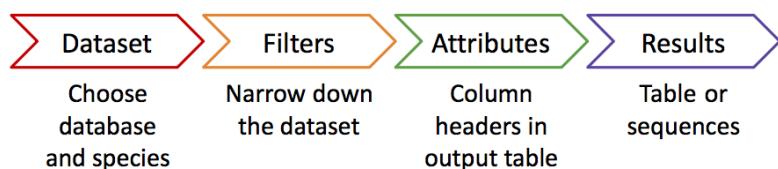


Exercise: Ensembl Fungi BioMart

Follow these instructions to guide you through BioMart to answer the following query:

- How many genes are found in *Fusarium solani* that do not have an orthologue in *Fusarium oxysporum*?
- How many of these are associated with a pathogenic phenotype of 'reduced virulence'?
- Export the gene name, locations and GO terms associated with these genes
- Export their cDNA sequences

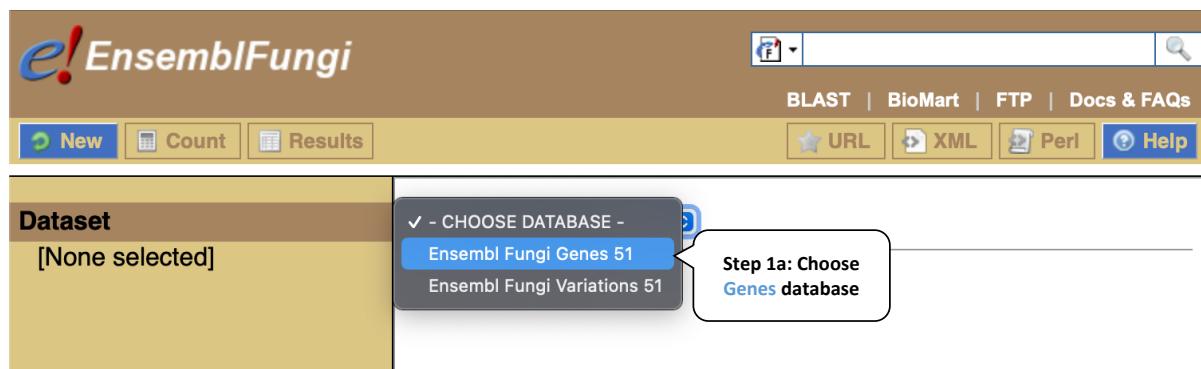
BioMart queries: The 4 step process



Click on **BioMart** in the top header of a fungi.ensembl.org page to go to: fungi.ensembl.org/biomart/martview

NOTE: These answers were determined using BioMart Ensembl Fungi 51

Step 1: Choose database and dataset



EnsemblFungi

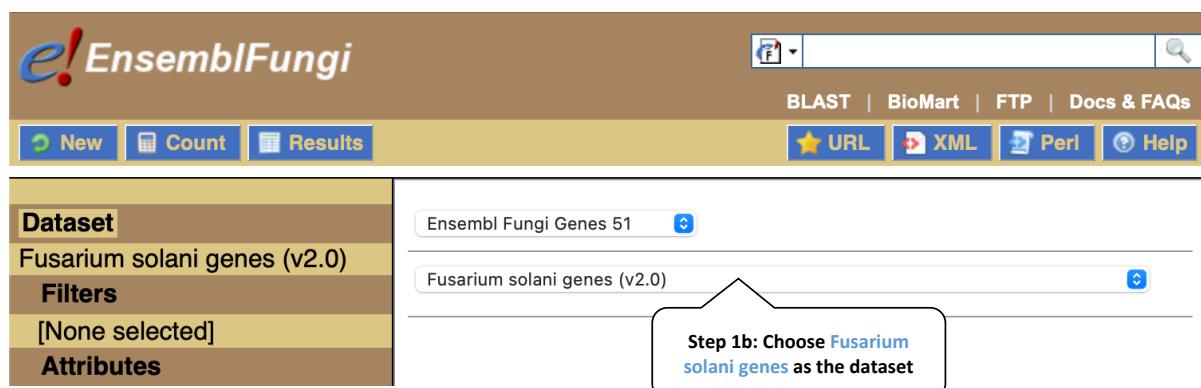
New Count Results BLAST | BioMart | FTP | Docs & FAQs URL XML Perl Help

