

Anatomy of the Ensembl Fungi homepage

1a: Log in to Ensembl

1: Website header

2: Main search box

3: Genome and species directory

1b: Quick search

4: Release details

5: Archive sites

The screenshot shows the Ensembl Fungi homepage with several key sections highlighted by orange boxes and numbered annotations:

- 1: Website header**: The top navigation bar includes the Ensembl Fungi logo, links to HMMER, BLAST, BioMart, Tools, Downloads, Help & Docs, and Blog. A search bar is located on the right with the text "Search Ensembl Fungi..." and a "Login/Register" link.
- 2: Main search box**: A large search area with a "Search:" label, a dropdown menu for "All species", a "Go" button, and a placeholder text "e.g. NAT2 or alcohol*".
- 3: Genome and species directory**: A section titled "All genomes" with a dropdown menu for "-- Select a species --" and a link to "View full list of all species". To the right, under "Favourite genomes", a list of species is shown with their respective icons and IDs: *Saccharomyces cerevisiae* (R64-1-1), *Schizosaccharomyces pombe* (ASM294v2), *Aspergillus nidulans* (ASM1142v1), *Puccinia graminis* (ASM14992v1), *Magnaporthe oryzae* (MG8), and *Zymoseptoria tritici* (MG2).
- 1b: Quick search**: A section titled "What's New in Release 50" listing updates: Genomes (EnsemblFungi currently has 1014 genomes in total; No new or updated genomes from last release), Updated data (Updated protein features for all species using InterProScan with version 81 of InterPro; Updated BioMarts for all gene and variation data; Updated pan-taxonomic gene trees and homologues), and a "Did you know...?" box about the e!REST service.
- 4: Release details**: A section titled "Join the *Zymoseptoria tritici* gene annotation team!" providing information about the collaborative effort and contact details for Marc-Henri Lebrun.
- 5: Archive sites**: A section titled "Archive sites" listing previous versions of data: Release 49 (December 2020), Release 45 (September 2019), Release 40 (July 2018), and Release 37 (October 2017), each with a corresponding Ensembl Fungi URL.

The footer of the page includes the Ensembl Fungi logo, a description of the project, and logos for EMBL-EBI, E!mpowered, and the Elixir Core Data Resource.

1: Website header

This section is present on all pages as you navigate around Ensembl Fungi. It contains quick links to commonly used tools, help and documentation pages and download options.

- 1a: Log into your Ensembl account

This is part of the header. By logging into Ensembl you will be able to save your queries on the Ensembl tools, such as the VEP to return to at a later date. You can also upload your own data or custom track-hubs to your account. You can also edit which species appear in section 3: Genome and species directory.

- 1b: Quick search

This is part of the header. This enables you to quickly search all of Ensembl Fungi from whatever page you are on. You can search for a species, a gene, a region or the help and documentation.

2: Main search box

This enables you to search the whole of Ensembl Fungi, you can specify the species or strain you are interested in from the drop-down menu, or simply search across all species.

3: Genome and species directory

Here are listed the most popular species in Ensembl. If you create an account with Ensembl Fungi (See Section 1a), you can edit which species appear here. You can also click the link to view a table listing all of the genomes available.

4: Release details

A new version of Ensembl Fungi is released approximately every 3 months. This is where we add new data or update existing data, this section details the highlights of the current release. It is important to know which version you are working with as if you return to Ensembl at a later date the data may have changed.

5: Archive sites

This section lists available Ensembl Fungi web archives frozen in time in case you wanted to go back to previous releases.

Anatomy of the Ensembl Fungi gene page

1: Selected genome

2: Location and feature tabs

3: Tab-specific pages

4: Customisation and download options

The screenshot displays the Ensembl Fungi interface for the gene **yfh7** (SPAC227.14) in **Schizosaccharomyces pombe** (ASM294v2). The page is annotated with five numbered callouts:

- 1: Selected genome** points to the organism dropdown menu.
- 2: Location and feature tabs** points to the 'Location: 1:520,174-522,766' and 'Gene: yfh7' tabs.
- 3: Tab-specific pages** points to the 'Gene-based displays' sidebar menu.
- 4: Customisation and download options** points to the 'Configure this page' and 'Custom tracks' buttons.
- 5: Feature overview** points to the 'Gene: yfh7' summary section.
- 5: Transcript table** points to the table listing transcripts for yfh7.
- 1: Main display** points to the genomic track visualization.

Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Gene alleles
- Sequence
- Secondary Structure
- Gene families
- Literature
- Fungal Compara
- Genomic alignments
- Gene tree
- Gene gain/loss tree
- Orthologues
- Paralogues
- Pan-taxonomic Compara
- Gene Tree
- Orthologues
- Ontologies
- FYPO: Phenotype
- GO: Biological process
- GO: Molecular function
- GO: Cellular component
- MOD: Protein modification
- Phenotypes
- Genetic Variation
- Variant table
- Variant image
- Structural variants
- Gene expression
- Pathway
- Regulation
- External references
- Supporting evidence
- ID History
- Gene history

Gene: yfh7 SPAC227.14

Description: uridine kinase Yfh7 (predicted) [Source:PomBase;Acc:SPAC227.14]

Location: [Chromosome 1: 520,174-522,766](#) forward strand.
ASM294v2:CU329670.1

About this gene: This gene has 1 transcript ([splice variant](#)), [323 orthologues](#) and is a member of [2 Ensembl protein families](#).

Transcripts: [Hide transcript table](#)

Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
yfh7	SPAC227.14.1	2407	235aa	Protein coding	Q9UTC5	NP_592968	

Summary

Name: [yfh7](#) (PomBase Gene Name)

UniProtKB: This gene has proteins that correspond to the following UniProtKB identifiers: [Q9UTC5](#)

Gene type: Protein coding

Annotation method: Genes annotated by [PomBase](#)

Go to [Region in Detail](#) for more tracks and navigation options (e.g. zooming)

Drag/Select: [←](#) [→](#)

Genes

Forward strand

Reverse strand

Contigs

Genes

1: Selected genome

This will show the species binomial Latin name and the strain/isolate identifier. Many species have more than one genome assembly. Clicking on this will take you to the information page for the genome assembly.

2: Page tabs

Tabs allow you to see the gene information at different scales and to change between views easily. The 'Gene' tab is selected and highlighted in white and shows specific information about the gene. The 'Location' tab will show the gene information at a larger scale, showing surrounding features in the genome, such as regulatory features and neighbouring genes. The 'Transcript' tab will show you information at a finer scale, specific to gene transcript, such as protein products and cDNA.

3: Gene-specific pages

This is the left-hand navigation panel for the gene-specific views. Here are listed pages that show gene information grouped by data type. This will stay the same for all gene pages for all genomes, but the selection will be different on the location and transcript tabs.

4: Customisation options

These buttons are present in every tab. The 'Configure this page' button will open a range of options to add data displays to a page, and the options change depending on the tab and page you are on. 'Custom tracks' allows you to add tracks from the Track-hub registry and your own data to the page you are on. 'Export data' allows you to download the data on the page in a range of different data formats. 'Share this page' will give you a stable URL which will link to the current page, but also include information about any extra data you have added using the Configure this Page or custom tracks options to share with a colleague. 'Bookmark this page' will save this page if you have an Ensembl account.

5: Feature overview including the transcript table

These will be present on all pages in the Gene and Transcript tabs. You can hide or show the transcript table by clicking on the brown button above the table

6: Main display

Main display presents data specific to the chosen page. Toggling between gene-specific pages will update this view.