

# Introduction to MycoCosm

MycoCosm is a fungal genomics portal developed by the US Department of Energy Joint Genome Institute (JGI) to support integration, analysis, and dissemination of fungal genome sequences and related omics data by providing interactive web-based tools. To get started, navigate to the MycoCosm Homepage in your web browser (<https://mycocosm.jgi.doe.gov/>)

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THE FUNGAL GENOMICS RESOURCE

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May 01, 2025  
*Collariella robusta* PSN 660 v1.0  
May 01, 2025  
*Diplocelasiospora inaequalis* CBS 436.74 v1.0  
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*Zopfiella marina* IMI 229743 v1.0  
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*Schizothecium carpinicola* IMI 314718 v1.0  
May 01, 2025  
*Apodus sp.* PSN 540 v1.0  
May 01, 2025  
*Lasiosphaeria similisorbina* ILLS00125647 v1.0  
[more...](#)  

To use the tree navigation click a branch name and select an organism from the list.  
For MycoCosm, please cite: Igor V. Grigoriev, Roman Nikitin, Sajeet Haridas, Alan Kuo, Robin Ohm, Robert Olliar, Robert Riley, Asaf Salamov, Xueling Zhao, Frank Korzeniewski, Tatyana Smirnova, Henrik Nordberg, Irina Dubchak, Igor Shabalov, MycoCosm portal: gearing up for 1000 fungal genomes, Nucleic Acids Research, Volume 42, Issue D1, 1 January 2014, Pages D699–D704, DOI:10.1093/nar/gkt1183  
For JGI Fungal Program, please cite: Igor V. Grigoriev, Daniel Cullen, Stephen B. Goodwin, David Hibbett, Thomas W. Jeffries, Christian P. Kubicek, Cheryl Kuske, Jon K. Magnuson, Francis Martin, Joseph W. Spatafora, Adrian Tsang & Scott E. Baker (2011) Fueling the future with fungal genomics, Mycology, 2:3, 192-209, DOI:10.1080/21501203.2011.584577

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**Click to login/register**

**Search MycoCosm** **Search for JGI Data**

**All MycoCosm Groups**

Pucciniomycotina  
Ustilaginomycotina  
Agaricomycetes  
Dacrymycetes  
Tremellomycetes  
Wallemycetes  
Pezizomycetes  
Orbiliomycetes  
Eurotiomycetes  
Dothideomycetes  
Leancomycetes  
Leotiomycetes  
Sordariomycetes  
Xylonomycetes  
Saccharomycotina  
Taphrinomycotina  
Glomeromycotina  
Mortierellomycotina  
Mucoromycotina  
Zoopagomycotina  
Kickxellomycotina  
Chytridiomycetes  
Blastocladiomycota  
Monoblepharidomycetes  
Neocallimastigomycetes  
Microsporidia  
Cryptomycota

**Provides:**

- data access
- visualization
- analysis tools

**Allows researchers to:**

- Explore gene models within species
- Compare gene content between species

You can also get to MycoCosm from the unified JGI Genome Portal

(<https://genome.jgi.doe.gov>)

**JGI** | **Genome Portal**

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- How to grant access to your proposal/project/genome? [Get Instructions](#).

Genomes OnLine Database (GOLD) - a resource for sequencing projects and associated metadata.

Integrated Microbial Genomes (IMG) and Metagenomes (IMG/M) - resources for comparative analysis and annotation.

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The new JGI Publication Policy requires inclusion of Proposal Award DOIs within the DOE auspice statement to improve our manuscript and impact tracking efforts. Proposal DOIs can be found at the top of the proposal info page on the JGI Genome Portal. [Click here](#) to learn how to find DOIs for the datasets you are interested in.

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The "Tree of Life"

Please use our powerful search or go to the "Tree of Life" if it is the most convenient way for you to reach your genomes/projects.

Phytozome - a hub for accessing, visualizing and analyzing plant genomes.

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## Sign In

JGI – Sign In

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Email (or User Name):

[Forgot your username?](#)

Password:

[Forgot your password?](#)

**SIGN IN**

**SIGN IN WITH GOOGLE** (LBL/JGI users)

**REGISTER**

Currently MycoCosm hosts 2700+ genomes, including those sequenced by JGI in collaboration with the community, as well as those imported from the public domain or privately from collaborators. Most JGI-sequenced genomes are products of the Community Science Program (CSP) or the 1000 Fungal Genomes Project (1KFG). The MycoCosm page has links to these as well as other Programs and Projects. Nominations for genomes to 1KFG may be directly submitted from here!

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May 01, 2025  
*Lasiosphaeria similisporina* ILLS00125647 v1.0

[more...](#)

**All MycoCosm Groups** ▾

**Fungi** (2,729 genomes)

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- [SMURF Clusters](#)
- [Antimash Clusters](#)
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To use the tree

**For MycoCosm**  
 Korzeniewski, T  
 42, Issue D1, 1

**For JGI Fungi**  
 Magnuson, Fra  
 DOI:10.1080/21

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A green arrow points from the 'Nominate New Species!' link in the sidebar to the 'Nominate new Species' link in the main content area. Another green arrow points from the 'Nominate New Species!' link in the sidebar to the 'Nominate new Species' link in the main content area.

Searching for organism portals, groups, and projects: The main search box on MycoCosm can be used to find organism genome portals using the default search parameters.



- Exercise: Find ‘Aspergillus’ on MycoCosm using the default parameters.

Using ‘Search for JGI Data’ will allow searching the Genome Portal.

- Exercise: Find ‘Lichen’ on the Genome Portal (<https://genome.jgi.doe.gov>) using ‘Search for JGI Data’. How does this compare to the default search on MycoCosm?

Note: A global search ('Anything') for the keyword is the default search parameter at the JGI genome portal

For the next part, we will use a single genome portal to explore tools available in MycoCosm.

