

Exploring the gene record page

Learning objectives

- Become familiar with gene page structure and content
- Navigate to and from the gene pages
- Use the site search to navigate to the gene record page of [Afu2g13260](#), which is a gene known to be important for the virulence of *Aspergillus fumigatus*.

1 - 1 of 1

1

2

3

Export as a Search Strategy
to download or mine your results

- 1 The panel on the left provides a summary of all record types that match Afu2g13260.
- 2 Click on the gene link to navigate to the gene record page for Afu2g13260.
- 3 Clicking on this button will transform your search into a search strategy.
Note: If the button is shaded/inactive, limit your search to a single data type using the Filter results panel on the left.

Gene page components

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

The screenshot shows the top section of a gene record page for **Afu2g13260**, a developmental regulator medA, putative. The page includes several components highlighted with numbered callouts:

- 1**: Add to basket button.
- 2**: Add to favorites button.
- 3**: Download Gene button.
- 4**: View user comment or add a comment button.
- 5**: Shortcuts panel.

The gene record page displays the following information:

- Name:** medA
- Gene Type:** protein coding gene
- Biotype Classification:** protein_coding
- Chromosome:** 2
- Location:** Chr2_A_fumigatus_Af293:3,408,135..3,413,423(-)
- Species:** *Aspergillus fumigatus*
- Strain:** Af293
- Status:** Curated Reference Strain
- Model Organism Database(s):** CGD: C3_01180C_A

The Shortcuts panel provides quick access to the following sections:

- Synteny
- Alignments
- SNPs
- Transcriptomics
- Protein Features
- Proteomics

Also see Afu2g13260 in the [Genome Browser](#) or [Protein Browser](#)

- 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 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 screenshot shows the **Contents** section for **Afu2g13260**. It includes a search box and a list of sections with checkboxes for customization.

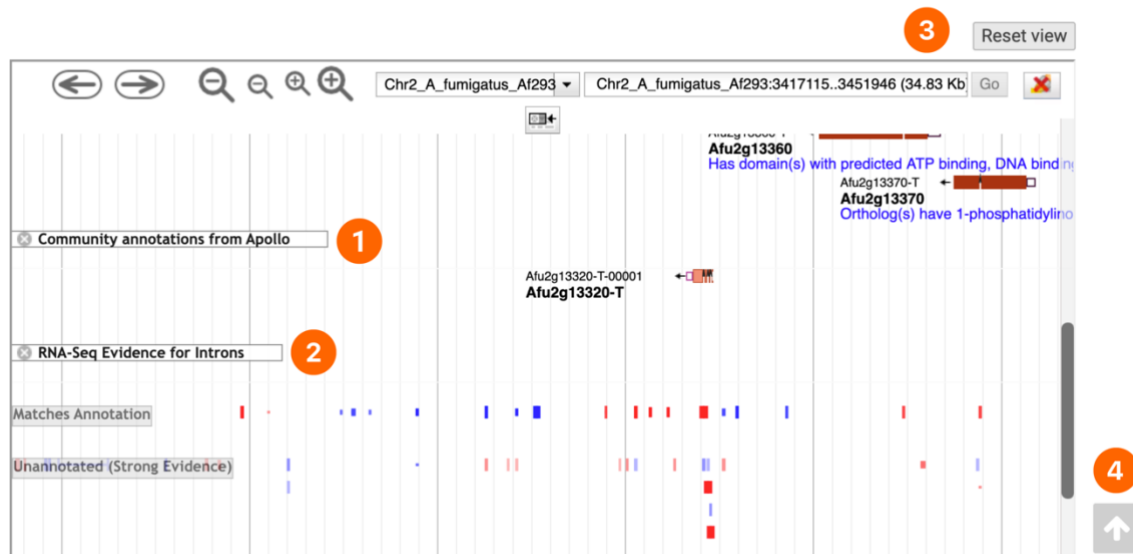
Search Box: Search section names...

Customize the Contents menu: Checkboxes next to each section name.

