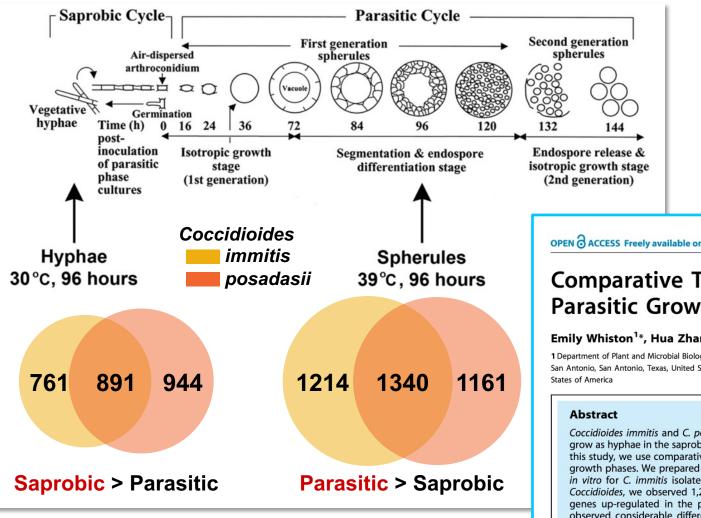
#### Coccidiomycosis (Valley Fever) **Coccidioides** Saprobic Life Cycle Parasitic Life Cycle immitis (free-living environmental form) (pulmonary inflammation, etc) Tubular posadasii structure emerges **Endospore converts** Day 5 (120h) to mycelium Spherule releases endospores Mycelia 🥯 Day 4 (96h) Arthroconidia **Endospores** form as alternate < form in the cells along the Conidia may Endospore spherule mycelia germinate continues and become cycle mycelia Arthroconidia Day 3 (72h) 3-5µm **Immature** spherule Day 2 (48h) Soil Free nuclear disturbed division Arthroconidia Day 1 (24h) are inhaled Arthroconidia enlarge Donovan et al. Ashraf et al, Mycopathologica 2020 Clin Microbiol Rev 2019

## Transcriptional differences between Parasitic & Saprobic stage C. immitis & C. posadasii



Fold difference*	Annotation						
185	Conserved protein (insect antifreeze protein repeat domain, predicted secreted)	CIMG_00925					
166	Acetyltransferase	CIMG_07556					
106	Acetamidase	CIMG_02374					
101	Conserved hypothetical protein (predicted secreted)	CIMG_03870					
94	Fungal hydrophobin (predicted secreted)	CIMG_06615					
75	Conserved protein (PAN domain, predicted secreted)	CIMG_09824					
53	Conserved protein (zinc-finger domain)	CIMG_00099					
53	Conserved hypothetical protein	CIMG_06344					
43	Putative serine proteinase	CIMG_09304					
41	Cell wall synthesis protein (beta-glucosidase domain, SUN family, predicted secreted)	CIMG_05254					
34	Hypothetical protein (predicted secreted)	CIMG_07839					
31	Hypothetical protein	CIMG_13374					
31	Helix-loop-helix transcription factor	CIMG_02390					
29	Conserved hypothetical protein (pyridine nucleotide-disulphide oxidoreductase domain, predicted secreted)	CIMG_07557					
24	Prp4 (CRoW domain-containing protein, predicted secreted)	CIMG_07303					

CIMG 09539

# Comparative Transcriptomics of the Saprobic and Parasitic Growth Phases in *Coccidioides* spp

provide context for studies in other fungal pathogens.