Dataset [None selected]

✓ - CHOOSE DATABASE -

Ensembl Fungi Genes 51
Ensembl Fungi Variations 51

Step 1a: Choose Genes database



EnsemblFungi

New Count Results BLAST | BioMart | FTP | Docs & FAQs URL XML Perl Help

Dataset

Fusarium solani genes (v2.0)

Filters

[None selected]

Attributes

Ensembl Fungi Genes 51

Fusarium solani genes (v2.0)

Step 1b: Choose Fusarium solani genes as the dataset

Step 2: Choose appropriate filters

We want to narrow down the dataset of all *F. solani* genes to a subset of genes matching our filters. We are interested in *F. solani* genes that **do not** have an orthologue with *Fusarium oxysporum*. We need to filter the dataset to find these genes.

The screenshot shows the BioMart search interface. On the left, under 'Dataset', it says 'Fusarium solani genes (v2.0)'. Under 'Filters', there is a link labeled 'Step 2a: Click on Filters'. On the right, there are several filter sections: 'REGION', 'GENE', 'PATHOGEN PHENOTYPES (PHI-BASE)', 'GENE ONTOLOGY', 'MULTI SPECIES COMPARISONS', and 'PROTEIN DOMAINS AND FAMILIES'. A callout box labeled 'Step 2b: Expand the MULTI SPECIES COMPARISONS sections' points to the 'MULTI SPECIES COMPARISONS' section. Another callout box labeled 'Top tip: Click Count to check if your filters work' points to the 'Count' button at the top.

The screenshot shows the BioMart search interface after applying filters. On the left, under 'Dataset', it says '6033 / 16464 Genes' and 'Fusarium solani genes (v2.0)'. Under 'Filters', it lists 'Orthologous Fusarium oxysporum Genes: Excluded' and other attributes like 'Gene stable ID' and 'Transcript stable ID'. A callout box labeled 'Step 2c: Choose Orthologous Fusarium oxysporum Genes' points to the 'Excluded' option in the 'Homologue filters' dropdown. Another callout box labeled 'Step 2d: Choose the Excluded option' points to the 'Excluded' radio button in the same dropdown. The 'Count' button is also visible.

Using the count function we can see that there are 6,033 *F. solani* genes (out of a total of 16,464) that do not have an orthologue in *F. oxysporum*. We also want to find out how many of these are associated with the PHI-base Pathogen phenotype ‘reduced virulence’.

Update the count

Please
(If filter values are true)

Step 2e: Expand the PATHOGEN PHENOTYPES (PHI-BASE) section

Step 2f: Choose the Reduced virulence option

Dataset 3 / 16464 Genes
Fusarium solani genes (v2.0)

Filters
Orthologous Fusarium oxysporum Genes: Excluded
Pathogenic phenotype (source: PHI-base): reduced virulence

Attributes
Gene stable ID
Transcript stable ID

Dataset
[None Selected]

REGION:

GENE:

PATHOGEN PHENOTYPES (PHI-BASE):

- Plant host (source: PHI-base) Pea
- Pathogenic phenotype (source: PHI-base) reduced virulence
- Experimental condition (source: PHI-base)

GENE ONTOLOGY:

MULTI SPECIES COMPARISONS:

Homologue filters Orthologous Fusarium oxysporum Genes

We can now see from the count information that we have three genes associated with this phenotype that do not have any orthologues with *F. oxysporum*.

