

Exploring the gene record page

Learning objectives

- Become familiar with gene page structure and content
- Navigate to and from the gene pages

Use a Gene ID to identify a gene record page.

1. Use the site search to navigate to the gene record page of [CNAG_01551](#), which is a positive regulator of titanization in *C. neoformans*.
2. Click on the card to be redirected to the gene record page.

The screenshot shows the FungiDB search results for the query "CNAG_01551". At the top, there is a search bar with the result "CNAG_01551" and a magnifying glass icon. Below the search bar is a navigation menu with links: My Strategies, Searches, Tools, My Workspace, Data, About, Help, and Contact Us. A blue button on the right says "Export as a Search Strategy" with the sub-instruction "To download or refine your results". The main content area is titled "Genes matching CNAG_01551" and shows a single result: "Gene - CNAG_01551 GATA family transcription factor". This result includes details: Gene name or symbol: GAT201; Gene type: protein coding gene; Organism: Cryptococcus neoformans var. grubii H99. Below this, a note states "Fields matched: Gene ID; Gene IDs; Names, IDs, and aliases". On the left, there are filter options for "Filter results" (Genome, Genes), "Filter Gene fields" (select all, clear all, Gene ID, Gene IDs, Names, IDs, and aliases), and "Filter organisms".

Gene page components

The top section of the gene record page provides a snapshot of the information available for this gene and also offers several shortcuts:

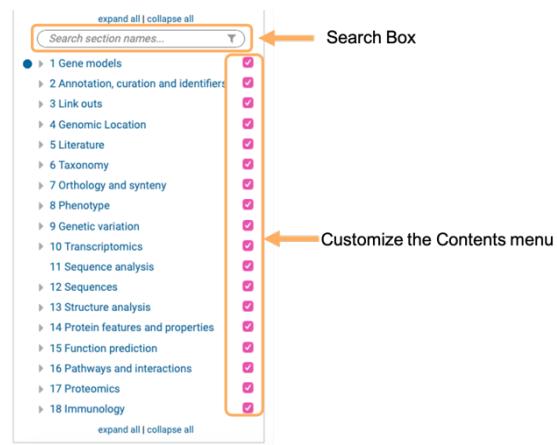
The screenshot shows the gene record page for CNAG_01551. At the top, there are three orange numbered circles: 1 (Add to basket), 2 (Add to favorites), and 3 (Download Gene). Below these are links: "Add to basket" with a basket icon, "Add to favorites" with a star icon, and "Download Gene" with a download icon. The main title is "CNAG_01551 GATA family transcription factor". To the right, there is a "Shortcuts" section with five icons: Synteny, Alignments, SNPs, Transcriptomics, Protein Features, and Proteomics. Below the "Shortcuts" section, a link says "Also see CNAG_01551 in the Genome Browser or Protein Browser". At the bottom left, there is a "View 1 user comment, or add a comment" link with a speech bubble icon, and a "View and update community annotations in Apollo" link. At the bottom right, there is a link "Collapse all sections for better performance" with a triangle icon. Numbered circles 4 and 5 are placed near the "View 1 user comment" link and the "Protein Features" shortcut respectively.

- 1 Add to basket: Save to basket if you want to download gene-specific information for selected genes.
- 2 Add to favorites: Saves genes in the private My favorites section, where you can add notes or keep track of your project.

- 3** Download Gene: Redirects to a download options page where gene records can be exported at text, FASTA, and GFF3 formats.
- 4** Submit a comment (e.g., add a PubMedID or annotated gene function) or annotate gene in Apollo, a web-based structural and functional gene annotation platform.
- 5** Shortcuts panel provides quick access to the selected section within the gene record page.

Explore the content of this gene record page. Below are the navigational highlights.

The **Contents** section contains a list of links to various sections in the gene record page and is searchable. Sub-sections of the Contents menu can be hidden by checking the box to the right.



