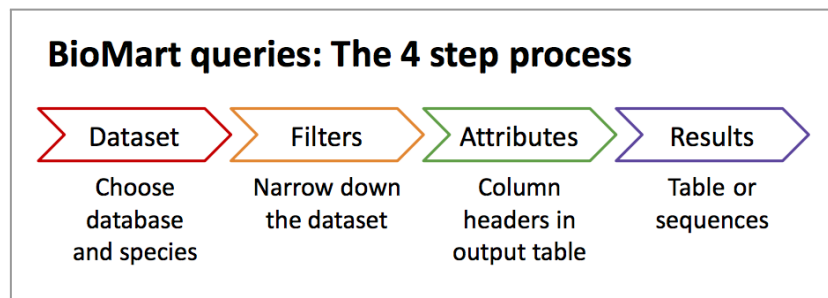


Exercise: Ensembl Fungi BioMart

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

- (a) How many genes within the 14:1128520-1142558 region are found in *Fusarium solani* that do not have an orthologue in *Fusarium verticillioides*?
- (b) Export the gene name, locations and GO terms associated with these genes
- (c) Export their cDNA sequences



Click on [BioMart](#) in the top header of a fungi.ensembl.org page to go to: <https://fungi.ensembl.org/biomart/martview/>

NOTE: These answers were determined using BioMart Ensembl Fungi 56

Step 1a: Choose [Ensembl Fungi Genes 56](#) as the database

The screenshot shows the Ensembl Fungi BioMart interface. The 'Dataset' dropdown menu is open, showing the following options:

- ✓ - CHOOSE DATABASE -
- Ensembl Fungi Genes 56 (selected)
- Ensembl Fungi Variations 56

Step 1b: Choose *Fusarium solani* genes (v2.0) as the dataset

The screenshot shows the Ensembl Fungi BioMart interface. The 'Dataset' dropdown menu is open, showing the following options:

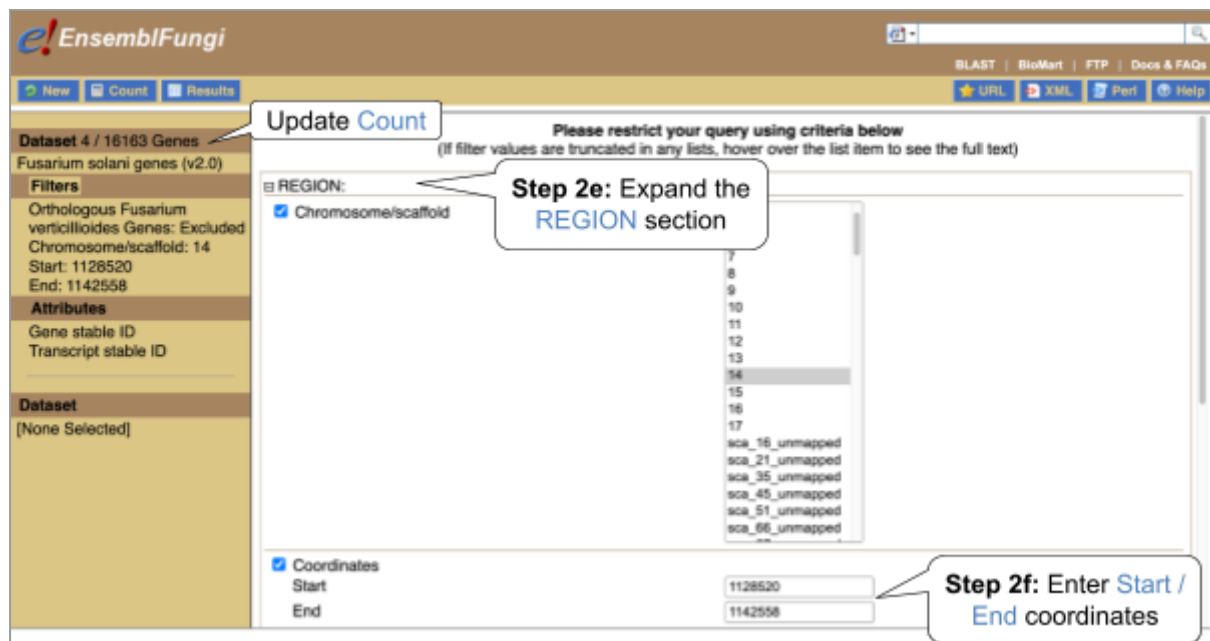
- Ensembl Fungi Genes 56
- Fusarium solani genes (v2.0) (selected)

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 *F. verticillioides*. We need to filter the dataset to find these genes.