Step 3: Select Attributes

Attributes (our desired output) are defined by what we would like to learn about the data. We want to find out more information about these genes, including:

1. Gene name
2. Locations
3. Associated GO terms
4. cDNA sequences

There are four main attribute types: Features, Structures, Homologues and Sequences. BioMart allows querying only one type at a time. We can answer points 1-3 in a single query as they can all be found under [Features](#), but we will need to build a second query to answer point 4 ([Sequence](#) type).

Step 3a: Click on Attributes

Step 3b: In the 'Features' section. Expand the GENE section

Dataset 3 / 16464 Genes
Fusarium solani genes (v2.0)

Filters
Orthologous Fusarium oxysporum Genes: Excluded
Pathogenic phenotype (source: PHI-base): reduced virulence

Attributes
Gene stable ID

Dataset

Features Homologues
Structures Sequences

GENE:

Ensembl:

- Gene stable ID
- Transcript stable ID
- Protein stable ID
- Exon stable ID
- Gene description
- Chromosome/scaffold name
- Gene start (bp)
- Gene end (bp)
- Strand
- Karyotype band
- Transcript start (bp)
- Transcript end (bp)
- Transcription start site (TSS)
- Transcript length (including UTRs and CDS)
- Gene name
- Source of gene name
- Transcript count
- Gene % GC content
- Gene type
- Transcript type
- Source (gene)
- Source (transcript)

EXTERNAL:

Make sure that [Features](#) is selected at the top of the page.
Expand the **GENE** section, **deselect Transcript stable ID**, and **select Chromosome/scaffold name**, **Gene start** and **Gene end**, and **Gene name**.

Step 3c: Expand the EXTERNAL section

Step 3d: Choose GO term accession and name

Dataset 3 / 16464 Genes
Fusarium solani genes (v2.0)

Filters
Orthologous Fusarium oxysporum Genes: Excluded
Pathogenic phenotype (source: PHI-base): reduced virulence

Attributes
Gene stable ID
Gene name
Chromosome/scaffold name
Gene start (bp)
Gene end (bp)
GO term accession
GO term name

GO
 GO term accession
 GO term name
 GO term definition

GOSlim GOA
 GOSlim GOA Accession(s) GOSlim GOA Description

Pathogen Phenotypes (source: PHI-base)
 PHI-base ID Pathogenic phenotype
 Plant host Experimental condition

External References (max 3)
 European Nucleotide Archive ID
 INSDC protein ID
 KEGG Pathway and Enzyme ID
 MEROPS - the Peptidase Database ID
 NCBI gene ID RFAM ID
 tRNAscan-SE ID
 UniParc ID
 UniProtKB/Swiss-Prot ID
 UniProtKB/TrEMBL ID

Expand the **EXTERNAL** section. This section contains lots of identifiers from databases outside of Ensembl. Select **GO term accession** and **GO term name**.

Step 4: Get results!

You can download the data if you'd like. The output table shows only 10 first rows by default.

Step 4a: Click Results

Step 4b: Change the number of rows to 20 to view all results

Dataset 3 / 16464 Genes
Fusarium solani genes (v2.0)

Filters
Orthologous Fusarium oxysporum Genes: Excluded
Pathogenic phenotype (source: PHI-base): reduced virulence

Attributes
Gene stable ID
Gene name
Chromosome/scaffold name
Gene start (bp)
Gene end (bp)
GO term accession
GO term name

Dataset
[None Selected]

