

Fungal Pathogen Genomics 2023

Ensembl Fungi

Nishadi De Silva, Manuel Carbajo and Aleena Mushtaq

Ensembl, EMBL-EBI

Tuesday, 9th May 2023



What is Ensembl?

Ensembl brings together information from a wide range of other databases in a single site.

```
AGTGCTTAATGTGGCTAGTGGCACCGGTTGGACAGCACAGCTGTAAAATGTTCCC  
ATCCTCACAGTAAGCTGTTACCGTTCAGGAGATGGGACTGAATTAGAATTCAAAC  
AAATTTCCAGCGCTTCTGAGTTACCTCAGTCACATAATAAGGAATGCATCCCT  
GTGTAAGTGCATTGGTCTTGTGAGACTTACCAAGCATTGGAGGA  
ATATCGTAGGTAAAAATGCCTATTGGATCAAAGAGAGGCCAACATTGGAAAT  
TTTAAGACACGCTGCAACAAAGCAGGTATTGACAAATTATATAACTTATAAAA  
TTACACCGAGAAAGTGTCTAAAAATGCTGCTAAAAACCCAGTACGTACAG  
TGTTGCTTAGAACATAACTGTTCTATGTGTGTATAAATCCAGTTAACACAT  
AATCATCGTTGCAGGTTAACACATGATAAATAGAACGTCTAGTGGATAAAGA  
GGAAACTGGCCCCTGACTAGCAGTAGGAACAATTACTAACAAATC
```



History of the Ensembl resources

	Ensembl	Ensembl Genomes	Ensembl COVID-19
Released	2000	2009	2020
Species	Vertebrates (fly, worm and yeast as outgroups)	Non-vertebrates (plants, fungi, metazoa, protists, bacteria)	SARS-CoV-2
Annotation	By Ensembl	In collaboration with the scientific communities	By Ensembl and imported from ENA
Website	www.ensembl.org	www.ensemblgenomes.org	covid-19.ensembl.org
REST API	rest.ensembl.org	rest.ensembl.org	N/A

Non-vertebrate species in Ensembl

EnsemblPlants

<https://plants.ensembl.org/>

Search: All species e.g. *Carboxy* or chs2B*

Wheat assemblies
Ensembl Plants hosts the *last wheat assembly* from the IWGSC (v1.0), including:
• The IWGSC RefSeq v1.0 gene annotation, with links to wheat-specific transcript and protein data;
• 14 wheat chromosomes (A, B, D and E) and 20 genome crosses;
• Alignment of ~370K high confidence genes from the TGAC1 annotation;
• Axom 20K, RDXN SNP arrays from *Cerezo et al.*, including QTL links in selected cases and Linkage Disequilibrium display; QTLs, earliness, biomass, yield, grain weight, protein content, seedling traits, resistance to Powdery mildew (coding regions) and Kornika (coding regions and promoters);
• Inter-Homologous Variants (IHVs) between the A, B and D genome components;
• Chromosome specific KASP markers were added from the Nottingham BBSRC Wheat Research Centre;
• Protein alignments between wheat, bread and durum; and
• Assembly-wide alignment mapping and per-chromosome QTL mapping to the previous TGAC1 assembly, archived at <http://wgs.csiro.au/tgac/>.
• Phylogenetic tree enabled, allowing users to view alignments among multiple wheat accessions (<https://wgs.csiro.au/tgac/>)

All genomes Favourite genomes *Arabidopsis thaliana* TAIR10
Oryza sativa Japonica IRGSP-1.0
Triticum aestivum IWGSC

EnsemblMetazoa

<https://metazoa.ensembl.org/>

Search: All species e.g. *CPDRA or chitin**

What's New in Release 53
Updated data
• Selected species
• All genomes
Favourite genomes *Anopheles gambiae* AgamP4
Drosophila melanogaster BDGP37
Apis mellifera DH4
View full list of all species

What's New in Release 53
Updated data
• Anophelis palpipes (Palaearctic) (OCA_005090785_1)
• Anophelis palpipes (Asia opaca) (OCA_005090785_1)
• Anophelis pseudopunctipennis (Common eastern banded) (OCA_000180935_4)
• Anopheles maculipennis (Monach long-horned beetle) (OCA_000300255_2)
• Anopheles stephensi (Stephensi) (OCA_014002326_1)
• Danacea pleopis (Monarch butterfly) (OCA_000731995_1)
• Glossina kordofana (Tsetse fly) (OCA_014003621_1)
• Sarcophaga crassimacula (Horsefly) (OCA_018027251_1)
• Sarcoptes scabei (Human itch mite) (OCA_014006071_1)
• Neophasma damarensis (Malaysian stick-eyed fly) (OCA_002237135_2)

New data
• Culex quinquefasciatus (Southern house mosquito) (OCA_017302785_1)
• Anolis scutellatus (Black-legged tick) (OCA_019020785_2)
• Demodex folliculorum (OCA_01339741_1)

EnsemblBacteria

<https://bacteria.ensembl.org/>

Search for a gene Search for a genome
Search for species Start typing the name of a genome...
e.g. *Escherichia coli**
View full list of all species