The screenshot shows the EnsemblFungi interface. On the left, the 'Dataset' section is set to 'Fusarium solani genes (v2.0)'. The 'Filters' section is currently empty, with '[None selected]' under 'Attributes'. A callout bubble labeled 'Step 2a: Click on Filters' points to the 'Filters' link in the left sidebar. The main panel, titled 'Please restrict your query using criteria below', contains several filter categories: 'GENE:', 'PATHOGEN PHENOTYPES (PHI-BASE):', 'GENE ONTOLOGY:', 'MULTI SPECIES COMPARISONS:', and 'PROTEIN DOMAINS AND FAMILIES:'. The 'MULTI SPECIES COMPARISONS' section is expanded, showing 'Paralogous Fusarium solani Genes' with radio buttons for 'Only' (selected) and 'Excluded'.

The screenshot shows the EnsemblFungi interface after applying filters. The 'Dataset' section now displays '6727 / 16163 Genes' and 'Fusarium solani genes (v2.0)'. The 'Filters' section shows 'Orthologous Fusarium verticillioides Genes: Excluded' under 'Attributes'. A callout bubble labeled 'Top tip: Click Count to check if your filters work' points to the 'Count' button in the top navigation bar. The main panel, titled 'Please restrict your query using criteria below', shows the 'MULTI SPECIES COMPARISONS' section expanded. The 'Orthologous Fusarium verticillioides Genes' section now has radio buttons for 'Only' and 'Excluded' (selected). A callout bubble labeled 'Step 2c: Choose Orthologous Fusarium verticillioides Genes' points to the 'Orthologous Fusarium verticillioides Genes' text. Another callout bubble labeled 'Step 2d: Choose the Excluded option' points to the 'Excluded' radio button. The 'Protein Domains and Families' section is also visible at the bottom.



Using the count function we can see that there are 4 *F. solani* genes (out of a total of 16,163) in the 14:1128520-1142558 region that do not have an orthologue in *F. verticillioides*.

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).

EnsemblFungi

BLAST | BioMart | FTP | Docs & FAQs

New | Count | Results

URL | XML | Perl | Help

Dataset 4 / 16163 Genes
Fusarium solani genes (v2.0)

Filters

Orthologous Fusarium verticillioides Genes: Excluded
Chromosome/scaffold: 14
Start: 1128520
End: 1142558

Attributes

Gene stable ID
Transcript stable ID
Chromosome/scaffold name
Gene start (bp)
Gene end (bp)
Gene name

Dataset

[None Selected]

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

☒ 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)
☐ Ensembl Canonical
☒ Gene name
☐ Source of gene name
☐ Transcript count
☐ Gene % GC content
☐ Gene type
☐ Transcript type
☐ Source (gene)
☐ Source (transcript)
☐ Gene Synonym

EXTERNAL:

PROTEIN DOMAINS AND FAMILIES:

Make sure that **Features** is selected at the top of the page.

Expand the **GENE** section, and select **Chromosome/scaffold name**, **Gene start** and **Gene end**, and **Gene name**.

EnsemblFungi

BLAST | BioMart | FTP | Docs & FAQs

New | Count | Results

URL | XML | Perl | Help

Dataset 4 / 16163 Genes
Fusarium solani genes (v2.0)

Filters

Orthologous Fusarium verticillioides Genes: Excluded
Chromosome/scaffold: 14
Start: 1128520
End: 1142558

Attributes

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

Dataset

[None Selected]

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

☒ Features ☐ Homologues ☐ Structures ☐ Sequences

GENE:

EXTERNAL:

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
☐ Host
☐ Pathogenic phenotype
☐ Experimental condition

External References (max 3)

☐ European Nucleotide Archive ID
☐ INSOC protein ID
☐ MEROPS - the Peptidase Database ID
☐ NCBI gene (formerly Entrezgene) description
☐ NCBI gene (formerly Entrezgene) accession
☐ NCBI gene (formerly Entrezgene) ID
☐ PDB ID
☐ RefSeq peptide predicted ID
☐ RFAM ID
☐ STRING 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.