Section	Customize
1 Gene models	<input checked="" type="checkbox"/>
2 Annotation, curation and identifiers	<input checked="" type="checkbox"/>
3 Link outs	<input checked="" type="checkbox"/>
4 Genomic Location	<input checked="" type="checkbox"/>
5 Literature	<input checked="" type="checkbox"/>
6 Taxonomy	<input checked="" type="checkbox"/>
7 Orthology and synteny	<input checked="" type="checkbox"/>
8 Phenotype	<input checked="" type="checkbox"/>
9 Genetic variation	<input checked="" type="checkbox"/>
10 Transcriptomics	<input checked="" type="checkbox"/>
11 Sequence analysis	<input checked="" type="checkbox"/>
12 Sequences	<input checked="" type="checkbox"/>
13 Structure analysis	<input checked="" type="checkbox"/>
14 Protein features and properties	<input checked="" type="checkbox"/>
15 Function prediction	<input checked="" type="checkbox"/>
16 Pathways and interactions	<input checked="" type="checkbox"/>
17 Proteomics	<input checked="" type="checkbox"/>
18 Immunology	<input checked="" type="checkbox"/>

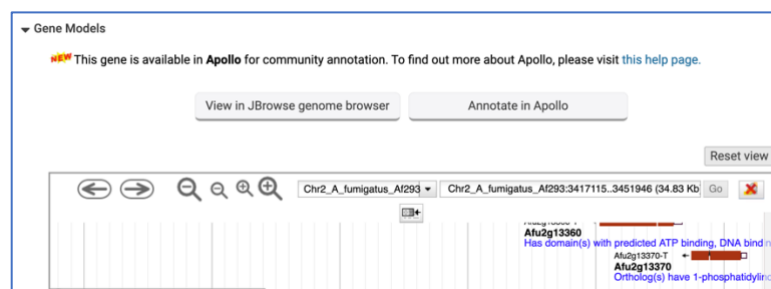
- **Explore the gene model section.**

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, introns, etc.) displayed within the genome browser JBrowse wrapper.



- 1 Community annotation from Apollo provides the latest annotation updates (within 24-48hrs after the changes were submitted to the curation team in Apollo)
- 2 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).
- 3 If you navigated away from the gene on interest while scrolling, click on the “Reset view” button to return to the default position within the JBrowse wrapper.
- 4 Click this button to navigate to the top of the gene record page.

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.



- **Explore the RNA-Seq Evidence for Introns track.**

Click on the intron. 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.

Chr2_A_fumigatus_Af293_3434523..3434611_0 details

Intron Junction Details

Intron Location Chr2_A_fumigatus_Af293:3434523..3434611 (+ strand)

Intron Spanning Reads (ISR) 7027

ISR per million (ISRPM) 2140.85

Gene assignment Afu2g13295 - annotated intron

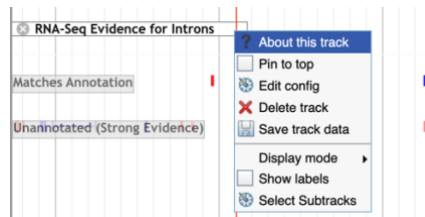
% of Most Abundant Intron (MAI) 100

Sample Details

Experiment	Sample	Unique	ISRPM	ISR/Cov	% MAI
Gene expression in WT, hrmA deletion, hrmA OE, hrmA_REV, EVOL under hypoxia and normoxia conditions	Delta hrmA hypoxia	64	33.07	5.61	100
	Delta hrmA normoxia	61	28.65	4.78	61.61

% 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:



- **Explore other contents within the page.**

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 (*e.g.* AspGD, Ensembl, *etc.*), or user-submitted data (user comments).

2 Annotation, curation and identifiers

Community annotations from Apollo [Data sets](#)

Product Descriptions [Download](#) [Data sets](#)

Alternate Product Descriptions [Data sets](#)

Gene Name or Symbol medA

Names, Previous Identifiers, and Aliases [Download](#) [Data sets](#)

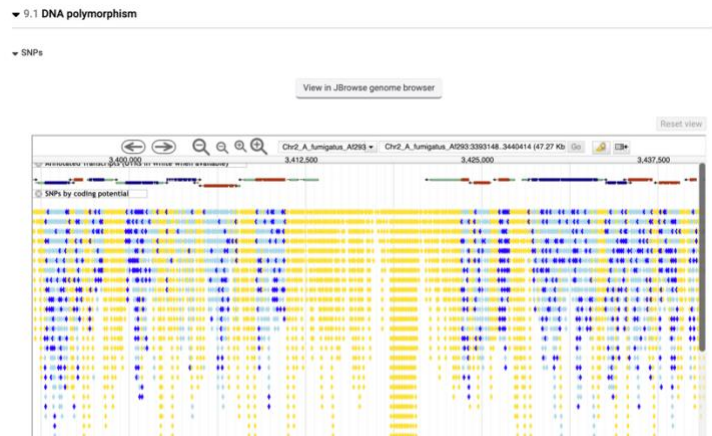
Search this table...