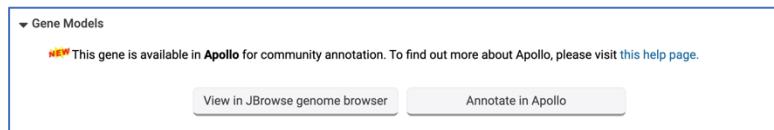
The **Gene Models** section is the first section of the gene record page, and it contains information about the structure of the gene (e.g. exon count, transcript number, annotated UTRs, community gene annotation in Apollo (if any), intron evidence, etc.) displayed within the genome browse JBrowse wrapper.



Introns that are matching transcript annotation for which there is an abundance of supporting data from aligned RNA-Seq reads are displayed in bold colours (Blue for a forward gene and red for a gene located on the reverse strand).

If you navigated away from the gene of interest while scrolling, click on the “Reset view” button to return to the default position within the JBrowse wrapper.

The “View in JBrowse genome browser” and “Annotate in Apollo” buttons open in separate tabs. In JBrowse, you can activate additional tracks and build custom evidence views. In Apollo, you can modify and create new genes to improve the genome annotation.



- Click on one of the introns within the **RNA-Seq Evidence for Introns** track. The pop-up window contains a table showing all experiments and samples that provide evidence for this intron junction (generated by in-house automated pipelines):

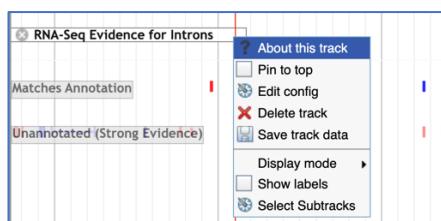
Intron Spanning Reads (ISR): The total number of uniquely mapped reads (all samples) which map across the junction and are on the appropriate strand. GSNAP uses splice site consensus sequences to determine the strand of the mapped read.

ISR per million (ISRPm): Intron Spanning Reads Per Million intron spanning reads and thus represents a normalized count of unique reads.

CP003830.1_260916_261076_1 details					
Intron Junction Details					
Intron Location	CP003830.1:260916..261076 (- strand)				
Intron Spanning Reads (ISR)	68276				
ISR per million (ISRPm)	17918.72				
Gene assignment	CNAG_01551 - annotated intron				
% of Most Abundant Intron (MAI)	100				
Sample Details					
Experiment	Sample	Unique ISRPM	ISR/Cov	% MAI	
Cell cycle transcriptome of Cryptococcus neoformans var. grubii	0 min	38	1.75	3.53	100
	10 min	5	0.27	0.8	25.23
	100 min	24	0.96	2.39	64.86

% of Most Abundant Intron (MAI): The percentage (ISRPM of this junction / ISRPM of maximum junction for this gene) of this junction over the maximum for this gene.

Note that the tracks within the JBrowse wrapper have a drop-down menu for further track customization:



The **Annotation, curation and identifiers** section offers alternate product descriptions, previous identifiers, and aliases, and is populated using data from internal curation, other fungal resources (if applicable), or user-submitted data (user comments).

