

## Exercise: Exploring host-pathogen interactions in Ensembl Fungi

*Zymoseptoria tritici*, also known as *Septoria tritici* and *Mycosphaerella graminicola*, is a fungal pathogen that causes septoria leaf blotch disease in wheat. This fungus is considered a major threat to wheat production world-wide, and its ability to rapidly adapt to fungicides and host plants makes it a significant challenge for disease management.

You can explore molecular interactions of genes in Ensembl Fungi, ranging from pathogen-host interactions to symbiotic relationships across microbes and other Ensembl species.

**Step 1:** Find all genes with molecular interactions for *Zymoseptoria tritici*.

From the endpoint API doc page <https://interactions.rest.ensembl.org>, search for all *zymoseptoria\_tritici* genes

[https://interactions.rest.ensembl.org/ensembl\\_gene?scientific\\_name=zymoseptoria tritici](https://interactions.rest.ensembl.org/ensembl_gene?scientific_name=zymoseptoria%20tritici)

You should get the following output:

```
zymoseptoria_tritici": ["Mycgr3G53658", "Mycgr3g88451",  
"Mycgr3G85040", "Mycgr3G40048", "Mycgr3G111221", "Mycgr3G103264",  
"Mycgr3G89160", "Mycgr3G80707", "Mycgr3G65552", "Mycgr3g105487",  
"Mycgr3G70181", "Mycgr3G46840", "Mycgr3G93828", "Mycgr3G31676",  
"Mycgr3G51018", "Mycgr3G36951", "Mycgr3G77528", "Mycgr3G39611",  
"Mycgr3G96592", "Mycgr3G86705", "Mycgr3G107320", "Mycgr3G74194",  
"Mycgr3G87000", "Mycgr3G100355", "Mycgr3G92404", "Mycgr3G69942"]
```

**Step 2:** Let's find out more about the gene *Mycgr3G65552* in Ensembl Fungi. On the homepage, enter the gene ID *Mycgr3G65552* in the top right-hand corner and hit **Search**. Click on the Gene ID *Mycgr3G65552* to open the Gene tab.

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HMMER | BLAST | More

Search: Mycgr3G65552

New Search Jobs

Search Ensembl Fungi

- New Search
- Gene (1)
  - Ensembl Fungi (1)

Configure this page

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### Search results for 'Mycgr3G65552'

Showing 1 Gene found in Ensembl Fungi

#### Mycgr3G65552

**Description** Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F9WWD1]

**Gene ID** [Mycgr3G65552](#)

**Species** [Zymoseptoria tritici](#)

**Location** [1:1786483-1788643](#)

**Gene trees** [EGGT00050000025158](#) (Pan-taxonomic Compara) [PTHR10587](#) (Fungi Compara)

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Search Ensembl Fungi...

Zymoseptoria tritici (MG2)

Location: 1:1,786,483-1,788,643 Gene: Mycgr3G65552 Transcript: Mycgr3T65552 Jobs

### Gene: Mycgr3G65552

**Description** Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F9WWD1]

**Location** [Chromosome 1: 1,786,483-1,788,643](#) reverse strand.  
MG2:ACPE01000001.1

**About this gene** This gene has 1 transcript ([splice variant](#)), [279 orthologues](#) and [4 paralogues](#).

**Transcripts** [Hide transcript table](#)

Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
-	<a href="#">Mycgr3T65552</a>	1868	<a href="#">471aa</a>	Protein coding	<a href="#">F9WWD1</a>	-	Ensembl Canonical

### Summary

**UniProtKB** This gene has proteins that correspond to the following UniProtKB identifiers: [F9WWD1](#)

**Gene type** Protein coding

**Annotation method** Protein coding genes annotated by the [JGI](#)

[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

22.16 kb Forward strand

Genes

- [Mycgr3T18164](#) > protein coding
- [Mycgr3T89063](#) > protein coding
- [Mycgr3T65551](#) > protein coding
- [Mycgr3T2868](#) > protein coding

Contigs

- [ACPE01000001.1](#) >
- [Mycgr3T23438](#) < protein coding
- [Mycgr3T65552](#) < protein coding
- [Mycgr3T107001](#) < protein coding
- [Mycgr3T107003](#) < protein coding

Molecular interactions

Configure this page

Custom tracks

Export data

Share this page

To find a list of species with which this particular *Z. tritici* gene has molecular interactions with, click on [Molecular interactions](#) in the left-hand panel. From this page, we can see that *Z. tritici* is known to interact with *Triticum aestivum* (wheat). Can you find the wheat Gene ID that Mycgr3G65552 interacts with? Look at the [Interacts with](#) table. The Gene ID is [UNDETERMINED](#). This means a molecular interaction has been experimentally verified between Mycgr3G65552 and wheat, but the former gene hasn't been identified yet.