## Navigating a genome portal

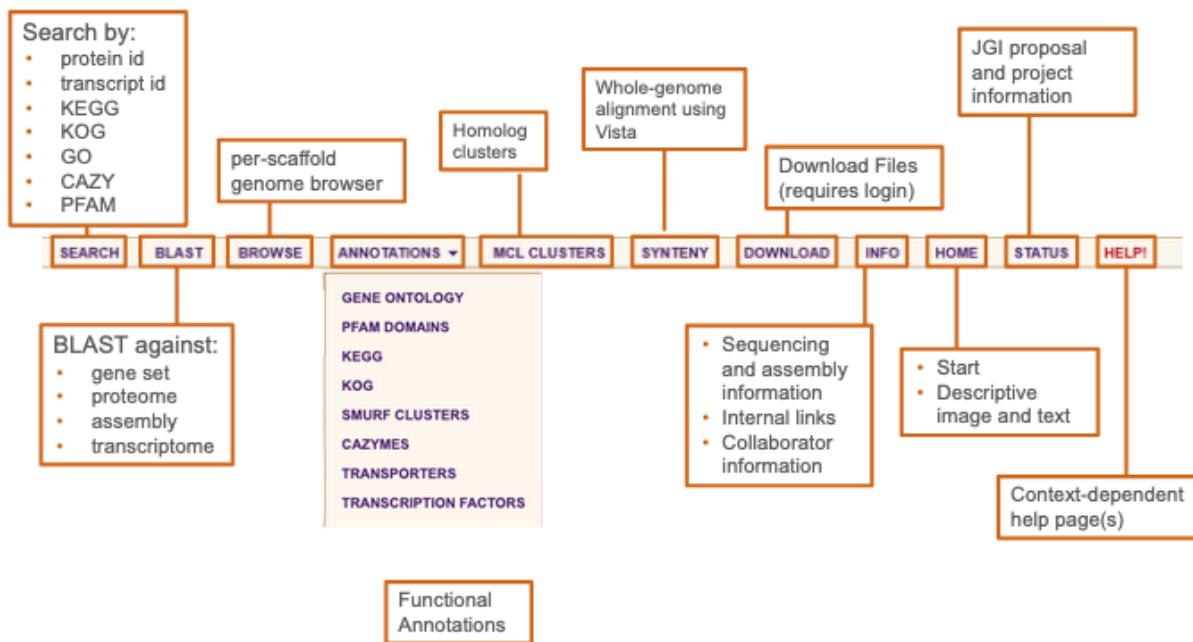
Choose one of the *Aspergillus* genome portals you identified in the exercise above. This will take you to the genome portal for that species. The data for that genome is stored in a database, which can be identified using the url for the genome portal. For example, the home page for *Aspergillus welwitschiae* is <https://mycocosm.jgi.doe.gov/Aspwel1>. In this case, the databaseID is **Aspwel1** (i.e. the part right after mycocosm.jgi.doe.gov/). JGI uses these databaseIDs as shorthand for the portal in various places, including urls, download files, genome annotation browsers, clustering, and many others.

A screenshot of a web browser displaying the homepage of the Aspergillus welwitschiae genome portal. The URL in the address bar is https://mycocosm.jgi.doe.gov/Aspwel1/Aspwel1.home.html. The page features the JGI logo and the MycoCosm logo. The main content area shows several circular growth assays of the fungus on different media (CREA, OAT, CYA, YES, MEA, OX, MEA) with labels indicating growth patterns. A text box provides information about the sequencing project. Below this is a section titled 'Genome Reference(s)' with citation details. At the bottom, there is a photo credit to Ellen Kirstine Lyhne.

Photo credit: Ellen Kirstine Lyhne

## The navigation toolbar

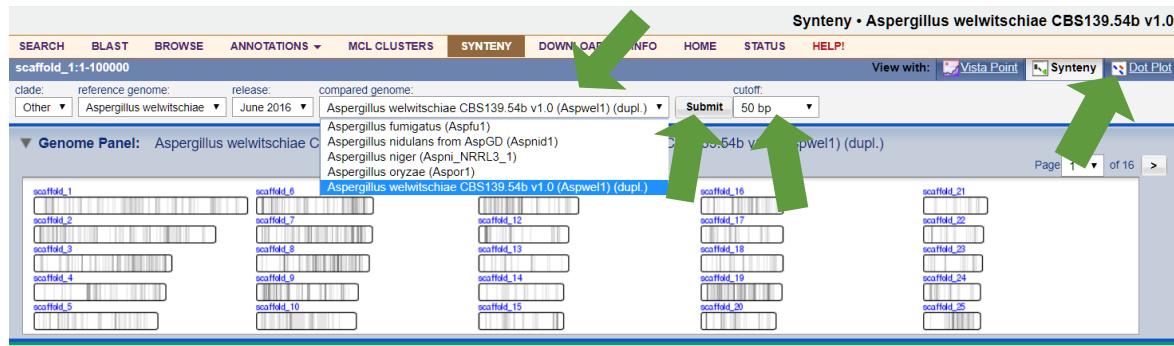
At the top of the genome portal is the navigation toolbar with the following functions.



We will explore most of the tools in a later exercise, but for now, let us investigate the **synteny browser**, the **genome browser**, and **protein pages**.

## Synteny

The synteny browser allows you to look at genome synteny at the nucleotide level using various filters.



Check out the basic functions of the synteny browser by clicking on the buttons and pulldowns marked by the arrows in the image above. To return from the ‘Dot Plot’ view, click ‘Synteny’ next to it. Note that self-alignment (main diagonal) is already removed in the dot plot if the genome is compared with itself, thus allowing you to observe other regions of duplication. We will explore this feature further in a later tutorial.

## Genome browser

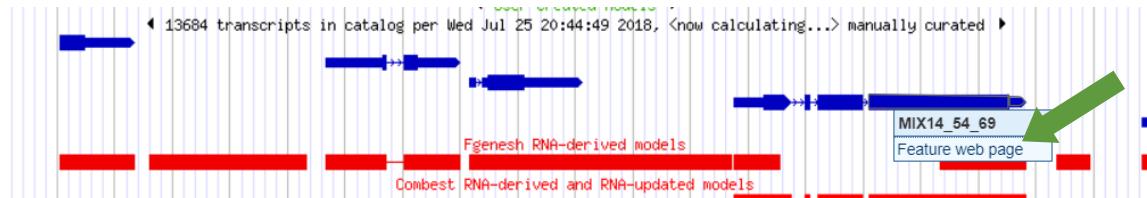
Now, we will explore the genome browser using the ‘BROWSE’ tab. On the browser, you can navigate using available navigation tools and explore multiple layers (or “tracks”) of information we superimpose upon scaffolds. These include GC%, nucleotide conservation with closely related genomes, RNAseq expression data and transcriptome support, homology support, a total set of predicted gene models, and a single final set of models. Certain portals may also include multi-omics related tracks, such as for ChIPseq. With multiple sources of information visible simultaneously, identifying potentially interesting regions, or locations which need further improvement through manual curation, is relatively straightforward. You can also customize your view by clicking ‘Open/Close Toolbar’ and updating track settings. With the Toolbar open, you can get additional help by clicking the ‘?’ button, or close the toolbar by clicking the ‘X’ button (both of these are next to the refresh button).



The nucleotide conservation tracks (based on vista alignment data) are a visual representation of alignments between two genomes. The peaks and valleys present on these curves represent percent conservation between aligned regions, and regions of high conservation are colored according whether that region corresponds to an exon (dark blue), UTR (light blue), or non-coding (pink) region in the aligned genome. You can click on any of these tracks to get more information/download data.

The browser can be a useful tool for identifying potentially interesting genes, or exploring the gene neighborhood surrounding a gene of interest. For example, let’s zoom in on one region of scaffold 1 to take a closer look. In the navigation tools, replace ‘scaffold\_1:1-100000’ with ‘scaffold\_1:352500-362500’ and press ‘Apply’ to zoom in. Alternatively, you can scroll (i.e. ‘<<<’ and ‘>>>’) and zoom (i.e. +1.5x, +3x, or +10x) using the available navigation tools. You can also expand any track by clicking on it. Try this now for the ‘GeneCatalog’, which

will allow you view this track with increased resolution. Click on any gene in the GeneCatalog and click on ‘Feature web page’. This will take you to the protein page.



## Protein page

On the protein page, detailed information is available regarding gene structure, functional annotation, homology to other organisms, etc. Almost everything on this page is click-able, bringing you to detailed descriptions of specific functional annotations. The top part of the page describes gene details, functional annotations and information on gene structure/domains present. Below this, BLAST alignments and scores (length, score, % identity, etc) are shown. Clicking on the alignment will allow you to view individual alignments, or clicking on the hit name will bring you to a page describing that protein in detail. Below you can select and retrieve protein sequences of either this protein, or any BLAST hit.

