

MycoCosm, *The Fungal Genomics Resource*

Igor Grigoriev

DOE Joint Genome Institute

FGC, March 18, 2011



- **Robust Annotation**

- Automated Pipeline



- **Multi-factorial Genomics Analysis**

- Genome Centric Depth
- Comparative Genomics Breadth



- **Community Resource**

- Integrated data (Community Hub)
- User tools (Community Annotation)



Fungal Genomics Program

Exploration of fungal diversity



Genomic Encyclopedia of Fungi

Plant Feedstock Health

- Myorrhizal Symbiosis
- Plant Pathogenicity
- Biocontrol

Biorefinery

- Lignocellulose Degradation
- Sugar Fermentation
- Industrial Organisms

Fungal Diversity

Announcements

- March 22-24, 2011
JGI User Meeting, Walnut Creek, CA
- March 15-20, 2011
Fungal Genetics Conference at
Asilomar, Pacific Grove, CA

60+ fungal genomes
500+ registered users
4000+ visitors/month

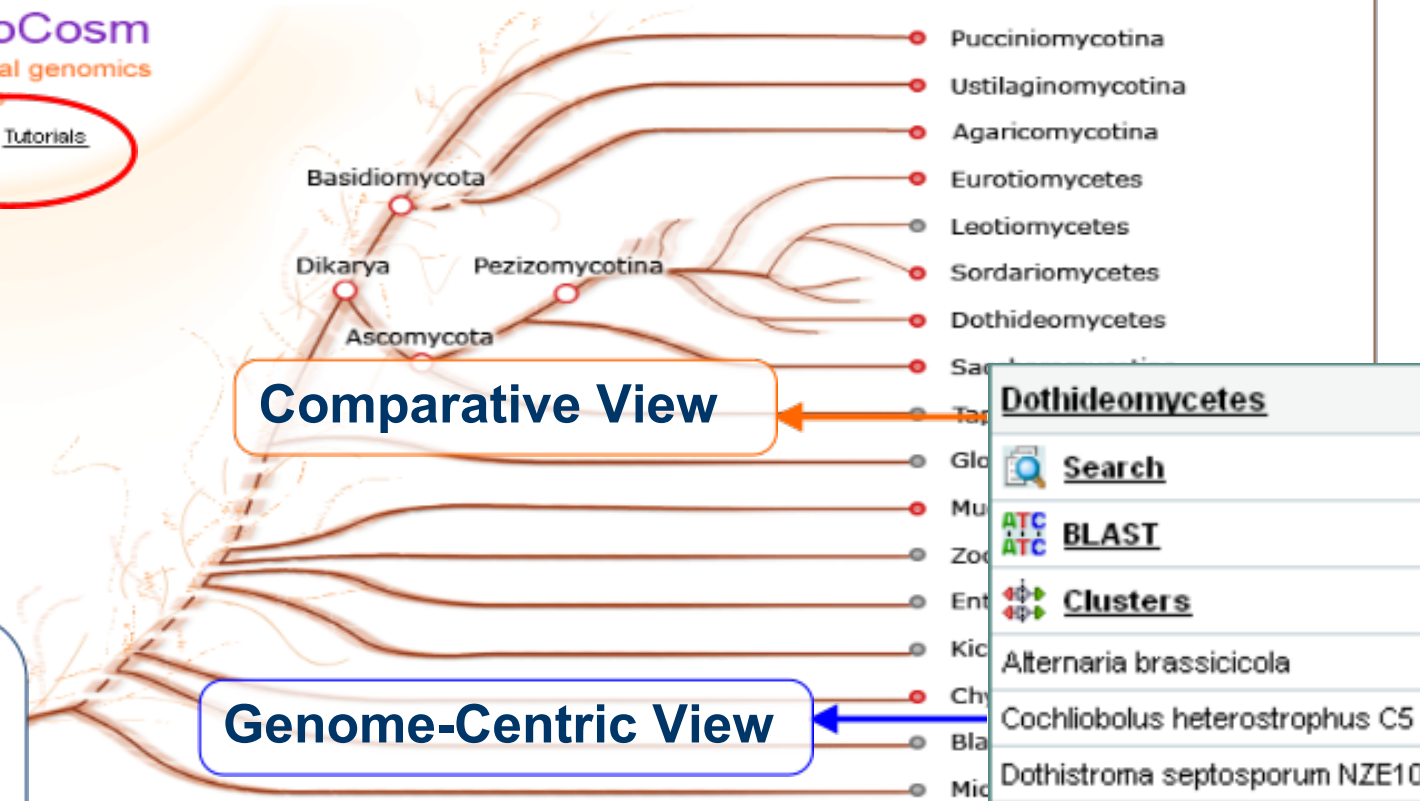
- January 10, 2011
Fomitiporia mediterranea v1.0
- January 5, 2011
Dichomitus squalens v1.0