Name/ID/Alias	Type	Source
746128.CADAFUBP00002828	alternate ID	STRING
EAL93620.1	alternate ID	protein_id
Q4X0J5	alternate ID	Uniprot/SPTREMBL
UPI000051EE09	alternate ID	UniParc
XM_750565.1	alternate ID	RefSeq_dna
XP_755658.1	alternate ID	RefSeq_peptide
medA	name	N/A
AFUA_2013260	previous ID	N/A
CADAFUAG00004866	previous ID	N/A

▼ Aspergillus fumigatus transcription factor KO collection Download Data sets										
No data available										
▼ PHI-base curated phenotypes Download Data sets										
PHI- base entry	Essential gene	Multiple mutants	Pathogen species	Pathogen strain	Host species	Host strain	Tissue	Mutant phenotype	Disease	
PHI-261	no	no	<i>Aspergillus fumigatus</i>	A2323	<i>Galleria mellonella</i> (reared greater wax moth)	N/A	larva	reduced virulence	Invasive pulmonary aspergillosis	no fou
▼ Phenotype (qualities or directionality + entity or biological process) Download Data sets										
Search this table... <input type="text"/>										
Modification	Allele	Phenotype	Further Information				PubMed	CHEBI Annotation Extension		
null mutant	meA::hygR	abnormal colony color	Details delay in brown pigmentation				19889063	N/A		
null mutant	meA::hygR	decreased amount biological adhesion	Condition:bioflocin coated wells				19889063	N/A		
null mutant	meA::hygR	decreased amount conidium formation	N/A				19889063	N/A		
null mutant	meA::hygR	decreased amount virulence	Virulence model immunosuppressed mouse pulmonary infection				19889063	N/A		
null mutant	meA::hygR	decreased amount virulence	Virulence model insect infection (<i>Galleria mellonella</i> larvae)				19889063	N/A		
null mutant	meA::hcrI	increased amount cell growth	Dentally slightly lower conidia and conidiospores				19889063	N/A		

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:

NGS_SNP.Chr2_A_fumigatus_Af293.3411010 details

SNP:

Location:

Gene:

Position in CDS:

Position in protein:

Type:

Number of strains:

NGS_SNP.Chr2_A_fumigatus_Af293.3411010

3411010

Afu2g13260

80

27

Coding (non-synonymous)

840

NA

AA

(frequency)

Af293 (reference):

Major Allele:

Minor Allele:

C

S

C

S

A

Y

(1)

(0)

OK

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

Add to basket Add to favorites Download SNP

SNP: NGS_SNP.Chr2_A_fumigatus_Af293.3411010

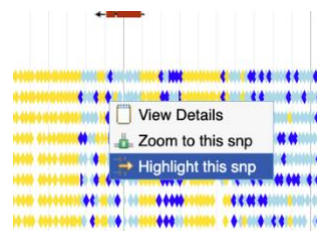
Organism: *Aspergillus fumigatus* Af293
 Location: Chr2_A_fumigatus_Af293: 3,411,010
 Type: coding
 Number of Strains: 840
 Gene ID: Afu2g13260
 Gene Strand: reverse
 Major Allele: G (1)
 Minor Allele: T (0)
 Distinct Allele Count: 2
 Reference Allele: G
 Reference Product: S 27
 Allele (gene strand): C
 SNP context: AGCCGATCCGTCTGCCTGCATTGGCCAAAGAGCAGCAGTGCTCAAGGAAGAAAGAGGGCA
 SNP context (gene strand): TGCCCTCTTTCTTCCTTGAGCACTGCTGCTCTTGGCAAATGCAGGCAGACGATGCTGCT

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

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).

Right click provides more options for JBrowse view:



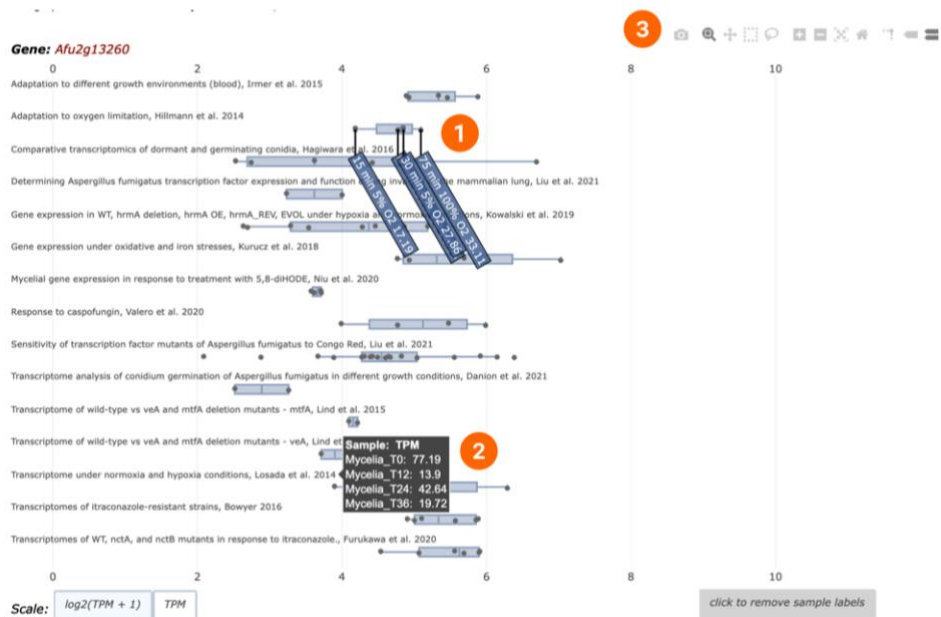
The **Transcriptomics** section (RNA-Seq and microarray data).

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 [Data sets](#)

▼ **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. \log_2 : 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.](#)



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.).

lsm-43d1300

Genotype	Transcript (TPM)	Mean (TPM)
WT_Neutro	~6.5	~6.5
WT_Itra	~8.5	~8.5
nctb_Neutro	~8.5	~8.5
nctb_Itra	~4.5	~4.5
nctb_Neutro	~3.5	~3.5

Full Dataset Description
[View in genome browser](#)

Coverage
 Non-unique mapping may be examined in the genome browser ([tutorial](#))

Table Data
[Search this table](#)

Gene	Sample	Value	Standard Error	Percentile 1	Percentile 2
Afu012280	WT_Neutro-unique	50.54	3.15	79.24	N/A
Afu012280	WT_Itra-unique	59.01	1.93	88.17	N/A
Afu012280	nctb_Neutro-unique	58.59	7.58	81.4	N/A
Afu012280	nctb_Itra-unique	22.49	3.95	68.33	N/A
Afu012280	nctb_Neutro-unique	22.21	5.31	72.12	N/A
Afu012280	nctb_Itra-unique	46.15	3.55	86.92	N/A
Afu012280	WT_Neutro	50.7	3.16	N/A	N/A
Afu012280	WT_Itra	59.23	1.95	N/A	N/A
Afu012280	nctb_Neutro	58.78	7.6	N/A	N/A
Afu012280	nctb_Itra	22.73	3.93	N/A	N/A
Afu012280	nctb_Neutro	22.31	5.32	N/A	N/A
Afu012280	nctb_Itra	46.32	3.59	N/A	N/A

Description
General Description Genome-wide gene expression profile was investigated in the wild-type and null nctb and nctb mutants. Strains were grown in the absence and presence of tetracycline [0.5 mg/L].

Methodology used Paired-end RNA-seq libraries were generated using the TruSeq Stranded mRNA assay (Illumina, Inc.) with three biological replicates.

X-axis
 Transcript abundance in Transcripts per Million (TPM). The percentile graph shows the ranking of expression for this gene compared to all others in this experiment.

Choose gene for which to display graph
 # Afu012280

Choose graph(s) to display
 # tpm : percentile

Graph options
☐ Show top 50 (not applicable for isoforms) tracks, percentile tracks or data tables

protein sequence database (NRDB), 3D structure prediction and similar Protein Data Bank (PDB) chains, when available, and visualization from AlphaFold

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 and 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 AspGD, MIPS, and others

For some genes, 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.

For example, Afu2g13260 is not associated with metabolic pathways but its neighbor ([Afu2g13250](#)) does:

Glycine, serine and threonine metabolism

Pathway Source: KEGG
Pathway ID: ec00260
Total Pathway Enzymes: 81
Total Pathway Compounds: 48

1 Pathways and interactions [S](#)

Show Contents [S](#)

▼ 1.1 Metabolic pathways

▼ Cytoscape Drawing

NOTE Click on nodes for more info. Nodes highlighted in orange are EC numbers that we have mapped to at least one gene. The nodes, as well as the info box, can be repositioned by dragging.