The protein page for *MIX14\_54\_69* is shown. The top section displays gene details and functional annotation, including:

- Name: MIX14\_54\_69
- Protein ID: 176767
- Location: scaffold\_1:51371-53916
- Strand: +
- Number of exons: 4
- Description: 54 EST updated Ab initio model
- Best Hit: iqlAspph1|247693 Cysteine proteinase (model%: 99, hit%: 99, score: 3332, %id: 98) [no tax name]
- total hits(shown): 111 (10)

Annotations include GO terms (ubiquitin-dependent protein catabolism), Interpro ID (IPR001394), and KOG ID (KOG1865).

**Structural information:** Shows the protein's length (2546 amino acids) and a schematic diagram of its domain architecture. Domains include PF00443: Ubiquitin carboxyl-terminal hydrolase (HMPFam), PS0205: Ubiquitin specific protease (USP) domain profile, and SSF54001: (SUPERFAMILY).

**Functional domains:** Lists various domains found in the protein, such as:

- PF00443: Ubiquitin carboxyl-terminal hydrolase (HMPFam)
- PS0205: Ubiquitin specific protease (USP) domain profile, [ProSiteProfiles]
- SSF54001: (SUPERFAMILY)

**Blast results:** Displays a table of BLAST alignments against the NCBI database. The table includes columns: FJip Start, End, Len, %C, XID, Score, and Description (TaxName). Some entries are:

| FJip Start | End | Len | %C   | XID | Score | Description (TaxName)  |
|------------|-----|-----|------|-----|-------|--|
| 1          | 638 | 638 | 100% | 98% | 3332  | nr_b_b_jgi Aspph1 247693 247693 Cysteine proteinase [no tax name]    |
| 7          | 561 | 561 | 99%  | 99% | 2969  | nr_b_b_jgi Asppn_NRR3_1 5027 5027 hypothetical protein [no tax name] |
| 7          | 556 | 556 | 99%  | 79% | 2348  | nr_b_b_jgi Aspkal_1 15194 15194 hypothetical protein [no tax name]   |
| 7          | 556 | 556 | 99%  | 79% | 2340  | nr_b_b_jgi Aspecul 414728 414728 Cysteine proteinase [no tax name]   |
| 7          | 556 | 556 | 99%  | 79% | 2333  | nr_b_b_jgi Aspppl 425235 425235 Cysteine proteinase [no tax name]    |
| 7          | 556 | 556 | 99%  | 79% | 2320  | nr_b_b_jgi Asptul 32206 32206 hypothetical protein [no tax name]     |
| 7          | 554 | 556 | 99%  | 78% | 2302  | nr_b_b_jgi Aspol 63691 63691 hypothetical protein [no tax name]      |
| 7          | 556 | 556 | 99%  | 78% | 2301  | nr_b_b_jgi Aspnedl 310946 310946 Cysteine proteinase [no tax name]   |
| 7          | 556 | 556 | 99%  | 78% | 2299  | nr_b_b_jgi Aspvadl 431945 431945 Cysteine proteinase [no tax name]   |
| 7          | 556 | 556 | 99%  | 78% | 2295  | nr_b_b_jgi Asposnl 276000 276000 Cysteine proteinase [no tax name]   |

## EXERCISES:

1. Go to the test portal for this course at [mycocosm.jgi.doe.gov/Rhoto1\\_AP2687\\_1/](http://mycocosm.jgi.doe.gov/Rhoto1_AP2687_1/)

2. Hide all gene model tracks except the Gene Catalog and make all SNP tracks visible on the browser. Identify genes that show SNP variation within coding sequence and explore the protein pages of those genes.
3. Using the navigation tools to scroll, compare the RNA coverage tracks (from different conditions) to identify additional genes that show different expression profiles and identify what those genes are.
4. Using the data displayed on the browser, identify and take note of regions which need manual curation. Note: curation privileges were granted only to this specific genome portal. We will learn more about manual curation tools in this workshop.

## MycoCosm Group Portals

In addition to single genome portals, MycoCosm also hosts groups of genomes in ‘Group portals.’ These groups are either based on phylogeny (‘PhyloGroups,’ e.g. ‘Pezizomycetes’) in an automatic way, or on a common feature such as a lifestyle (‘EcoGroups,’ e.g. ‘Plant Pathogens’) in a more curated effort. We will look at phylogenetic groups in this exercise by starting at the MycoCosm home page.

Browse the cartoon phylogeny by clicking on a node or leaf. Each node and leaf has a menu of links to the associated Group Portal, several Group tools, and each member Genome Portal. The Pezizomycetes are an important class of Ascomycota that includes truffles and morels, and both saprobes and mycorrhizal symbionts. Let’s find out more about them by clicking on the ‘Pezizomycetes’ leaf, and selecting the top ‘Pezizomycetes’ link in the menu.

The screenshot shows the MycoCosm home page with a phylogenetic tree on the left. A green arrow points to the 'Pezizomycetes' node, which is highlighted with a green box. A dropdown menu for 'All MycoCosm Groups' is open, showing a list of phylogenetic groups. The 'Pezizomycetes' group is listed first, followed by other groups like Agaricomycotina, Dikarya, Mucoromycotina, Zoopagomycotina, Chytridiomycotina, and Fungi. To the right of the tree, there is a search bar for JGI Data and a search button for MycoCosm. Below the tree, there is a section for 'Latest Additions' with a list of new fungal species. At the bottom, there is contact information and logos for the U.S. Department of Energy Office of Science.

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To use the tree navigation click a b

For MycoCosm, please cite: Igor Riley, Asaf Salamov, Xueling Zhao, MycoCosm portal: gearing up for 1 D699–D704, DOI:10.1093/nar/gkt1

For JGI Fungal Program, please Jeffries, Christian P. Kubicek, Cher Baker (2011) Fueling the future with

J. Kuo, Robin Ohm, Robert Otillar, Robert Nordberg, Inna Dubchak, Igor Shabalov, volume 42, Issue D1, 1 January 2014, Pages 10.1080/21501203.2011.584577

Goodwin, David Hibbett, Thomas W. Philip W. Spathafora, Adrian Tsang & Scott E. 10.1080/21501203.2011.584577

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## Anatomy of a MycoCosm Group Portal

The default view of a Group Portal shows a hyperlinked list of all of the member genomes, basic statistics of each genome, and the primary associated publication, if any. Genome names are linked to their Genome Portals, and publications to PubMed. The Pezizomycetes Group currently consists of 80 genomes, 27 of which are published.