Archive sites
The following archive sites are available to access previous versions of data:
• Release 40, December 2020 <https://bacteria.ensembl.org/40>
• Release 45, September 2019 <https://bacteria.ensembl.org/45>
• Release 40, July 2018 <https://bacteria.ensembl.org/40>
• Release 37, October 2017 <https://bacteria.ensembl.org/37>

Ensembl Bacteria
Ensembl Bacteria is a browser for bacterial and archaeal genomes. These are drawn from the databases of the International Nucleotide Sequence Database Collaboration, the European Nucleotide Archive at the EBI, Genbank at the US National Center for Biotechnology Information and the Collection of Aspergillus

Data access
Data can be visualised through the Ensembl genome browser and accessed programmatically via our Perl and RESTful APIs. Data is also accessible via the Ensembl API, which provides a standard interface to access bacterial genomes as defined by Ensembl set out by UniProt. See more details about the update in our [blog post](#).

EnsemblProtists

<https://protists.ensembl.org/>

Search: All species e.g. *PF3907_8532506 or cyst**

All genomes Favourite genomes *Plasmodium falciparum* 3D7
Dicystidium discoidale dyc-2.7
Phytophthora infestans Inf-1
Lishmania major AS9427v1

View full list of all species

What's New in Release 53
No updated genomes from last release
• Updated data
• Updated feature for all species using <https://rest.ensembl.org/> with version 86 of InterPro®
• Updated features for all gene and variant data
• Updated interactions, gene trees and orthologues

Ensembl Rapid Release
New assemblies with gene and protein annotation every two weeks.
Now, species that already exist on the site will continue to be updated with the full range of annotations.
The Ensembl Rapid Release website provides annotation for recently produced, publicly available vertebrate and non-vertebrate genomes from biodiversity initiatives such as the Tree of Life, the Vertebrate Genomes Project and the Earth BioGenome Project.
[Read the press release on our blog](#)

EnsemblFungi

<https://fungi.ensembl.org/>

Search: All species e.g. *NAT2 or alcohol**

All genomes Favourite genomes *Baccharomyces cerevisiae* RPK-1
Saccharomyces pombe AS9424v2
Aspergillus nidulans AS9411v1
Puccinia graminis AS9406v1

View full list of all species

What's New in Release 53
Ensembl is adding ~100 genomes to its database every two weeks. This includes genomes imported from NCBI (<https://www.ncbi.nlm.nih.gov/genome/>) and UniProt (<https://rest.ensembl.org/>).
• 14 genomes imported from UniProt
• Updated data
• Updated feature for all gene and variant data
• Updated interactions, gene trees and homologues

Ensembl Rapid Release
New assemblies with gene and protein annotation every two weeks.
Now, species that already exist on the site will continue to be updated with the full range of annotations.
The Ensembl Rapid Release website provides annotation for recently produced, publicly available vertebrate and non-vertebrate genomes from biodiversity initiatives such as the Tree of Life, the Vertebrate Genomes Project and the Earth BioGenome Project.

EnsemblCOVID-19

<https://covid.ensembl.org/>

SARS-CoV-2

Reference Genome
The complete genome of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) isolate Wuhan-Hu-1, release of the disease COVID-19.

Genome assembly: **ASMB5888v3** [GCA_000208085.3](https://www.ncbi.nlm.nih.gov/assembly/GCA_000208085.3/) v3
Sequencer: MN908947

View in Genome browser
• Example gene
• Example protein summary
• Whole genome

COVID-19 resources
The EnsemblGENCODE human protein coding gene set linked to COVID-19 can be found at <https://covid.ensembl.org/>