EnsemblFungi

Step 4a: Click **Results**

Step 4b: Change the number of rows to **All** to view all results in a new tab

Export all results to: File

Email notification to:

View: 10 rows per page Unique results only

| Gene stable ID | Transcript stable ID | Chromosome/scaffold name | Gene start (bp) | Gene end (bp) | Gene name | GO term accession | GO term name |
|----------------|----------------------|--------------------------|-----------------|---------------|-----------|-------------------|---|
| NechaG73960 | NechaT73960 | 14 | 1129115 | 1131280 | PEP5 | GO:0016021 | integral component of membrane |
| NechaG73960 | NechaT73960 | 14 | 1129115 | 1131280 | PEP5 | GO:0022857 | transmembrane transporter activity |
| NechaG73960 | NechaT73960 | 14 | 1129115 | 1131280 | PEP5 | GO:0050885 | transmembrane transport |
| NechaG73960 | NechaT73960 | 14 | 1129115 | 1131280 | PEP5 | GO:0016020 | membrane |
| NechaG64937 | NechaT64937 | 14 | 1131753 | 1133840 | PDA1 | GO:0016021 | integral component of membrane |
| NechaG64937 | NechaT64937 | 14 | 1131753 | 1133840 | PDA1 | GO:0004497 | monooxygenase activity |
| NechaG64937 | NechaT64937 | 14 | 1131753 | 1133840 | PDA1 | GO:0020037 | heme binding |
| NechaG64937 | NechaT64937 | 14 | 1131753 | 1133840 | PDA1 | GO:0016706 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen |
| NechaG64937 | NechaT64937 | 14 | 1131753 | 1133840 | PDA1 | GO:0005506 | iron ion binding |
| NechaG64937 | NechaT64937 | 14 | 1131753 | 1133840 | PDA1 | GO:0016020 | membrane |

Each attribute becomes a column in the results table

Dataset: [None Selected]

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.

EnsemblFungi

Step 3.2b: Click on **Sequences**

Please select the output and hit 'Results' when ready

☐ Features ☐ Homologues
☐ Structures ☒ Sequences

SEQUENCES:

Sequences (max 1)

☐ Unspliced (Transcript)

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

Upstream flank
☐ Upstream flank

Downstream flank
☐ Downstream flank

HEADER INFORMATION:

Step 3.2a: Click on **Attributes** again

Step 3.2c: Select **cDNA sequences**

Dataset: [None Selected]

Also expand the **HEADER INFORMATION** section and **select Gene name**.

Step 4.2: View results for the sequences

The screenshot shows the EnsemblFungi BioMart interface. A callout box labeled "Step 4.2a: Click on Results again" points to the "Results" button in the top navigation bar. The main content area displays search results for "Dataset 4 / 16163 Genes" (Fusarium solani genes (v2.0)). The left sidebar shows filters and attributes. The main table displays a list of genes with their cDNA sequences. The first gene shown is "Necha73960 | Necha73960 | PEP5". The sequence is displayed in FASTA format.

Dataset 4 / 16163 Genes
Fusarium solani genes (v2.0)

Filters
Orthologous Fusarium verticillioides Genes: Excluded
Chromosome/scaffold: 14
Start: 1128520
End: 1142558

Attributes
Gene stable ID
Transcript stable ID
Gene name
cDNA sequences

Dataset
[None Selected]

Export all results to: File (FASTA) Unique results only Go

Email notification to: [Empty field]

