

Anatomy of the Ensembl Fungi homepage

1: Website header

2: Main search box

3: Genome and species directory

1a: Ensembl login

1b: Quick search

4: Release highlights

5: Archive sites

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

- 1: Website header:** The top navigation bar containing the Ensembl Fungi logo, links to HMMER, BLAST, BioMart, Tools, Downloads, Help & Docs, and Blog, a search bar, and a Login/Register button.
- 2: Main search box:** A search area with a dropdown menu set to "All species", a text input field, a "Go" button, and a suggestion "e.g. NAT2 or alcohol*".
- 3: Genome and species directory:** A section with two columns: "All genomes" (with a species selector and a link to "View full list of all species") and "Favourite genomes" (listing Saccharomyces cerevisiae, Schizosaccharomyces pombe, Aspergillus nidulans, Puccinia graminis, Magnaporthe oryzae, and Zymoseptoria tritici).
- 1a: Ensembl login:** The Login/Register button in the header.
- 1b: Quick search:** The search bar in the header.
- 4: Release highlights:** A section titled "What's New in Release 58" listing updates to Genomes, Updated data, and a "Rapid Release" section with a "Go" button.
- 5: Archive sites:** A section titled "Archive sites" listing previous versions of data, such as Release 56 (February 2023) and Release 52 (December 2021).

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 Ensembl's 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 below.

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

Listed here are the most popular species in Ensembl Fungi. If you create an account with Ensembl Fungi (see Section 1a above), you can edit which species to appear here. You can also click the link 'View full list of all species' to view a table listing all of the genomes available in Ensembl Fungi.

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

Ensembl Fungi | HMMER | BLAST | BioMart | Tools | Downloads | Help & Docs | Blog

Search Ensembl Fungi...

Schizosaccharomyces pombe (ASM294v2)

Location: 1:520,174-522,766 | Gene: yfh7 | Transcript: yfh7

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
- Molecular interactions
- 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 I: 520,174-522,766](#) forward strand.

ASM294v2:CU329670.1

About this gene: This gene has 1 transcript ([splice variant](#)), [284 orthologues](#) and [5 paralogues](#).

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	-	Ensembl Canonical

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)

Add/remove tracks | Custom tracks | Share | Resize image | Export image | Reset configuration | Reset track order | Drag/Select: ++

Forward strand

Genes

512,500 515,000 517,500 520,000 522,500 525,000 527,500 530,000 532,500

yfh1-antisense-1 - SPNCRNA.657.1 > ncRNA

ma4 - SPAC227.12.1 > protein coding

SPNCRNA.658.1 > ncRNA

reg1 - SPAC227.15.1 > protein coding

psf3-antisense-1 - SPNCRNA.659.1 > ncRNA

sno28 - SPSNORNA.02.1 > snoRNA

sno27 - SPSNORNA.03.1 > snoRNA

sno25 - SPSNORNA.04.1 > snoRNA

ENSRNA049676807-T1 > snoRNA

sno24 - SPSNORNA.05.1 > snoRNA

sno23 - SPSNORNA.06.1 > snoRNA

gim4 - SPAC227.10.1 > protein coding

fol3 - SPAC227.09.1 > protein coding

yfh7 - SPAC227.14.1 > protein coding

5a: Feature overview

5b: Transcript table

6: Main display

1: Selected genome

This will show the species' binomial Latin name and the strain and/or 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 the cDNA and proteins.

3: Gene-specific pages

This is the left-hand navigation panel for the gene-specific views. Listed here are pages that show gene-specific 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. The 'Custom tracks' button 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

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