Sequence and annotation data
• Download data

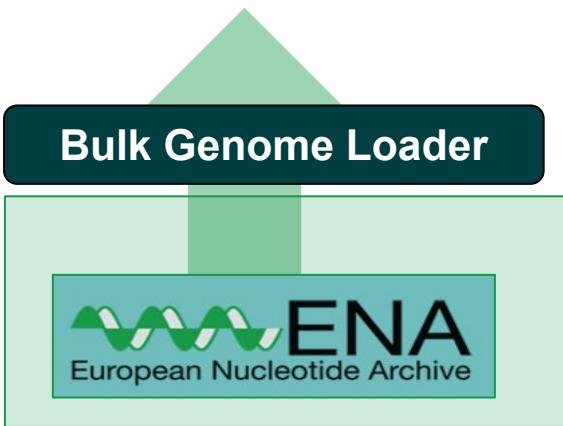
Assemblies and annotation



Data generators and
collaborators, in-house
annotation

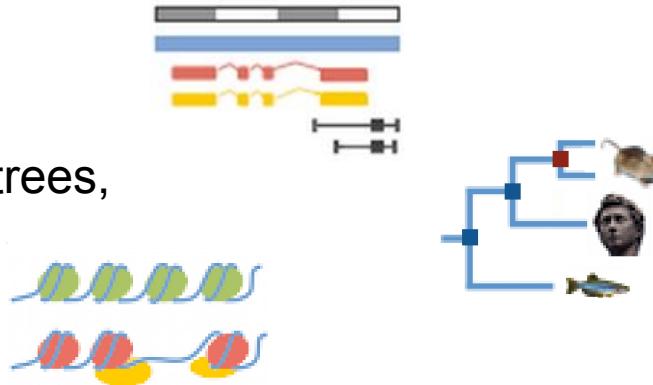


ROTHAMSTED
RESEARCH



Ensembl Fungi features

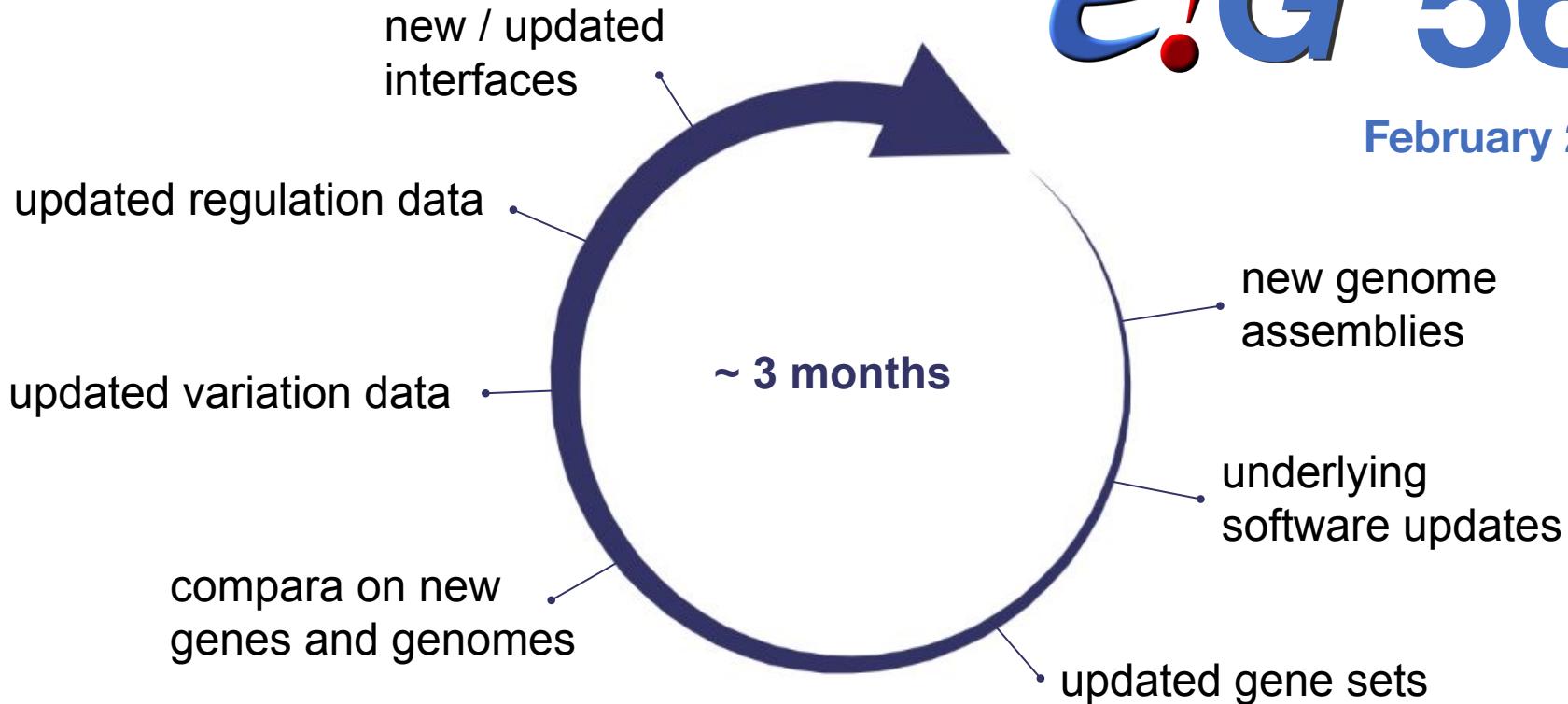
- Genome assemblies and annotation
- Variation data and VEP
- Comparative genomics (alignments, gene trees, homologues)
- Cross-species molecular interactions
- Microarray data (2 species)
- TrackHubs (RNA-Seq data)
- BioMart (data query))
- Display your own data
- Programmatic access via APIs
- Completely Open Source (FTP, GitHub)



Ve!P



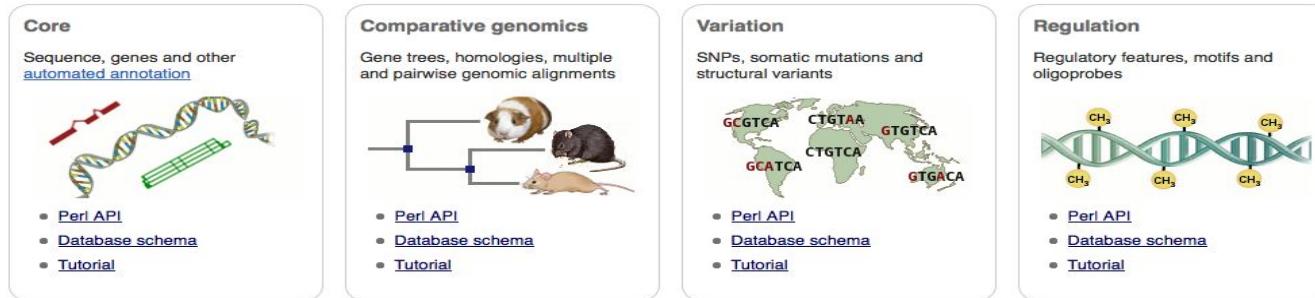
Ensembl Release Cycle



e!G 56

February 2023

Use the Ensembl infrastructure



Genome browser



Bulk data retrieval + bespoke queries



Programmatic data retrieval



Variant effect prediction

The Track Hub Registry

Community gene annotation

Display external RNA-Seq data

Training

The Ensembl genome browser

e! EnsemblFungi ▾ HMMER | BLAST | BioMart | Tools | Downloads | Help & Docs | Blog