[more >>](#)

MycoCosm

the fungal genomics resource

[Video Tutorials](#)

 by keyword Search Genome


Comparative View

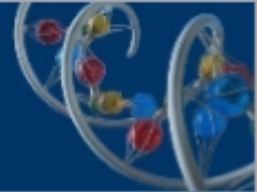
Genome-Centric View

- Dothideomycetes**
- [Search](#)
 - [BLAST](#)
 - [Clusters](#)
 - Alternaria brassicicola
 - Cochliobolus heterostrophus C5
 - Dothistroma septosporum NZE10
 - Hysterium pulicare
 - Mycosphaerella fijiensis v2.0
 - Mycosphaerella graminicola v2.0
 - Pyrenophora tritici-repentis
 - Rhizidhysterium rufulum
 - Septoria musiva SO2202 v1.0
 - Stagonospora nodorum SN15

www.jgi.doe.gov/fungi



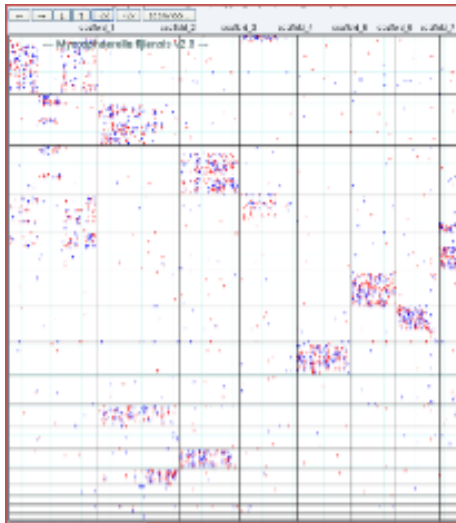
New Comparative View



[Home](#)
[Mycocosm](#)
[Projects](#)
[Login](#)
Dothideomycetes

[SEARCH](#)
[BLAST](#)
[CLUSTERS](#)
[DOWNLOAD](#)
[INFO](#)
[HELP!](#)

- Altbr1 [Alternaria brassicicola](#)
- CocheC5_1 [Cochliobolus heterostrophus C5](#)
- Dotse1 [Dothistroma septosporum NZE10 v1.0](#)
- Hyspu1 [Hysterium pulicare](#)
- Lepmu1 [Leptosphaeria maculans](#)
- Mycf2 [Mycosphaerella fijiensis v2.0](#)
- Mycgr3 [Mycosphaerella graminicola v2.0](#)
- Pytr1 [Pyrenophora tritici-repentis](#)
- Rhyru1 [Rhytidhysterium rufulum](#)
- Sepmu1 [Septoria musiva SO2202 v1.0](#)
- Stano1 [Stagonospora nodorum SN15](#)



[scaffold_1](#)
[scaffold_2](#)
[scaffold_3](#)
[scaffold_4](#)
[scaffold_5](#)