Emily Whiston's, Hua Zhang	<b>Table 2.</b> Top 15 genes with significantly higher expression (up-regulated) in the parasitic ph	ase.
1 Department of Plant and Microbial Biology,	Up in PARASITIC stage Coccidioides immitis	& C.posadasii
San Antonio, San Antonio, Texas, United Stat	Fold difference* Annotation	Gene ID

Conserved hypothetical protein (DUF 536)

#### Heat shock protein 30 (Hsp20/alpha-crystallin domain) CIMG\_01749 Abstract Conserved hypothetical protein CIMG\_12822 Conserved hypothetical protein (YCII-related domain) CIMG\_07089 Coccidioides immitis and C. pos Conserved hypothetical protein CIMG\_13084 grow as hyphae in the saprobic this study, we use comparative 28 Hypothetical protein CIMG 11522 Hypothetical protein CIMG\_05235 growth phases. We prepared III 28 in vitro for C. immitis isolate R 26 Polysaccharide deacetylase (Arp2/3 complex subunit Arc16) CIMG\_02628 Coccidioides, we observed 1,29 24 Conserved hypothetical protein (predicted secreted) CIMG\_00509 genes up-regulated in the par 23 Hypothetical protein CIMG\_11203 observed considerable differen Spherule outer-wall glycoprotein (SOWgp, predicted secreted) CIMG\_04613 observed differential expression Conserved hypothetical protein CIMG 10488 pathogens. These included alph Hypothetical protein CIMG 10670 observed differential expression Sphingosine hydroxylase CIMG\_01209 comparative genomics studies. Conserved hypothetical protein CIMG\_04740 and virulence in Coccidioides. The 17

dil

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Curation and

Annotation





## Search for...

#### expand all I collapse all

Filter the searches below...

#### Genes

- Annotation, curation and identifiers
- **Function prediction**
- Gene models
- Genetic variation
- Genomic Location
- Immunology
- Orthology and synteny
- Pathways and interactions
- Phenotype
- Protein features and properties
- Protein targeting and localization
- **Proteomics**
- Sequence analysis
- Structure analysis
- Taxonomy
- Text
- Transcriptomics

## Organisms

## Overview of Resources and To







## **Getting Started**

VEuPathDB is packed with data, tools and v workflows, and present the results for you to

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Annotation, curation and identifiers

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Differential Expression

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- Genomic Sequences
- **Genomic Segments**
- SNPs
- **ESTs**
- Metabolic Pathways
- Compounds

## **Tutorials and Exercises**

#### Apollo: Manual gene annotation

Structural and functional community curation with Apollo, a real time collaborative genome

## Gene Pages

Explore the data and images on gene pages

Gene Pages















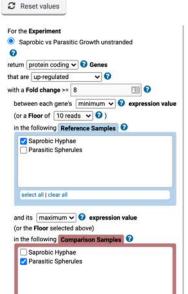




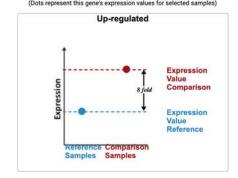
Identify Genes based on C. posadasii C735 delta SOWgp Saprobic vs Parasitic Growth RNA-Seq (fold change)

8

Downloads



select all I clear all



Example showing one gene that would meet search criteria

1

How to Submi

Data

For each gene, the search calculates:

comparison expression value

and returns genes when fold change >= 8.

You are searching for genes that are up-regulated between one reference sample and one comparison sample.

Get Answer

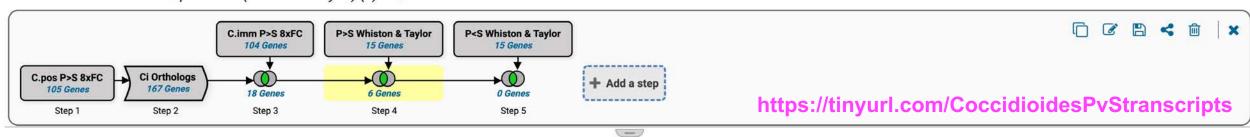
Build a Web Services URL from this Search &gt>