Login/Register

Magnaporthe oryzae (MG8) ▾

Location: 2:2,789,925-2,792,654 Gene: MGG_01236 Transcript: MGG_01236T0

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

Gene: MGG_01236

Description WD repeat-containing protein slp1 [Source:UniProtKB/TrEMBL;Acc:G4MXK2]

Location Chromosome 2: 2,789,925-2,792,654 reverse strand.
MG8:CM001236T0

About this gene This gene has 1 transcript (splice variant), 280 orthologues and 2 paralogues.

Transcripts Show transcript table

Summary

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 | Drag>Select: ↕

2.78Mb 2.79Mb 2.80Mb

Forward strand

Genes

Contigs

Genes

AACU03000075.1 >

< MGG_01233T0 protein coding

< MGG_01235T0 protein coding

< MGG_01236T0 protein coding

< MGG_01238T0 protein coding

The Ensembl genome browser

[Login/Register](#)

Ensembl Fungi • Magnaporthe oryzae (MG8) ▾

Location: 2:2,789,925-2,792,654 Gene: MGG_01236 Transcript: MGG_01236T0

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 - GO: Biological process
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- External references
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Gene: MGG_01236

Description WD repeat-containing protein slp1 [Source:UniProtKB/TrEMBL;Acc:[G4MXK2](#)]

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MG8:CM001232.1

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Transcripts [Show transcript table](#)

Summary ⓘ

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

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

2.78Mb 2.79Mb 2.80Mb

22.73 kb

Forward strand

Genes

Contigs

Genes

< MGG_01233T0 protein coding

< MGG_01236T0 protein coding

< MGG_01238T0 protein coding

AACU03000075_1 >

The Ensembl genome browser

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Search Ensembl Fungi...

Login/Register

Magnaporthe oryzae (MG8) ▾

Location: 2:2,789,925-2,792,654 Gene: MGG_01236 Transcript: MGG_01236T0

Gene-based displays

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Transcripts [Show transcript table](#)

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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 | Drag>Select:

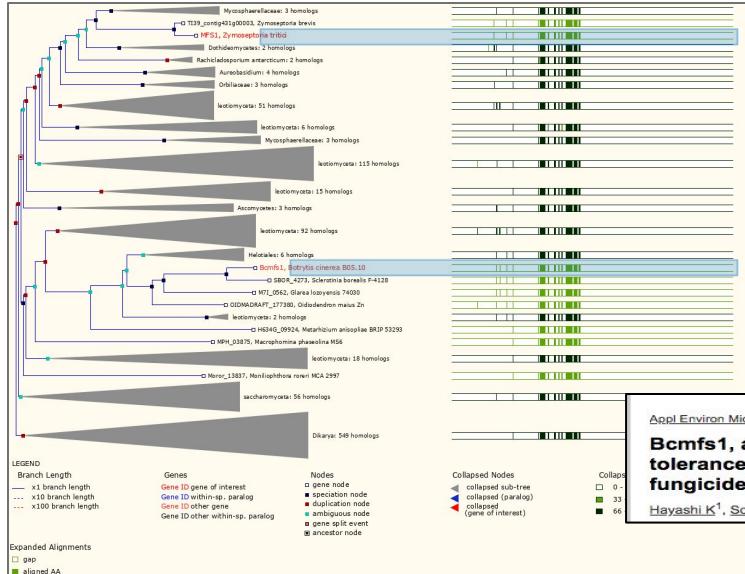
Genes

2.78Mb 2.79Mb 2.80Mb Forward strand

Contigs

AACU03000075.1 >

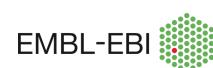
Explore behaviour in other pathogens



Regularly generate gene trees showing orthologous relationships



<https://training.ensembl.org/events/>



Botrytis cinerea infections

Pest Manag Sci. 2013 Jun;69(6):667-78. doi: 10.1002/ps.3506. Epub 2013 Apr 10.

French vineyards provide information that opens ways for effective resistance management of *Botrytis cinerea* (grey mould).

Walker AS¹, Micoud A, Rémyson F, Grosman J, Gredt M, Leroux P.

Appl Environ Microbiol. 2013 Jan;79(1):159-67. doi: 10.1128/AEM.02655-12. Epub 2012 Oct 19.

Gray mold populations in german strawberry fields are resistant to multiple fungicides and dominated by a novel clade closely related to *Botrytis cinerea*.

Leroch M¹, Plesken C, Weber RW, Kauff F, Scalliet G, Hahn M.

Appl Environ Microbiol. 2002 Oct;68(10):4996-5004.