PFAM domains

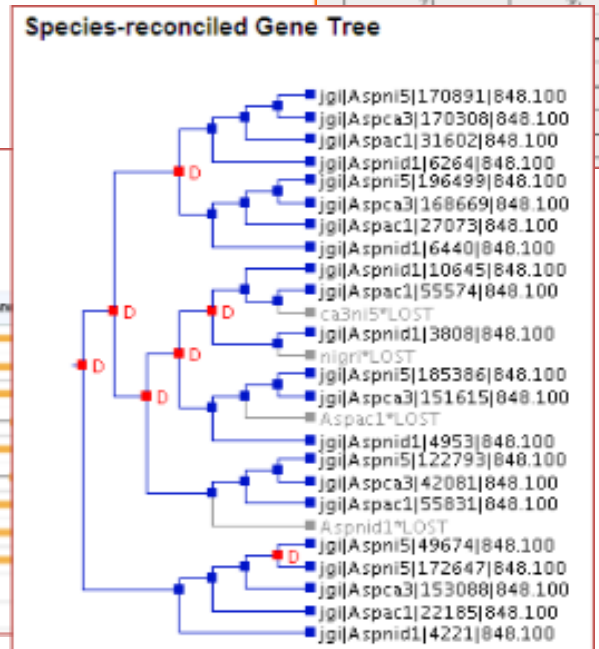
PhosPP00088

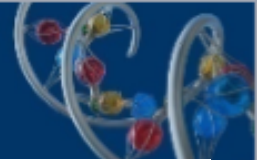
Cluster 136

download selected proteins Do Cluster 11 proteins found

Protein ID	Location	Score	Expect	Number of domains	Members	SEQUENCE	CONTIG	ORF
21426	scf010_1_002108-032788	1283	107	1	11	Dothistroma		
61941	scf010_2_220743-102541	1733	202	1	8	Dothistroma		
133245	scf010_11109530-150837	1065	188	1	11	Dothistroma		
130303	scf010_6_3115218-3126423	1233	346	1	8	Dothistroma		
134052	scf010_11317706-1131838	1128	114	1	11	Dothistroma		
42759	scf010_21346426-2147615	1133	346	1	7	Dothistroma		
43426	scf010_21512735-2152882	1273	341	1	7	Dothistroma		
113388	scf010_2_481921-4830621	1131	297	1	7	Dothistroma		
120673	scf010_8_201943-18330	1348	318	1	7	Dothistroma		
181581	scf010_1_5132126-5123422	1348	338	0	7	Dothistroma		
185181	scf010_7_543391-545313	1843	338	0	7	Dothistroma		

nodes in Sordariomycetes v1.0 (tax 1)	nodes in Dothideomycetes v1.0 (tax 1)	nodes in Dothideomycetes v1.0 (tax 1)
241	239	424
26	24	29
26	22	25
35	27	34
26	26	28
35	32	39
22	21	26
48	45	52
21	16	22
		18
		164
		54
		25
		30
		119





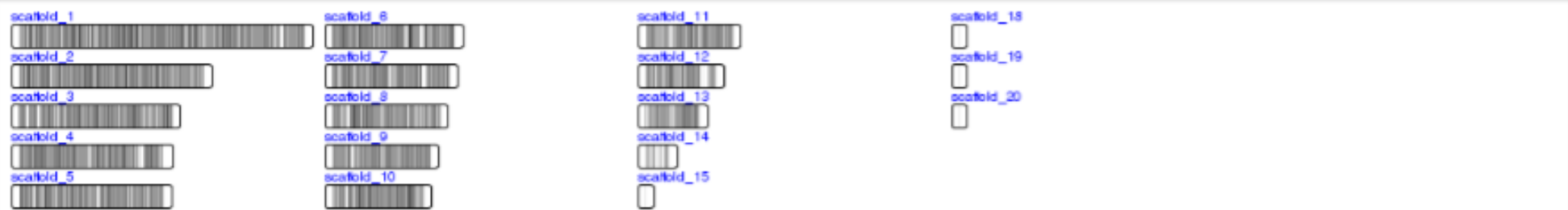
Dothistroma septosporum NZE10 v1.0 (Dotse1) vs. Mycosphaerella fijiensis v2.0 (Mycf2)

View with: Vista Point Synteny Dot Plot

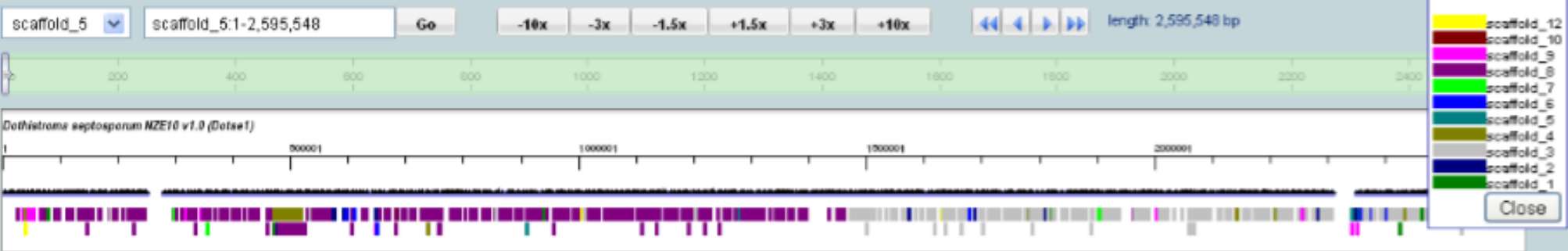
clade: reference genome: release: compared genome: cutoff:

Other Dothistroma septosporum Aug 2010 Mycosphaerella fijiensis v2.0 (Mycf2) Submit 50 bp

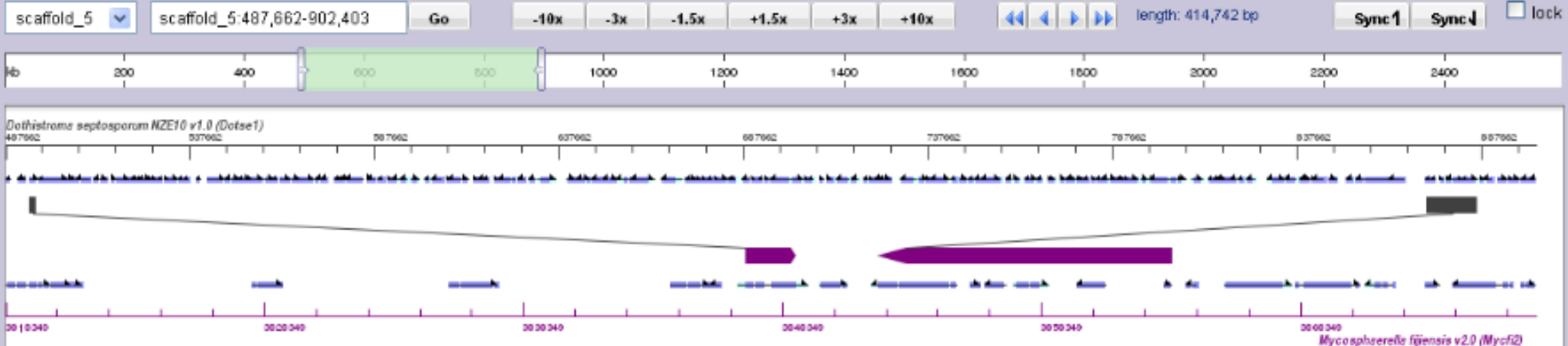
▼ **Genome Panel:** Dothistroma septosporum NZE10 v1.0 (Dotse1) vs. Mycosphaerella fijiensis v2.0 (Mycf2)



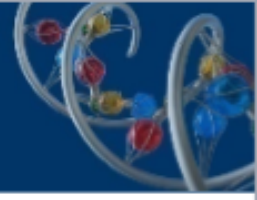
▼ **Chromosome Panel:** Dothistroma septosporum NZE10 v1.0 (Dotse1) (scaffold_5) vs. Mycosphaerella fijiensis v2.0 (Mycf2)



▼ **Comparison Panel:** Dothistroma septosporum NZE10 v1.0 (Dotse1) (scaffold_5) vs. Mycosphaerella fijiensis v2.0 (Mycf2) (scaffold_8)



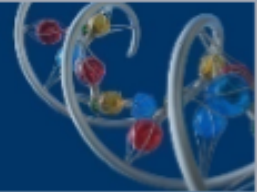
Dot Plot



Dothistroma septosporum NZE10 v1.0 (Dotse1) vs. Mycosphaerella fijiensis v2.0 (Mycf12) View with: Vista Point Synteny Dot Plot