View: 10 rows as FASTA Unique results only

>Necha73960 | Necha73960 | PEP5
GCCTATCCAAGTTCAGCAATGTCGGAGCATCGGACAAGGTCGACGACGAGCCCAACGC
AGTTGGGGTTGAACCTCTCGCTCGCAACGAGGATGAAACTACCAAGGGCTTACATTGAA
ATGTGTTCTGGTCTATCTGTCTATTCTTATCGGTTGCACTGCACAGGTACTCGCTATTGT
TGCAACTGGCGGCTTTGCGAAGACGTGGCCGCCAGCGCTCGGTGAGCAAGACAATATAT
CTGGATCCCTCAAGGCTGATCACTCGGTTACCTTCACGGCAGCCCAATTGCGCAGGC
GTCGGATTCTGGGGTCGAGAGTACCCATCTCTCAATTCACAGCCCTCTGCTTCATCGG
TTCGCTTCTGATAAGCAGGGCGGTTTCCATGACCATGGCGATTGCTGAGTGTCTGGTC
GGTGTAGGATCAGGATCGTCTCATTTACTGTATGCAAGTTCATCAGAGATCATGCGGAGG
CGATATCGACCAATCGCTCAAGCCGGAGTCAACATTGCCAATTCACCTGGAGGAATATTC
ACACTGCTCGCCGCTTCTGCTCTTGTCAAGAAGAGTGACGAAGGCTTTGCGGTTGTCTAG
TACATTAGCACAAAGATTTTTCGCCATCACTTTATCGCTATCTGTTCTCTTCAAGCG
CCCAAGCGGCGCTCGAAGTATCTTTGAGCTTTCGGCAGAACTCAAGGCTCTCGACTGG
ATAGGATACATGCTATTCTCTATCGGAATGATTCTGTTACGATGGGCTGACATGGGCC
AACAACCCCTATCCCTGGAAGGATGCTCATGTGCTCAGCACCTTTATTGTGCGGCTAGGT
TTTATCGCCCTCACTGTCATGTGGGAGGTCAAGAAGAGGACGGATTCTGTCAACATGCT
CTTTTGAACAGCGCGCAACTTCGCCCTTGGCTTATCTTGTCTTTCGCGCAAGGAGTT
GCAATTCACGCTGTCAACAACCTTCTCCCTTTGCTATTTTGGCTCTTTTGTGAGACCGAT
CAATTCAAGGCGGGGTTTTGGTCTCCATGCTCTTATTGGCGGGGAGCTTCATCCGTG
GTGGCGGCTTTACTCTTCAAGACAAAAGGGTTGACCGCCCTTGATGGCTGGAATG
GGGCTCTTTCTCAGCTATTTTGCATGTATGGCTACCATCAAGCTCAACCAAGTCAGCTGCC

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 RJ, Kähäri A, Haider S, et al. [Ensembl BioMart: a hub for data retrieval across taxonomic space](#). Database : the Journal of Biological Databases and Curation. 2011;2011:bar030. DOI: 10.1093/database/bar030. PMID: 21785142; PMCID: PMC3170168.

Additional BioMart Exercise 1 – Export orthologues

Use Ensembl Fungi BioMart to retrieve all *Zymoseptoria tritici* genes associated with the GO term detoxification located on chromosome 1. Export the gene IDs, names, homology type and confidence of their orthologues in *Blumeria graminis*, *Botrytis cinerea*, *Cryptococcus neoformans* and *Saccharomyces cerevisiae*.

- 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?
- Can you find an orthologue in *Cryptococcus neoformans* with high orthology confidence? What is the Gene ID? We will explore more about this orthologue in the exercise section for the Evolutionary Analysis module.

EnsemblFungi

BLAST | BioMart | FTP | Docs & FAQs

New | Count | Results

URL | XML | Perl | Help

Dataset 18 / 11091 Genes
Zymoseptoria tritici genes (MG2)

Filters
Chromosome/scaffold: 1
GO Term Name [e.g. regulation of biological process]: detoxification

Attributes
Gene stable ID
Transcript 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

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)

REGION:

GENE:

PATHOGEN PHENOTYPES (PHI-BASE):

GENE ONTOLOGY:

☐ GO Term Accession (e.g. GO:0050789) [Max 500 advised]

☒ GO Term Name [e.g. regulation of biological process] detoxification

☐ GO Evidence code

MULTI SPECIES COMPARISONS:

PROTEIN DOMAINS AND FAMILIES:

VARIANT:

EnsemblFungi

BLAST | BioMart | FTP | Docs & FAQs

New | Count | Results

URL | XML | Perl | Help

Dataset 18 / 11091 Genes
Zymoseptoria tritici genes (MG2)

Filters
Chromosome/scaffold: 1
GO Term Name [e.g. regulation of biological process]: detoxification

Attributes
Gene stable ID
Transcript 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

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
☐ %id. query gene identical to target Blumeria graminis 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]

Candida albicans Orthologues

☐ Candida albicans gene stable ID
☐ Candida albicans gene name
☐ Candida albicans protein or transcript stable ID
☐ Candida albicans chromosome/scaffold name

☐ Query protein or transcript ID
☐ Last common ancestor with Candida albicans
☐ Candida albicans homology type
☐ %id. target Candida albicans gene identical to query gene

Gene stable ID
Transcript 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
homolog type

[illegible]

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 Transmembrane domains/helices. Include the Ensembl Gene ID and description.