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**Zymoseptoria tritici (MG2)**

Location: 1:1,786,483-1,788,643 | Gene: Mycgr3G65552 | Transcript: Mycgr3T65552 | Jobs

**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
  - GO: Cellular component
  - GO: Biological process
  - GO: Molecular function
  - PHI: Phibase identifier
- Phenotypes
- Genetic Variation
  - Variant table
  - Variant image
  - Structural variants
- Gene expression
- Pathway
- Molecular Interactions**
- Regulation

**Gene: Mycgr3G65552**

**Description** Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F9WWDD1.6]

**Location** Chromosome 1: 1,786,483-1,788,643 reverse strand.  
MG2:ACPE01000001.1

**About this gene** This gene has 1 transcript (splice variant), 279 orthologues and 4 paralogues.

**Transcripts** [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
-	Mycgr3T65552	1868	471aa	Protein coding	F9WWDD1.6	-	Ensembl Canonical

**Molecular interactions**

**This species**

Species	Gene ID	Interactor	Identifier
Zymoseptoria tritici	Mycgr3G65552	protein	uniprot:F9WWDD1

**Interacts with** [Show metadata](#)

Species	Gene ID	Interactor	Identifier	Source DB
Triticum aestivum	UNDETERMINED	protein	UNDETERMINED	PHI-base

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Can you find out what the phenotype for this interaction is? Click on [Show metadata](#) at the top right-hand corner of the **Interacts with** table. Based on PHI-base, the interaction is associated with [Loss of pathogenicity](#).

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**Zymoseptoria tritici (MG2)**

Location: 1:1,786,483-1,788,643 | Gene: Mycgr3G65552 | Transcript: Mycgr3T65552 | Jobs

**Gene: Mycgr3G65552**

**Description** Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F9WWDD1.6]

**Location** Chromosome 1: 1,786,483-1,788,643 reverse strand.  
MG2:ACPE01000001.1

**About this gene** This gene has 1 transcript (splice variant), 279 orthologues and 4 paralogues.

**Transcripts** [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
-	Mycgr3T65552	1868	471aa	Protein coding	F9WWDD1.6	-	Ensembl Canonical

**Molecular interactions**

**This species**

Species	Gene ID	Interactor	Identifier
Zymoseptoria tritici	Mycgr3G65552	protein	uniprot:F9WWDD1

**Interacts with** [Show metadata](#)

Species	Gene ID	Interactor	Identifier	Source DB
Triticum aestivum	UNDETERMINED	protein	UNDETERMINED	PHI-base

**Experimental evidence** gene complementation

**Interaction type** interspecies interaction

**Interaction phenotype** PHIPO-0000010

**Disease name** PHIDO-0000331

**Pathogen protein modification** gene deletion: full

**PHI-base high level term** Loss of pathogenicity

**Pathogen experimental strain** IPO323

**Host experimental strain** cv. Riband

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**Step 3:** Next, let's find all fungal orthologues. There are several ways of doing this. One way is to go to [Fungal Compara: Orthologues](#) in the left-hand panel.

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Search Ensembl Fungi

Location: 11,786,485-1,786,643 Gene: Mycgr3G65552 Transcript: Mycgr3T65552 Job: v

Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Gene alleles
- Sequence
- Secondary Structure
- Gene families
- Literature
- Gene Comparisons
- Genomic alignments
- Gene tree
- Gene gain/loss tree
- Orthologues
- Phylogenetic
- Phylogenetic Comparisons
- Gene Tree
- Orthologues
- Ontologies
- GO Biological process
- GO Molecular function
- GO Cellular component
- Phylogenetic identifier
- Phylogenetic
- Genetic Variation
- Variant table
- Variant image
- Structural variants
- Gene expression
- Pathway
- Molecular interactions
- Regulation
- External references
- Supporting evidence
- ID History
- Gene history

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 "Configure this page" to choose a custom list of species.