Filter alignments: Show everything Length: 30,209,431 x 74,141,167





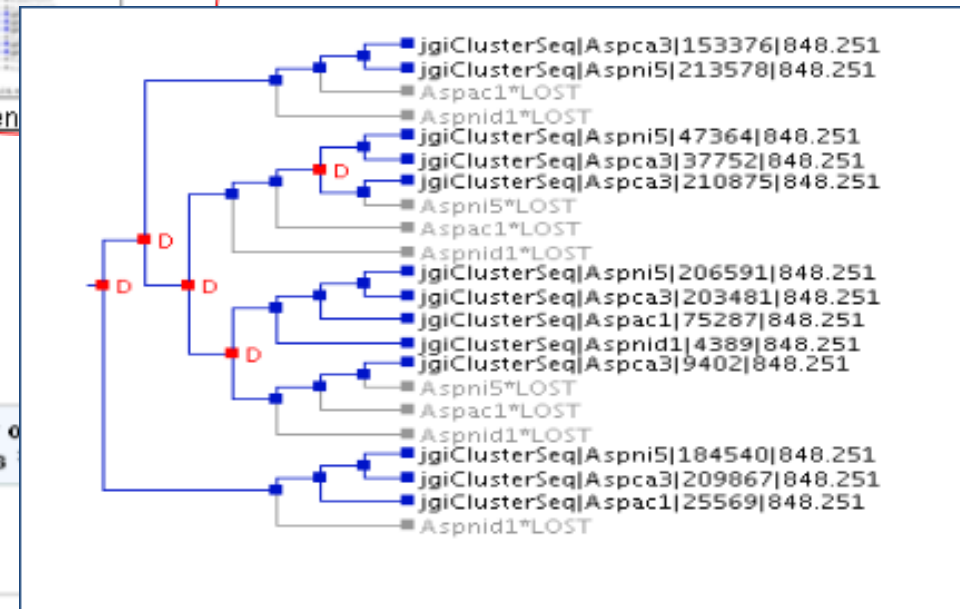
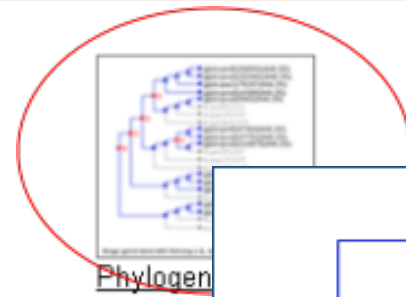
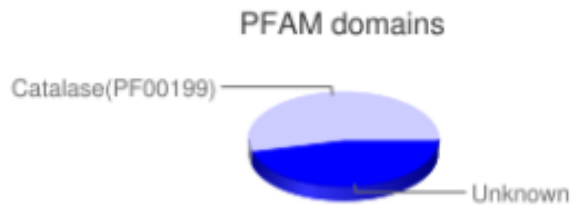
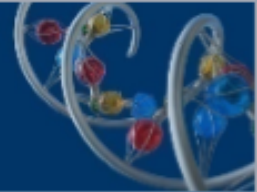
Run

Number Of Clusters	Cluster Size			Standard Deviation
	Minimum	Maximum	Average	
11032	1	280	4.0198	7.0343

Find a gene in Protein Id:

MCL inflation parameter: 3 4875 clusters found

<input type="text" value="1+"/> Cluster	<input type="text" value="1+"/> A. aculeatus v1.0 FilteredModels6	<input type="text" value="1"/> A. nidulans from AspGD AspGD_genes	<input type="text" value="1+"/> A. niger v3.0 FrozenGeneCatalog071508	<input type="text" value="1+"/> Aspergillus carbonarius v3.0 FilteredModels6	<input type="text" value="filter"/> Total
Totals	5282	4875	5433	5617	21207
76	9	1	10	5	25
144	4	1	7	6	18
177	5	1	6	4	16
205	4	1	5	5	15
207	1	1	3	10	15
216	3	1	6	4	14
224	3	1	5	5	14
229	4	1	3	6	14
236	4	1	4	4	13
251	2	1	4	6	13