- @ Give this search a name (optional
- Give this search a weight (optional

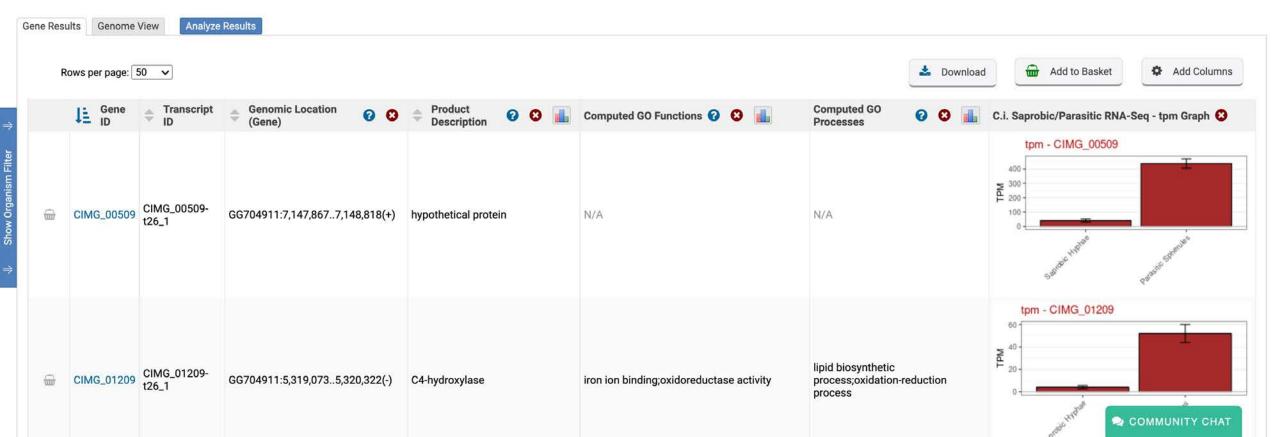


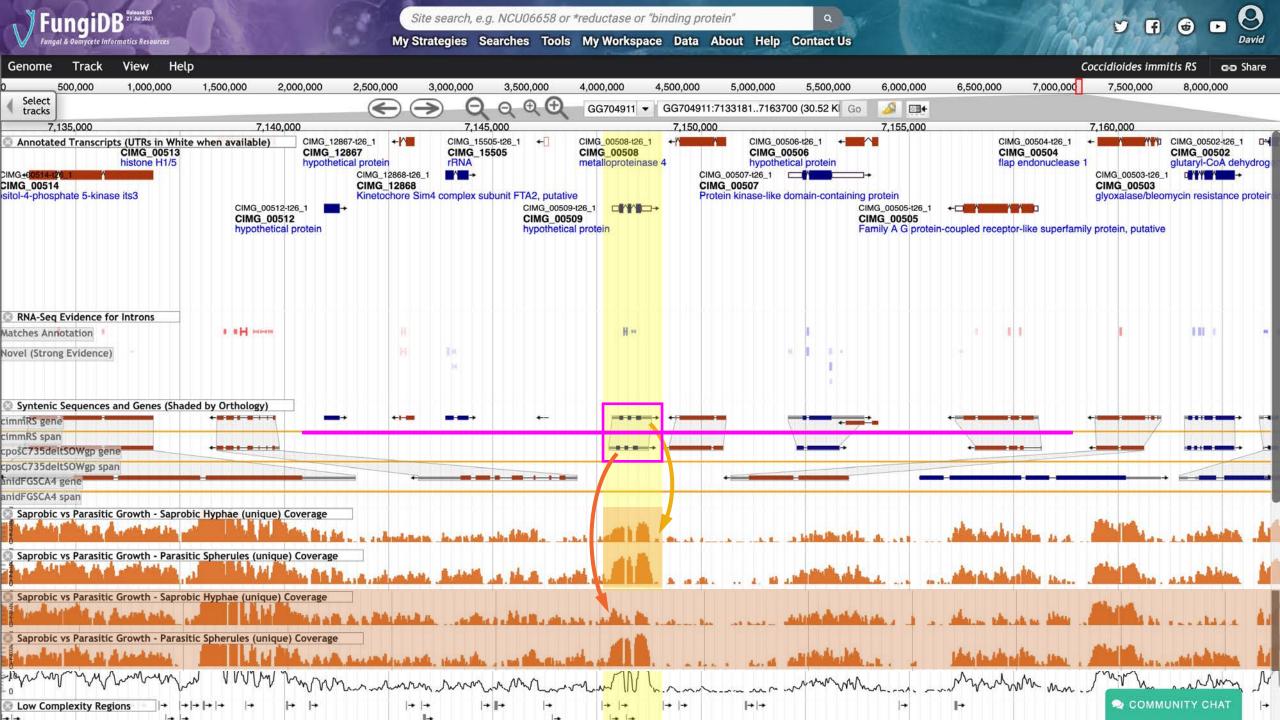
#### All (312) Public (70) Help Opened (1)