EnsemblFungi

BLAST | BioMart | FTP | Docs & FAQs

New Count Results URL XML Perl Help

Dataset
Magnaporthe oryzae genes (MG8)

Filters
Chromosome/scaffold: 4
With Transmembrane helices: Only

Attributes
Gene stable ID
Transcript stable ID

Dataset
[None Selected]

REGION:
☒ Chromosome/scaffold
Coordinates
Start: 1
End: 10000000
☐ Multiple regions (Chr:Start:End:Strand) [Max 500 advised]
e.g. 1:100:10000:-1, 1:100000:200000:1
Choose File no file selected

GENE:
PATHOGEN PHENOTYPES (PHI-BASE):
GENE ONTOLOGY:
MULTI SPECIES COMPARISONS:
PROTEIN DOMAINS AND FAMILIES:
☒ Limit to genes ...
With Transmembrane helices: ☒ Only ☐ Excluded

New Count Results URL XML Perl Help

Dataset 297 / 13470 Genes
Magnaporthe oryzae genes (MG8)

Filters
Chromosome/scaffold: 4
With Transmembrane helices: Only

Attributes
Gene stable ID
Gene description

Dataset
[None Selected]

Export all results to: File HTML Unique results only Go

Email notification to:

View: 10 rows as HTML Unique results only

| 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. 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 |

The screenshot shows the EnsemblFungi BioMart interface. The left sidebar shows the dataset 'Schizosaccharomyces pombe genes (ASM294v2)' and the filter 'UniProtKB/Swiss-Prot ID(s)'. The main panel shows the query criteria:

- 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]

The main panel shows the query criteria:

- REGION:** (empty)
- GENE:**
 - ☐ Limit to genes (external references)...
 - ☒ Input external references ID list [Max 500 advised]
- Transcript count >=** (empty)
- Transcript count <=** (empty)
- Gene type**
 - ☐ ncRNA
 - ☐ protein_coding
 - ☐ pseudogene
 - ☐ RNase_MRP_RNA
 - ☐ RNase_P_RNA
- Transcript type**
 - ☐ ncRNA
 - ☐ protein_coding
 - ☐ pseudogene
 - ☐ RNase_MRP_RNA
 - ☐ RNase_P_RNA

The UniProtKB/Swiss-Prot ID(s) list is populated with the following IDs: P31411, O13742, O60159, O94287.

