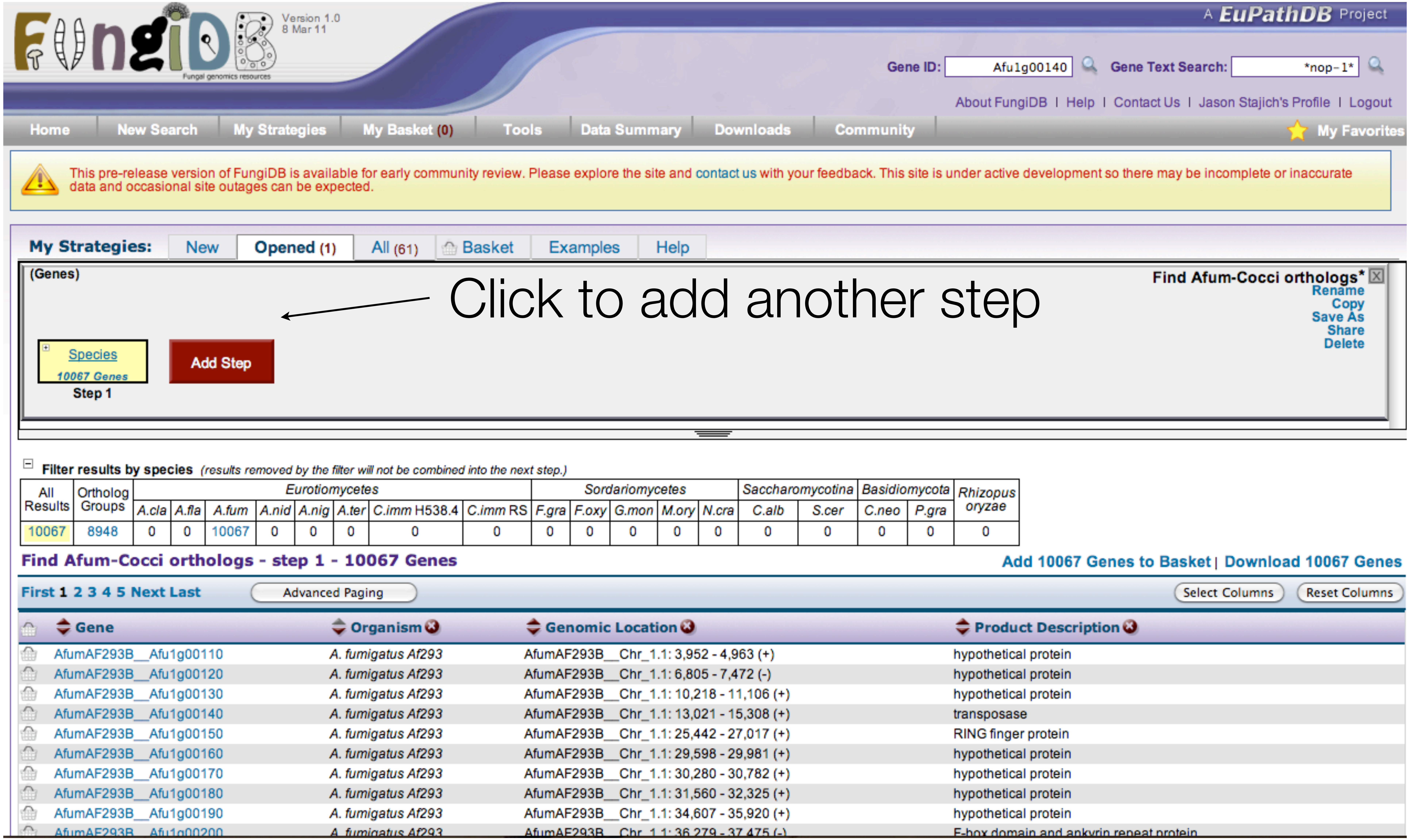
Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
10067	8948	0	0	10067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Find Afum-Cocci orthologs - step 1 - 10067 Genes

Gene	Organism	Genomic Location	Product Description
AfumAF293B__Afu1g00110	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 3,952 - 4,963 (+)	hypothetical protein
AfumAF293B__Afu1g00120	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 6,805 - 7,472 (-)	hypothetical protein
AfumAF293B__Afu1g00130	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 10,218 - 11,106 (+)	hypothetical protein
AfumAF293B__Afu1g00140	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 13,021 - 15,308 (+)	transposase
AfumAF293B__Afu1g00150	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 25,442 - 27,017 (+)	RING finger protein
AfumAF293B__Afu1g00160	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 29,598 - 29,981 (+)	hypothetical protein
AfumAF293B__Afu1g00170	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 30,280 - 30,782 (+)	hypothetical protein
AfumAF293B__Afu1g00180	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 31,560 - 32,325 (+)	hypothetical protein
AfumAF293B__Afu1g00190	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 34,607 - 35,920 (+)	hypothetical protein
AfumAF293B__Afu1g00200	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 36,279 - 37,475 (-)	F-box domain and ankyrin repeat protein

10,067 *A.fumigatus* genes



Gene ID: Afu1g00140

Gene Text Search: *nop-1*

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Click to add another step

Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm H538.4*	*C.imm RS*	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
10067	8948	0	0	10067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Find Afum-Cocci orthologs - step 1 - 10067 Genes

Add 10067 Genes to Basket | Download 10067 Genes

Gene	Organism	Genomic Location	Product Description
AfumAF293B__Afu1g00110	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 3,952 - 4,963 (+)	hypothetical protein
AfumAF293B__Afu1g00120	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 6,805 - 7,472 (-)	hypothetical protein
AfumAF293B__Afu1g00130	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 10,218 - 11,106 (+)	hypothetical protein
AfumAF293B__Afu1g00140	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 13,021 - 15,308 (+)	transposase
AfumAF293B__Afu1g00150	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 25,442 - 27,017 (+)	RING finger protein
AfumAF293B__Afu1g00160	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 29,598 - 29,981 (+)	hypothetical protein
AfumAF293B__Afu1g00170	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 30,280 - 30,782 (+)	hypothetical protein
AfumAF293B__Afu1g00180	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 31,560 - 32,325 (+)	hypothetical protein
AfumAF293B__Afu1g00190	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 34,607 - 35,920 (+)	hypothetical protein
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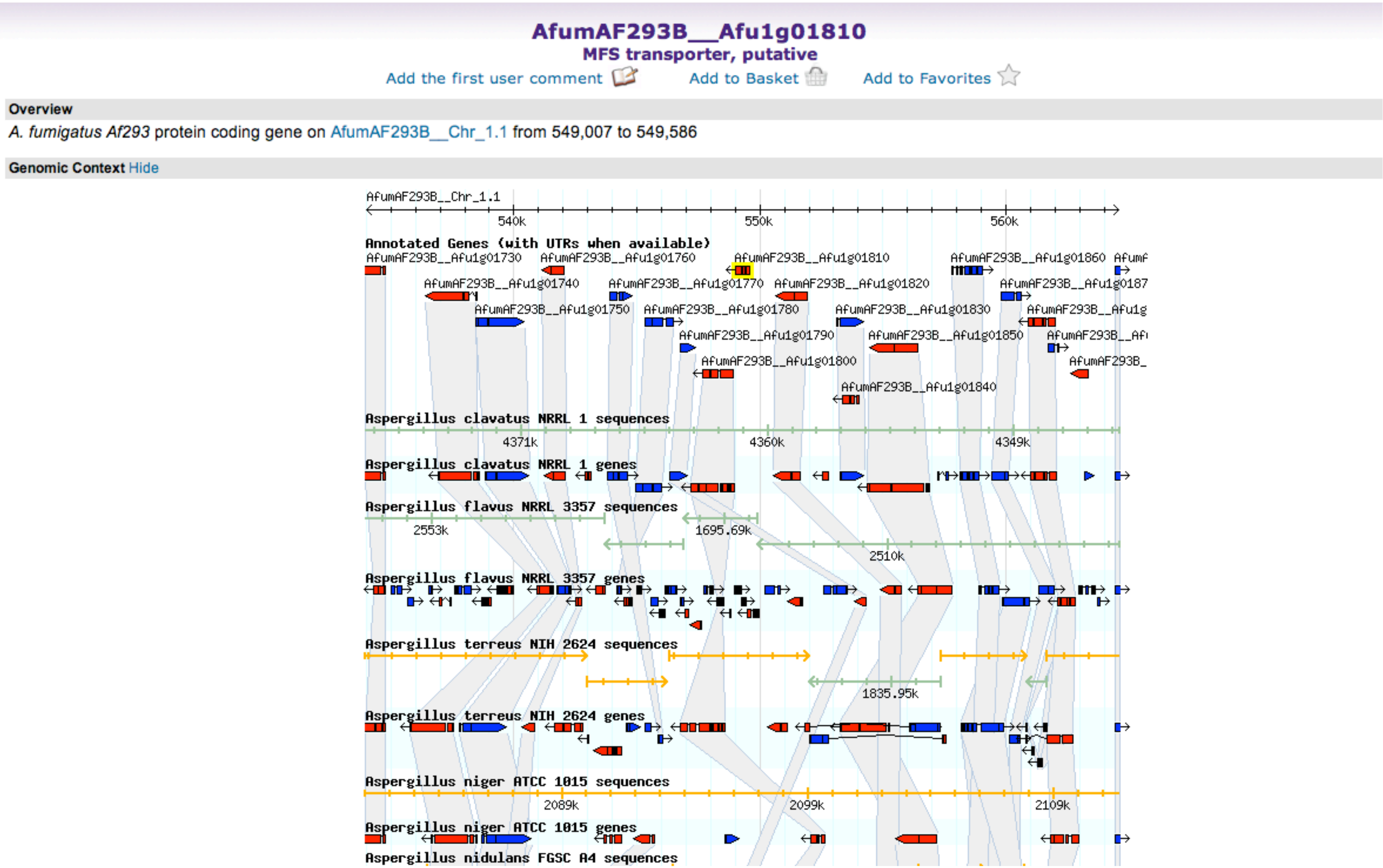