Run 848

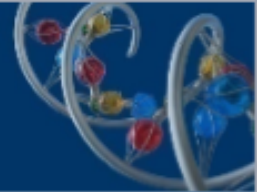
Cluster 251

download selected proteins

Do Clustalw

13 proteins found

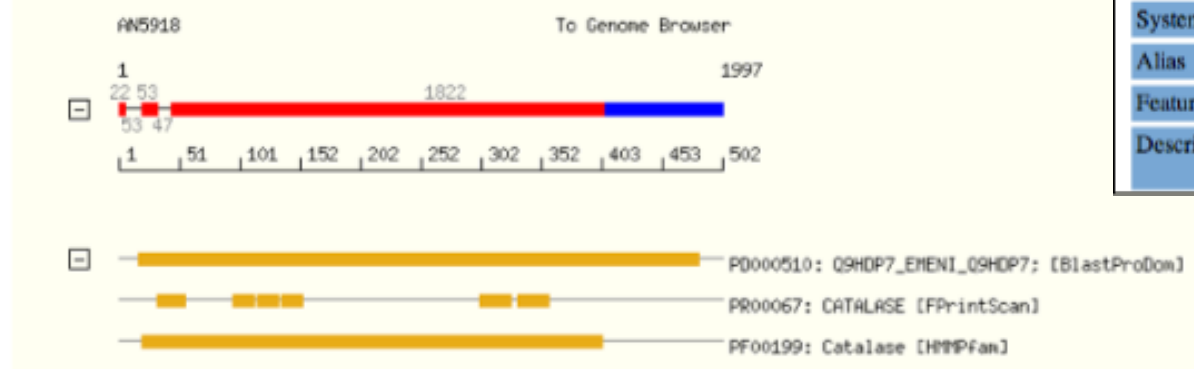
Protein Id <input type="checkbox"/>	Location <input type="checkbox"/>	Gene length <input type="checkbox"/>	Protein length <input type="checkbox"/>	Number of domains		
37752 <input type="checkbox"/>	scaffold_1:989148-991047	1900	521	1		
9402 <input type="checkbox"/>	scaffold_18:8926-10536	1611	517	1	Aspergillus carbonarius v3.0	517
4389 <input type="checkbox"/>	Chr1_A.nidulans FGSC_A4:1815930-1817926	1997	502	1	A. nidulans from AspGD	502
203481 <input type="checkbox"/>	scaffold_2:1292891-1294883	1993	500	1	Aspergillus carbonarius v3.0	500
210875 <input type="checkbox"/>	scaffold_18:42812-45123	2312	492	1	Aspergillus carbonarius v3.0	492



Name: AN5918
 Protein ID: 4389
 Location: [ChrI_A_nidulans_FGSC_A4:1815930-1817926](#)
 Strand: -
 Number of exons: 3
 Description:
 AspGD: [Link to AN5918 in the Aspergillus Genome Database \(AspGD\)](#)
 Best Hit: [ani:AN5918.2_hypothetical_protein](#) (model%: 99, hit%: 100, score: 2734, %id: 100) [Asper]
 total hits(shown) 263 (10)

ASPECT	GO Id	GO Desc	Interpro Id	Inter
Molecular Function	0004096	catalase activity	IPR002226	Catala
			IPR011614	Catala
Biological Process	0006118	electron transport	IPR002226	Catala
	0006979	response to oxidative stress	IPR011614	Catala
			IPR002226	Catala
			IPR011614	Catala
KOG GROUP	KOG Id	KOG Class	KOG	CO
Metabolism	KOG0047	Inorganic ion transport and metabolism		Cat

[View nucleotide and 3-frame translation](#) [To Genome Browser](#)
 NCBI blast [Predicted number of transmembrane domains: 0](#)



Quick Search:

[Site Map](#) | [Search Options](#) | [Help](#) | [Contact AspGD](#) | [Home](#)

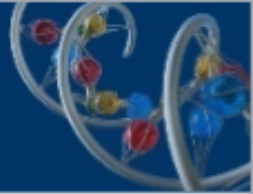
[Community Info](#) | [Submit Data](#) | [BLAST](#) | [Primers](#) | [PatMatch](#) | [Gene/Seq Resources](#) | [Advanced Search](#)

A. nidulans *catC*/AN5918 Summary [Help](#)

[Summary](#) | [Locus History](#) | [Literature](#) | [Gene Ontology](#) | [Phenotype](#) | [Protein](#)

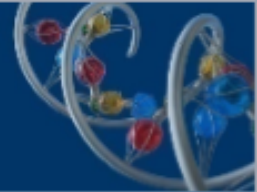
catC BASIC INFORMATION [[View References](#)]

Standard Name	<i>catC</i> ¹
Systematic Name	AN5918
Alias	ANID_05918, ANIA_05918
Feature Type	ORF, Verified
Description	Putative catalase with a predicted role in gluconic acid and gluconate metabolism (2)



