

Demo: Ensembl Fungi gene trees and homologues

Let's look at the homologues of *Saccharomyces cerevisiae* YPR140W aka Taz1. This gene is involved in stress response and conserved across different taxonomic domains. Search for the gene and go to the Gene tab.

Click on [Fungal compara: Gene tree](#), which will display the current gene in the context of a phylogenetic tree used to determine orthologues and paralogues.

Summary statistics

GeneTree [ENSGT0093000005979](#) Unique gene tree ID

Number of genes	186
Number of speciation nodes	158
Number of duplication nodes	18
Number of ambiguous nodes	9
Number of gene split events	0

Highlight annotations Hide annotations table

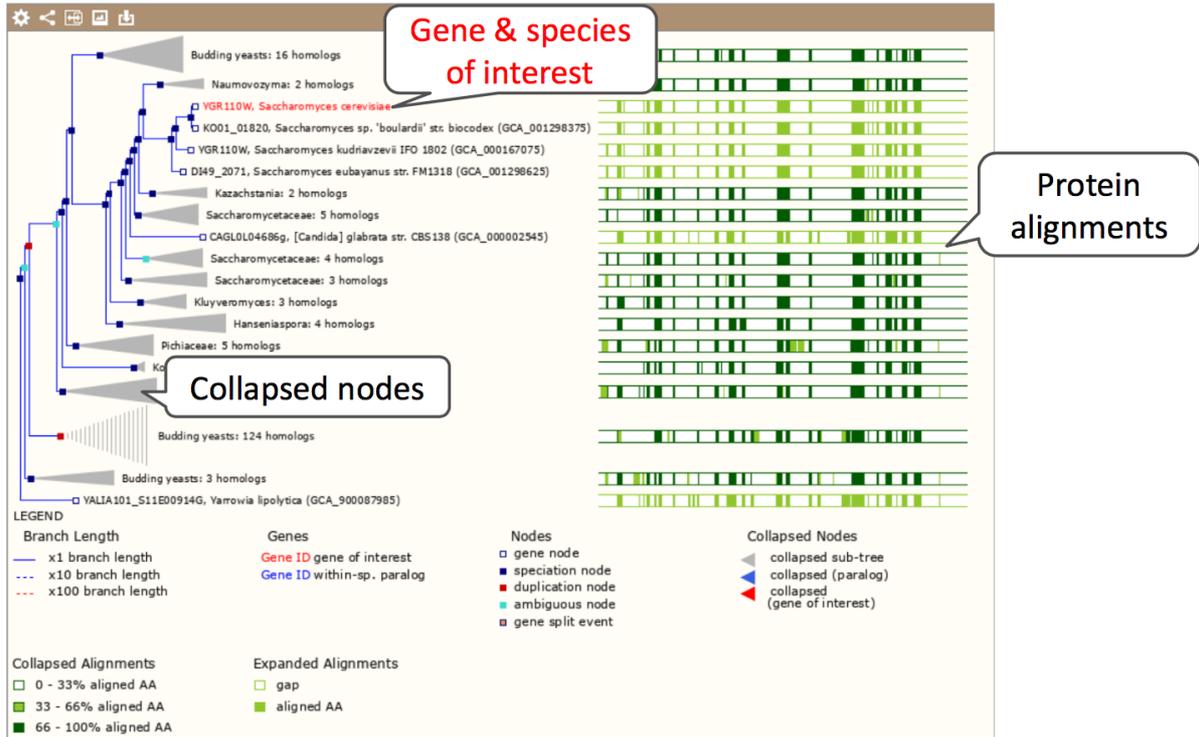
Show INTERPRO GO

Show 10 entries Filter

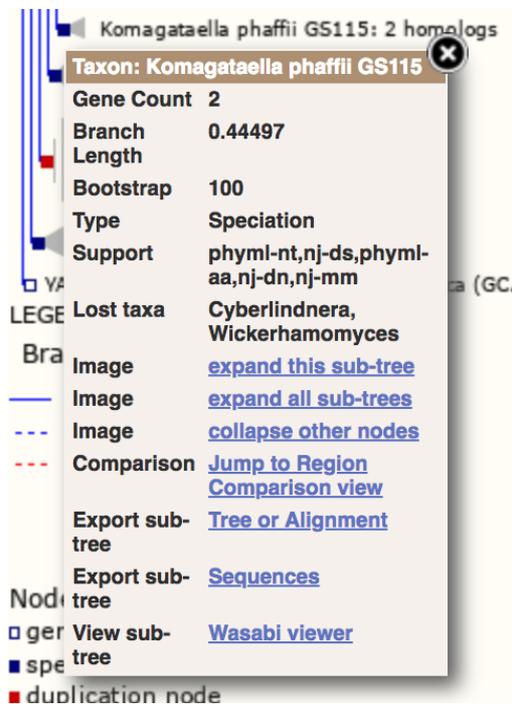
highlight	Accession	Description
72 members	GO:0003674	molecular_function
48 members	GO:0003824	catalytic activity
56 members	GO:0008150	biological_process
56 members	GO:0016787	hydrolase activity
56 members	GO:0006629	lipid metabolic process
56 members	GO:0006644	phospholipid metabolic process
56 members	GO:0006650	glycerophospholipid metabolic process
56 members	GO:0006793	phosphorus metabolic process
56 members	GO:0006796	phosphate-containing compound metabolic process
56 members	GO:0008152	metabolic process

Showing 1 to 10 of 80 entries << < 1 2 3 4 5 > >>

Filter tree by GO terms or Interpro protein domains



Funnels indicate collapsed nodes. Click on a node (coloured square) to get a pop-up. We can then see what type of node this is, some statistics and options to expand or export the sub-tree.



There are some quick filtering options below the image, where you can add paralogues, and quickly expand or collapse nodes.