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<p>▼ Notes from Annotator Download Data sets</p> <p>Search this table... ▼ ?</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left; padding: 5px;">Date</th> <th style="text-align: left; padding: 5px;">Note</th> <th style="text-align: left; padding: 5px;">Transcript ID(s)</th> </tr> </thead> <tbody> <tr> <td style="padding: 5px;">N/A</td><td style="padding: 5px;">Biological role: Regulation of anti-phagocytic mechanisms (PMID:25970403); date_20171207</td><td style="padding: 5px;">CNAG_01551-t26_1</td></tr> <tr> <td style="padding: 5px;">N/A</td><td style="padding: 5px;">Deletion of GAT201 exhibited a hypcapsular phenotype with severely reduced capsule thickness (PMID:25644834; IMP); date_20171211</td><td style="padding: 5px;">CNAG_01551-t26_1</td></tr> <tr> <td style="padding: 5px;">N/A</td><td style="padding: 5px;">It is a core virulence-regulating transcription factor and it is required for both the lung and brain infections (PMID:32251295; IMP); date_20200501</td><td style="padding: 5px;">CNAG_01551-t26_1</td></tr> <tr> <td style="padding: 5px;">N/A</td><td style="padding: 5px;">Translation loaded from EMBL</td><td style="padding: 5px;">CNAG_01551-t26_1</td></tr> <tr> <td style="padding: 5px;">N/A</td><td style="padding: 5px;">When deleted, GAT201 mutant is avidly phagocytosed by human macrophages and exhibited a phagocytic index of 1.77 (PMID:25970403); eupathdb_uc=100057903; date_20171207</td><td style="padding: 5px;">CNAG_01551-t26_1</td></tr> </tbody> </table>	Date	Note	Transcript ID(s)	N/A	Biological role: Regulation of anti-phagocytic mechanisms (PMID:25970403); date_20171207	CNAG_01551-t26_1	N/A	Deletion of GAT201 exhibited a hypcapsular phenotype with severely reduced capsule thickness (PMID:25644834; IMP); date_20171211	CNAG_01551-t26_1	N/A	It is a core virulence-regulating transcription factor and it is required for both the lung and brain infections (PMID:32251295; IMP); date_20200501	CNAG_01551-t26_1	N/A	Translation loaded from EMBL	CNAG_01551-t26_1	N/A	When deleted, GAT201 mutant is avidly phagocytosed by human macrophages and exhibited a phagocytic index of 1.77 (PMID:25970403); eupathdb_uc=100057903; date_20171207	CNAG_01551-t26_1	<p>Names, Previous Identifiers, and Aliases Download Data sets</p> <p>Search this table... ▼ ?</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left; padding: 5px;">Name/ID/Alias</th> <th style="text-align: left; padding: 5px;">Type</th> <th style="text-align: left; padding: 5px;">Source</th> </tr> </thead> <tbody> <tr> <td style="padding: 5px;">AFR97756.1</td><td style="padding: 5px;">alternate ID</td><td style="padding: 5px;">protein_id</td></tr> <tr> <td style="padding: 5px;">J9VWG0</td><td style="padding: 5px;">alternate ID</td><td style="padding: 5px;">Uniprot/SPTREMBL</td></tr> <tr> <td style="padding: 5px;">UPI00027E690C</td><td style="padding: 5px;">alternate ID</td><td style="padding: 5px;">UniParc</td></tr> <tr> <td style="padding: 5px;">XM_012197203.1</td><td style="padding: 5px;">alternate ID</td><td style="padding: 5px;">RefSeq_dna</td></tr> <tr> <td style="padding: 5px;">XP_012052593.1</td><td style="padding: 5px;">alternate ID</td><td style="padding: 5px;">RefSeq_peptide</td></tr> <tr> <td style="padding: 5px;">GAT201</td><td style="padding: 5px;">name</td><td style="padding: 5px;">N/A</td></tr> </tbody> </table>	Name/ID/Alias	Type	Source	AFR97756.1	alternate ID	protein_id	J9VWG0	alternate ID	Uniprot/SPTREMBL	UPI00027E690C	alternate ID	UniParc	XM_012197203.1	alternate ID	RefSeq_dna	XP_012052593.1	alternate ID	RefSeq_peptide	GAT201	name	N/A
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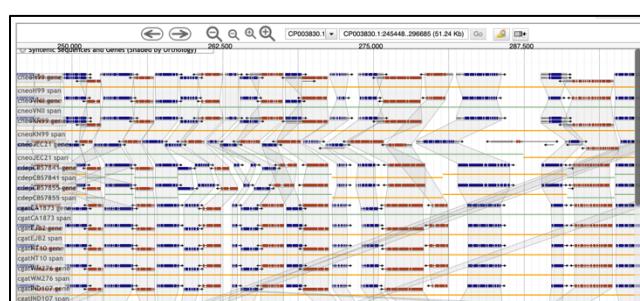
The **Link outs** section offers redirection to other resources (*e.g.*, CGD, Ensembl, MycoCosm, *etc.*).

The **Orthology and synteny** section provides a table of Orthologs and Paralogs within FungiDB produced by OrthoMCL (www.orthomcl.org).