AfumAF293B__Afu1g01810

MFS transporter, putative

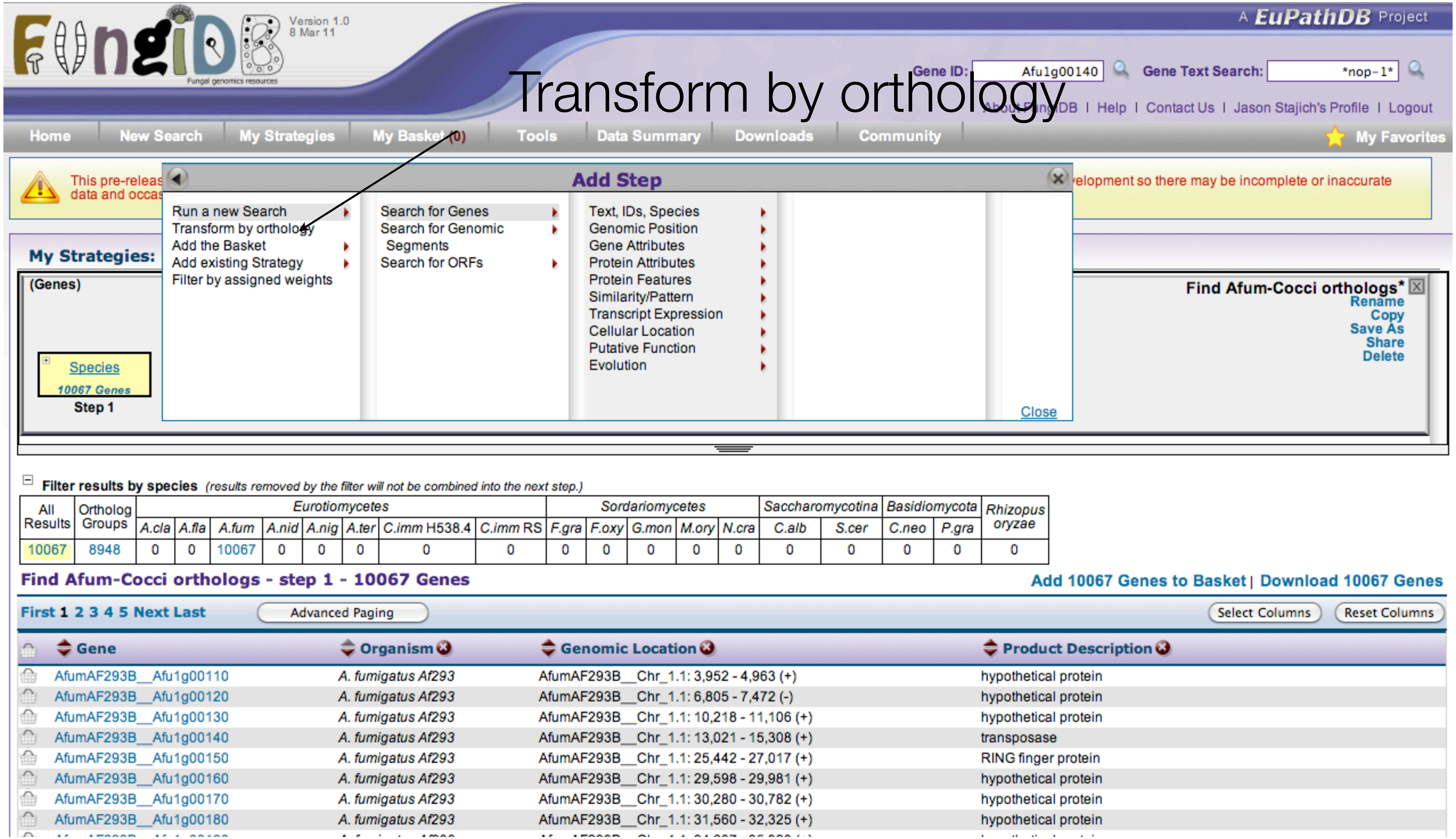
Add the first user comment Add to Basket Add to Favorites

Overview

A. fumigatus Af293 protein coding gene on AfumAF293B__Chr_1.1 from 549,007 to 549,586

Genomic Context Hide

Transform by orthology



Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm H538.4*	*C.imm RS*	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
10067	8948	0	0	10067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Find Afum-Cocci orthologs - step 1 - 10067 Genes

Gene	Organism	Genomic Location	Product Description
AfumAF293B__Afu1g00110	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 3,952 - 4,963 (+)	hypothetical protein
AfumAF293B__Afu1g00120	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 6,805 - 7,472 (-)	hypothetical protein
AfumAF293B__Afu1g00130	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 10,218 - 11,106 (+)	hypothetical protein
AfumAF293B__Afu1g00140	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 13,021 - 15,308 (+)	transposase
AfumAF293B__Afu1g00150	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 25,442 - 27,017 (+)	RING finger protein
AfumAF293B__Afu1g00160	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 29,598 - 29,981 (+)	hypothetical protein
AfumAF293B__Afu1g00170	*A. fumigatus Af293*	AfumAF293B__Chr_1.1: 30,280 - 30,782 (+)	hypothetical protein
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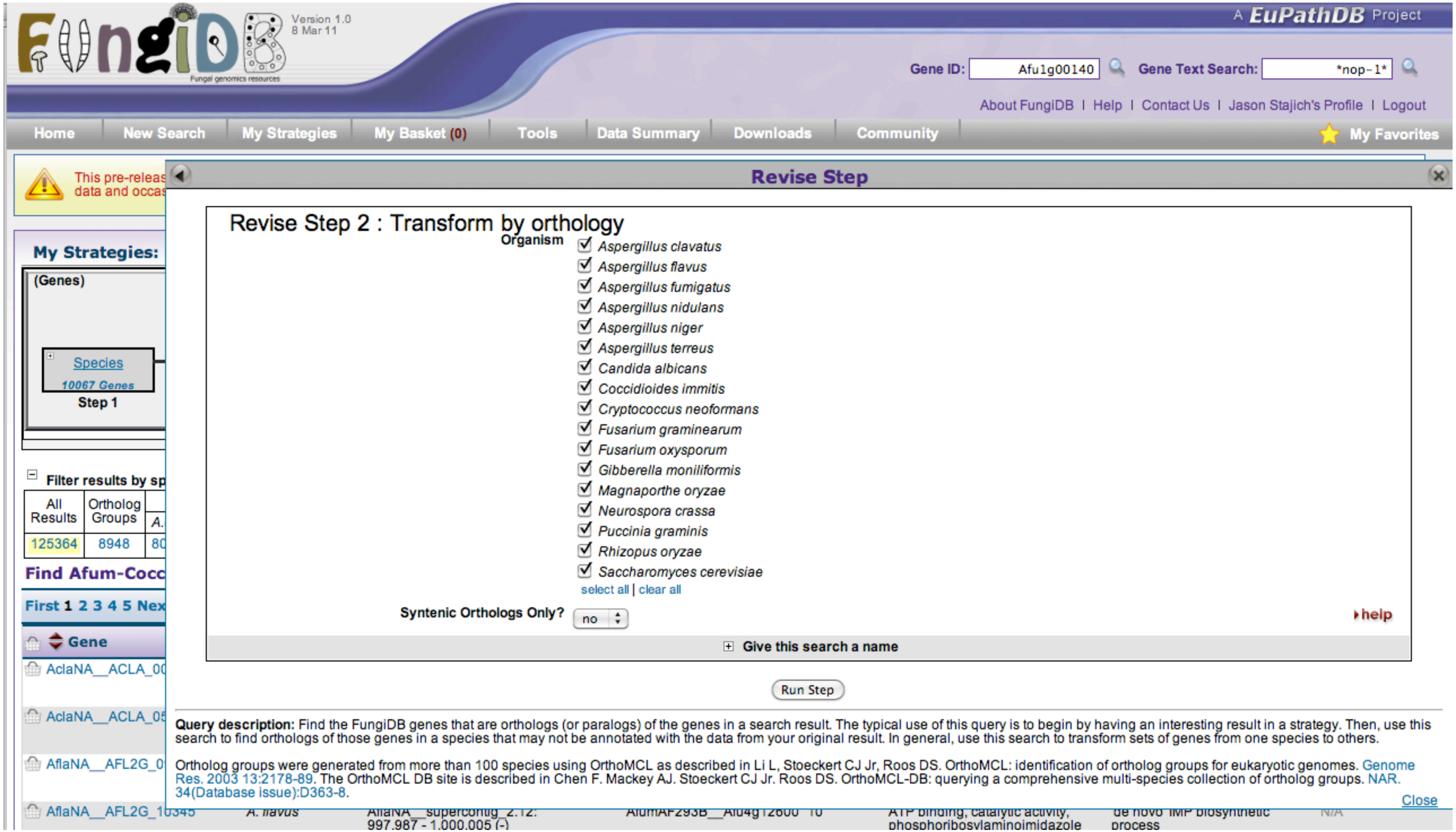