Bcmfs1, a novel major facilitator superfamily transporter from *Botrytis cinerea*, provides tolerance towards the natural toxic compounds camptothecin and cercosporin and towards fungicides.

Hayashi K¹, Schoonbeek HJ, De Waard MA.

The Ensembl genome browser

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Magnaporthe oryzae (MG8) ▾

Location: 2:2,789,925-2,792,654 Gene: MGG_01236 Transcript: MGG_01236T0

Gene-based displays

- Summary**
 - Splice variants
 - Transcript comparison
 - Gene alleles
- Sequence**
 - Secondary Structure
 - Gene families
 - Literature
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 - GO: Cellular component
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 - Variant table
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 - Structural variants
- Gene expression
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- External references
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Gene: MGG_01236

Description WD repeat-containing protein slp1 [Source:UniProtKB/TrEMBL;Acc:[G4MXK2](#)]

Location Chromosome 2: 2,789,925-2,792,654 reverse strand.
MG8:CM001232.1

About this gene This gene has 1 transcript ([splice variant](#)), [280 orthologues](#) and [2 paralogues](#).

Transcripts [Show transcript table](#)

Summary ⓘ

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)

Genes

2.78Mb 22.73kb 2.79Mb 2.80Mb

Contigs

2.78Mb 22.73kb 2.79Mb 2.80Mb

AACU03000075_1 >

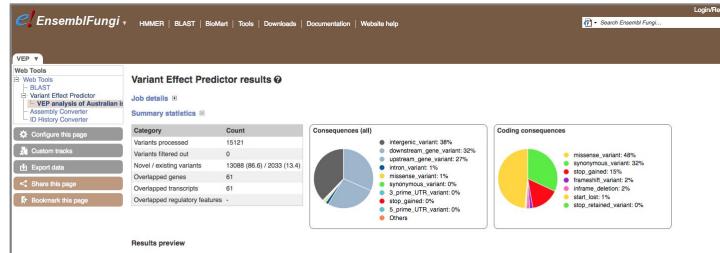
< MGG_01233T0 protein coding < MGG_01235T0 protein coding < MGG_01236T0 protein coding < MGG_01238T0 protein coding

Add/remove tracks | **Custom tracks** | **Share** | **Resize image** | **Export image** | **Reset configuration** | **Reset track order** | Drag>Select: ↕ ↖ ↘ ↙

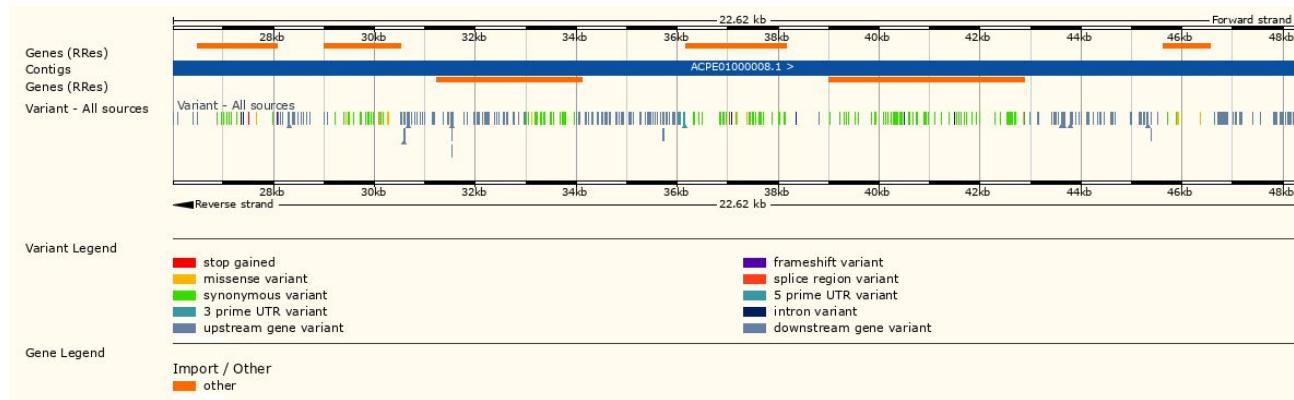
Explore your own variation data



Ensembl Variant Effect Predictor



Quick VEP run showing predicted consequences of variants from 13 Australian *Z. tritici* isolates obtained from
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4825649/>



Customise what you see (“tracks”)

EnsemblFungi ▾ HMMER | BLAST | BioMart | Tools | Downloads | Help & Docs | Blog

Login register

Magnapo Location: 2:2,789,871 Location-based display

- Whole genome
- Chromosome summary
- Region overview
- Region in detail
 - Comparative Genomics
 - Synteny
 - Alignments (image)
 - Alignments (text)
 - Region Comparison
 - Genetic Variation
 - Variant table
 - Resequencing
 - Linkage Data
 - Markers

Configure Region Image Configure Overview Image Configure Chromosome Image Personal Data

Find a track Active tracks Favourite tracks Track order Search results Sequence and assembly (2/4) Genes and transcripts (2/2) mRNA and protein alignments (0/4) EST alignments (0/1) RNA alignments (0/3) Comparative genomics (0/1) Repeat regions (0/8) Information and decorations (8/10) Display options