Orthologues

[Download orthologues](#)

Summary of orthologues of this gene [Hide](#)

Click on 'Show details' to display the orthologues for one or more groups of species. Alternatively, click on 'Cont' species.

Orthologue types (mouse over for definitions)

Summary of orthologues by taxonomic group

Species set	Show details	With 1:1 orthologues	With 1:many orthologues	With many:many orthologues	Without orthologues
All (487 species)	<input checked="" type="checkbox"/>	53	6	0	428
Acidomyces (1 species)	<input type="checkbox"/>	0	0	0	1
Agaricales (24 species)	<input type="checkbox"/>	0	0	0	24
Atheliales (2 species)	<input type="checkbox"/>	0	0	0	2
Blastocladales (2 species)	<input type="checkbox"/>	0	0	0	2
Boletales (10 species)	<input type="checkbox"/>	0	0	0	10
Botryosphaerales (4 species)	<input type="checkbox"/>	0	0	0	4
Cantharellales (3 species)	<input type="checkbox"/>	0	0	0	3
Caenodiales (14 species)	<input type="checkbox"/>	0	0	0	14

Choose a taxon of interest

Similarity metrics

Filter table

Orthologue details per species

Species	Type	Orthologue	dN/dS	Target %id	Query %id	GOC Score	WGA	...
[Candida] auris str. 6684 (GCA_001189475)	1-to-1	QG37_03321	n/a	37.96 %	36.85 %	n/a	n/a	n/a
[Candida] glabrata str. CBS138 (GCA_000002545)	1-to-1	CAGL0L04686g	n/a	46.34 %	46.97 %	n/a	n/a	n/a
Ascoidea rubescens DSM 1968 (GCA_001661345)	1-to-1	ASCRUDRAFT_74793	n/a	29.16 %	33.48 %	n/a	n/a	n/a

Scroll to the bottom of the page to see a list of the species that do not have any orthologues with taz1 in *Saccharomyces cerevisiae*... there's a lot!

Species without orthologues

460 species are not shown in the table above because they don't have any orthologue with YPR140W.