The table has a search box for creating a custom display of orthologs and also deploy the ClustalOmega analysis. The output of this tool can be used to build phylogenetic trees (e.g., iTOL).

Use the search box to limit species to *Kwoniella* and run Clustal Omega

The Orthology and Synteny section also contains synteny graphs in JBrowse:

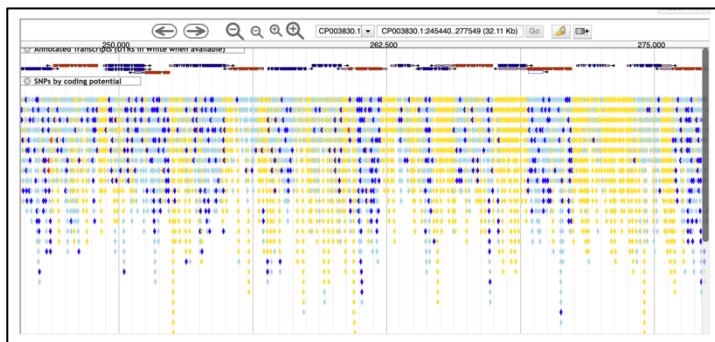


In the screenshot above, the syntenic genes are highlighted in grey.

The **Phenotype** section offers curated information, including annotations from the Pathogen-Host Interactions database, and inhouse manual annotation efforts.

The **Genetic variation** section summarizes integrated SNP data for a given region and classifies SNPs based on the effect on gene function:

- noncoding (yellow diamonds)
- non-synonymous (dark blue)
- synonymous (light blue)
- nonsense (red)



Note that you can interact with the SNP records by using left and right clicking options on your mouse/touch pad.

Left click brings up a pop-up window containing more information about a particular SNP:

Click on the SNP record linked in blue. It is linked to the SNP record page, which contains summary of the SNP across different isolates and samples.

SNP:	NGS_SNP.CP003830.1.257542
Location:	257542
Gene:	CNAG_01549
Position in CDS	424
Position in protein	142
Type:	Coding (non-synonymous)
Number of strains:	590
	NA AA (frequency)
H99 (reference):	T S
Major Allele:	T S (.82)
Minor Allele:	C P (.18)

Major allele is the most common allele in the studied population/isolates.

Add to basket Add to favorites Download SNP

SNP: NGS_SNP.CP003830.1.257542

Organism: Cryptococcus neoformans var. grubii H99
Location: CP003830.1: 257,542
Type: coding
Number of Strains: 590
Gene ID: CNAG_01549
Gene Strand: forward
Major Allele: T (0.82)
Minor Allele: C (0.18)
Distinct Allele Count: 2
Reference Allele: T
Reference Product: S 142
SNP context: ATGGTAGCTGACTGGAGCACAGCCCTTGATTCGGTATTCTCTGGTAGGAAGCCTACGGCA

Minor allele frequency is the frequency of the second most common allele. Minor allele frequency is useful when looking for rare variants or disease-causing SNPs. However, there can be exceptions when minor allele frequency increases under selective pressure (e.g., development of drug resistance).

The **Transcriptomics** section (RNA-Seq and microarray data).