Export all results to Unique results only

Email notification to

View

Gene stable ID	Gene name	Chromosome/scaffold name	Gene start (bp)	Gene end (bp)	GO term accession	GO term name
NechaG64937	PDA1	14	1131753	1133840	GO:0005506	iron ion binding
NechaG64937	PDA1	14	1131753	1133840	GO:0020037	heme binding
NechaG64937	PDA1	14	1131753	1133840	GO:0004497	monooxygenase activity
NechaG64937	PDA1	14	1131753	1133840	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
NechaG64937	PDA1	14	1131753	1133840	GO:0016020	membrane
NechaG64937	PDA1	14	1131753	1133840	GO:0016021	integral component of membrane
NechaG64937	PDA1	14	1131753	1133840	GO:0016491	oxidoreductase activity
NechaG64937	PDA1	14	1131753	1133840	GO:0046872	metal ion binding
NechaG64937	PDA1	14	1131753	1133840	GO:0055114	oxidation-reduction process
NechaG73962	PEP2	14	1141191	1142037		
NechaG73960	PEP5	14	1129115	1131280	GO:0016021	integral component of membrane
NechaG73960	PEP5	14	1129115	1131280	GO:0055085	transmembrane transport
NechaG73960	PEP5	14	1129115	1131280	GO:0016020	membrane

Gene 1 Gene 3

Each attribute becomes a column in the table

We can see that all of these genes are located in the same region. Perhaps this has something to do with why they are not found in *F. oxysporum*...? You can click on the location links and explore the synteny between the two species.

What about the last point? ‘Export their cDNA sequences?’

In the **Attributes** section there are some ‘radio buttons’. If you’d like to export Sequence data, you need to build a separate query.

Step 3.2: Let’s go back to step 3: Selecting attributes

From the results page, click back to [Attributes](#) in the left-hand navigation panel – there's no need to start from scratch.

Dataset 3 / 16464 Genes
Fusarium solani genes (v2.0)
Filters
Orthologous Fusarium oxysporum Genes: Excluded
Pathogenic phenotype (source: PHI-base): reduced virulence
Attributes
Gene stable ID
Transcript stable ID
Data type
[None Selected]

Please select columns to be included in the output and hit 'Results' when ready

Features Homologues
 Structures Sequences

SEQUENCES:

Sequences (max 1)

Unspliced (Transcript)
 Spliced (Gene)
 Unspliced (Transcript)
 Spliced (Gene)
 5'-coding region (Transcript)
 5'-coding region (Gene)

Upstream flank
 Upstream flank

5' UTR
 3' UTR
 Exon sequences
 cDNA sequences
 Coding sequence
 Peptide

Also expand the **HEADER INFORMATION** section and **deselect** Transcript stable ID and **select** Gene name.

Step 4.2: View results for the sequences

Dataset 3 / 16464 Genes
Fusarium solani genes (v2.0)
Filters
Orthologous Fusarium oxysporum Genes: Excluded
Pathogenic phenotype (source: PHI-base): reduced virulence
Attributes
Gene stable ID
cDNA sequences
Gene name

Export all results to File Unique results only
Email notification to

View rows as Unique results only

```
>NechaG73960 | PEP5
GCCATATCCAAGTTCAAGCAATGTGGGACATCGCAGACAAGGTCGACGACGAGGCCAACGC
AGTTGGGGTTGAACTCTCTCTGGGAACGAGGATGAAAACATACCAAGGGCTTACATTGAA
ATGTGTTCCTGGCTATCTGCTATTCTTATCGGTGCACTGCACAGGTACTCGCTTATTGT
TCCAACTGGCCCTTTCGAGAAACGTGGCCAGCGCTCGGTGAGCAAGACAAAAATATA
CTGGATCCCTCAAGGCTGATCATCTGGTGTACCTTCAGGGCAGCCCCATTGCGCAGGC
GTCGGATTTCCTGGGGTGGAGTACCCATCTCATTTCACAGGCCCTTGCTTACATCGG
TTGGCTTCGATAAGCAGGGCGGTTCCATGACCATGGCGATTGCTGAGTGTGCTGGTC
GGTGTAGGATCAGGATCGTCCCTCATTAATGTTGAGTGCAGTTGATCAGAGATCATGCCAGG
CGATATGCCAAATGGCTCAAGGCCAGCTAACATTGCGAAATTGCACTTGGCACCAATTG
```

What did you learn about these genes in this exercise?

Could you learn these things from the Ensembl browser? Would it take longer?