Revise Step 2 : Transform by orthology

Organism

- ☑ *Aspergillus clavatus*
- ☑ *Aspergillus flavus*
- ☑ *Aspergillus fumigatus*
- ☑ *Aspergillus nidulans*
- ☑ *Aspergillus niger*
- ☑ *Aspergillus terreus*
- ☑ *Candida albicans*
- ☑ *Coccidioides immitis*
- ☑ *Cryptococcus neoformans*
- ☑ *Fusarium graminearum*
- ☑ *Fusarium oxysporum*
- ☑ *Gibberella moniliformis*
- ☑ *Magnaporthe oryzae*
- ☑ *Neurospora crassa*
- ☑ *Puccinia graminis*
- ☑ *Rhizopus oryzae*
- ☑ *Saccharomyces cerevisiae*

select all | clear all

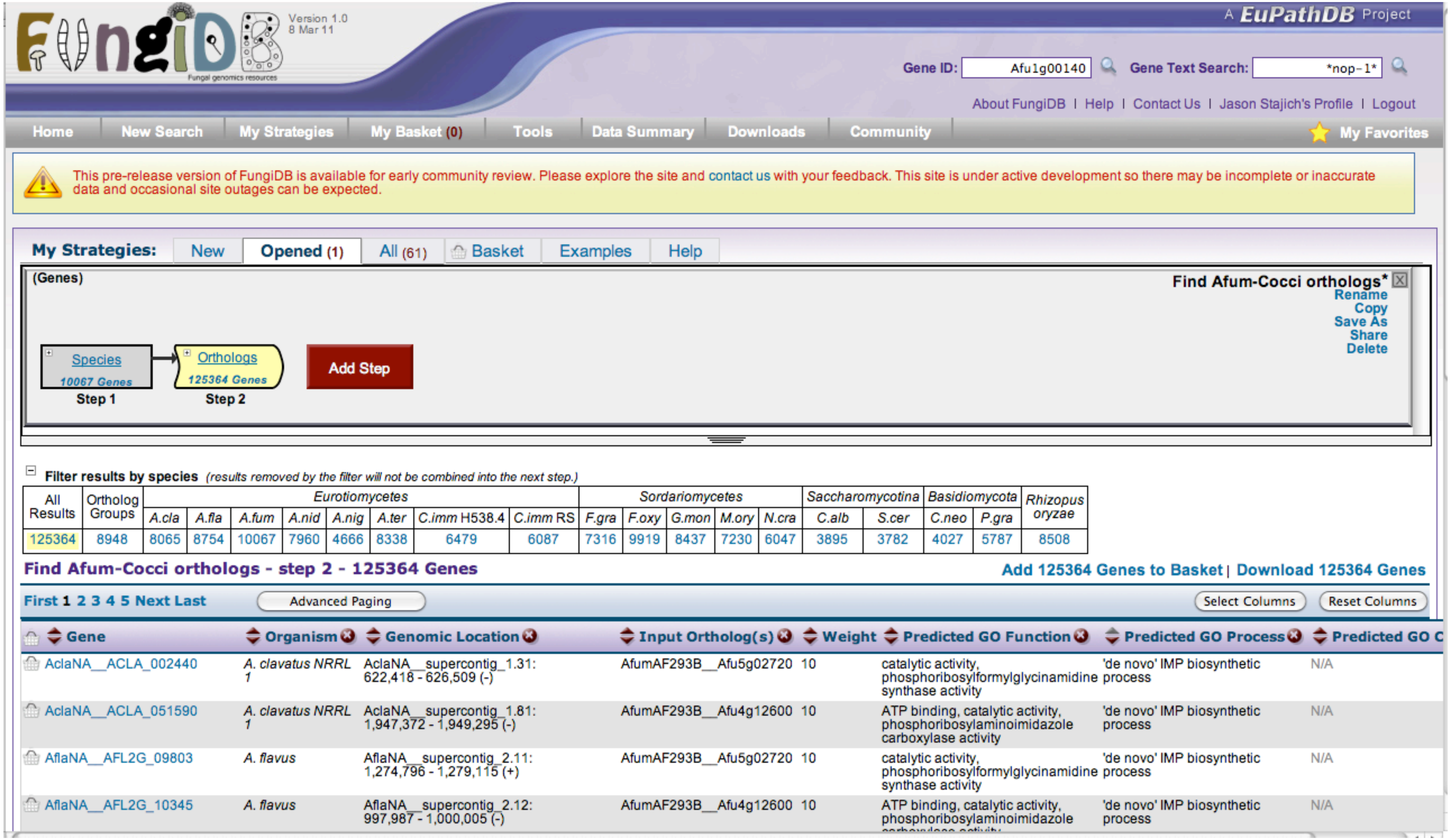
Syntenic Orthologs Only? no

Query description: Find the FungiDB genes that are orthologs (or paralogs) of the genes in a search result. The typical use of this query is to begin by having an interesting result in a strategy. Then, use this search to find orthologs of those genes in a species that may not be annotated with the data from your original result. In general, use this search to transform sets of genes from one species to others.

Ortholog groups were generated from more than 100 species using OrthoMCL as described in Li L, Stoeckert CJ Jr, Roos DS. OrthoMCL: identification of ortholog groups for eukaryotic genomes. Genome Res. 2003 13:2178-89. The OrthoMCL DB site is described in Chen F. Mackey AJ. Stoeckert CJ Jr. Roos DS. OrthoMCL-DB: querying a comprehensive multi-species collection of ortholog groups. NAR. 34(Database issue):D363-8.