Select from available configurations: Default

Active tracks

Sequence and assembly

- Contigs
- Sequence

Genes and transcripts

- Genes
- ncRNA genes

Information and decorations

- Scale bar
- Ruler
- Alignment Difference Legend
- Gene Legend
- Display in-track labels
- Highlight current feature
- Disabled track summary
- Information

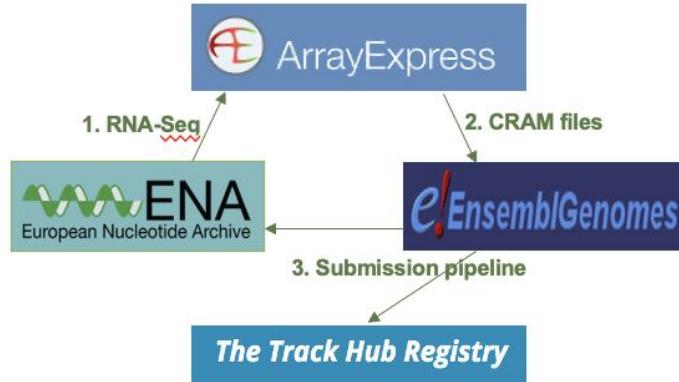
Looking for more data? Search the [Trackhub Registry](#) for external sources of annotation

Genes

View publicly available RNA-Seq alignments

Study: PRJEB15490
The plant pathogen genomics RNA-Seq identification, alignment and visualisation pipeline
View: Project XML Study XML
Submitting Centre EMBL EBI
Download: Project XML Study XML
Name Plant pathogen RNA-Seq alignment
Sample accession(S) SRP017351
Description The analysis was performed by the EMBL-EBI Gene Expression team (<http://www.ebi.ac.uk/about/people/robert-petryszak>) using the IRAP pipeline (<http://runonfseca.github.io/irap/>). Quality-filtered reads were aligned to the latest genome reference from Ensembl via TopHat version 2 (<https://ccb.jhu.edu/software/tophat/index.shtml>). The resulting BAM file was then converted to CRAM.
<http://www.ebi.ac.uk/ena/software/cram-tools/> format.
Navigation Analysis Files Portal Attributes

Bulk Download File (If the app doesn't open, please use Firefox to launch the bulk downloader app.)
Download: 1 + 379 of 279 results in TEXT
Select columns
Showing results 1 - 10 of 279 results
Analysis accession Study accession Sample accession Secondary sample accession Tax ID Scientific name Submitted files (FTP) Submitted files (Galaxy)
ERZ23209 PRJEB15490 SAMP00272635 SRS991732 31870 Colletotrichum graminicola CRAM File 1 CRAM File 1
ERZ23210 PRJEB15490 SAMP004012982 SRS1045933 31870 Colletotrichum graminicola CRAM File 1 CRAM File 1
ERZ232101 PRJEB15490 SAMP004012974 SRS1045941 31870 Colletotrichum graminicola CRAM File 1 CRAM File 1



<https://training.ensembl.org/events/>



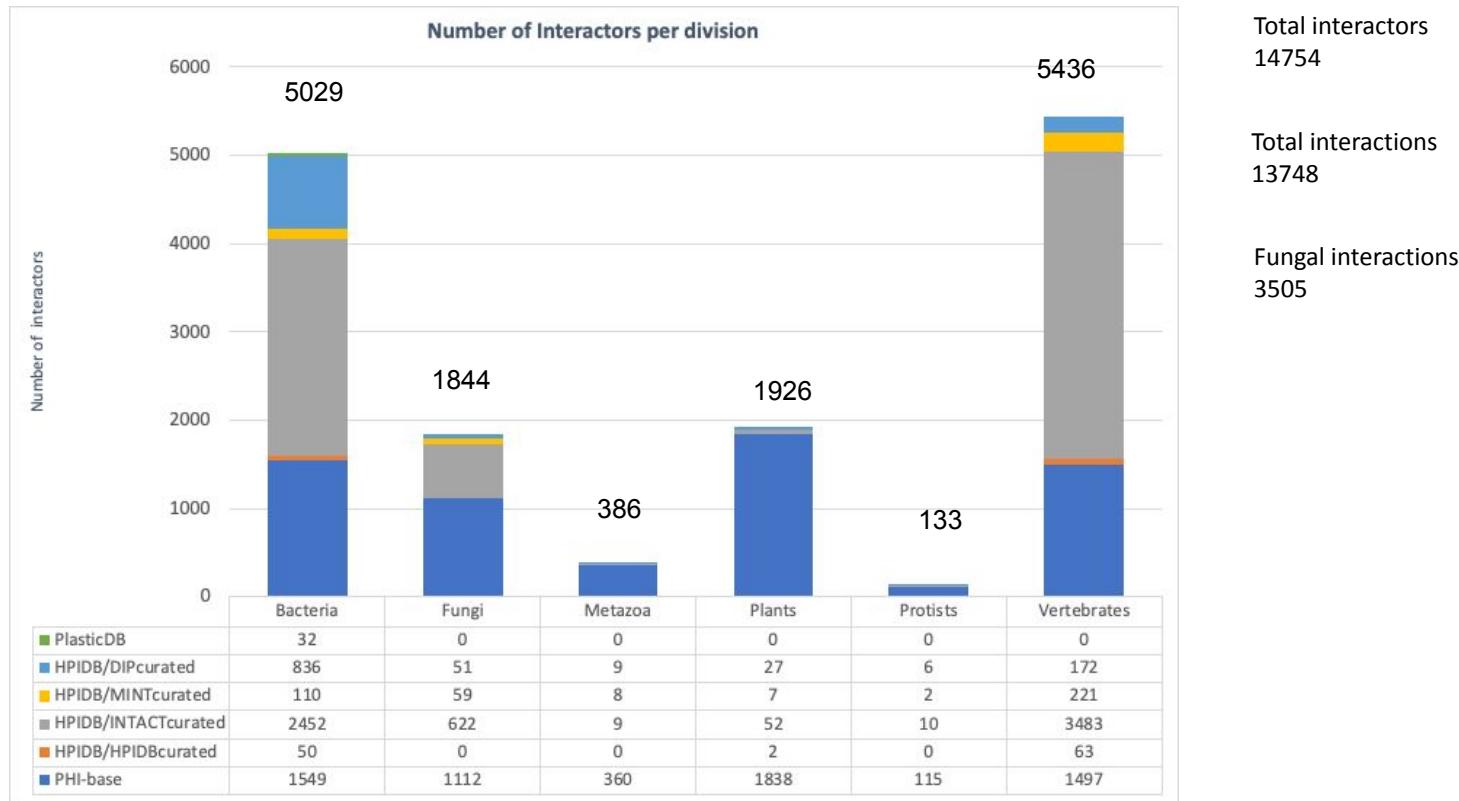
About Cross Species Molecular interactions