For more details on BioMart, have a look at this publication:

Kinsella, R.J. *et al*

Ensembl BioMarts: a hub for data retrieval across taxonomic space.

Database (Oxford) 2011;bar030

Additional BioMart Exercise 1 – Export PHI-base data and Orthologues

Use Ensembl Fungi BioMart to retrieve all *Zymoseptoria tritici* genes that have been linked to a loss of pathogenicity. Export the gene IDs, names, homology type and confidence of their orthologues in *Blumeria graminis*, *Botrytis cinerea*, *Cryptococcus neoformans* and *Saccharomyces cerevisiae*.

(a) Do all of these *Z. tritici* genes have an orthologue in the other species? Which of these species are pathogenic? Do you see a correlation?

(b) Find the only orthologue in *Cryptococcus neoformans*. Is this a high confidence orthologue?

We will explore more about this orthologue in the exercise section for Comparative Genomics.

The screenshot shows the Ensembl Fungi BioMart interface. The search bar at the top contains the query "Zymoseptoria tritici genes (MG2)". Below the search bar are tabs for "New", "Count", and "Results". The "Results" tab is selected, displaying a table of orthologous genes across four species: Blumeria graminis, Botrytis cinerea, Cryptococcus neoformans, and Saccharomyces cerevisiae.

Blumeria graminis Orthologues:

- Blumeria graminis gene stable ID
- Blumeria graminis gene name
- Blumeria graminis protein or transcript stable ID
- Blumeria graminis chromosome/scaffold name
- Blumeria graminis chromosome/scaffold start (bp)
- Blumeria graminis chromosome/scaffold end (bp)
- Query protein or transcript ID
- Last common ancestor with Blumeria graminis
- Blumeria graminis homology type
- %id. target Blumeria graminis gene identical to query gene
- Blumeria graminis orthology confidence [0 low, 1 high]

Botrytis cinerea B05.10 Orthologues:

- Botrytis cinerea B05.10 gene stable ID
- Botrytis cinerea B05.10 gene name
- Botrytis cinerea B05.10 protein or transcript stable ID
- Botrytis cinerea B05.10 chromosome/scaffold name
- Botrytis cinerea B05.10 chromosome/scaffold start (bp)
- Botrytis cinerea B05.10 chromosome/scaffold end (bp)
- Query protein or transcript ID
- Last common ancestor with Botrytis cinerea B05.10
- Botrytis cinerea B05.10 homology type
- %id. target Botrytis cinerea B05.10 gene identical to query gene
- %id. query gene identical to target Botrytis cinerea B05.10 gene
- Botrytis cinerea B05.10 orthology confidence [0 low, 1 high]

Colletotrichum gloeosporioides Orthologues:

- Colletotrichum gloeosporioides gene stable ID
- Colletotrichum gloeosporioides gene name
- Colletotrichum gloeosporioides protein or transcript stable ID
- Colletotrichum gloeosporioides chromosome/scaffold name
- Colletotrichum gloeosporioides chromosome/scaffold start (bp)
- Colletotrichum gloeosporioides chromosome/scaffold end (bp)
- Query protein or transcript ID
- Last common ancestor with Colletotrichum gloeosporioides
- Colletotrichum gloeosporioides homology type
- %id. target Colletotrichum gloeosporioides gene identical to query gene
- %id. query gene identical to target Colletotrichum gloeosporioides gene
- Colletotrichum gloeosporioides orthology confidence [0 low, 1 high]

Colletotrichum graminicola Orthologues:

- Colletotrichum graminicola gene stable ID
- Colletotrichum graminicola gene name
- Colletotrichum graminicola protein or transcript stable ID
- Colletotrichum graminicola chromosome/scaffold name
- Query protein or transcript ID
- Last common ancestor with Colletotrichum graminicola
- Colletotrichum graminicola homology type
- %id. target Colletotrichum graminicola gene identical to query gene

Dataset: 6 / 11199 Genes (Zymoseptoria tritici genes (MG2))