All Results	Ortholog Groups
125364	8948

Gene
AclaNA__ACLA_00
AclaNA__ACLA_05
AflaNA__AFL2G_0
AflaNA__AFL2G_10345



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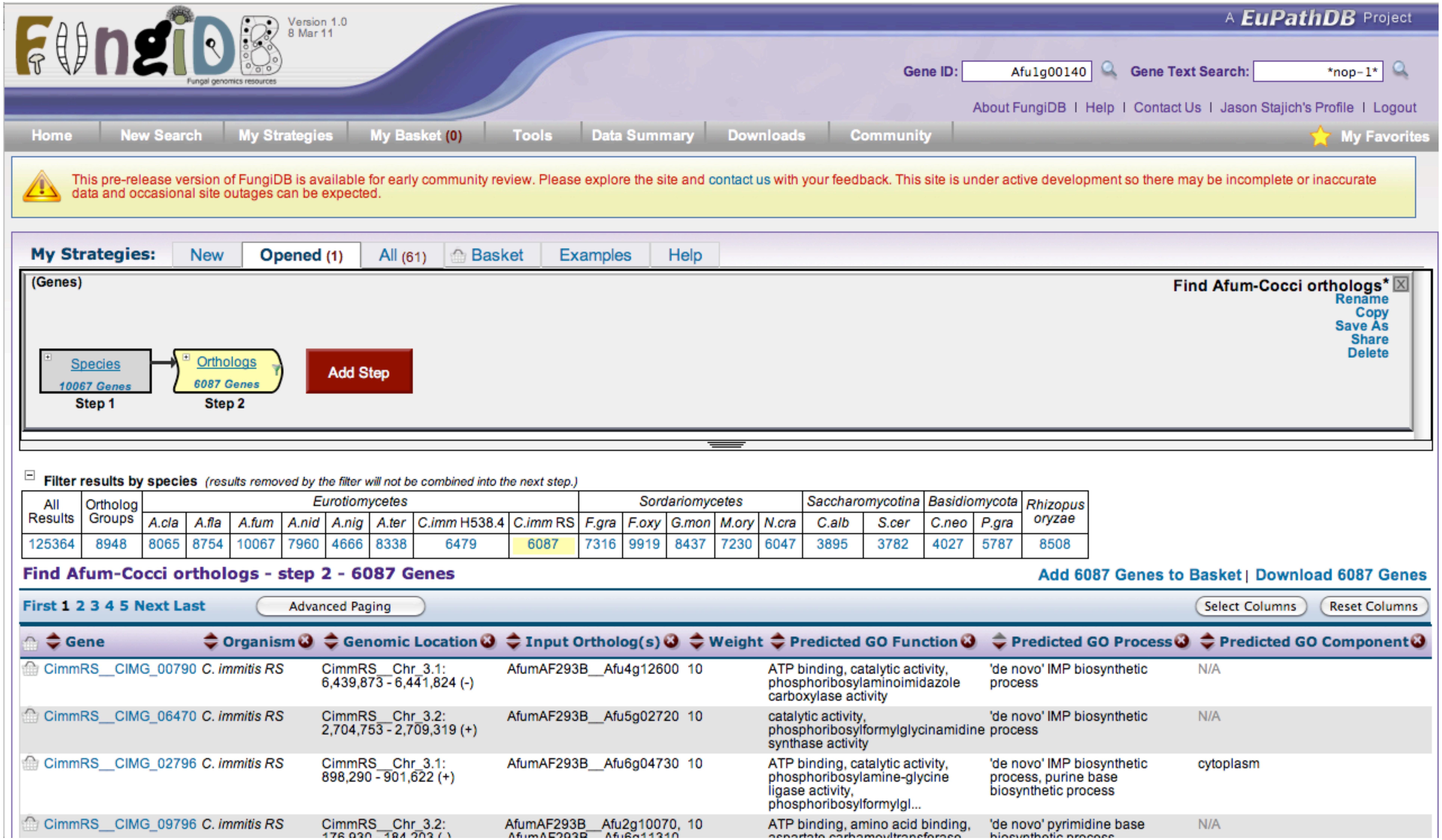
125364	8948	8065	8754	10067	7960	4666	8338	6479	6087	7316	9919	8437	7230	6047	3895	3782	4027	5787	8508

Find Afum-Cocci orthologs - step 2 - 125364 Genes

Gene	Organism	Genomic Location	Input Ortholog(s)	Weight	Predicted GO Function	Predicted GO Process	Predicted GO C
AclaNA__ACLA_002440	*A. clavatus NRRL 1*	AclaNA__supercontig_1.31: 622,418 - 626,509 (-)	AfumAF293B__Afu5g02720	10	catalytic activity, phosphoribosylformylglycinamidine synthase activity	'de novo' IMP biosynthetic process	N/A
AclaNA__ACLA_051590	*A. clavatus NRRL 1*	AclaNA__supercontig_1.81: 1,947,372 - 1,949,295 (-)	AfumAF293B__Afu4g12600	10	ATP binding, catalytic activity, phosphoribosylaminoimidazole carboxylase activity	'de novo' IMP biosynthetic process	N/A
AflaNA__AFL2G_09803	*A. flavus*	AflaNA__supercontig_2.11: 1,274,796 - 1,279,115 (+)	AfumAF293B__Afu5g02720	10	catalytic activity, phosphoribosylformylglycinamidine synthase activity	'de novo' IMP biosynthetic process	N/A
AflaNA__AFL2G_10345	*A. flavus*	AflaNA__supercontig_2.12: 997,987 - 1,000,005 (-)	AfumAF293B__Afu4g12600	10	ATP binding, catalytic activity, phosphoribosylaminoimidazole	'de novo' IMP biosynthetic process	N/A

6087 Orthologs between *A.fumigatus* & *C.immitis* Fall into 8948 Ortholog groups



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Filter results by species *(results removed by the filter will not be combined into the next step.)*

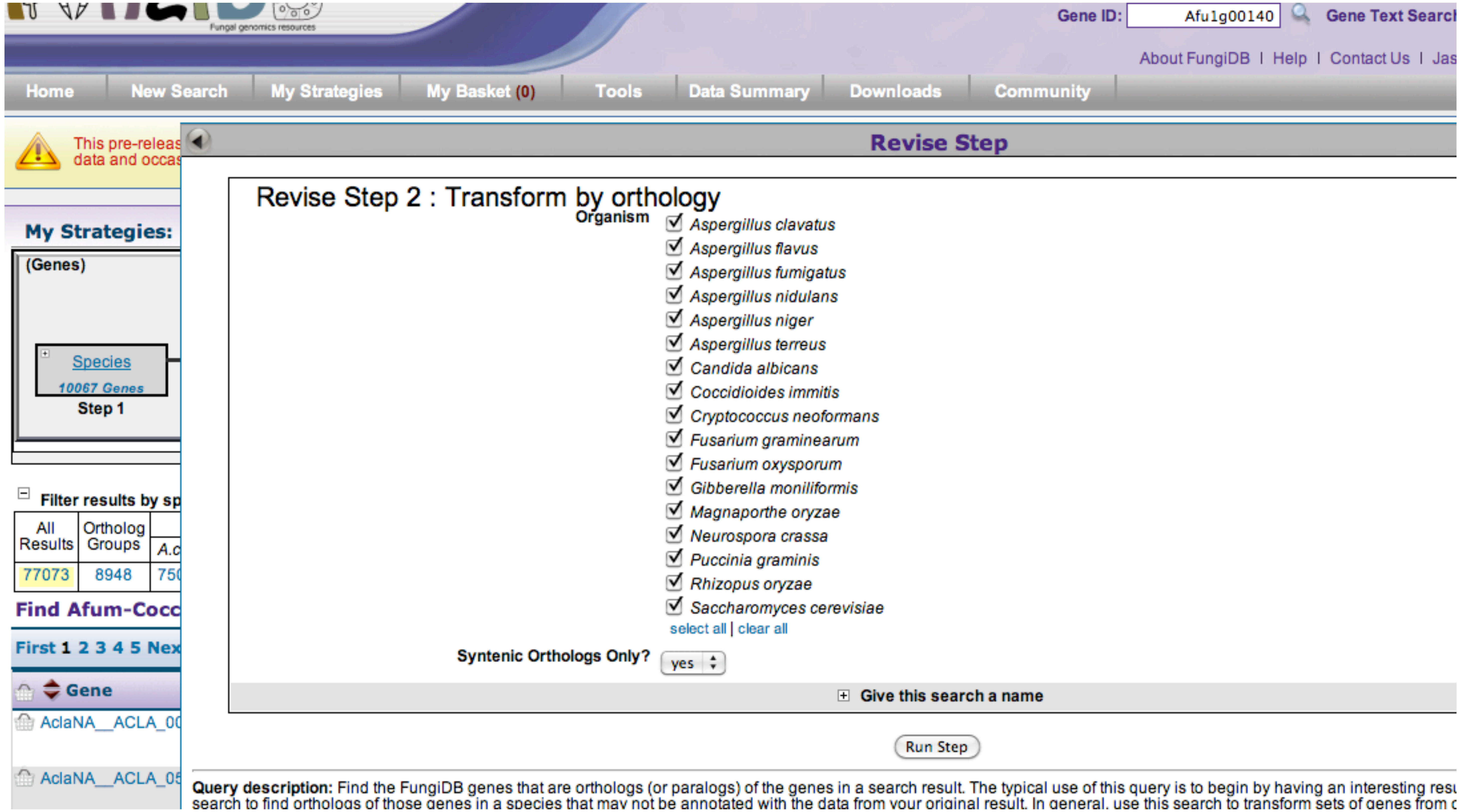
All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
125364	8948	8065	8754	10067	7960	4666	8338	6479	6087	7316	9919	8437	7230	6047	3895	3782	4027	5787	8508