| Info • Pezizomycetes  |             |        |  |          |              |             |          |      |       |
|---|-------------|--------|--|----------|--------------|-------------|----------|------|-------|
| TREE  | SEARCH      | BLAST  | ANNOTATIONS ▾                              | PATHWAYS | MCL CLUSTERS | GEO MAPPING | DOWNLOAD | INFO | HELP! |
| <b>## Name</b> <b>Assembly Length</b> <b># Genes</b> <b>Published</b> |             |        |  |          |              |             |          |      |       |
| 1 <a href="#">Anthracobia sp. CZU v1.0</a>                            | 53,428,419  | 14,194 |  |          |              |             |          |      |       |
| 2 <a href="#">Ascobolus immersus RN42 v1.0</a>                        | 59,529,874  | 17,877 | <a href="#">Murat C et al., 2018</a>       |          |              |             |          |      |       |
| 3 <a href="#">Ascodesmis nigricans CBS 389.68 v1.0</a>                | 27,385,218  | 9,622  | <a href="#">Lütkenhaus R et al., 2019</a>  |          |              |             |          |      |       |
| 4 <a href="#">Caloscypha fulgens ATCC 42695 v1.0</a>                  | 44,839,139  | 9,203  |  |          |              |             |          |      |       |
| 5 <a href="#">Choiromyces venosus 120613-1 v1.0</a>                   | 126,035,033 | 17,986 | <a href="#">Murat C et al., 2018</a>       |          |              |             |          |      |       |
| 6 <a href="#">Disciotis venosa NRRL 24433 v1.0</a>                    | 45,269,384  | 11,264 |  |          |              |             |          |      |       |
| 7 <a href="#">Geopyxis carbonaria CBS 144460 v1.0</a>                 | 49,454,325  | 11,663 | <a href="#">Steindorff AS et al., 2022</a> |          |              |             |          |      |       |
| 8 <a href="#">Gyromitra esculenta CBS101906 v1.0</a>                  | 45,046,303  | 11,202 | <a href="#">Dirks AC et al., 2025</a>      |          |              |             |          |      |       |
| 9 <a href="#">Gyromitra infula GyrinfSpk-SM18 v1.0</a>                | 45,877,806  | 11,121 | <a href="#">Dirks AC et al., 2025</a>      |          |              |             |          |      |       |
| 10 <a href="#">Kalaharituber pfeilii F3 v1.0</a>                      | 78,991,937  | 15,190 | <a href="#">Miyauchi S et al., 2020</a>    |          |              |             |          |      |       |
| 11 <a href="#">Kalapuya brunnea GMNB372 v1.0</a>                      | 189,316,756 | 11,095 |  |          |              |             |          |      |       |
| 12 <a href="#">Leucangium carthusianum GMNB180 v1.0</a>               | 114,191,169 | 12,369 |  |          |              |             |          |      |       |
| 13 <a href="#">Mattirolomyces terfezioides MAT_tt4AIII v1.0</a>       | 50,061,460  | 10,894 |  |          |              |             |          |      |       |
| 14 <a href="#">Morchella americana PhC 192 v1.0</a>                   | 63,616,142  | 11,032 |  |          |              |             |          |      |       |
| 15 <a href="#">Morchella anatolica PhC 233 v1.0</a>                   | 57,520,386  | 10,630 |  |          |              |             |          |      |       |
| 16 <a href="#">Morchella angusticeps Mel-15 v1.0</a>                  | 56,785,355  | 11,637 |  |          |              |             |          |      |       |
| 17 <a href="#">Morchella arbutiphila PhC 291 v1.0</a>                 | 54,167,150  | 11,179 |  |          |              |             |          |      |       |
| 18 <a href="#">Morchella brunnea JGI1270818 v1.0</a>                  | 54,761,096  | 11,196 |  |          |              |             |          |      |       |
| 19 <a href="#">Morchella brunnea NRRL 20869 v1.0</a>                  | 56,688,582  | 10,595 |  |          |              |             |          |      |       |
| 20 <a href="#">Morchella conifericola Mel-32 v1.0</a>                 | 52,567,085  | 10,590 |  |          |              |             |          |      |       |
| 21 <a href="#">Morchella crassipes M84 v1.0</a>                       | 54,774,707  | 10,480 |  |          |              |             |          |      |       |
| 22 <a href="#">Morchella deliciosa PhC 191 v1.0</a>                   | 56,658,686  | 11,470 |  |          |              |             |          |      |       |
| 23 <a href="#">Morchella diminutiva Mes-2 v1.0</a>                    | 53,423,193  | 10,998 |  |          |              |             |          |      |       |
| 24 <a href="#">Morchella disparilis PhC 293 v1.0</a>                  | 50,421,455  | 10,570 |  |          |              |             |          |      |       |
| 25 <a href="#">Morchella dunali PhC 240 v1.0</a>                      | 50,708,236  | 10,363 |  |          |              |             |          |      |       |
| 26 <a href="#">Morchella eohespera Mel-19 v1.0</a>                    | 52,040,391  | 10,683 |  |          |              |             |          |      |       |
| 27 <a href="#">Morchella esculenta PhC 158 v1.0</a>                   | 51,151,225  | 10,777 |  |          |              |             |          |      |       |

Note the navigation tool bar at the top of the Group Page. Here it contains many of the same viewing, searching, and browsing functions as in the single genome portal, however with the notable absence of home, synteny, and genome browser tools (as these do not make sense for group portals). You can similarly find the context-dependent ‘HELP!’ function, that provides useful information specific to the current page. The ‘DOWNLOAD’ function is also available, from which you may, if registered and logged in, download files from all genomes in this Group, including genomic and transcriptomic assemblies, as well as structural and functional annotations.

Click on SEARCH to try the text-based search tool for all genomes in this group.

The default search is for keywords in the Default Analysis Track (the accepted gene model set) of each genome in the group. Pulldown menus allow choices other than the default settings.

Search • Pezizomyces

TREE SEARCH BLAST ANNOTATIONS PATHWAYS MITOCHONDRIA MCL CLUSTERS GEO MAPPING DOWNLOAD INFO ADMIN HELP!

Search By: Across: Terms:

Keywords Model Name default exact - fast

Model Name  
Protein Id  
Transcript Id  
Track  
Go Terms  
Go Terms and Descriptions  
Go Lineage  
Go Lineage and Descriptions  
PFAM Terms  
PFAM Terms and Descriptions  
KOG Terms  
KOG Terms and Description  
KOG Function and Description  
KEGG Terms  
KEGG Terms and Descriptions  
KEGG Pathway and Descriptions  
CAZY Terms  
CAZY Terms and Description  
User annotations

impressed by Gzip

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Multiple search terms are combined using a logical ‘AND’, meaning that a search for the terms ‘pheromone receptor’ will return only results containing both ‘pheromone’ and ‘receptor’. Try it! The basic anatomy of search output is shown below.