Species set	Show details	With 111 orthologues	With 1 many orthologues	With many many orthologues	Without orthologues
All (370 species)	<input type="checkbox"/>	139	91	11	129
Ascomycetes (1 species)	<input type="checkbox"/>	1	0	0	0
Agaricales (2 species)	<input type="checkbox"/>	0	19	0	2
Atheliales (2 species)	<input type="checkbox"/>	0	1	1	0
Blastocladales (1 species)	<input type="checkbox"/>	0	0	0	1
Boliales (1 species)	<input type="checkbox"/>	0	9	0	0
Bolialesphaerales (2 species)	<input type="checkbox"/>	2	0	0	0
Cantharellales (3 species)	<input type="checkbox"/>	0	3	0	0
Cephalosporiales (11 species)	<input type="checkbox"/>	9	2	0	0
Chaetothyriomycetidae (9 species)	<input type="checkbox"/>	7	0	0	1
Chytridiomycota (6 species)	<input type="checkbox"/>	0	1	0	5
Corticiales (1 species)	<input type="checkbox"/>	0	0	0	1
Cryptomycota (2 species)	<input type="checkbox"/>	0	0	0	2
Decrymycetales (3 species)	<input type="checkbox"/>	0	3	0	0
Dortheales (1 species)	<input type="checkbox"/>	1	0	0	0
Dortheomycetes (3 species)	<input type="checkbox"/>	3	0	0	0
Erysiphales (3 species)	<input type="checkbox"/>	3	0	0	0
Eurotiales (17 species)	<input checked="" type="checkbox"/>	17	0	0	0
Fungi (112 species)	<input type="checkbox"/>	3	8	0	5

Can you find out if there are any orthologues in *Aspergillus fumigatus* with molecular interactions entries?

**Step 4:** You can hide the [Summary of orthologues of this gene](#) table by clicking the [Hide](#) button. Enter *Aspergillus fumigatus* in the filter box on the top right-hand corner of the Orthologues table.

Selected orthologues [Hide](#)

Show [All](#) entries

Show/hide columns

Filter

Species	Type	Orthologue	Target %id	Query %id	GOC Score	WGA Coverage	High Confidence
Aspergillus fumigatus A293	1-to-1	<a href="#">AFUA_7G02500</a> 7-680,932-683,084-1 <a href="#">View Sequence Alignments</a>	54.37 %	42.25 %	n/a	n/a	Yes
Aspergillus fumigatus A1163	1-to-1	<a href="#">AFUA_089042</a> DS499601678,603-680,755-1 <a href="#">View Sequence Alignments</a>	54.37 %	42.25 %	n/a	n/a	Yes

There are two orthologues in *A. fumigatus*. Click each of the gene IDs to find out which one has an entry under the [Molecular interactions](#) Gene-based display. Molecular interactions are available for the second orthologue, [AFUA\\_7G02500](#). What is the phenotype of the interaction for this orthologue with mice?

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Aspergillus fumigatus Af293 (ASM265v1)

Location: 7:680,932-683,084

Gene: AFUA\_7G02500

Transcript: EAL84644

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

GO: Biological process

GO: Cellular component

GO: Molecular function

PHI: Phibase identifier

Phenotypes

Genetic Variation

Variant table

Variant image

Structural variants

Gene expression

Pathway

Molecular interactions

Regulation

External references

Supporting evidence

Gene: AFUA\_7G02500

Description

polysaccharide synthase Cps1, putative

Location

[Chromosome 7: 680,932-683,084](#) reverse strand.  
ASM265v1:CM000175.1

About this gene

This gene has 1 transcript ([splice variant](#)), [279 orthologues](#) and [6 paralogues](#).