A new Ensembl resource:

- 2 molecules + experimentally verified + published + curated
- Cross species (species-species OR species-synthetic molecules)
- Imported from external interaction databases:
PHI-base, PlasticDB, HPIDB, IntAct, DIP, Mint
- Conservative import of exact protein/strain matches
- Data interlaced with other Ensembl resources



Unique interactors per division and source DB



Accessing molecular interactions

The screenshot shows a web browser displaying the Ensembl protein-protein interaction search results for the query "Drosophila melanogaster". The main content area is titled "Protein-protein interactions" and lists several interactions between proteins from the Drosophila melanogaster genome. The results are presented in a table with columns for "Protein A", "Protein B", "Score", and "P-value". The table includes rows for interactions such as "Drosophila melanogaster|Drosophila melanogaster", and "Drosophila melanogaster|Drosophila melanogaster". The "Score" column shows values like 1000.000000000000, 1000.000000000000, 1000.000000000000, 1000.000000000000, 1000.000000000000, and 1000.000000000000. The "P-value" column shows values like 0.000000000000000, 0.000000000000000, 0.000000000000000, 0.000000000000000, 0.000000000000000, and 0.000000000000000.

Protein A	Protein B	Score	P-value
Drosophila melanogaster	Drosophila melanogaster	1000.000000000000	0.000000000000000
Drosophila melanogaster	Drosophila melanogaster	1000.000000000000	0.000000000000000
Drosophila melanogaster	Drosophila melanogaster	1000.000000000000	0.000000000000000
Drosophila melanogaster	Drosophila melanogaster	1000.000000000000	0.000000000000000
Drosophila melanogaster	Drosophila melanogaster	1000.000000000000	0.000000000000000
Drosophila melanogaster	Drosophila melanogaster	1000.000000000000	0.000000000000000

Accessing molecular interactions

- Through the Ensembl browser

 **EnsemblFungi** ▾ HMMER | BLAST | BioMart | Tools | Downloads | Help & Docs | Blog

Phaeosphaeria nodorum (ASM14691v1) ▾

Location: supercont1.10:1,101,626-1,102,347 Gene: SNOG_20078 Transcript: SNOT_20078

Gene-based displays

- Summary
 - Splice variants
 - Transcript comparison
 - Gene alleles
- Sequence
 - Secondary Structure
 - Gene families
 - Literature
- Fungal Compara
 - Genomic alignments
 - Gene tree
 - Protein loss tree
 - Orthologues
 - Paralogues
- Pan-taxonomic Compara
 - 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
- ID History
 - Gene history

Gene: SNOG_20078

Description Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:[A9JX75](#);rf]

Location SuperContig supercont1.10:1,101,626-1,102,347 reverse strand.
ASM14691v1:CH445334.1

About this gene This gene has 1 transcript ([splice variant](#)).

Transcripts [Show transcript table](#)

Molecular interactions Cross-species interactions imported from PHI-base, HPIDB and PlasticDB with exact matches to proteins in Ensembl.

This species

Species	Gene ID	Interactor	Identifier
Phaeosphaeria nodorum	SNOG_20078	protein	uniprot:A9JX75
SN15			

Interacts with [Show metadata](#)

Species	Gene ID	Interactor	Identifier	Source DB
Triticum aestivum	UNDETERMINED	protein	UNDETERMINED	PHI-base
Triticum aestivum	TraesCS1B02G004100	protein	uniprot:W5AB81	PHI-base
Triticum aestivum	TraesCS1B02G004100	protein	uniprot:W5AB81	PHI-base

[Configure this page](#)
[Custom tracks](#)
[Export data](#)
[Share this page](#)

Accessing molecular interactions

- API REST endpoints: <https://interactions.rest.ensembl.org>

The screenshot shows the Swagger UI interface for the Ensembl Interactions REST API. At the top, there's a header with the Swagger logo, the URL <https://interactions.rest.ensembl.org/>, and a green 'Explore' button. Below the header, the title 'API interactions doc v1' is displayed, along with a note about the base URL and a link to the OpenAPI specification.