Links to

- protein page
- annotation page
- genome browser

Search • Phanerochaete chrysosporum RP-78 v2.2

| Gene  | Gene Ontology  | Annotations   | User Annotations   |
|---|--|---|--|
| Portal: Phchr2<br>Portal Name: Phanerochaete chrysosporum RP-78 v2.2<br>Protein id: 2912118<br>Transcript id: 2912333<br>Location: scaffold_10_92485_9269 [ ]<br>Model Name: e_gw1.10.150.1<br>Track: Genewise1Plus | GO:0005199 • structural constituent of cell wall<br>GO:0005618 • cell wall | PF01185 • Fungal hydrophobin<br>IPR001338 • Hydrophobin |  |
| Portal: Phchr2<br>Portal Name: Phanerochaete chrysosporum RP-78 v2.2<br>Protein id: 3027085<br>Transcript id: 3027300<br>Location: scaffold_6_1957160_1957677 [ ]<br>Model Name: gmt5302_g<br>Track: Genemark1      | GO:0005199 • structural constituent of cell wall<br>GO:0005618 • cell wall | PF01185 • Fungal hydrophobin<br>IPR001338 • Hydrophobin |  |
| Portal: Phchr2<br>Portal Name: Phanerochaete chrysosporum RP-78 v2.2<br>Protein id: 3027111<br>Transcript id: 3027326<br>Location: scaffold_10_94466_95058 [ ]<br>Model Name: gmt7326_g<br>Track: Genemark1         | GO:0005199 • structural constituent of cell wall<br>GO:0005618 • cell wall | PF01185 • Fungal hydrophobin<br>IPR001338 • Hydrophobin |  |
| Portal: Phchr2<br>Portal Name: Phanerochaete chrysosporum RP-78 v2.2<br>Protein id: 3030349<br>Transcript id: 3030555<br>Location: scaffold_12_679129_679642 [ ]<br>Model Name: gmt8557_g<br>Track: Genemark1       | GO:0005199 • structural constituent of cell wall<br>GO:0005618 • cell wall | PF01185 • Fungal hydrophobin<br>IPR001338 • Hydrophobin | Name: Pch12 ( <a href="#">Ursula Kies</a> , 2011-08-15)<br>Description: class I hydrophobin ( <a href="#">Ursula Kies</a> , 2011-08-15)<br>Define: class I hydrophobin ( <a href="#">Ursula Kies</a> , 2011-08-15) |

Links to external databases

Manual annotations from users

The search output provides links to the genome portals, genome browser, protein pages, and functional annotations.

Exercise: Use the ‘Lichens’ group identified in the previous exercise for this exercise ([mycocosm.jgi.doe.gov/lichens](http://mycocosm.jgi.doe.gov/lichens)). How many genes in these genomes have Pfam annotations?

Hint: You can find this using the prefix ‘HMMPfam’ common to all Pfam annotations in MycoCosm.

There are multiple additional ways to investigate the Group. For example, the navigation bar’s BLAST function will perform a Blast search against all genomes at once. Additional ANNOTATION functions include:

- MCL CLUSTERS – draft gene families clustered using Blastp and MCL
- PFAM DOMAINS - identified using InterProScan
- SMURF CLUSTERS – predicted secondary metabolism gene clusters based on Pfam domains
- CAZYMES – carbohydrate-active enzyme annotations done by the CAZy team ([www.cazy.org](http://www.cazy.org))
- PEPTIDASES – assignments made by Blastp against the highly curated MEROPS database ([www.ebi.ac.uk/merops](http://www.ebi.ac.uk/merops))
- TRANSPORTERS - assignments made by Blastp against the highly curated Transporter Classification Database ([www.tcdb.org](http://www.tcdb.org))
- TRANSCRIPTION FACTORS - assignments made by Blastp against an in-house curated database

We will explore a few of these in subsequent exercises. Now let’s look a little more closely at PEPTIDASES. Click on the tab in the menu bar to go to the PEPTIDASES page. Each row represents a Merops clan or family, and may be expanded or collapsed; clicking on the clan or family goes to the cognate Merops web page. Each column represents a genome and has a unique databaseID; the databaseID is short and often obscure, but the species and gene model set may be revealed by hovering over the databaseID. The number in each cell is the number of proteins in that genome with the assigned Merops classification. Clicking on it will present details about those proteins. For large groups like this one, you may need to scroll to the right to view the rest of the table.

Peptidases • Pezizomyctetes

TREE SEARCH BLAST ANNOTATIONS MCL CLUSTERS GEO MAPPING DOWNLOAD INFO HELP!

Search for: To Default Expand All

Any Keywords Exact Filter Clear

Annotations/Genomes

|          | Antsp2 | Ascm1 | Ascn1 | Cafu1 | Chov1 | Diven1 | Gesc1 | Gyres1 | Gyrinf1 | Kalbru1 | Katife1 | Leuca1 | Matter1 | Mordun1 | Moren1 | Mores1 | Moresx1 | Morem1 | Morflu1 | Mora11 | Moris1 | Morimp1 | Mortak1 | Mora11 | Morp1 |    |   |   |
|----------|--------|-------|-------|-------|-------|--------|-------|--------|---------|---------|---------|--------|---------|---------|--------|--------|---------|--------|---------|--------|--------|---------|---------|--------|-------|----|---|---|
| ↳ Merops | 221    | 218   | 177   | 188   | 217   | 219    | 225   | 210    | 243     | 192     | 209     | 193    | 228     | 200     | 203    | 205    | 201     | 200    | 221     | 203    | 232    | 209     | 210     | 205    | 211   |    |   |   |
| ↳ AA     | 6      | 5     | 5     | 6     | 9     | 6      | 7     | 7      | 8       | 5       | 5       | 6      | 9       | 8       | 6      | 6      | 5       | 5      | 6       | 5      | 6      | 6       | 4       | 5      | 7     | 5  |   |   |
| ↳ AC     | 1      |       |       |       |       |        |       | 2      | 1       |         |         |        |         |         | 1      | 2      | 1       | 1      | 1       | 1      | 1      | 3       | 2       | 1      | 3     | 1  |   |   |
| ↳ AD     | 4      | 4     | 3     | 3     | 4     | 6      | 2     | 2      | 3       | 2       | 3       | 2      | 3       | 2       | 3      | 2      | 1       | 3      | 2       | 2      | 2      | 2       | 1       | 1      | 1     |    |   |   |
| ↳ CA     | 24     | 19    | 18    | 25    | 23    | 22     | 28    | 24     | 21      | 21      | 26      | 22     |         |         | 3      | 24     | 24      | 23     | 27      | 25     | 24     | 28      | 21      | 24     | 27    | 24 |   |   |
| ↳ CD     | 3      | 2     | 2     | 2     | 2     | 2      | 2     | 2      | 2       | 2       | 2       | 4      | 2       |         | 2      | 2      | 2       | 2      | 2       | 2      | 2      | 2       | 2       | 2      | 2     |    |   |   |
| ↳ CE     | 1      | 2     |       | 1     | 3     | 2      | 2     | 1      | 1       | 1       | 1       | 1      |         |         | 1      | 2      | 1       | 1      | 1       | 11     | 2      | 2       | 2       | 1      | 1     | 1  |   |   |
| ↳ CF     | 1      | 1     | 1     | 1     | 1     | 1      | 1     | 1      | 1       | 1       | 1       | 1      |         |         | 1      | 1      | 1       | 1      | 1       | 1      | 1      | 1       | 1       | 1      | 1     | 1  |   |   |
| ↳ CO     | 1      | 2     | 1     | 1     | 1     |        |       |        |         |         |         |        |         |         |        | 1      | 1       | 1      | 1       | 1      | 1      | 1       | 1       | 1      | 1     | 1  | 1 |   |
| ↳ CP     | 1      | 1     | 1     | 1     | 1     | 1      |       |        |         |         |         |        |         |         |        |        | 1       | 1      | 1       | 1      | 1      | 1       | 1       | 1      | 1     | 1  | 1 | 1 |
| ↳ GA     |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |
| ↳ GB     |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |
| ↳ L      |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |
| ↳ Kazal  |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |
| ↳ ID     |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |
| ↳ IL     |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |
| ↳ IV     |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |
| ↳ JC     |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |
| ↳ JE     |        |       |       |       |       |        |       |        |         |         |         |        |         |         |        |        |         |        |         |        |        |         |         |        |       |    |   |   |

Annotations/Genomes

Search by Keywords or Annotations

Click on number to go to web page with details about those proteins

Expand Merops classifications or click ID to go to clan/family page

Hover over to reveal organism

Scroll to the right to view last columns; total count and Annotation Description

Let's search for a specific type of protein by entering 'subtilase' in the 'Search for:' textbox and clicking on 'Filter'. This search by 'Keywords' will look for matches to domain descriptions. Now only subtilase-related clans and families are shown (and inhibitors thereof). Note that the S08.115 peptidases are found only in a handful of organisms, mostly saprobes. To search by the specific Merops ID, enter 'S08.115' in the Search box, change the dropdown selection to 'Annotation', and click 'Filter'. The right-most column of numbers are totals for that Merops row, so let us click on the '10' to learn more about these proteases.