Find Afum-Cocci orthologs - step 2 - 6087 Genes

Add 6087 Genes to Basket | **Download 6087 Genes**

Gene	Organism	Genomic Location	Input Ortholog(s)	Weight	Predicted GO Function	Predicted GO Process	Predicted GO Component
CimmRS__CIMG_00790	*C. immitis RS*	CimmRS__Chr_3.1: 6,439,873 - 6,441,824 (-)	AfumAF293B__Afu4g12600	10	ATP binding, catalytic activity, phosphoribosylaminoimidazole carboxylase activity	'de novo' IMP biosynthetic process	N/A
CimmRS__CIMG_06470	*C. immitis RS*	CimmRS__Chr_3.2: 2,704,753 - 2,709,319 (+)	AfumAF293B__Afu5g02720	10	catalytic activity, phosphoribosylformylglycinamidine synthase activity	'de novo' IMP biosynthetic process	N/A
CimmRS__CIMG_02796	*C. immitis RS*	CimmRS__Chr_3.1: 898,290 - 901,622 (+)	AfumAF293B__Afu6g04730	10	ATP binding, catalytic activity, phosphoribosylamine-glycine ligase activity, phosphoribosylformylgl...	'de novo' IMP biosynthetic process, purine base biosynthetic process	cytoplasm
CimmRS__CIMG_09796	*C. immitis RS*	CimmRS__Chr_3.2:	AfumAF293B__Afu2g10070,	10	ATP binding, amino acid binding,	'de novo' pyrimidine base	N/A

Find Syntenic Orthologs between *A.fumigatus* & *C.immitis*



Gene ID: Afu1g00140

This pre-releas
data and occas

Filter results by sp

All Results	Ortholog Groups	A.c
77073	8948	750

Revise Step 2 : Transform by orthology

Organism
- ☑ *Aspergillus clavatus*
- ☑ *Aspergillus flavus*
- ☑ *Aspergillus fumigatus*
- ☑ *Aspergillus nidulans*
- ☑ *Aspergillus niger*
- ☑ *Aspergillus terreus*
- ☑ *Candida albicans*
- ☑ *Coccidioides immitis*
- ☑ *Cryptococcus neoformans*
- ☑ *Fusarium graminearum*
- ☑ *Fusarium oxysporum*
- ☑ *Gibberella moniliformis*
- ☑ *Magnaporthe oryzae*
- ☑ *Neurospora crassa*
- ☑ *Puccinia graminis*
- ☑ *Rhizopus oryzae*
- ☑ *Saccharomyces cerevisiae*

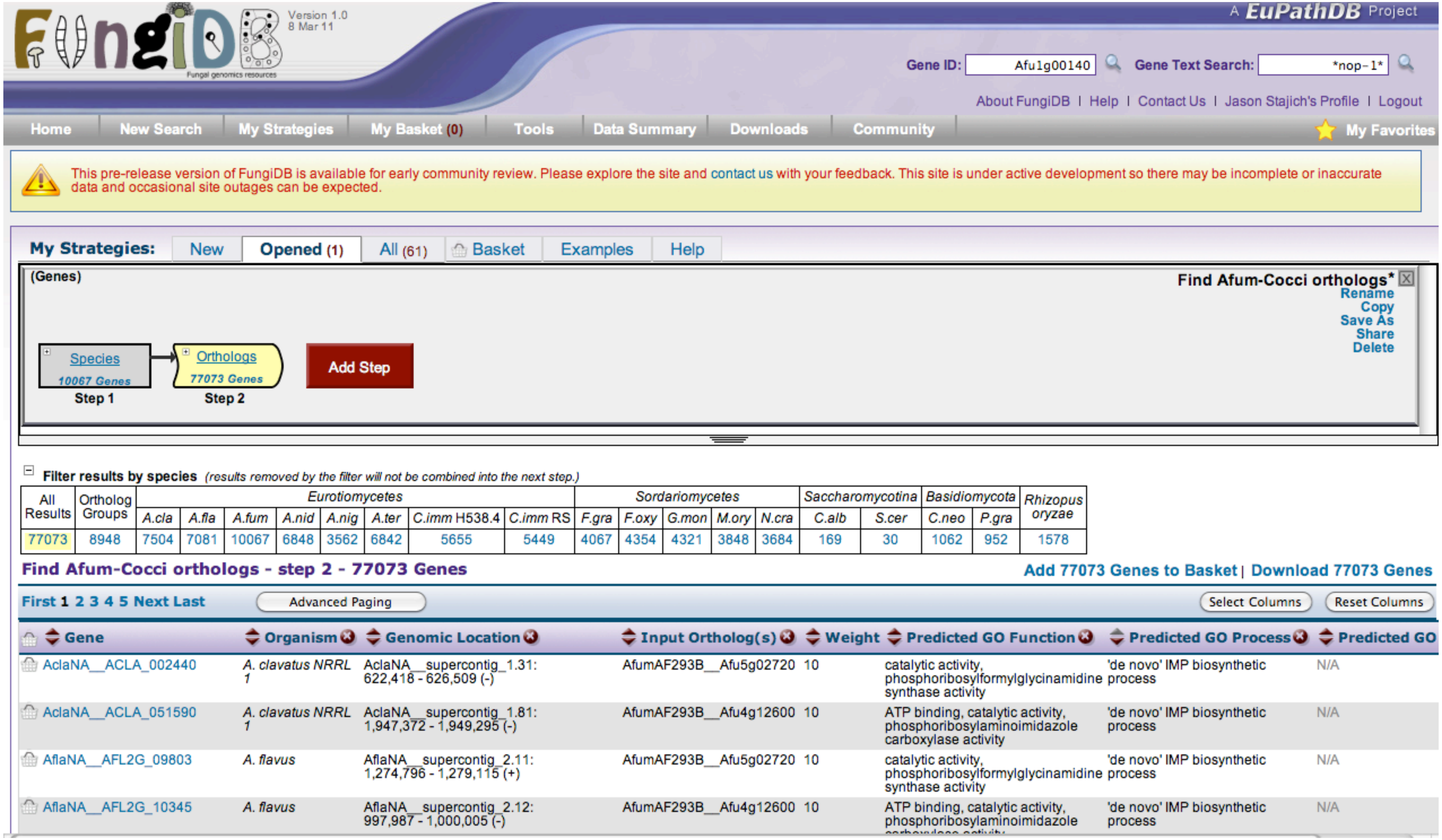
select all | clear all

Syntenic Orthologs Only? yes

⊞ Give this search a name

Query description: Find the FungiDB genes that are orthologs (or paralogs) of the genes in a search result. The typical use of this query is to begin by having an interesting resu
search to find orthologs of those genes in a species that may not be annotated with the data from your original result. In general, use this search to transform sets of genes from c

5449 Syntenic Orthologs between *A.fumigatus-C.immitis*



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Filter results by species *(results removed by the filter will not be combined into the next step.)*