Attributes: Gene stable ID, Gene name, Blumeria graminis gene stable ID, Blumeria graminis gene name, Blumeria graminis homology type, Blumeria graminis orthology confidence [0 low, 1 high], Botrytis cinerea B05.10 gene stable ID, Botrytis cinerea B05.10 gene name, Botrytis cinerea B05.10 homology type, Botrytis cinerea B05.10 orthology confidence [0 low, 1 high], Colletotrichum gloeosporioides gene stable ID, Colletotrichum gloeosporioides gene name, Colletotrichum gloeosporioides homology type, Colletotrichum graminicola gene stable ID, Colletotrichum graminicola gene name, Colletotrichum graminicola homology type, Cryptococcus neoformans var. neoformans gene stable ID, Cryptococcus neoformans var. neoformans gene name, Cryptococcus neoformans var. neoformans homology type, Cryptococcus neoformans var. neoformans orthology confidence [0 low, 1 high], Saccharomyces cerevisiae gene stable ID, Saccharomyces cerevisiae gene name, Saccharomyces cerevisiae homology type, Saccharomyces cerevisiae orthology confidence [0 low, 1 high].

Additional BioMart Exercise 2 – Finding genes by protein domain

Generate a list of all *Magnaporthe oryzae* genes on chromosome 4 that are annotated to contain a Transmembrane domains/helices. Include the Ensembl Gene ID and description.

The screenshot shows the EnsemblFungi BioMart search interface. The search criteria are set to find genes on Chromosome/scaffold 4 with Transmembrane helices. The results section shows a table of genes with their stable IDs and descriptions.

Gene stable ID	Gene description
MGG_17084	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4N801]
MGG_03684	Mitochondrial distribution and morphology protein 38 [Source:UniProtKB/TrEMBL;Acc:G4N6R1]
MGG_09963	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4N9P1]
MGG_03644	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4N713]
MGG_06510	Cytochrome b5 [Source:UniProtKB/TrEMBL;Acc:G4N6W6]
MGG_09720	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4NAH4]
MGG_03721	Urea transporter [Source:UniProtKB/TrEMBL;Acc:G4N6H1]
MGG_13659	Dicarboxylic amino acid permease [Source:UniProtKB/TrEMBL;Acc:G4NAK4]
MGG_08498	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4NAP3]
MGG_13624	ABC transporter CDR4 [Source:UniProtKB/TrEMBL;Acc:G4N9L5]

The screenshot shows the EnsemblFungi BioMart search interface. The search criteria are set to find genes on Chromosome/scaffold 4 with Transmembrane helices. The results section shows a table of genes with their stable IDs and descriptions.

Gene stable ID	Gene description
MGG_17084	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4N801]
MGG_03684	Mitochondrial distribution and morphology protein 38 [Source:UniProtKB/TrEMBL;Acc:G4N6R1]
MGG_09963	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4N9P1]
MGG_03644	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4N713]
MGG_06510	Cytochrome b5 [Source:UniProtKB/TrEMBL;Acc:G4N6W6]
MGG_09720	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4NAH4]
MGG_03721	Urea transporter [Source:UniProtKB/TrEMBL;Acc:G4N6H1]
MGG_13659	Dicarboxylic amino acid permease [Source:UniProtKB/TrEMBL;Acc:G4NAK4]
MGG_08498	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:G4NAP3]
MGG_13624	ABC transporter CDR4 [Source:UniProtKB/TrEMBL;Acc:G4N9L5]

Additional BioMart Exercise 3 – Convert IDs

For a list of *Schizosaccharomyces pombe* UniProt (UniProtKB/Swiss-Prot) IDs, export the Gene name and description, as well as the PomBase IDs.

(a) Do these 36 protein IDs correspond to 36 genes?