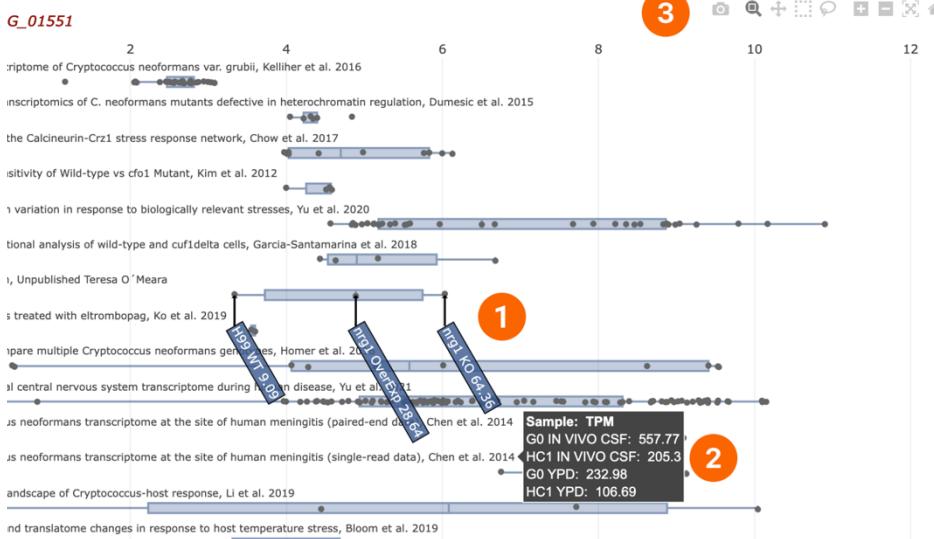
The Transcript Expression Summary section provides a big picture of gene expression across different samples and experiments, and helps identify experiments in which the current gene is highly regulated.

▼ RNA-Seq Transcription Summary 

▼ Summary of expression values. Each row represents a distinct RNA-Seq experiment. [Click to read more...](#)

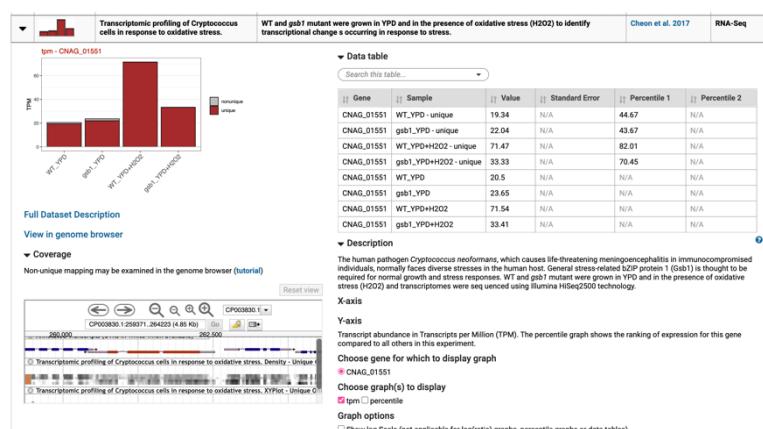
- Each black dot represents expression in a sample. A boxplot is shown, with the box representing the median and upper/lower quartiles, and the whiskers representing the max/min values (or 1.5 times the interquartile range, in which case values beyond the whiskers are considered outliers).
- Hover over the experiment name to show a table of sample names and values.
- Click on a boxplot to show labels and values for each sample in an experiment. Click again on the boxplot to hide labels and values. A button at the bottom-right removes labels and values for all experiments.
- Use the toggle button at the bottom-left to switch from Log Scale to Linear Scale.
- Log Scale values are $\log_2(\text{TPM}+1)$ for these reasons:
 1. TPM+1: to de-emphasize low noisy TPM values (i.e., <1).
 2. log₂: so that each unit on the x-axis represents a 2-fold difference.
- Navigation buttons appear at the above-right when hovering over the graph. If the buttons do not appear, reload the page.
- Zoom in with the navigation button or click and drag within the graph. Zoom out with the navigation button or double-click within the graph.
- This graph was created with Plotly. [Get more help at their website.](#)

expression values. Each row represents a distinct RNA-Seq experiment. [Click to read more...](#)