FEATURES	Location/Qualifiers
<code>source</code>	<code>1..2740984</code> <code>/organism="Scheffersomyces stipitis CBS 6054"</code> <code>/mol_type="genomic DNA"</code> <code>/strain="CBS 6054"</code> <code>/db_xref="taxon:322104"</code> <code>/chromosome="2"</code>
<u>gene</u>	<code>1613..>8355</code> <code>/gene="ADD3.2"</code> <code>/locus_tag="PICST_66748"</code>
<u>mRNA</u>	<code>1613..>8355</code> <code>/gene="ADD3.2"</code> <code>/locus_tag="PICST_66748"</code> <code>/product="ATP-dependent DNA helicase"</code> <code>/note="Has EST support"</code>
<u>CDS</u>	<code>1876..8355</code> <code>/gene="ADD3.2"</code> <code>/locus_tag="PICST_66748"</code> <code>/codon_start=1</code> <code>/transl_table=12</code> <code>/product="ATP-dependent DNA helicase"</code> <code>/protein_id="ABN64199.2"</code> <code>/db_xref="GI:149384933"</code> <code>/db_xref="JGIDB:Picst3 66748"</code>

Genome-Centric View



JGI Tree of Life Genome Projects **Login**

SEARCH ADVANCED SEARCH BLAST BROWSE

Position: scaffold_1:1-100000 Apply

Size: 100000 Feature: Get Scaffold Info

Base Position 10000 20000

GC Content 54.49

Vista_Thite1 Vista Sporotrichum thermophile vs. Thielavia terrestris conservation

Scaffold scaffold_1 Contigs in Scaffolds

FilteredModels1

Concordia_ESTs ESTs 404.00

Spoth1_EstClusters BLAT

Spoth1_Ests BLAT

Thite1_FilteredModels2 Blastx

..odels_BroadGeneModels Blastx

Repeats

JGI — Sign In

Email (or User Name):

Password:

Sign In

[Forgot your password?](#) | [Help](#)

[Register now!](#)

Sporotrichum thermophile v1.0

HOME HELP!