Input list of IDs:

Q92338	Q9US55	P78847	O74964
O13728	O14075	O94418	O14026
P49776	O94574	O94526	O74630
O74769	O94380	Q9UTG2	O14356
Q09170	P87172	O14326	O13339
Q9USK4	Q9USP5	Q9URZ3	P31411
O14040	Q9P7Y8	P42657	O13742
Q9Y804	Q9Y7Z8	P08647	O60159
O94552	Q10331	O74335	O94287

EnsemblFungi

New Count Results URL XML Perl Help

Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)

Dataset: Schizosaccharomyces pombe genes (ASM294v2)

Filters: UniProtKB/Swiss-Prot ID(s) [e.g. A0ZWU1]; [ID-list specified]

Attributes: Gene stable ID, Transcript stable ID

Dataset: [None Selected]

REGION:

GENE:

Limit to genes (external references)... With ChEMBL ID(s) Only Excluded

Input external references ID list [Max 500 advised] UniProtKB/Swiss-Prot ID(s) [e.g. A0ZWU1] Choose File no file selected

Transcript count >=

Transcript count <=

Gene type ncRNA, protein_coding, pseudogene, RNase_MRP_RNA, RNase_P_RNA

Transcript type ncRNA, protein_coding, pseudogene, RNase_MRP_RNA, RNase_P_RNA

New Count Results URL XML Perl Help

Dataset 36 / 7268 Genes: Schizosaccharomyces pombe genes (ASM294v2)

Filters: UniProtKB/Swiss-Prot ID(s) [e.g. A0ZWU1]; [ID-list specified]

Attributes: Gene stable ID, Gene name, Gene description, PomBase ID

Dataset: [None Selected]