Transcripts

Show transcript table

Molecular interactions

This species

Species	Gene ID	Interactor	Identifier
Aspergillus fumigatus Af293	<a href="#">AFUA_7G02500</a>	protein	<a href="#">uniprot.Q4WAU2</a>

Interacts with

[Show metadata](#)

Species	Gene ID	Interactor	Identifier	Source DB
Mus musculus	UNDETERMINED	protein	UNDETERMINED	<a href="#">PhI-base</a>
Mus musculus	UNDETERMINED	protein	UNDETERMINED	<a href="#">PhI-base</a>

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## Additional host-pathogen exercise 1 – Exploring GO terms and phenotypes

*Botrytis cinerea* is a necrotrophic fungus that infects a wide range of crops and ornamental plants, causing significant economic losses in agriculture and horticulture industries. It is known to cause botrytis bunch rot in various species. Use Ensembl Fungi to find out more information about molecular interactions in the species and answer the following questions:

- Using the Ensembl REST API, can you retrieve all genes with molecular interactions information for *B. cinerea*?
- Open the Molecular interactions page for the Bcin07g00720 gene in *B. cinerea*. What plant species does the gene interact with?
- Can you find the phenotype that is reported for each of the species the gene interacts with?
- Find all fungal orthologues. Is there any orthologue in *Magnaporthe oryzae* for Bcin07g00720? For which orthologue is molecular interaction information available?
- Which species does the *M. oryzae* orthologue interact with?
- Compare the Molecular interaction phenotypes between the *B. cinerea* and *M. oryzae* orthologues. Can you find any common molecular functions that may explain this phenotype?

### Answers:

(a) From the endpoint [https://interactions.rest.ensembl.org/interactions\\_by\\_proddname/](https://interactions.rest.ensembl.org/interactions_by_proddname/). Search for **botrytis\_cynerea**, which will give you the following output:

```
"botrytis_cinerea": ["Bcin07g00720", "Bcin02g02570", "Bcin12g04900",  
"Bcin16g00630", "Bcin02g06770", "Bcin03g07190", "Bcin09g02390",  
"Bcin09g01800", "Bcin07g03050", "Bcin08g05150", "Bcin10g01250",  
"Bcin14g01870", "Bcin06g04870", "Bcin06g00240", "Bcin06g03440",  
"Bcin03g07900", "Bcin03g06840", "Bcin10g02530", "Bcin08g02990",  
"Bcin07g02610", "Bcin03g08710", "Bcin10g05590", "Bcin16g01820",  
"Bcin03g01540", "Bcin14g00650", "Bcin09g05460", "Bcin10g02650",  
"Bcin02g02780", "Bcin05g03080", "Bcin08g00160", "Bcin01g06010",  
"Bcin01g11360", "Bcin15g00450", "Bcin03g04600", "Bcin09g01910",  
"Bcin09g05050", "Bcin15g03580", "Bcin05g02590"]
```

(b) Go to the Ensembl Fungi homepage and search for **Bcin07g00720**. In the results, click on the **Gene ID** to open the Gene tab.

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Bcin07g00720

New Search | Jobs

Search Ensembl Fungi

- New Search
- Gene (1)
  - Ensembl Fungi (1)

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### Search results for 'Bcin07g00720'

Showing 1 Gene found in Ensembl Fungi

**Bcin07g00720**

Description: n/a

Gene ID: [Bcin07g00720](#)

Species: [Botrytis cinerea B05.10](#)

Location: [7:260067-264879](#)

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In the left-hand panel, click on [Molecular interactions](#) to open the page.

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Zymoseptoria tritici (MG2)

Location: 1:1,786,483-1,788,643 | Gene: Mycgr3G65552 | Transcript: Mycgr3T65552 | Jobs

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
  - GO: Cellular component
  - GO: Biological process
  - GO: Molecular function
  - PHI: Phibase identifier
- Phenotypes
- Genetic Variation
  - Variant table
  - Variant image
- Structural variants
- Gene expression
- Pathway
- Molecular interactions**
- Regulation
- External references
- Supporting evidence
- ID History
  - Gene history

### Gene: Mycgr3G65552

Description: Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:[F9WWD1](#)]

Location: [Chromosome 1: 1,786,483-1,788,643](#) reverse strand.  
MG2:ACPE01000001.1

About this gene: This gene has 1 transcript ([splice variant](#)), [279 orthologues](#) and [4 paralogues](#).