nalink Add custom tracks

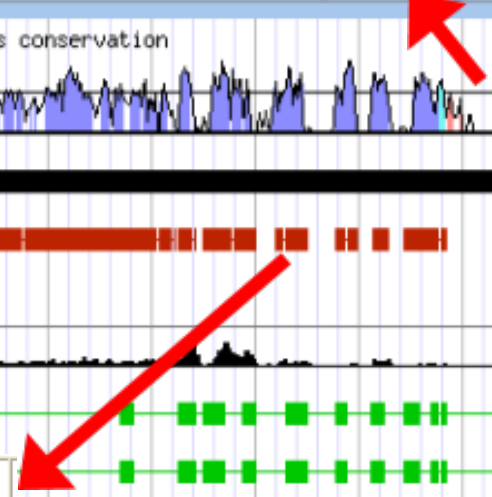
Open / Close Toolbar

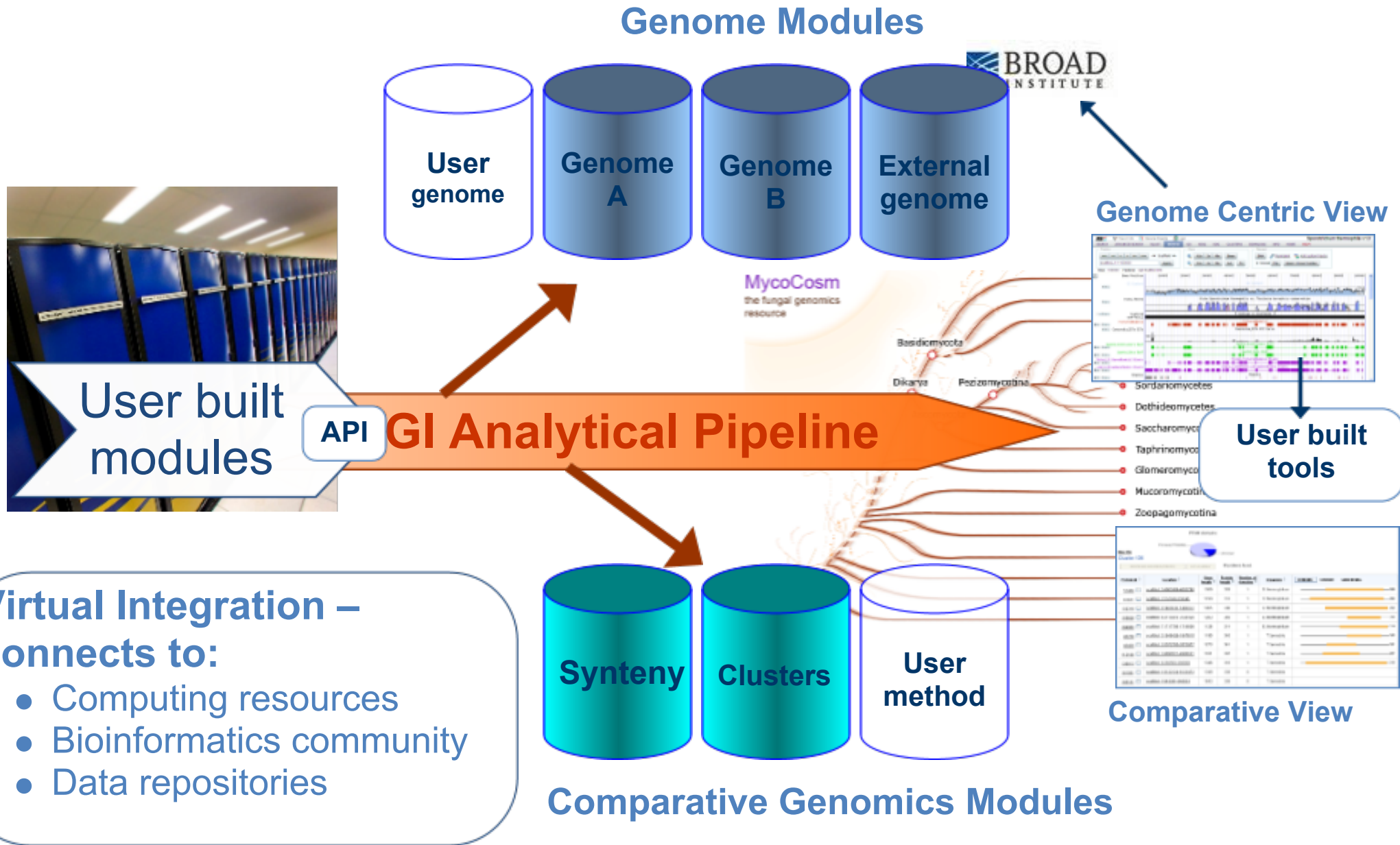
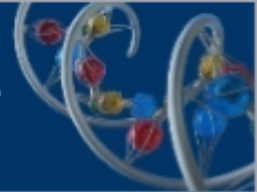
Sequence (softmasked)
length: 17,731 bp

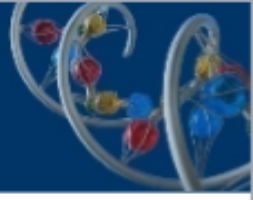
[Vista Browser](#)

[JGI T. terrestris Browser](#)

Attribute	Value	Creator	Action
Name	SPT97310	SCOTT.BAKER@PNL.GOV	add
Description	non-ribosomal peptide synthetase	SCOTT.BAKER@PNL.GOV	add
Define	non-ribosomal peptide synthetase	SCOTT.BAKER@PNL.GOV	add
Disposition	Catalog	AUTOMATIC	add edit
Literature			add

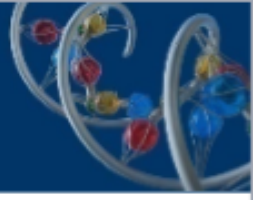






MycoCosm

- **Integrates genomic data and analytical tools for energy and environment fungi**
- **Offers community annotation tools and data repository**
- **Aims to integrate into global system of genomics data and tools**



Genomics Team:

Andrea Aerts

Alan Kuo

Robert Otillar

Robin Ohm

Robert Riley

Asaf Salamov

Kemin Zhou

Frank Korzeniewski

Xueling Zhao

Portal Team:

Igor Shabalov

Henrik Nordberg

Serge Dusheyko

Arkady Voloshin

Simon Minovitsky

Mike Cantor

Igor Ratnere

Tatyana Smirnova

Inna Dubchak

JGI User Community