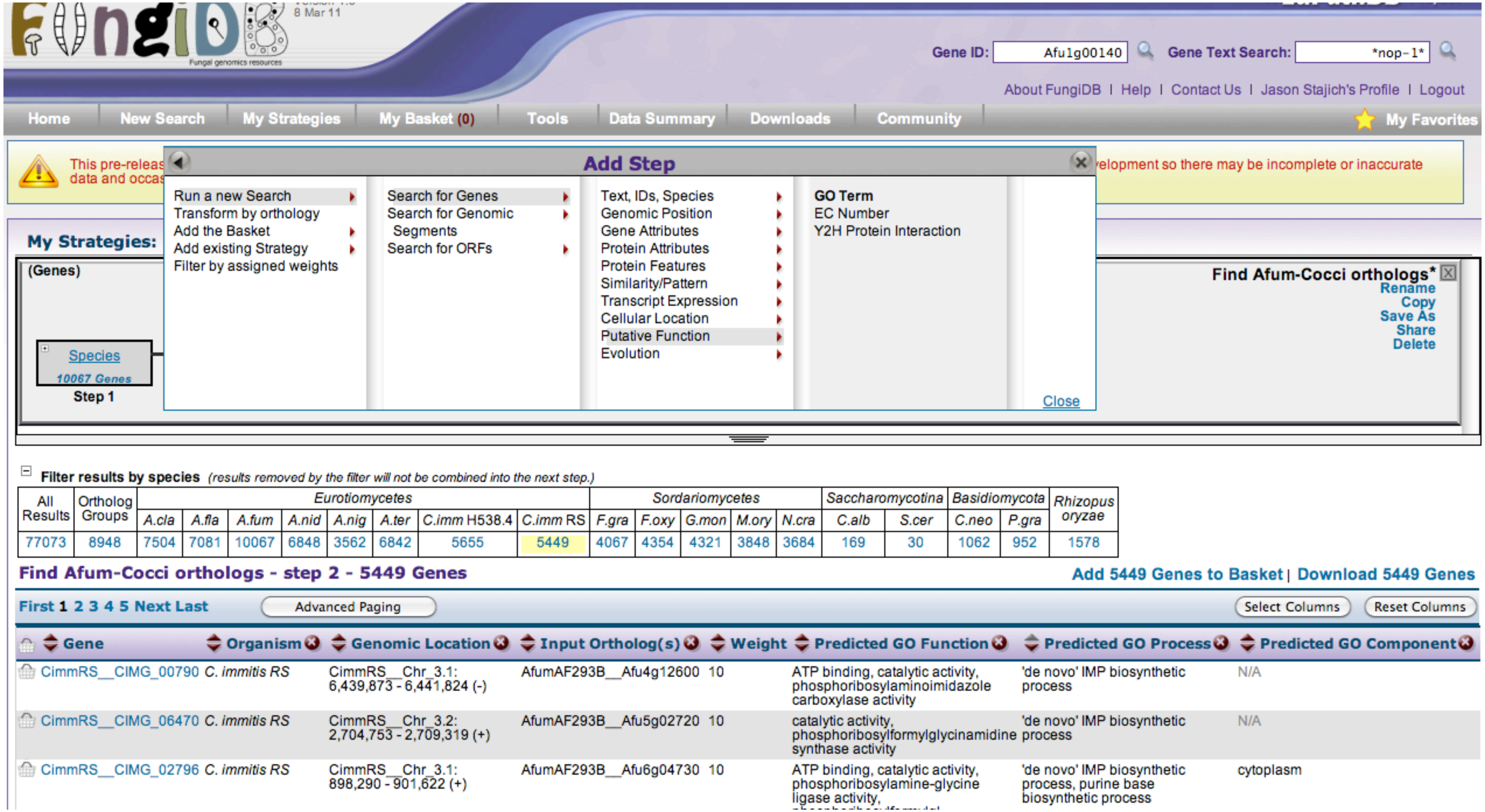
All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
77073	8948	7504	7081	10067	6848	3562	6842	5655	5449	4067	4354	4321	3848	3684	169	30	1062	952	1578

Find Afum-Cocci orthologs - step 2 - 77073 Genes

Gene	Organism	Genomic Location	Input Ortholog(s)	Weight	Predicted GO Function	Predicted GO Process	Predicted GO
AclaNA__ACLA_002440	*A. clavatus NRRL 1*	AclaNA__supercontig_1.31: 622,418 - 626,509 (-)	AfumAF293B__Afu5g02720	10	catalytic activity, phosphoribosylformylglycinamidine synthase activity	'de novo' IMP biosynthetic process	N/A
AclaNA__ACLA_051590	*A. clavatus NRRL 1*	AclaNA__supercontig_1.81: 1,947,372 - 1,949,295 (-)	AfumAF293B__Afu4g12600	10	ATP binding, catalytic activity, phosphoribosylaminoimidazole carboxylase activity	'de novo' IMP biosynthetic process	N/A
AflaNA__AFL2G_09803	*A. flavus*	AflaNA__supercontig_2.11: 1,274,796 - 1,279,115 (+)	AfumAF293B__Afu5g02720	10	catalytic activity, phosphoribosylformylglycinamidine synthase activity	'de novo' IMP biosynthetic process	N/A
AflaNA__AFL2G_10345	*A. flavus*	AflaNA__supercontig_2.12: 997,987 - 1,000,005 (-)	AfumAF293B__Afu4g12600	10	ATP binding, catalytic activity, phosphoribosylaminoimidazole	'de novo' IMP biosynthetic process	N/A

For all pairwise, syntenic orthologs

			Acla	*Afum*	*Afla*	*Anid*	*Ater*	*Anig*	*CimmRS*	*CimmH538.4*	*Fgra*	*Foxy*	*Gmon*	*Mory*	*Ncra*	*Cneo*	*Pgra*	*Rory*	*Calb*	*Scer*
Eurotiomycetes	*Aspergillus*	*clavatus*	9114	7383	6801	6655	6628	3407	5548	5764	3795	3927	3944	3730	3592	858	783	994	143	26
			+299	7504	6718	6822	6579	3386	5798	5296	4223	3826	3778	3530	4502	785	455	747	76	39
	Aspergillus	*fumigatus*		9887	7081	6848	6842	3562	5449	5655	4067	4354	4321	3848	3684	1062	952	1578	169	30
				+180	6780	6829	6592	3384	5624	5144	4159	3854	3745	3401	4354	777	483	768	117	37
	Aspergillus	*flavus*			12471	6852	7024	3744	5290	5516	3779	4153	4094	3538	3296	765	758	950	174	20
					+259	7160	6999	3790	5663	5046	4419	4047	3920	3487	4360	802	455	768	173	29
	Aspergillus	*nidulans*				10691	6957	3588	5529	5746	4103	4454	4372	3842	3671	1042	868	1721	245	106
						+174	6663	3439	5706	5176	4367	3969	3859	3520	4417	788	480	830	307	117
	Aspergillus	*terreus*					10402	3478	5175	5429	3437	3737	3729	3328	3148	353	304	916	84	21
							+162	3532	5544	4943	4218	3824	3772	3368	4279	330	185	806	28	28
	Aspergillus	*niger*						6398	2575	2690	1687	1835	1802	1538	1390	696	744	468	8	3
								+281	2766	2398	2074	1844	1773	1546	2147	823	444	359	5	3
	Coccidioides	*immitis* RS							9757	8008	3989	4085	4168	3991	3761	1113	987	1651	224	171
									+121	8622	3824	3534	3495	3303	4270	738	478	774	177	155
	Coccidioides	*immitis* H538.4								10524	2868	2894	2923	2879	2811	504	467	446	21	32
										+116	3748	3464	3436	3287	4151	701	495	634	13	14
Sordariomycetes	*Fusarium*	*graminearum*									13279	10274	10068	6095	5594	1126	947	1498	85	39
											+326	9569	9469	5645	6037	774	397	738	152	30
	Fusarium	*oxysporum*						**SYNTENIC**				17466	11070	5676	5305	797	740	976	87	7
								ORTHOLOGS				+0	11103	5746	6093	786	396	726	160	5
	Gibberella	*moniliformis*						75 -100%					14161	5589	5231	770	699	956	75	33
								50 - 75%					+296	5711	6090	802	394	684	133	7
	Magnaporthe	*oryzae*						25 - 50%						11041	5690	715	768	924	27	13
								10 - 25%						+344	6277	746	419	658	34	24
	Neurospora	*crassa*						5 - 10%							9372	1031	857	1450	81	8
								0 - 5%							+422	679	367	630	63	60
Basidiomycota	*Cryptococcus*	*neoformans*						protein coding								6967	1181	1194	4	4
								non-coding								+154	894	860	4	5
	Puccinia	*graminis*															20534	708	3	7
																	+531	1026	3	7
Rhizopus	*Rhizopus*	*oryzae*																17413	4	0
																		+239	46	0
Saccharomycotina	*Candida*	*albicans*									-->(syntenic) *S. cerevisiae* orthologs of *C. albicans* genes								6203	875
											-->(syntenic) *C. albicans* orthologs of S. cerevisiae genes								+241	689
	Saccharomyces	*cerevisiae*																		6607
																				+319



Gene ID: Afu1g00140

Gene Text Search: *nop-1*

Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
77073	8948	7504	7081	10067	6848	3562	6842	5655	5449	4067	4354	4321	3848	3684	169	30	1062	952	1578