Transcripts: [Hide transcript table](#)

Show/hide columns (1 hidden) | Filter

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
-	<a href="#">Mycgr3T65552</a>	1868	<a href="#">471aa</a>	Protein coding	<a href="#">F9WWD1</a>	-	Ensembl Canonical

### Summary

UniProtKB: This gene has proteins that correspond to the following UniProtKB identifiers: [F9WWD1](#)

Gene type: Protein coding

Annotation method: Protein coding genes annotated by the [JGI](#)

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

22.16 kb | Forward strand

Genes

Mycgr3T18164 > protein coding | Mycgr3T89063 > protein coding | Mycgr3T18164 > protein coding | Mycgr3T89063 > protein coding | Mycgr3T18164 > protein coding | Mycgr3T89063 > protein coding | Mycgr3T18164 > protein coding | Mycgr3T89063 > protein coding | Mycgr3T18164 > protein coding | Mycgr3T89063 > protein coding

In the Molecular interactions page, you can find all species the gene interacts with in the right-hand table. These include *Solanum lycopersicum* (tomato), *Vitis vinifera* (grape),

*Cucumis sativus* (cucumber) and *Malus domestica* (apple).

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**Botrytis cinerea B05.10** (ASM83294v1)

Location: 7,260,067-264,879 | Gene: Bpk3 | Transcript: Bcin07g00720.1 | Jobs

**Gene-based displays**

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

**Gene: Bpk3** Bcin07g00720

Gene Synonyms

Location: [Chromosome 7: 260,067-264,879](#) forward strand.  
ASM83294v1-CP009811.1

About this gene: This gene has 1 transcript ([splice variant](#)) and 313 orthologues.

Transcripts: [Hide transcript table](#)

Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
Bcin07g00720.1	4551	952aa	Protein coding	AGAS84JLH6	A6RYB86	-	Ensembl Canonical

**Molecular interactions**

This species

Species	Gene ID	Interactor	Identifier
Botrytis cinerea B05.10	Bcin07g00720	protein	uniprot:A6RYB8

Interacts with [Show metadata](#)

Species	Gene ID	Interactor	Identifier	Source DB
Solanum lycopersicum	UNDETERMINED	protein	UNDETERMINED	<a href="#">PHI-base</a>
Vitis vinifera	UNDETERMINED	protein	UNDETERMINED	<a href="#">PHI-base</a>
Cucumis sativus	UNDETERMINED	protein	UNDETERMINED	<a href="#">PHI-base</a>
Malus domestica	UNDETERMINED	protein	UNDETERMINED	<a href="#">PHI-base</a>

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(c) Click on [Show metadata](#) in the right-hand corner of the Interacts with table. You can find associated phenotypes under [PHI-base high level term](#). The gene is associated with “Reduced virulence” and / or “Loss of pathogenicity”.

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**Zymoseptoria tritici (MG2)**

Location: 1,178,483-1,786,643 | Gene: Mycgr3G65552 | Transcript: Mycgr3T65552 | Jobs

**Gene: Mycgr3G65552**

Description: Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:FWWWD16]

Location: [Chromosome 1: 1,178,483-1,786,643](#) reverse strand.  
MG2-ACPE21000001.1

About this gene: This gene has 1 transcript ([splice variant](#)), 279 orthologues and 4 paralogues.

Transcripts: [Hide transcript table](#)

Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
Mycgr3T65552	1868	471aa	Protein coding	FWWWD16	-	-	Ensembl Canonical

**Molecular interactions**

This species

Species	Gene ID	Interactor	Identifier
Zymoseptoria tritici	Mycgr3G65552	protein	uniprot:FWWWD1

Interacts with [Show metadata](#)

Species	Gene ID	Interactor	Identifier	Source DB
Triticum aestivum	UNDETERMINED	protein	UNDETERMINED	<a href="#">PHI-base</a>

**Experimental evidence**

gene complementation	
Interaction type	Interspecies interaction
Interaction phenotype	PHIPO:0000010
Disease name	PHIDO:0000331
Pathogen protein modification	gene deletion: full
PHI-base high level term	Loss of pathogenicity
Pathogen experimental strain	IP0323
Host experimental strain	cv. Riband

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(d) To retrieve all fungal orthologues, go to [Fungal Compara: Orthologues](#) in the left-hand panel.