Coccidioides Parasitic > Saprobic FC (Whiston & Taylor) (6) \*



### 6 Genes (6 ortholog groups)











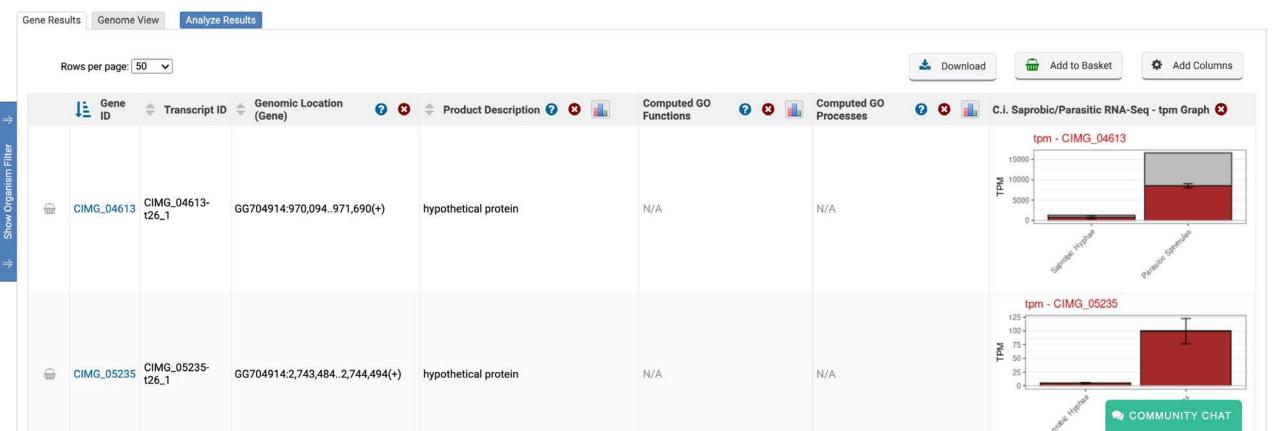
All (312) Public (70) Help Opened (1)

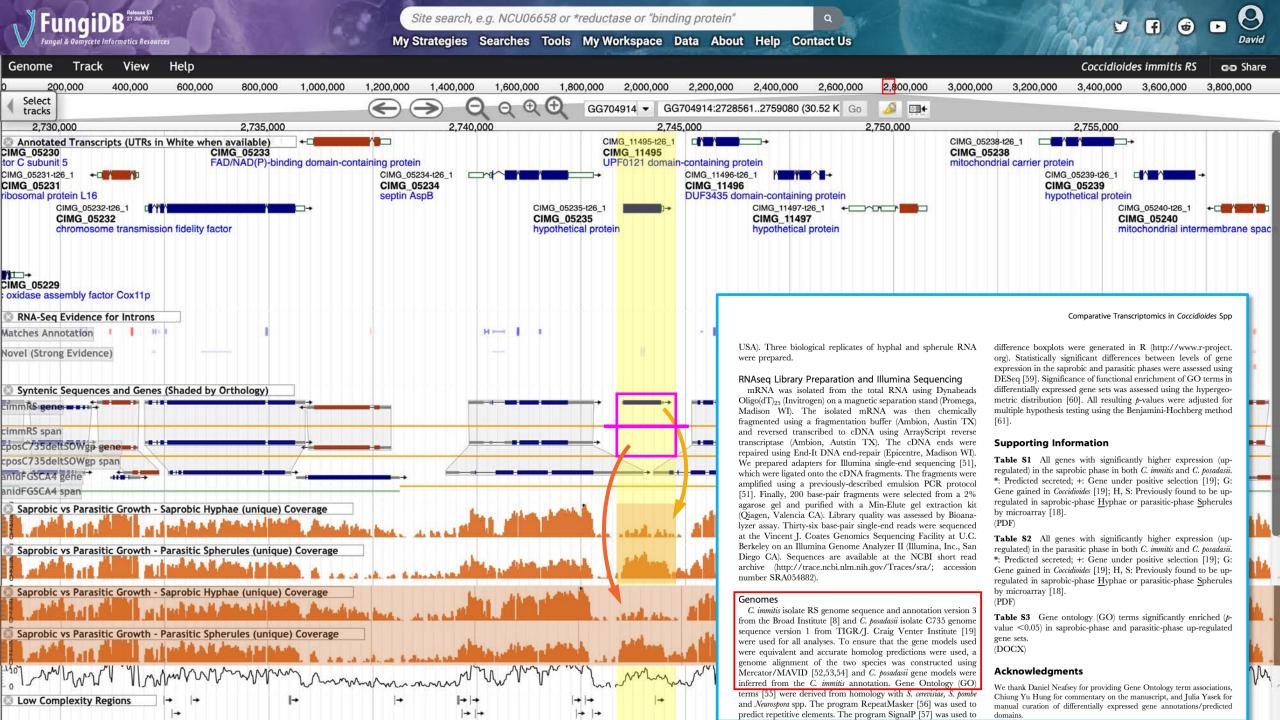
Coccidioides Parasitic > Saprobic FC (Whiston & Taylor) (6) \*