The main content area is organized into sections: 'Schemes' (set to HTTPS), 'Authorize' (with a lock icon), and a search bar labeled 'Filter by tag'. The API documentation is presented in a tree-like structure:

- display_by_gene**:
 - GET /display_by_gene/{ens_stbl_id}** (marked as `display_by_gene_read`)
- ensembl_gene**:
 - GET /ensembl_gene** (marked as `ensembl_gene_list`)
 - GET /ensembl_gene/ensembl_name** (marked as `ensembl_gene_ensembl_name_list`)
- interaction**:
 - GET /interaction** (marked as `interaction_list`)

Accessing molecular interactions

- API REST endpoints: <https://interactions.rest.ensembl.org/interaction>

?species_A=zymoseptoria tritici

&species_B=Triticum aestivum

&meta_key=disease

Filters

Field filters

Interaction id:

interactor name:

ensembl stable id:

species A:
zymoseptoria tritici

species B:
triticum aestivum

Source db:

meta value:

meta key:
disease

Submit



```
[  
  {  
    "interaction_id": 18174,  
    "interactor_1": "uniprot:F9WR1",  
    "interactor_2": "uniprot:UNDETERMINED_PHI:4966_Triticum_aestivum",  
    "ensembl_gene_1": "Mycgr3G53658",  
    "ensembl_gene_2": "UNDETERMINED_PHI:4966_Triticum_aestivum",  
    "species_1": "zymoseptoria tritici",  
    "species_2": "Triticum aestivum",  
    "doi": "26092798",  
    "source_db": "PHI-base"  
  },  
  {  
    "interaction_id": 18254,  
    "interactor_1": "uniprot:F9X056",  
    "interactor_2": "uniprot:UNDETERMINED_PHI:2442_Triticum_aestivum",  
    "ensembl_gene_1": "Mycgr3G88451",  
    "ensembl_gene_2": "UNDETERMINED_PHI:2442_Triticum_aestivum",  
    "species_1": "zymoseptoria tritici",  
    "species_2": "Triticum aestivum",  
    "doi": "19522561",  
    "source_db": "PHI-base"  
  },  
  {  
    "interaction_id": 18277,  
    "interactor_1": "uniprot:F9X7N2",  
    "interactor_2": "uniprot:UNDETERMINED_PHI:4943_Triticum_aestivum",  
    "ensembl_gene_1": "Mycgr3G85040",  
    "ensembl_gene_2": "UNDETERMINED_PHI:4943_Triticum_aestivum",  
    "species_1": "zymoseptoria tritici",  
    "species_2": "Triticum aestivum",  
    "doi": "26092796",  
    "source_db": "PHI-base"  
  }]
```

Exercises

You will learn about all these features of Ensembl Fungi as you go through this course

Time (BST)	Tuesday 9 May 2023	Wednesday 10 May 2023	Thursday 11 May 2023	Friday 12 May 2023	Saturday 13 May 2023	Time (BST)
09:00	Arrival & Registration	Breakfast	Breakfast	Breakfast	Breakfast	09:00
09:30		SNPs & Variants	Enrichment analysis	Pathways & Metabolites	Group projects (continued)	09:30
10:00						10:00
10:30	Welcome, Instructor Introductions					10:30
11:00	Database Introductions	Tea break	Tea break	Pathways & Metabolites (continued)	Group presentations - 12 min/team	11:00
11:30		Comparative Genomics & Orthology	Enrichment analysis (continued)			11:30
12:00				Group projects		12:00
12:30		Introduction to Group Projects				12:30
13:00-14:00	Lunch	Lunch	Lunch	Lunch	Lunch & Departure	13:00-14:00
14:00	Introduction to Database Queries	Comp Gx & Orthology (continued)	Sanger Tour (optional)	Group projects (continued)		14:00
14:30						14:30
15:00						15:00
15:30			Tea break			15:30
16:00	Tea break	NGS data analysis (Intro & setup)	NGS data analysis II	Tea break		16:00
16:30		Background, Intro to VEuPathDB Galaxy	RNAseq analysis	Variant calling (parallel sessions)		16:30
17:00	Transcriptomics & Proteomics	RNAseq analysis	Variant calling (parallel sessions)			17:00
17:30						17:30
18:00						18:00
18:30						18:30
19:00-20:00	Welcome reception & Dinner	Dinner	Dinner	Dinner		19:00-20:00
20:00-21:00	Participant presentations: flash presentations - 2 min each	Research Seminar: Michel Bromley, MRC	Research Seminar: Ester Gaya, Kew	Free time (or time for project prep)		20:00-21:00
	Adjourn (bar open)	Adjourn (bar open)	Adjourn (bar open)	Adjourn (bar open)		

Ensembl staff at this course



Manuel Carbajo – Ensembl Microbes



Aleena Mushtaq – Ensembl outreach



Nishadi De Silva – Ensembl Microbes



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