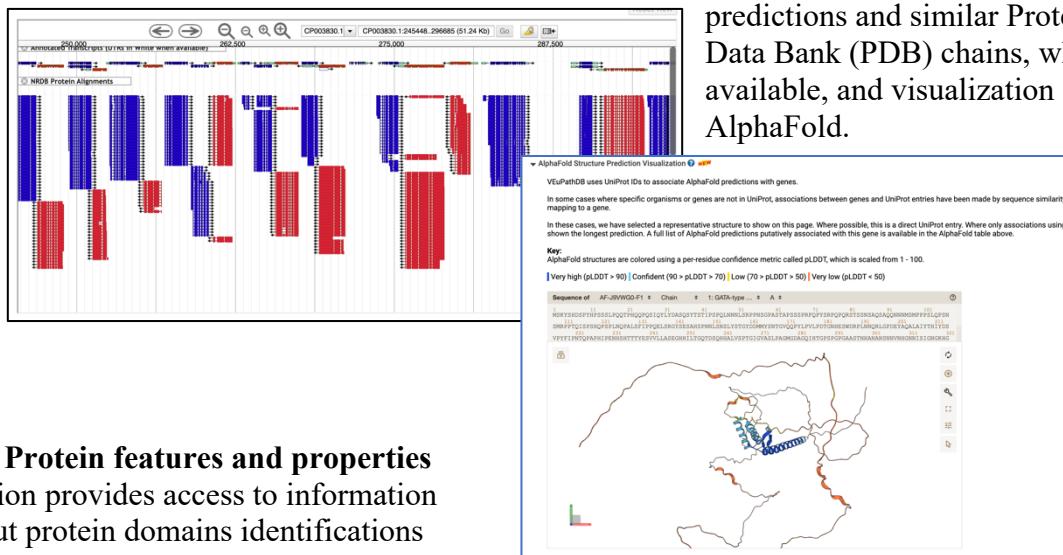
1. Clicking on the box plot will bring up sample labels.
2. Hovering over the experiments will display sample names.
3. The buttons above the summary graph provide additional options (e.g., download data in PNG, zoom, pan, etc.).

The **Transcript Expression** section, which is located under the RNA-Seq summary section, can be expanded to view the expression graph (TPM), data table, full dataset description, coverage plots, a link to the dataset in JBrowse.



The **Sequence analysis, Sequences, and Structure analysis** sections offer sequence information (DNA, RNA, and protein), an interactive summary of EST alignments and BLAT hits against the nonredundant protein sequence database (NRDB), 3D structure

predictions and similar Protein Data Bank (PDB) chains, when available, and visualization from AlphaFold.



The **Protein features and properties** section provides access to information about protein domains identifications (InterPro), signal and transmembrane predictions graphics, BLASTP hits, and other tools that can be deployed directly from the gene record page using the amino acid sequence of interest:

14 Protein features and properties

- ▶ Attributes and Protein Browser
- ▶ BLASTP (protein-protein BLAST)
- ▶ GPI anchor prediction: big-PI Predictor
- ▶ InterPro Domains
- ▶ InterProScan: Run on EBI site
- ▶ MitoProt
- ▶ STRING: functional protein association networks
- ▶ WoLF PSORT

The **Function Prediction** section features Gene Ontology (GO) assignments that have been either downloaded from Gene Ontology databases or manually curated by FungiDB. GO Slim terms, Enzyme Commission (EC) numbers with links to EC number and GO terms description and relevant publications are available as well.

Gene ontology provides statements for describing the functions of genes along with three aspects: Molecular function, Biological process, and Cellular component, and it is organized in hierarchies. The GO terms table above provides GO IDs and terms associated with a particular gene and additional metadata that are available for these associations such as source, evidence code (e.g. IDA, IMP, etc.) and reference (PubMed ID).

There are three classes of GO terms in FungiDB:

1. Automatically assigned by InterPro2GO
2. Assigned by FungiDB curators
3. Obtained from external resources such as MIPS

The **Pathways and interactions** section provides information about metabolic pathways loaded from the KEGG and MetaCyc repositories. Genes are linked to individual pathways

by EC numbers when this data is available and clicking on any of the links redirects to an interactive metabolic pathway viewer where the user can explore individual reactions or export all known data for a given pathway. EC numbers are inferred by the OrthoMCL pipeline automatically. As with any automated analysis, use caution when interpreting this data.

The Proteomics section is populated when Mass Spec evidence data and phosphoproteomics datasets become available in FungiDB.