Rows: 10 25 rows per page

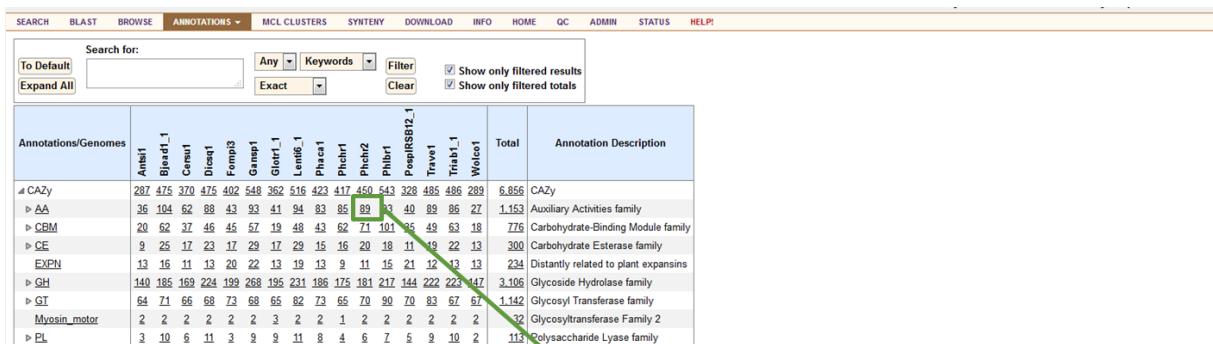
| Protein Id     | Location                       | Gene Length | Protein Length | Merops Annotations    | Domains                                     | Models Domains           |
|----------------|--------------------------------|-------------|----------------|-----------------------|---|--------------------------|
| Ascm1_321137   | scaffold_3:818,001-819,568     | 1,568       | 401            | • S08.115             | • Subtilase family                          | 213 189 423 109 84 185   |
| Ascm1_326276   | scaffold_34:203,990-205,048    | 1,059       | 276            | • S08.115             |   | 84 76 60 87 58           |
| Ascm1_211249   | scaffold_57:190,517-189,456    | 1,062       | 306            | • S08.115             | • Subtilase family                          | 108 49 408 49 54 79      |
| Ascn1_363694   | scaffold_7:535,694-537,533     | 1,840       | 453            | • S08.115             | • Subtilase family • Peptidase inhibitor I9 | 406 90 89 54 423         |
| Ascn1_359457   | scaffold_19:313,495-311,891    | 1,605       | 419            | • cerevisin • S08.115 | • Subtilase family • Peptidase inhibitor I9 | 516 96 791 57 380        |
| Morpon1_602957 | scaffold_99:102,934-101,805    | 1,130       | 251            | • S08.115             | • Subtilase family                          | 485 52 120 81 363 252 33 |
| Morpr1_711690  | scaffold_5:2,218,063-2,220,014 | 1,952       | 480            | • S08.115             | • Subtilase family • Peptidase inhibitor I9 | 156 271 200 56 326       |
| Sarco1_402179  | scaffold_8:110,499-109,257     | 1,243       | 379            | • S08.115             | • Subtilase family • Peptidase inhibitor I9 | 532 499 289 337 190      |
| Sarco1_418028  | scaffold_283:11,576-10,133     | 1,444       | 415            | • cerevisin • S08.115 | • Subtilase family • Peptidase inhibitor I9 | 234 55 51 623 144        |
| Tubb1_1_876549 | scaffold_441:86,341-86,006     | 336         | 112            | • S08.115             |   | 413 57 47 45 336 50      |

The list of proteins shows basic information of the underlying gene models. The left-most column is the databaseID and proteinId, which together provide a unique identifier for the gene model in MycoCosm. The next 5 columns are self-explanatory, but note that Location is linked to the Browse view of that Genome Portal, and Merops and Domains are linked to the corresponding page on Merops and Pfam domains on EBI's InterPro site. The right-most column is by default in 'Models' mode and shows the exon-intron structure of each gene.

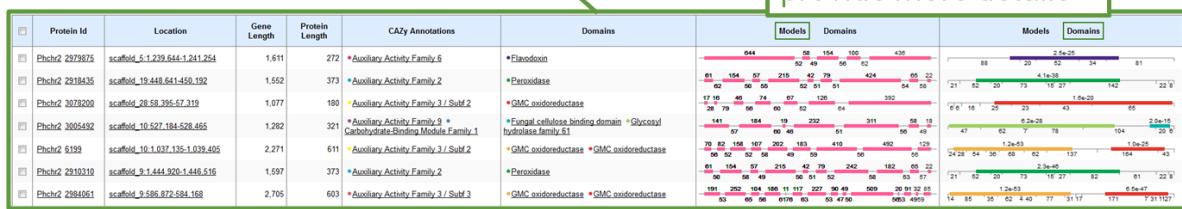
Click on ‘Domains’ to view the domain structure of the proteins. As is often the case with subtilases, the gene product is a pre-protein with a peptidase inhibitor domain that likely must be cleaved off before the mature proteinase can function as such.

| Protein Id     | Location                       | Gene Length | Protein Length | Merops Annotations  | Domains                                   | Models              | Domains         |
|----------------|--------------------------------|-------------|----------------|---------------------|---|---------------------|-----------------|
| Ascim1_321137  | scaffold_3:818.001-819.568     | 1,568       | 401            | •S08.115            | •Subtilase family                         |                     | 1.7e-22         |
| Ascim1_326276  | scaffold_34:203.980-205.048    | 1,059       | 276            | •S08.115            |   | 71 63 141 37 29 62  |                 |
| Ascim1_211249  | scaffold_57:190.517-189.456    | 1,062       | 306            | •S08.115            | •Subtilase family                         |                     | 3.8e-51         |
| Ascn1_363694   | scaffold_7:535.694-537.533     | 1,840       | 453            | •S08.115            | •Subtilase family •Peptidase inhibitor I9 | 3.3e-06 264 79      | 5.0e-37         |
| Ascn1_359457   | scaffold_19:313.495-311.891    | 1,605       | 419            | •cerevisin •S08.115 | •Subtilase family •Peptidase inhibitor I9 | 136 40 27 121 84 11 | 1.2e-15 5.0e-69 |
| Morpop1_602957 | scaffold_99:102.934-101.805    | 1,130       | 251            | •S08.115            | •Subtilase family                         | 62 91 109           | 5.1e-27         |
| Morpra1_711690 | scaffold_5:2,218.063-2,220.014 | 1,952       | 480            | •S08.115            | •Subtilase family •Peptidase inhibitor I9 | 154 167 97 64       | 6.2e-07 4.2e-20 |
| Sarco1_402179  | scaffold_8:110.499-109.257     | 1,243       | 379            | •S08.115            | •Subtilase family •Peptidase inhibitor I9 | 78 94 208           | 1.2e-15 2.4e-71 |
| Sarco1_418028  | scaffold_283:11.576-10.133     | 1,444       | 415            | •cerevisin •S08.115 | •Subtilase family •Peptidase inhibitor I9 | 138 36 31 165 48    | 1.2e-15 3.7e-60 |
| Tubb1_1_876549 | scaffold_441:86.341-86.006     | 336         | 112            | •S08.115            |   |                     | 112             |

A similar set of tools is available for other functional annotations. For example, the tools in CAZYMES are shown below.