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Botrytis cinerea B04.10 (MAG2024v1) v Gene Bp33 3,898,532-3,902,777 (MAG\_06393T0) 07 Search Ensembl Fungi...

Gene-based displays

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Gene: Bp33 (B04.10)MAG2024v1

Gene Synonyms

Location

Chromosome 7: 3,898,532-3,902,777 forward strand.

Annotation: MAG2024v1 CPO00811.1

About this gene

This gene has 1 transcript ([splice variant](#)) and 313 orthologues.

Transcripts

Hide transcript table

Showhide columns (1 hidden)

Name	Transcript ID	tp	Protein	UniProt	RefSeq	Flags
Bp33	B04.10	4531	4531	Q52EB3	Q52EB3	Ensembl Canonical

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 'Configure this page' to choose a custom list of species.

Species set	Show details	With 11 orthologues	With 1 binary orthologues	With many many orthologues	Without orthologues
All (370 species)		270	16	0	23
Ascomycota (1 species)		1	0	0	0
Agaricales (1 species)		4	0	0	11
Albionales (2 species)		1	0	0	1
Blasidiales (1 species)		0	1	0	0
Boliales (1 species)		3	0	0	0
Bryophytes (2 species)		2	0	0	0
Cantharellales (3 species)		9	2	0	0
Cephalosporiales (1 species)		8	0	0	1
Chytridiomycota (1 species)		3	3	0	0
Corticiales (1 species)		0	0	0	1
Cryptophytes (2 species)		2	0	0	0
Dactylospora (2 species)		3	0	0	0
Dulidiales (1 species)		1	0	0	0
Dulidiales (2 species)		3	0	0	0
Erysiphales (1 species)		3	0	0	0
Eurotiales (17 species)		17	0	0	0
Fungi (14 species)		13	0	0	1
Geotrichales (1 species)		1	0	0	0
Geotrichales (1 species)		1	0	0	0
Gloiosporales (2 species)		0	1	0	1
Gloiosporales (2 species)		6	1	0	0
Helotiales (9 species)		8	1	0	0
Hymenochaetales (2 species)		0	0	0	2
Hymenochaetales (2 species)		30	0	0	0
Jaspliales (1 species)		0	0	0	1
Magnaportheales (4 species)		4	0	0	0
Microsporidia (4 species)		4	0	0	0

Scroll down to the Orthologues table and use the filter box in the top right-hand corner to search for *Magnaporthe oryzae*.

Selected orthologues Hide

Species	Type	Orthologue	Target %id	Query %id	GOC Score	WGA Coverage	High Confidence
Magnaporthe poae	1-to-1	MAGS_07887 supercont1.7:832,004-836,478-1 <a href="#">View Sequence Alignment</a>	51.17 %	36.87 %	n/a	n/a	Yes
Magnaporthe oryzae	1-to-1	M_0632_EuGene_0042871 BP32_scaff400003.3:066,924-3,069,846-1 <a href="#">View Sequence Alignment</a>	50.05 %	49.58 %	n/a	n/a	Yes
Gaeumannomyces grisei RD-111a-1	1-to-1	G010_08136 supercont2.4:2,261,817-2,266,643-1 <a href="#">View Sequence Alignment</a>	49.49 %	50.63 %	n/a	n/a	Yes
Magnaporthe oryzae	1-to-1	ATG1_MGG_06393 4:3,898,532-3,902,777-1 <a href="#">View Sequence Alignment</a>	49.90 %	51.47 %	n/a	n/a	Yes

Click on each of the orthologue gene IDs to open their respective gene tab and find out if the **Molecular interactions** Gene-based display is available. Molecular interactions information is available for the orthologue ATG1 (MGG\_06393).