Accessing JBrowse

Browse can be accessed from the main menu and also from gene record pages

The screenshot shows the FungiDB main menu with the 'Tools' tab selected. Other tabs include 'My Workspace', 'Data', and 'About'. The 'Tools' section lists several options: Apollo, BLAST (multi-query capable), Companion, CRISPR guide design tool, Galaxy, Genome browser (which is underlined in blue), PubMed and Entrez, Sequence retrieval, and Web services.

Gene Models

This gene is available in Apollo for community annotation. To find out more about Apollo, please visit [this help page](#).

[View in JBrowse genome browser](#) [Annotate in Apollo](#)

Navigate to the top of the gene record page and click on the “View in JBrowse genome browser” button to be redirected to the JBrowse view for [CNAG_01551](#). Here are a few general navigation tips:

The JBrowse interface for the *Fusarium graminearum* PH-1 genome. The top navigation bar includes links for My Strategies, Searches, Tools, My Workspace, Data, About, Help, Contact Us, and a Guest account. The genome name is displayed as *Fusarium graminearum* PH-1. The main area shows a genomic track for the region 4,465,000 to 4,490,000. The track displays various gene models and their annotations. A yellow highlighter is used to mark specific regions of interest. The bottom navigation bar contains icons for zooming, panning, and highlighting, along with a reference sequence selector and a search bar.

Menu bar includes the Genome menu, Track menu, View menu, Help menu and the Sharing link.

Current genome is indicated above the tracks

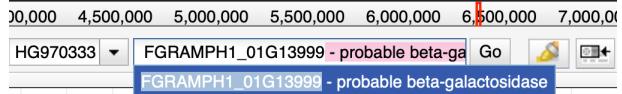
Customised JBrowse views can be shared via a URL generated by clicking on the *Share* button

Select additional tracks to view (transcriptomics, SNPs, etc.)

Navigation bar contains zooming (magnifying glass icons), panning (left/right arrows) and highlighting (yellow highlighter) buttons, reference sequence selector (drop down with sequences from the selected genome sorted by length), a text box to search for features such as gene IDs and overview bar which shows the location of the region in view.

Genome view area

Note: If you navigated away from the gene, you can type your gene ID directly in the location search box and select the highlighted match to return to your original position. You can also double click on the gene to re-centre your view.



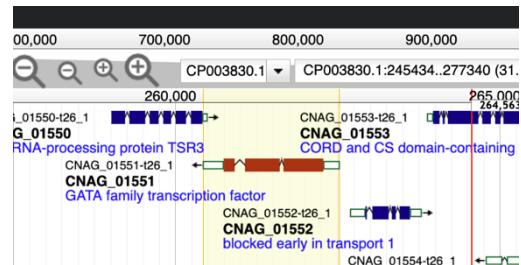
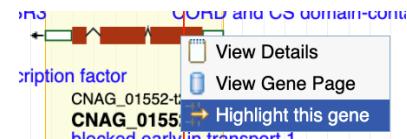
Gene Details

Gene	CNAG_01551
Gene Name	GAT201
Taxon	Cryptococcus neoformans var. grubii H99
Sequence Ontology	protein_coding_gene
Biotype Classification	protein_coding
Description	GATA family transcription factor
Position	CP003830.1:260426..262535 (- strand)
OrthoMCL	OG6_531912
Links	JBrowse Gene Page Apollo

- Left-click on the gene and a pop-up window will display the coordinates of CDS, 3' and 5' UTRs (when available), etc. You can also export CDS and protein sequences or navigate to the gene record page.

- Highlight this gene for easy tracking.

Right-click (or control click) on the gene feature to display the context menu which provides quick links to highlighting, navigation to the gene record page). You can also get the more details by selecting the View Details option, which will bring up the pop-up box shown above.

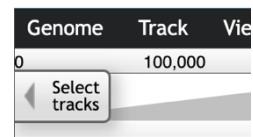


- Click on the “Select tracks” tab on the left to select a list of tracks mentioned below:

Select the following tracks:

Hint: Click on “Clear All Filter” button to clear filters (but not tracks) between your track selections.

- Intron Evidence (if not selected by default already).