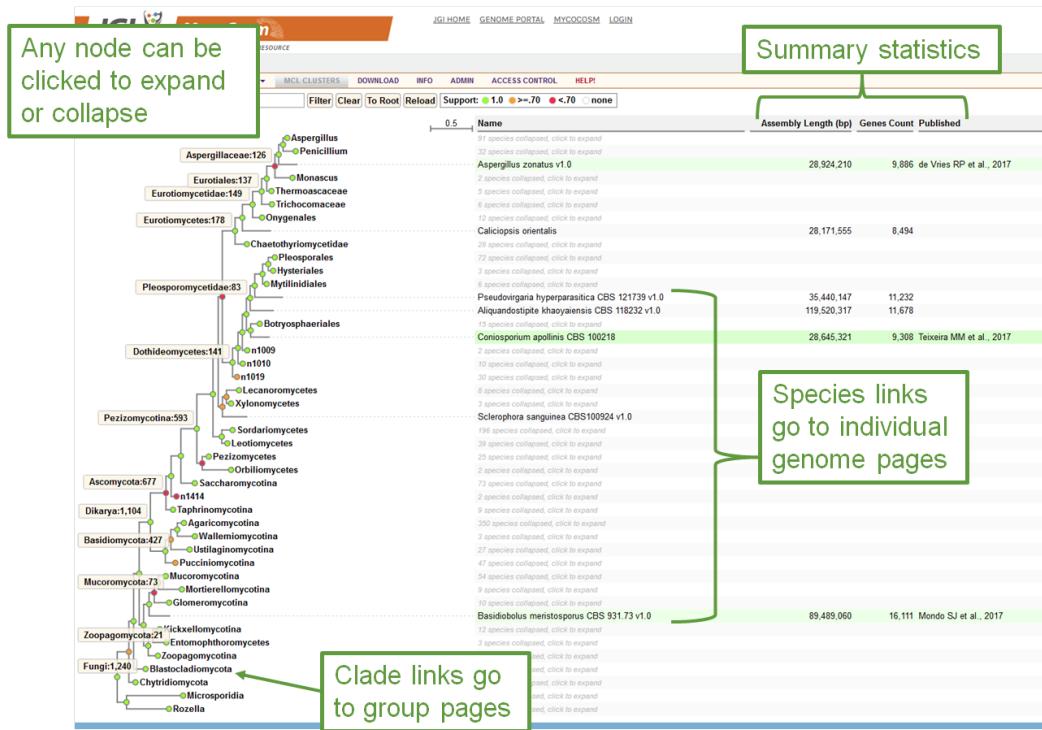


Click on counts to provide more details



So far, we have browsed the Group based on common (or uncommon) functional annotation. Another way to browse is based on phylogeny, and may be accessed through the Menu bar's Tree Item. Click on it:

Unlike the cartoon on the MycoCosm home page, this tree, and others associated with each Group, is calculated by JGI using the clusters mentioned above, followed by MAFFT alignment of presumptive orthologs and FastTree modeling. Sometimes unexpected branchings appear that contradict other resources such as NCBI Taxonomy, but not in this case. The nodes are selectable, collapsible, and expandable. The table to the right of the tree recapitulates the Group data we saw earlier. The basic tools available in the tree view are shown below using the whole MycoCosm fungal tree as an example.



Let's take a look at a larger tree, the Eurotiomycetes. The main driver for the growth in Eurotiomycetes is JGI's *Aspergillus* Whole-Genus Sequencing Project, with the goal of sequencing ~300 species of *Aspergillus*.

Click on the MycoCosm link at the top of the page, above the Menu bar, to go back to the MycoCosm home page. From there, go to the Eurotiomycetes Group Portal. Or even better, on the leaf's menu click on 'Search' rather than the Group link, to go straight to the Group's Search tool. This way we don't have to wait for the entire list of genomes to load. Next, look for the known *Aspergillus nidulans* septin. Enter the GeneID "AN8182" into the Search box. We get a single gene, as expected.

Search • Eurotiomycetes

---

[TREE](#) [SEARCH](#) [BLAST](#) [ANNOTATIONS](#) [PATHWAYS](#) [MITOCHONDRIA](#) [MCL CLUSTERS](#) [GEO MAPPING](#) [DOWNLOAD](#) [INFO](#) [ADMIN](#) [HELP!](#)

AN8182

Search By:
Across:
Terms:

Keywords
Default
exact - fast

Download
as CSV
compressed by Gzip

Total genes found: 1

| Gene  | Gene Ontology   | Annotations   | User Annotations |
|---|---|---|------------------|
| Portal: <a href="#">Aspnid1</a><br>Portal Name: <b>Aspergillus nidulans</b><br><b>Protein Id:</b> <a href="#">1633</a> <br>Transcript Id: <a href="#">1813</a><br>Location: <a href="#">ChrII_A_nidulans_FGSC_A4:1046574-1048647(-)</a><br>Model Name: <b>AN8182</b><br>Track: <a href="#">AspGD_genes</a> | <b>GO:0004182</b> • obsolete carboxypeptidase A activity<br><b>GO:0005515</b> • protein binding<br><b>GO:0005525</b> • GTP binding<br><b>GO:0006508</b> • proteolysis<br><b>GO:0007049</b> • cell cycle<br><b>GO:0008270</b> • zinc ion binding<br><b>GO:0031105</b> • septin complex | <b>KOG2655</b> • Septin family protein (P-loop GTPase)<br><b>PF00735</b> • Septin<br><b>IPR000038</b> • missing_ipr000038<br><b>IPR016491</b> •<br><b>IPR000834</b> • |                  |

Click on the Protein ID 1633. This show the protein page for this gene and protein, which is part of the Aspnid1 Genome Portal. We will see more of the protein page in later exercises. *A. nidulans* was not sequenced at JGI. Instead this genome was imported from AspGD ([www.aspergillusgenome.org](http://www.aspergillusgenome.org)). This genome has also been imported by FungiDB, and again this page has a link to the corresponding FungiDB page. Try it!