- Absidia glauca
- Acidomyces richmondensis BFW
- Acremonium chrysogenum ATCC 11550
- Agaricus bisporus var. burnettii JB137-S8
- Allomyces macrogynus ATCC 38327
- Alternaria alternata
- Amanita muscaria Koide BX008

Saccharomyces cerevisiae is part of Pan-compara, which compares a subset of fungal species with species from other taxa, such as plants, bacteria and vertebrates.

Click on [Pan-taxonomic compara > Orthologues](#). Let's see if there are any orthologues of this gene in plants. Click the 'Show details' box for plants.

Species set	Show details	With 1:1 orthologues	With 1:many orthologues	With many:many orthologues	Without orthologues
All (187 species)	<input type="checkbox"/>	8	1	1	177
Vertebrates (0 species)	<input type="checkbox"/>	0	0	0	0
Metazoa (22 species)	<input type="checkbox"/>	0	0	0	22
Plants (9 species)	<input checked="" type="checkbox"/>	2	0	0	7
Fungi (6 species)	<input type="checkbox"/>	5	0	0	1
Protists (14 species)	<input type="checkbox"/>	1	1	1	11
Bacteria (98 species)	<input type="checkbox"/>	0	0	0	98
Archaea (25 species)	<input type="checkbox"/>	0	0	0	25

Selected orthologues [Hide](#) 

Species	Type	Orthologue	dN/dS	Target %id	Query %id	GOC Score	WGA Coverage	High Confidence
Chlamydomonas reinhardtii	1-to-1	CHLRE_01g000300v5 1:54,136-57,919:1 View Gene Tree View Sequence Alignments	n/a	13.07 %	16.63 %	n/a	n/a	No
Cyanidioschyzon merolae	1-to-1	CML191C 12:479,112-480,413:1 View Gene Tree View Sequence Alignments	n/a	20.09 %	19.55 %	n/a	n/a	No

There are two orthologues in plants, both are species of algae.

Exercises: Ensembl Fungi gene trees, homologues and alignments

Compara Exercise 1 – Orthologues for the *Schizosaccharomyces pombe mcm6* gene

- How many orthologues are predicted for this gene in Fungal Compara? What about in Pan-compara?
- Filter the second table to view the human orthologue. How much sequence identity does the human protein have to the pombe one? Click on the [Alignment](#) link next to the [Ensembl identifier](#) column to view a protein alignment in Clustal format.

Compara Exercise 2 - *Zymoseptoria* orthologues

Exploring an orthologue that we identified using BioMart, exercise 2. We identified 6 genes with a pathogenic phenotype of 'Loss of pathogenicity' in *Zymoseptoria tritici*. We then found a single gene low confidence gene orthologue in *Cryptococcus neoformans* which we will now explore further.

Search for CNC06590 in *Cryptococcus neoformans* var. *Neoformans* JEC21 to go to the gene page. Click on the gene ID [CNC06590](#) to go to the gene page.

- Does this gene in *C. neoformans* have a PHI-Base annotation?
- Is it the same as that in *Z. tritici* (loss of pathogenicity)? What host species was this linked to?
- Find the *Z. tritici* orthologue in the [Orthologues](#) page and view a protein alignment.
- At which end of the protein (3' or 5') does the alignment between these two genes become worse?

Compara Exercise 3 - Mushroom genes

We're going to take a look at the gene CC1G_05700 in *Coprinopsis cinerea* okayama7#130.

(a) From the gene tab, click to view the [Gene tree](#). At the bottom of the image click to collapse all the nodes at the taxonomic rank of [Class](#).

- What do you notice about the types of fungi shown in the gene tree?
- Does this match with what you would expect from the gene description?
- Based on the protein alignment shown at the right, can you predict which end of the gene/protein is most conserved?

(b) Click to view the [Orthologues](#) page. In the Selected orthologues table, find the entry for the species *Amanita thiersii* and click to view a protein alignment.

- Does this support your conclusion about the conserved region of the gene/protein?