Export all results to File HTML Unique results only Go

Email notification to

View 50 rows as HTML Unique results only

Gene stable ID	Gene name	Gene description	PomBase ID
SPBC29A3.14c	trt1	telomerase reverse transcriptase 1 protein Trt1 [Source:PomBase;Acc:SPBC29A3.14c]	SPBC29A3.14c.1
SPAC15A10.08	ain1	alpha-actinin [Source:PomBase;Acc:SPAC15A10.08]	SPAC15A10.08.1
SPAC16E8.07c	vph1	V-type ATPase V0 subunit a (predicted) [Source:PomBase;Acc:SPAC16E8.07c]	SPAC16E8.07c.1
SPAC29B12.02c	set2	histone lysine methyltransferase Set2 [Source:PomBase;Acc:SPAC29B12.02c]	SPAC29B12.02c.1
SPAC2C4.07c	dis32	3'-5' exonuclease activity Dis3L2 [Source:PomBase;Acc:SPAC2C4.07c]	SPAC2C4.07c.1
SPACUNK4.10		glyoxylate reductase (predicted) [Source:PomBase;Acc:SPACUNK4.10]	SPACUNK4.10.1
SPBC16E9.11c	pub3	HECT-type ubiquitin-protein ligase E3 Pub3 [predicted] [Source:PomBase;Acc:SPBC16E9.11c]	SPBC16E9.11c.1
SPBC3D0D10.10c	tor1	phosphatidylinositol kinase Tor1 [Source:PomBase;Acc:SPBC3D0D10.10c]	SPBC3D0D10.10c.1
SPBC19C7.11		CIC chloride channel (predicted) [Source:PomBase;Acc:SPBC19C7.11]	SPBC19C7.11.1
SPBC17F3.01c	rpa5	Rho-type GTPase activating protein Rpa5 [Source:PomBase;Acc:SPBC17F3.01c]	SPBC17F3.01c.1
SPCC23B6.03c	tel1	ATM checkpoint kinase [Source:PomBase;Acc:SPCC23B6.03c]	SPCC23B6.03c.1
SPBC24C6.08c	bhd1	folliculin/Birt-Hogg-Dubé syndrome ortholog Bhd1 [Source:PomBase;Acc:SPBC24C6.08c]	SPBC24C6.08c.1
SPBC4B4.03	rsc1	RSC complex subunit Rsc1 [Source:PomBase;Acc:SPBC4B4.03]	SPBC4B4.03.1
SPBC88T.02		CIC chloride channel (predicted) [Source:PomBase;Acc:SPBC88T.02]	SPBC88T.02.1
SPBC1604.15	gpi16	pig-T, Gpi16 (predicted) [Source:PomBase;Acc:SPBC1604.15]	SPBC1604.15.1
SPCC1620.11	nup97	nucleoporin N96 homolog [Source:PomBase;Acc:SPCC1620.11]	SPCC1620.11.1
SPBC609.02	ptn1	phosphatidylinositol-3,5-trisphosphate3-phosphatase Ptn1 [Source:PomBase;Acc:SPBC609.02]	SPBC609.02.1
SPCC18.18c	fum1	fumarate hydratase (predicted) [Source:PomBase;Acc:SPCC18.18c]	SPCC18.18c.1
SPBC1773.17c		glyoxylate reductase (predicted) [Source:PomBase;Acc:SPBC1773.17c]	SPBC1773.17c.1
SPAC17H9.09c	ras1	GTPase Ras1 [Source:PomBase;Acc:SPAC17H9.09c]	SPAC17H9.09c.1
SPAC637.05c	vma2	V-type ATPase V1 subunit B [Source:PomBase;Acc:SPAC637.05c]	SPAC637.05c.1
SPAC17A2.13c	rad25	14-3-3 protein Rad25 [Source:PomBase;Acc:SPAC17A2.13c]	SPAC17A2.13c.1
SPCC4G3.02	aph1	bis(5'-nucleosidyl)-tetraphosphatase [Source:PomBase;Acc:SPCC4G3.02]	SPCC4G3.02.1
SPCC290.03c	nup186	nucleoporin Nup186 [Source:PomBase;Acc:SPCC290.03c]	SPCC290.03c.1
SPBC3D6.07	gpi3	pig-A, phosphatidylinositol N-acetylglucosaminyltransferase subunit Gpi3 (predicted) [Source:PomBase;Acc:SPBC3D6.07]	SPBC3D6.07.1
SPCC18B5.11c	cds1	replication checkpoint kinase Cds1 [Source:PomBase;Acc:SPCC18B5.11c]	SPCC18B5.11c.1
SPBC42B.01c	nup107	nucleoporin Nup107 [Source:PomBase;Acc:SPBC42B.01c]	SPBC42B.01c.1
SPBC2D10.18	abc1	ABC1 kinase family ubiquinone biosynthesis protein Abc1/Cqg2 [Source:PomBase;Acc:SPBC2D10.18]	SPBC2D10.18.1
SPAPYUG7.03c	mid2	medial ring protein Mid2 [Source:PomBase;Acc:SPAPYUG7.03c]	SPAPYUG7.03c.1
SPAC869.10c	put4	proline specific plasma membrane permease Put4 (predicted) [Source:PomBase;Acc:SPAC869.10c]	SPAC869.10c.1
SPAC1002.03c	gls2	glucosidase II alpha subunit Gls2 [Source:PomBase;Acc:SPAC1002.03c]	SPAC1002.03c.1
SPCC4B3.14	cwf20	complexed with Cdc5 protein Cwf20 [Source:PomBase;Acc:SPCC4B3.14]	SPCC4B3.14.1
SPCC11E10.02c	gpi8	pig-K [Source:PomBase;Acc:SPCC11E10.02c]	SPCC11E10.02c.1
SPAC1805.15c	pub2	HECT-type ubiquitin-protein ligase E3 Pub2 [Source:PomBase;Acc:SPAC1805.15c]	SPAC1805.15c.1
SPBC146.13c	myo1	myosin type I [Source:PomBase;Acc:SPBC146.13c]	SPBC146.13c.1
SPBC146.06c	fan1	Fanconi-associated nuclease Fan1 [Source:PomBase;Acc:SPBC146.06c]	SPBC146.06c.1