|                    |  |  |                                       |                                   |
|--------------------|--|--|---------------------------------------|-----------------------------------|
| Name:              | AN8182   |  |                                       |                                   |
| Protein ID:        | 1633   |  |                                       |                                   |
| Location:          | <a href="#">ChrII_A_nidulans_FGSC_A4:1046574-1048647</a>   |  |                                       |                                   |
| Strand:            | -  |  |                                       |                                   |
| Number of exons:   | 7  |  |                                       |                                   |
| Description:       |  |  |                                       |                                   |
| FungiDB:           | <a href="#">Link to AN8182 in FungiDB</a>  |  |                                       |                                   |
| AspGD:             | <a href="#">Link to AN8182 in the Aspergillus Genome Database (AspGD)</a>  |  |                                       |                                   |
| Best Hit:          | gi 259480955 ipe CBF-74054.1  TPA; Septin Fragment [Source:UniProtKB/TrEMBL;Acc:Q9C1M2] [Aspergillus nidulans FGSC A4] (model%: 99, hit%: 100, score: 1918, %id: 100) [Aspergillus nidulans FGSC A4] |  |                                       |                                   |
| total hits(shown)  | 347 (10)   |  |                                       |                                   |
| <b>ASPECT</b>      | <b>GO Id</b>   | <b>GO Desc</b>   | <b>Interpro Id</b>                    | <b>Interpro Desc</b>              |
| Molecular Function | 0005515  | protein binding  | IPR016491                             | Septin                            |
|                    | 0005525  | GTP binding  | IPR000038                             | Cell division/GTP binding protein |
|                    | 0004182  | carboxypeptidase A activity                              | IPR000834                             | Peptidase M14, carboxypeptidase A |
| Biological Process | 0008270  | zinc ion binding   | IPR000834                             | Peptidase M14, carboxypeptidase A |
|                    | 0006508  | proteolysis and peptidolysis                             | IPR000834                             | Peptidase M14, carboxypeptidase A |
|                    | 0007049  | cell cycle   | IPR000038                             | Cell division/GTP binding protein |
| <b>KOG GROUP</b>   | <b>KOG Id</b>  | <b>KOG Class</b>   | <b>KOG Desc</b>                       |                                   |
| Metabolism         | KOG2655  | Cell_cycle_control_cell_division_chromosome_partitioning | Septin family protein (P-loop GTPase) |                                   |

Finally, for additional resources outside of this workshop, there are video tutorials available to the public on the MycoCosm homepage that walkthrough different features of the portal.

**JGI**  **MycoCosm**   
THE FUNGAL GENOMICS RESOURCE

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**1000 Fungal Genomes project**  
[Nominate New Species!](#)

**Genomic Encyclopedia of Fungi**  
[Submit CSP proposal](#)

**Myco-Ed Genomics Initiative**

**Announcements**

Jun 2-6, 2025  
Fungal Pathogen Genomics Virtual Course:  
Fungal Pathogen Genomics

Jun 28-Jul 2, 2025  
Mycological Society of America meeting  
Madison, WI

**Latest Additions**

May 01, 2025  
*Collariella robusta* PSN 660 v1.0

May 01, 2025  
*Diplogelasinopora inaequalis* CBS 436.74 v1.0

May 01, 2025  
*Zopfiella marina* IMI 229743 v1.0

May 01, 2025  
*Schizothecium carpinicola* IMI 314718 v1.0

May 01, 2025  
*Apodus* sp. PSN 540 v1.0

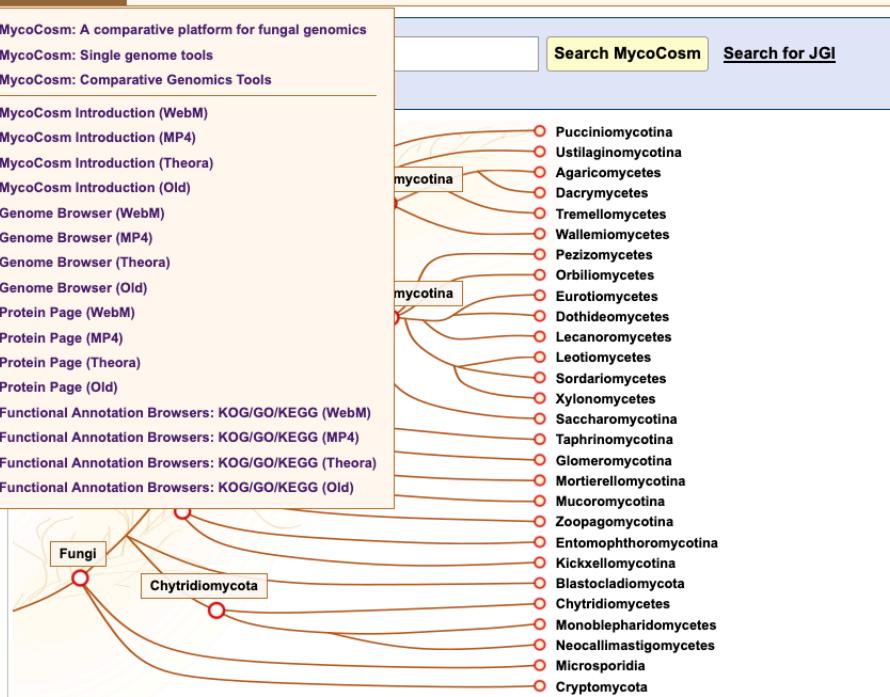
May 01, 2025  
*Lasiophaeria similiisorbina* ILLS00125647 v1.0

[more...](#)

**Video Tutorials**

- MycoCosm: A comparative platform for fungal genomics
- MycoCosm: Single genome tools
- MycoCosm: Comparative Genomics Tools
- MycoCosm Introduction (WebM)
- MycoCosm Introduction (MP4)
- MycoCosm Introduction (Theora)
- MycoCosm Introduction (Old)
- Genome Browser (WebM)
- Genome Browser (MP4)
- Genome Browser (Theora)
- Genome Browser (Old)
- Protein Page (WebM)
- Protein Page (MP4)
- Protein Page (Theora)
- Protein Page (Old)
- Functional Annotation Browsers: KOG/GO/KEGG (WebM)
- Functional Annotation Browsers: KOG/GO/KEGG (MP4)
- Functional Annotation Browsers: KOG/GO/KEGG (Theora)
- Functional Annotation Browsers: KOG/GO/KEGG (Old)

**Search MycoCosm** **Search for JGI**



To use the tree navigation click a branch name and select an organism from the list.

**For MycoCosm, please cite:** Igor V. Grigoriev, Roman Nikitin, Sajeet Haridas, Alan Kuo, Robin Ohm, Robert Otiilar, Robert Riley, Asaf Salamov, Xueling Zhao, Frank Korzeniewski, Tatjana Smirnova, Henrik Nordberg, Inna Dubchak, Igor Shabalov, MycoCosm portal: gearing up for 1000 fungal genomes, Nucleic Acids Research, Volume 42, Issue D1, 1 January 2014, Pages D699–D704, DOI:10.1093/nar/gkt1183

**For JGI Fungal Program, please cite:** Igor V. Grigoriev, Daniel Cullen, Stephen B. Goodwin, David Hibbett, Thomas W. Jeffries, Christian P. Kubicek, Cheryl Kuske, Jon K. Magnuson, Francis Martin, Joseph W. Spatafora, Adrian Tsang & Scott E. Baker (2011) Fueling the future with fungal genomics, Mycology, 2:3, 192-209, DOI:10.1080/21501203.2011.584577

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Mycocsm Portal version:19.317 myco-web-1.jgi.lbl.gov Release Date:15-May-2025 15:06:31 PST Current Date:15-May-2025 19:30:47.661 PDT