| | | | |
|---|--|-----------|--|
| <div>⌕ NewCountResults</div> <div>★ URLXMLPrintHelp</div> | | | |
| <div>Dataset 36 / 7268 Genes</div> <div>Schizosaccharomyces pombe genes (ASM294v2)</div> <div>Filters</div> <div>UniProtKB/Swiss-Prot ID(s) [e.g. A0ZWU1]: [ID-list specified]</div> <div>Attributes</div> <div>Gene stable ID</div> <div>Gene name</div> <div>Gene description</div> <div>PomBase ID</div> <div>Dataset</div> <div>[None Selected]</div> | <div>Export all results to<div>FileHTMLUnique results onlyGo</div></div> <div>Email notification to</div> <div>View<div>50rows asHTMLUnique results only</div></div> | | |
| | Gene stable ID | Gene name | Gene description |
| | SPBC29A3.14c | trt1 | telomerase reverse transcriptase 1 protein Trt1 [Source:PomBase;Acc:SPBC29A3.14c] |
| | SPAC15A10.08 | ain1 | alpha-actinin [Source:PomBase;Acc:SPAC15A10.08] |
| | SPAC16E8.07c | vph1 | V-type ATPase V0 subunit a (predicted) [Source:PomBase;Acc:SPAC16E8.07c] |
| | SPAC29B12.02c | set2 | histone lysine methyltransferase Set2 [Source:PomBase;Acc:SPAC29B12.02c] |
| | SPAC2C4.07c | dis32 | 3'-5'-exoribonuclease activity Dis3L2 [Source:PomBase;Acc:SPAC2C4.07c] |
| | SPACUNK4.10 | | glyoxylate reductase (predicted) [Source:PomBase;Acc:SPACUNK4.10] |
| | SPBC16E9.11c | pub3 | HECT-type ubiquitin-protein ligase E3 Pub3 (predicted) [Source:PomBase;Acc:SPBC16E9.11c] |
| | SPBC30D10.10c | tor1 | phosphatidylinositol kinase Tor1 [Source:PomBase;Acc:SPBC30D10.10c] |
| | SPBC19C7.11 | | ClC chloride channel (predicted) [Source:PomBase;Acc:SPBC19C7.11] |
| | SPBC17F3.01c | rga5 | Rho-type GTPase activating protein Rga5 [Source:PomBase;Acc:SPBC17F3.01c] |
| | SPCC23B6.03c | tel1 | ATM checkpoint kinase [Source:PomBase;Acc:SPCC23B6.03c] |
| | SPBC24C6.08c | bhd1 | folliculin/Birt-Hogg-Dube syndrome ortholog Bhd1 [Source:PomBase;Acc:SPBC24C6.08c] |
| | SPBC4B4.03 | rsc1 | RSC complex subunit Rsc1 [Source:PomBase;Acc:SPBC4B4.03] |
| | SPBC887.02 | | ClC chloride channel (predicted) [Source:PomBase;Acc:SPBC887.02] |
| | SPBC1604.15 | gpi16 | pig-T, Gpi16 (predicted) [Source:PomBase;Acc:SPBC1604.15] |
| | SPCC1620.11 | nup97 | nucleoporin Nic96 homolog [Source:PomBase;Acc:SPCC1620.11] |
| | SPBC609.02 | ptn1 | phosphatidylinositol-3,4,5-trisphosphate3-phosphatase Ptn1 [Source:PomBase;Acc:SPBC609.02] |
| | SPCC18.18c | fum1 | fumarate hydratase (predicted) [Source:PomBase;Acc:SPCC18.18c] |
| | SPBC1773.17c | | glyoxylate reductase (predicted) [Source:PomBase;Acc:SPBC1773.17c] |
| | SPAC17H9.09c | ras1 | GTPase Ras1 [Source:PomBase;Acc:SPAC17H9.09c] |
| | SPAC637.05c | vma2 | V-type ATPase V1 subunit B [Source:PomBase;Acc:SPAC637.05c] |
| | SPAC17A2.13c | rad25 | 14-3-3 protein Rad25 [Source:PomBase;Acc:SPAC17A2.13c] |
| | SPCC4G3.02 | aph1 | bis(5'-nucleosidyl)-tetraphosphatase [Source:PomBase;Acc:SPCC4G3.02] |
| | SPCC290.03c | nup186 | nucleoporin Nup186 [Source:PomBase;Acc:SPCC290.03c] |
| | SPBC3D6.07 | gpi3 | pig-A, phosphatidylinositol N-acetylglucosaminyltransferase subunit Gpi3 (predicted) [Source:PomBase;Acc:SPBC3D6.07] |
| | SPCC18B5.11c | cds1 | replication checkpoint kinase Cds1 [Source:PomBase;Acc:SPCC18B5.11c] |
| | SPBC428.01c | nup107 | nucleoporin Nup107 [Source:PomBase;Acc:SPBC428.01c] |
| | SPBC2D10.18 | abc1 | ABC1 kinase family ubiquinone biosynthesis protein Abc1/Csq8 [Source:PomBase;Acc:SPBC2D10.18] |
| | SPAPYUG7.03c | mid2 | medial ring protein Mid2 [Source:PomBase;Acc:SPAPYUG7.03c] |
| | SPAC869.10c | put4 | proline specific plasma membrane permease Put4 (predicted) [Source:PomBase;Acc:SPAC869.10c] |
| | SPAC1002.03c | glis2 | glucosidase II alpha subunit Glis2 [Source:PomBase;Acc:SPAC1002.03c] |
| | SPCC4B3.14 | cwf20 | complexed with Cdc5 protein Cwf20 [Source:PomBase;Acc:SPCC4B3.14] |
| | SPCC11E10.02c | gpi8 | pig-K [Source:PomBase;Acc:SPCC11E10.02c] |
| | SPAC1805.15c | pub2 | HECT-type ubiquitin-protein ligase E3 Pub2 [Source:PomBase;Acc:SPAC1805.15c] |
| | SPBC146.13c | myo1 | myosin type I [Source:PomBase;Acc:SPBC146.13c] |
| | SPBC146.06c | fan1 | Fanconi-associated nuclease Fan1 [Source:PomBase;Acc:SPBC146.06c] |