9 Genes (9 ortholog groups)

Some Genes in your combined result have Transcripts that were not returned by one or both of the two input searches. Explore





* My Tracks X Currently Active		Back to browser X Clear All Filters		Contains text 24 matching tracks					
Recently Used	V	Name		Category	Subcategory	Dataset	Track Type	RNA-Seq Alignment	RNA-Seg Strand
Category 1 Comparative Genomics	1		recripts (UTRs in White:	Gene Models	Transcripts		Processed Transcript	-	=
2 Gene Models 6 Sequence Analysis 15 Transcriptomics	1	C. immitis RS 1	E (Kirkland et al)	Sequence Analysis	Sequence sites, features and motifs	-	Segments	-	-
- Subcategory	4	CimmitiaRS cor	mbined RNAseq plot	Transcriptomics	RNA-Seq	Combined all RNA-Seq data for CimmitisRS	Multi XY plot	Unique	
2 (no data) 1 Orthology and Synteny	4	Community an	notations from Apolio	Gene Models	7/	-	Processed transcript from Apolio	m	
15 RNA-Seq 1 Sequence assembly	mposition,		Sequence Analysis	Sequence composition, complexity and repeats	-	XYPlot	75	-	
3 Sequence composition, complexity and repeats	1			Sequence Analysis	Sequence composition, complexity and repeats		Segments		-
<ol> <li>Sequence sites, features and motifs</li> </ol>	1	RNA-Seq Evide	nce for introns	Transcriptomics	RNA-Seq	-	Predicted Intron Junctions	141	:#
1 Transcripts  - Dataset	7	Reference Seg	uence	Sequence Analysis	181		Reference Sequence	***	
10 (no data) 1 Combined all RNA-Seq data	(2)	Saprobic vs Pa Spherules (unit	rasitic Growth - Parasitic que) Coverage	Transcriptomics	RNA-Seq	Saprobic vs Parasitic Growth	Coverage	unique	not strand specific
for CimmitisRS 4 Saprobic vs Parasitic Growth		Saprobic vs Pa Hyphae (uniqu	rasitic Growth - Saprobic.	Transcriptomics	IINA-Seq	Saprobic vs Parasitic Growth	Coverage	unique	not strand specific
<ol> <li>Transcriptional analysis of Coccidioides immitis mycelia and spherules</li> </ol>	1		rasitic Growth Density -	Transcriptomics	RNA-Seq	Saprobic vs Parasitic Growth	Multi-Density	unque	-
• Track Type	4	Saprobic vs Pa Unique Only	ranitic Growth XYPlot -	Transcriptomics	RNA-Seq	Saprobic vs Parasitic Growth	Multi XY plot	unique	-
11 Coverage 2 Multi XY plot	4	Scaffolds and I	Sape	Sequence Analysis	Sequence assembly		Segments		-
Multi-Density     Predicted Intron Junctions	4	Syntenic Segui by Orthology)	ences and Genes (Shaded	Comparative Genomics	Orthology and Synteny		Segments	***	*
Processed Transcript     Processed transcript from Apollo	7	Tandem Repea	ts	Sequence Analysis	Sequence composition, complexity and repeats	Table 1	Segments	W.	
Reference Sequence     Segments     XYPlot.		immitis myceli	analysis of Coccidioides a and spherules - Mature que forward) Coverage	Transcriptomics	RNA-Seq	Transcriptional analysis of Coccidendes immits mycella and spherules	Coverage	unique	forward