- RNA-Seq (Dataset: “Transcriptional landscape of Cryptococcus-host response”). Select all tracks.
- Orthology and Synteny (the “Syntenic Sequence and Genes (Shaded by Orthology)”).

Select Tracks

My Tracks		Category	Subcategory
Category	Currently Active		
Recently Used			
Category		Name	Category
1 Comparative Genomics		Syntenic Sequences and Genes (Shaded by Orthology)	Comparative Genomics
Subcategory			Orthology and Synteny
1 Orthology and Synteny			
Dataset			
1 (no data)			
Track Type			
1 Segments			
RNASeq Alignment			
1 (no data)			
RNASeq Strand			
1 (no data)			

Category	X
10 Transcriptomics	X
Subcategory	X
10 RNA-Seq	X
Dataset	X
50 Cell cycle transcriptome of Cryptococcus neoformans var. grubii	
14 Comparative transcriptomics of C. neoformans mutants defective in heterochromatin regulation	
12 Expression of the Calmodulin-Cet1 stress response network	
6 Fluconazole Sensitivity of Wild-type vs cfo1 Mutant	
72 Gene expression variation in response to biologically relevant stimuli	
6 Global transcriptional analysis of wild-type and cut1delta cells	
5 Ngt1 expression	
6 RNA-Seq of cells treated with etrömopag	
22 RNA-Seq to compare multiple Cryptococcus genotypes	
230 The Cryptococcus central nervous system transcriptome during human disease	
4 The Cryptococcus neofornans transcriptome at the site of human meningitis (paired-end data)	
6 The Cryptococcus neofornans transcriptome at the site of human meningitis (single-read data)	
10 Transcriptional landscape of Cryptococcus-host response	

- Click on the “Back to browser” button to go back to JBrowse.

You should have a view that looks something like this:



To be able to evaluate the RNA-Seq and other evidence for this gene, pin the “Annotate Transcripts (UTRs in White when available)” track to the top:

This screenshot shows the same JBrowse interface as above, but with a specific track pinned to the top. The track 'Annotated Transcripts (UTRs in White when available)' is now at the very top of the stack. A context menu is open over a gene entry for 'CNAG_01551', showing options such as 'About this track', 'Pin to top', 'Edit config', 'Delete', 'Save track data', 'Display mode', and 'Show labels'.

Now, when you scroll down, the gene model track will move with you along the screen.

Note: You can customize the **Syntenic Sequences and Genes (Shaded by Orthology)** track using the drop-down. To do this, choose the “Select Subtracks” option, unselect current tracks, use the filter to identify “Cryptococcus” only and then click on the “Save” button at the bottom.

Label	Species	Kingdom	Genus	Phylum	Class	syntype	taxon
cneoH99 gene	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	gene	Cryptococcus neoformans var. grubii H99
cneoH99 span	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	span	Cryptococcus neoformans var. grubii H99
cneoVIII gene	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	gene	Cryptococcus neoformans strain:VIII
cneoVIII span	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	span	Cryptococcus neoformans strain:VIII
cneoKN99 gene	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	gene	Cryptococcus neoformans var. grubii KN99
cneoKN99 span	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	span	Cryptococcus neoformans var. grubii KN99
chedJEC21 gene	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	gene	Cryptococcus neoformans var. grubii
chedJEC21 span	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	span	Cryptococcus neoformans var. grubii
cdsPCBS7841 gene	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	gene	Cryptococcus neoformans var. grubii B-3501A
cdsPCBS7841 span	Cryptococcus neoformans	Fungi	Cryptococcus	Basidiomycota	Tremellomycetes	span	Cryptococcus neoformans var. grubii B-3501A

Having this information in hand and using JBrowse track view, answer the following questions:

- In which tissue sample, this gene’s expression is the highest? Is this consistent with what is known about titan cell biology and dissemination pattern?
- What do you think about UTR annotations for this gene? How would you go about confirming or correcting UTRs, if needed?
- Is this gene well conserved in other *Cryptococcus* species?
- Is there evidence of alternative splicing?
- How would you go about generating a link to this view in JBrowse?