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Magnaporthe oryzae (MG8) v Location: 4:3,898,532-3,902,777 Gene: ATG1 Transcript: MGG\_06393T0

Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Gene alleles
- Sequence
- Secondary Structure
- Gene families
- Literature
- Fungal Compare
- Genomic alignments
- Gene tree
- Gene gain/loss tree
- Orthologues
- Paralogues
- Pan-taxonomic Compare
- Gene Tree
- Orthologues
- Ontologies
- GO: Biological process
- GO: Molecular function
- GO: Cellular component
- PHI: Phibase identifier
- Phenotypes
- Genetic Variation
- Variant table
- Variant image
- Structural variants
- Gene expression
- Pathway
- Molecular interactions
- Regulation
- External references
- Supporting evidence

Gene: ATG1 MGG\_06393

Description

Serine/threonine-protein kinase ATG1 [Source:UniProtKB/Swiss-Prot;Acc:Q52EB3]

Location

Chromosome 4: 3,898,532-3,902,777 reverse strand.

MG8:CM001234.1

About this gene

This gene has 1 transcript ([splice variant](#)) and 313 orthologues.

Transcripts

Show transcript table

Summary

Name

ATG1 (UniProtKB Gene Name)

UniProtKB

This gene has proteins that correspond to the following UniProtKB identifiers: [Q52EB3](#)

Gene type

Protein coding

Annotation method

Protein coding genes annotation from the [Broad Institute](#)

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

Genes

Contigs

Genes

3.89Mb 3.90Mb 3.91Mb

MGG\_06394T0 > protein coding

AACU03000115 3 >

MGG\_06393T0 > protein coding

MGG\_06393T0

(e) Click on **Molecular interactions** in the left-hand panel. The ATG1 protein interacts with *Hordeum vulgare* (barley) and *Oryza sativa* (rice).

**Gene: ATG1** MGG\_06393

Description: Serine/threonine-protein kinase ATG1 [Source:UniProtKB/Swiss-Prot;Acc:Q52EB3]

Location: Chromosome 4: 3,898,532-3,902,777 reverse strand. MGG\_CM001234.1

About this gene: This gene has 1 transcript (splice variant) and 313 orthologues.

Transcripts: Hide transcript table

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
-	MGG_06393T0	3957	982aa	Protein coding	Q52EB3	-	Ensembl Canonical

**Molecular interactions**

This species

Species	Gene ID	Interactor	Identifier
Magnaporthe oryzae 70-15	MGG_06393	protein	uniprot:Q52EB3

Interacts with

Species	Gene ID	Interactor	Identifier	Source DB
Hordeum vulgare	UNDETERMINED	protein	UNDETERMINED	PHI-base
Oryza sativa	UNDETERMINED	protein	UNDETERMINED	PHI-base
Oryza sativa	UNDETERMINED	protein	UNDETERMINED	PHI-base

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(f) Click on **Show metadata** to view the phenotypes associated with the molecular interactions. In *B. cinerea*, the phenotype is “Loss of pathogenicity” and in *M. oryzae* the phenotype is “Loss of pathogenicity” and “Reduced virulence”.

(g) Go to **Ontologies: GO: Molecular function** for both *B. cinerea* and *M. oryzae*. Comparing the GO terms for the two orthologues we can see that they have identical GO annotations: “nucleotide binding”, “protein kinase activity”, “protein serine/threonine kinase activity”, “ATP binding”, “kinase activity”, “transferase activity” and “protein serine kinase activity”.

**Gene: Bpk3** Bcin07g00720

Gene Synonyms: Bpk3

Location: Chromosome 7: 260,067,264-879 forward strand. ASM83294v1.CPO09811.1

About this gene: This gene has 1 transcript (splice variant) and 313 orthologues.

Transcripts: Hide transcript table

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
-	Bcin07g00720.1	4551	952aa	Protein coding	A0A384JLJ4	A6RYB8	Ensembl Canonical

**GO: Molecular function**

Accession	Term	Evidence	Annotation source	Transcript IDs
GO:0001668	nucleotide binding	IEA	UniProt	Bcin07g00720.1
GO:0004672	protein kinase activity	IEA		Bcin07g00720.1
GO:0004674	protein serine/threonine kinase activity	IEA		Bcin07g00720.1
GO:0005524	ATP binding	IEA		Bcin07g00720.1
GO:0016301	kinase activity	IEA	UniProt	Bcin07g00720.1
GO:0016749	transferase activity	IEA	UniProt	Bcin07g00720.1
GO:0106310	protein serine kinase activity	IEA	RHEA	Bcin07g00720.1