RNA-Seq Alignment			analysis of Coccidoides						
10 (no data) 1 Unique	•	immitis mycelia		Transcriptomics	RNA-Seq	Transcriptional analysis of Coccidedes immitis mycelia and spherules	Coverage	unque	reverse
13 unique • RNA-Seq Strand	12	Transcriptional immitis mycelli	analysis of Coccidioides a and spherules - Mycella	Transcriptomics	RNA-Seq	Transcriptional analysis of Cocciderdes immits mycela and spherules	Coverage	unique	forward
13 (no data) 6 forward		(unique forwar	d) Coverage			www.tis mycesa and spheruses			
2 not strand specific 3 reverse	(V)	immitis mycelii (unque forwar	analysis of Coccidedes s and spherules - Mycella d) Coverage	Transcriptomics	RNA-Seq	Transcriptional analysis of Coccidioides immitis mycella and spherules	Coverage	unique	forward
	•	Transcriptional immitis mycelli (unique forwar	analysis of Coccidioides a and spherules - Mycelia d) Coverage	Transcriptomics	RNA-Seq	Transcriptional analysis of Coccidoides immitis mycelia and spherules	Coverage	unque	forward
	•	Transcriptional immitis mycella (unique forwar		Transcriptomics	RNA-Seq	Transcriptional analysis of Coccidioides immitis mycella and spherules	Coverage	unque	forward
	(2)	Transcriptional immitis reycelli (unique revers		Transcriptomics	RNA-Seq	Transcriptional analysis of Coccidioides immitis mycella and spherules	Coverage	unique .	reverse
	Z	immitis myceli	analysis of Coccidioides and spherules - Young que forward) Coverage	Transcriptomics	RNA-Seq	Transcriptional analysis of Coccidoides investis mycelia and spherules	Coverage	unque	forward
	v	immitis mycelia	analysis of Coccidioides a and spherules - Young our reverse) Coverage	Transcriptomics	RNA-Seq.	Transcriptional analysis of Coccidioides immits mycella and spherules	Coverage	unique	- 4

GG704914_2740379_2740677_0 details					
ntron Junction Details					
Intron Location GG704914:27403792740677 (	+ strand)				
Intron Spanning Reads (ISR) 56					
ISR per million (ISRPM) 28					
Gene assignment CIMG_05234 - annotated intr	on				
% of Most Abundant Intron (MAI) 33.83					
Sample Details					
Experiment	Sample	Uniqu	e ISRPA	A ISR/Cov	% MAI
Transcriptional analysis of Coccidioides immitis mycelia a spherules	nd Mature spherules	1	0.54	0.38	9.08
	Mycelia	41	23.6	1.07	33.88
	Young spherules	14	3.86	1.74	53.84

Intron Locati	n	GG7049	914:27403	7927406	68 (+ str	and)				
Intron Spann	ng R	eads (	ISR) 18							
ISR per millio	n (15	RPM)	9.73							
Gene assignn	ent	CIMG	_05234							
% of Most Ab	ndar	nt Intr	on (MAI)	11.76						
Sample Details										
		Experi	ment			Sample	Unique	ISRPM	ISR/Cov	, M
Transcriptional analysis of Coccidioides immitis mycelia and spherules					ature herules	1	0.54	0.38	9.0	
					м	ycelia	15	8.64	0.39	12.
						oung oherules	2	0.55	0.25	7.6

GG704914\_2740379\_2740668\_0 details