Find Afum-Cocci orthologs - step 2 - 5449 Genes

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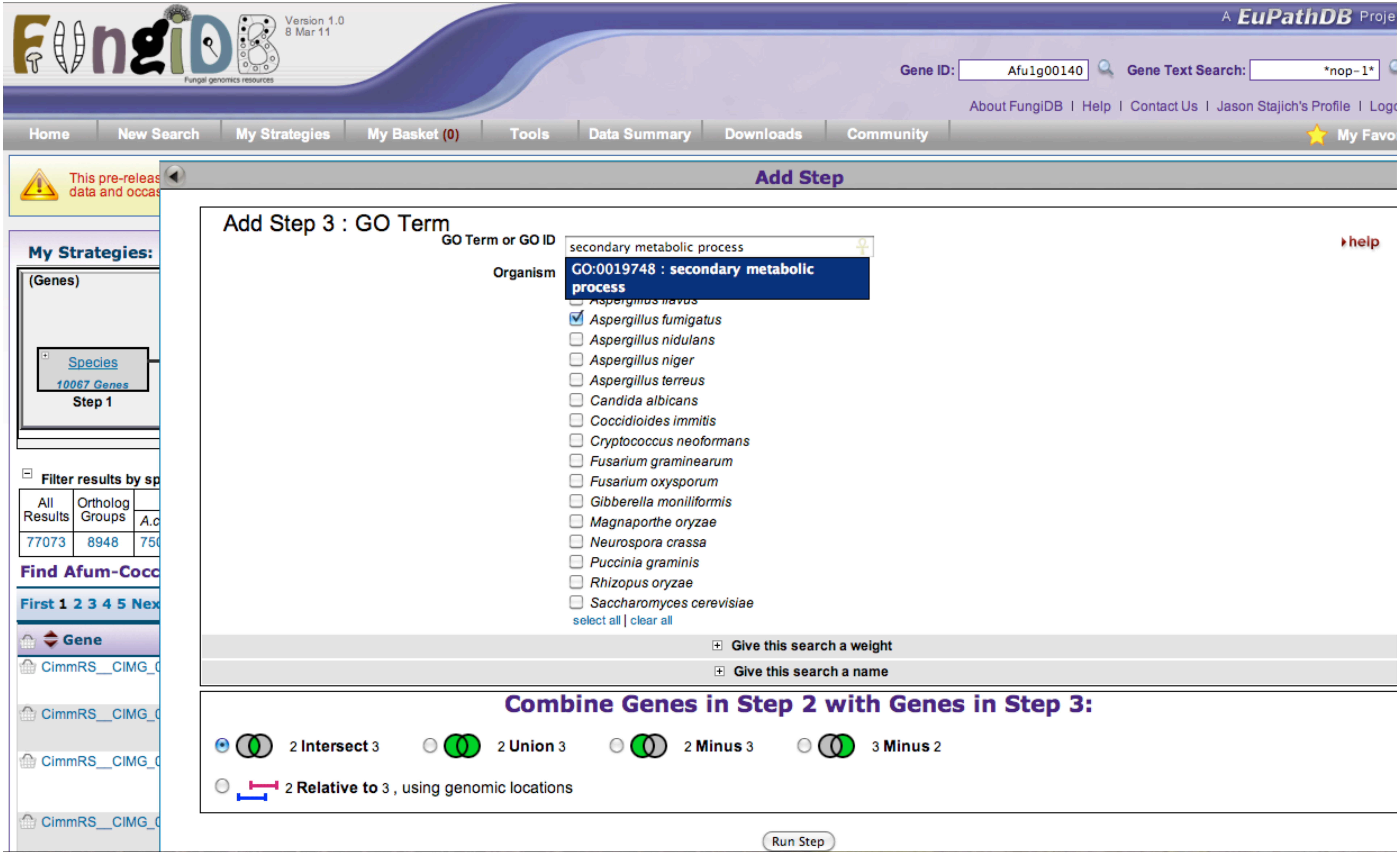
First 1 2 3 4 5 Next Last

Gene	Organism	Genomic Location	Input Ortholog(s)	Weight	Predicted GO Function	Predicted GO Process	Predicted GO Component
CimmRS__CIMG_00790	*C. immitis RS*	CimmRS__Chr_3.1: 6,439,873 - 6,441,824 (-)	AfumAF293B__Afu4g12600	10	ATP binding, catalytic activity, phosphoribosylaminoimidazole carboxylase activity	'de novo' IMP biosynthetic process	N/A
CimmRS__CIMG_06470	*C. immitis RS*	CimmRS__Chr_3.2: 2,704,753 - 2,709,319 (+)	AfumAF293B__Afu5g02720	10	catalytic activity, phosphoribosylformylglycinamidine synthase activity	'de novo' IMP biosynthetic process	N/A
CimmRS__CIMG_02796	*C. immitis RS*	CimmRS__Chr_3.1: 898,290 - 901,622 (+)	AfumAF293B__Afu6g04730	10	ATP binding, catalytic activity, phosphoribosylamine-glycine ligase activity,	'de novo' IMP biosynthetic process, purine base biosynthetic process	cytoplasm



All Results	Ortholog Groups	A.c
77073	8948	75(

Add Step 3 : GO Term

GO Term or GO ID: secondary metabolic process

GO:0019748 : secondary metabolic process

Organism

- ☐ Aspergillus flavus
- ☑ *Aspergillus fumigatus*
- ☐ *Aspergillus nidulans*
- ☐ *Aspergillus niger*
- ☐ *Aspergillus terreus*
- ☐ *Candida albicans*
- ☐ *Coccidioides immitis*
- ☐ *Cryptococcus neoformans*
- ☐ *Fusarium graminearum*
- ☐ *Fusarium oxysporum*
- ☐ *Gibberella moniliformis*
- ☐ *Magnaporthe oryzae*
- ☐ *Neurospora crassa*
- ☐ *Puccinia graminis*
- ☐ *Rhizopus oryzae*
- ☐ *Saccharomyces cerevisiae*

select all | clear all

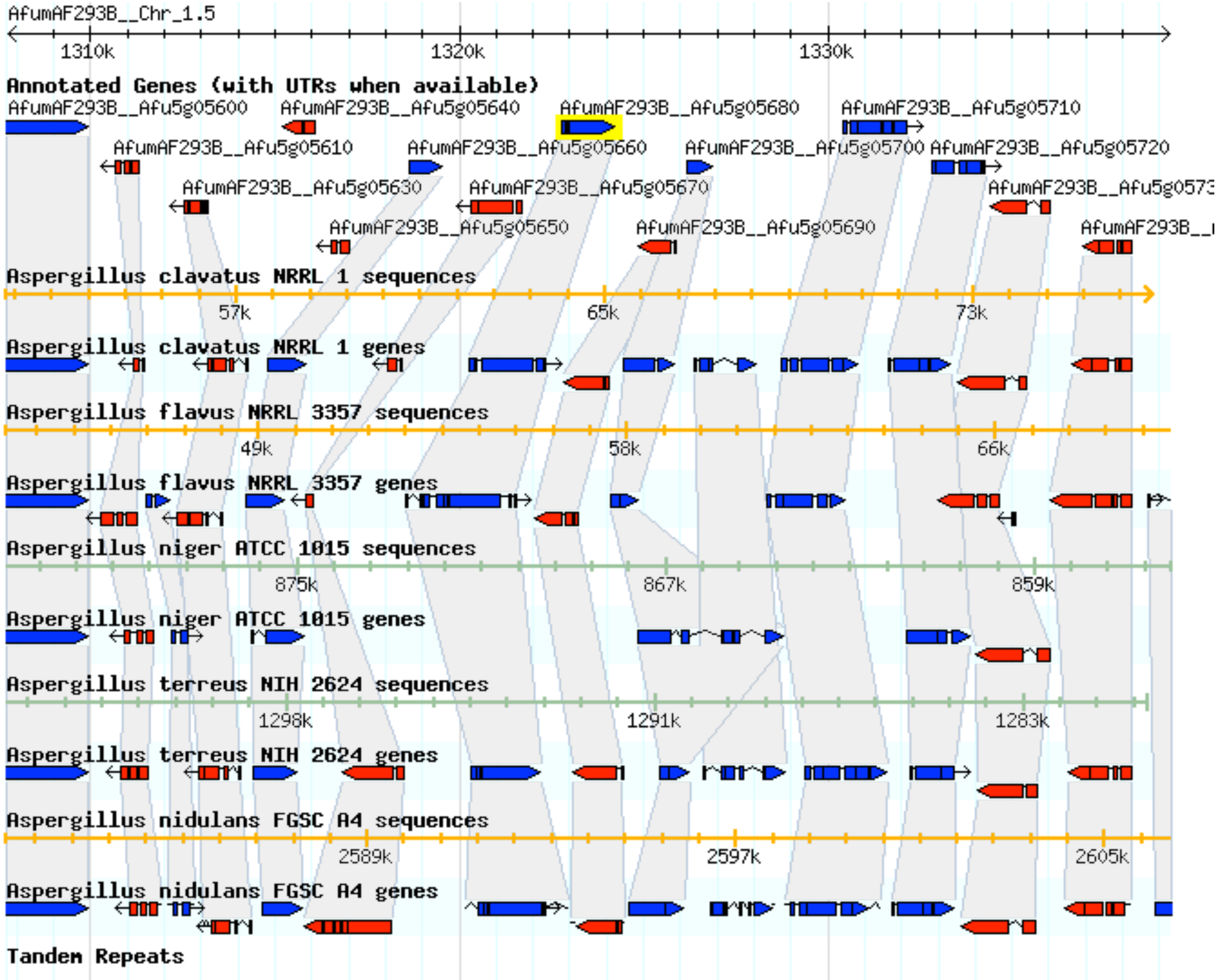
Combine Genes in Step 2 with Genes in Step 3:

● 2 **Intersect** 3 ○ 2 **Union** 3 ○ 2 **Minus** 3 ○ 3 **Minus** 2

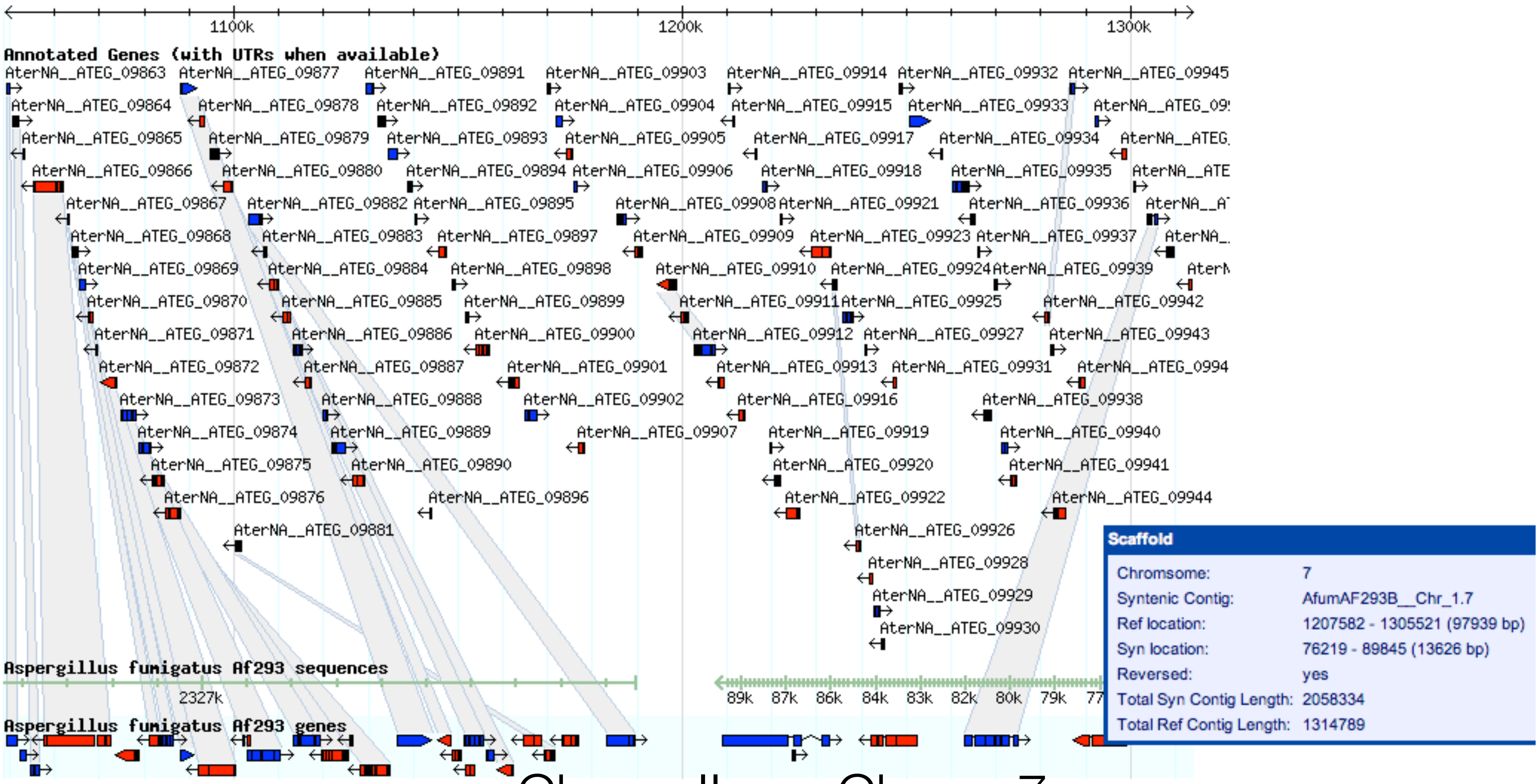
○ 2 **Relative to** 3 , using genomic locations

Visualizing Synteny in Gbrowse

Colinearity among Aspergillus genomes



Synteny decay at the Telomeres

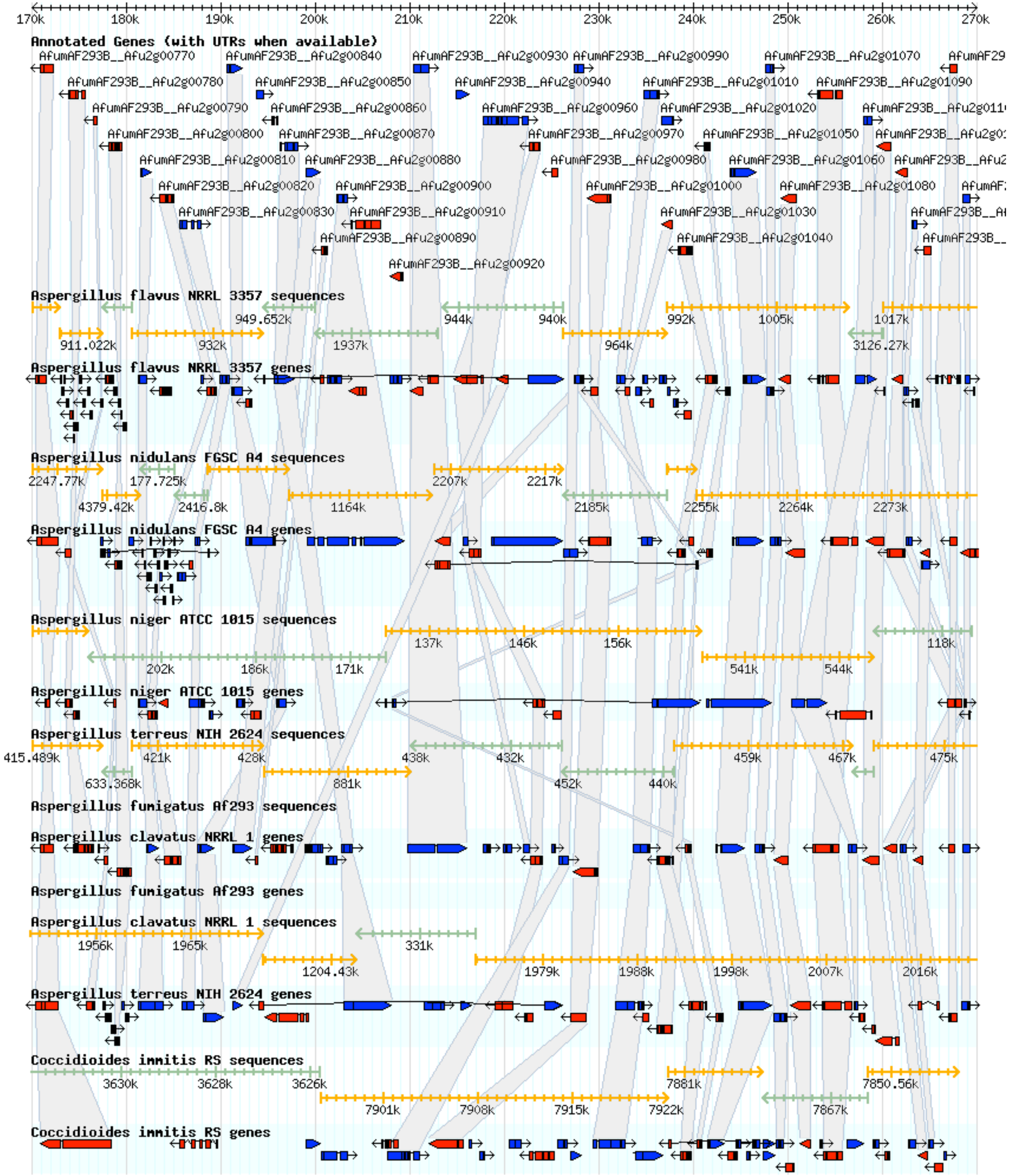


Scaffold

Chromsome: 7
Syntenic Contig: AfumAF293B__Chr_1.7
Ref location: 1207582 - 1305521 (97939 bp)
Syn location: 76219 - 89845 (13626 bp)
Reversed: yes
Total Syn Contig Length: 2058334
Total Ref Contig Length: 1314789

Chrom II Chrom 7

Synteny out to *Coccidioides*



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Brian Brunk

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