

Welcome to the GrameneMart Tutorial

A tool for batch data sequence retrieval

1. Select a Gramene dataset to search against.
2. Add filters to the dataset to increase its specificity.
3. Choose the fields to include in the report.
4. Generate a batch report in a format that can be imported into local tools, such as Excel.

Tutorial Tips



If you are viewing this tutorial with Adobe Acrobat Reader, click the “pages” on the left hand side of the Reader for easier navigation.

Note! Although we continually work to make Gramene compatible with all browsers, there are problems with some browser versions. If you're having difficulty viewing Gramene, try using a different browser. Please report any problems with browsers through Gramene Feedback.



GrameneMart is based upon BioMart.

The “Mart” tool is particularly suited for providing the 'data mining like” searches of complex descriptive (e.g. biological) data, and is optimized for large databases, such as genomic sequence or microarray experiments.

BioMart software is completely Open Source, licensed under the LGPL, and freely available to anyone without restrictions

GrameneMart

- Built upon BioMart, GrameneMart allows you to search the genes from many of the available genomes at Gramene.
- These genes can be filtered by chromosome or region, as well as other gene and protein data available for these genes.
- Results can be downloaded

Gramene Home Page

The screenshot shows the Gramene Home Page interface. At the top, the logo 'GRAMENE' is followed by the tagline 'A Resource for Comparative Grass Genomics' and the version 'v23 (November 2006)'. A navigation bar contains links for Search, Genomes, Species, Download, Resources, About, Help, and Feedback. The main content area is divided into several sections: 'Quick Search' with a search box and 'All Available' dropdown; 'Have Questions...?' with a list of links to tutorials, feedback, and FAQ; 'Gramene Tip:' with a note about AGI Maize FPC maps; 'Quick Start' with a list of links to various databases and tools; 'Featured News' with a list of recent releases and conferences; and 'Visit with us at' with links to Data Warehouse Technologies and Plant and Animal Genome XV Conference. A callout box with a green background and black border points to the 'All-GrameneMart' link in the 'Quick Start' section, containing the text 'Click here to open GrameneMart Home Page'. The bottom of the page features a 'SPECIES' section with images of various grasses and logos for USDA, OAS, and other institutions. A footer contains the date 'Last modified: Wed Nov 8 13:09:58 2006' and navigation links for Home, Site Map, About, and Cite.

Select a dataset

1) Select a **database** for this query, and the datasets will open up.

Select a **dataset** for this query, these are the available datasets within the database you selected..

After selecting your dataset, you may need to wait a few moments for this page to load.

“Count”

Click the “Count” button at any point to see how many results you have. Clicking on Count as you apply each filter will update the summary .

The screenshot shows a web interface with a top navigation bar containing buttons for 'New', 'Count', and 'Results'. Below the navigation bar, there is a section for 'Dataset' showing '58406 / 58406 Genes'. To the right of this, there are dropdown menus for 'Gramene 26' and 'Oryza sativa genes (TIGR5)'. Below the dataset information, there are sections for 'Filters' (showing '[None selected]'), 'Attributes' (listing 'Ensembl Gene ID' and 'Ensembl Transcript ID'), and another 'Dataset' section (showing '[None Selected]').

You have the whole dataset of 58406 Oryza sativa japonica genes, because no filters have been applied at this point.

Click “Filters” to see your options (next slide)

Default results options may display here under “Attributes”

After each filter selection click on “**Count**” to update your summary, but remain on the filter page.

Formulate the Filters:

New Count Results XML Perl Help

Dataset 58406 / 58406 Genes

Filters
[None selected]

Attributes
[None selected]

Dataset
[None Selected]

Please restrict your query using criteria below

- ⊕ REGION:
- ⊕ GENE:
- ⊕ GENE ONTOLOGY:
- ⊕ MULTISPECIES COMPARISONS:
- ⊕ PROTEIN:

Remember the summary shows the number of records matching your query and filters. Continue to add filters until the number becomes a manageable size.

Click on the expand icon in front of a filter to open that category to be able to apply aspects of that filter.

Formulate the Filters: Optionally Filter by Region

The screenshot shows a web-based interface for genomic data analysis. At the top, there are tabs for 'New', 'Count', and 'Results', along with 'XML', 'Perl', and 'Help' links. The main content area is divided into several sections. On the left, there is a 'Dataset' section showing '4198 Genes' and '58406 Genes'. Below this is a 'Filters' section with a 'Chromosome' dropdown set to '12'. The main panel on the right is titled 'Please restrict your query using the filters below'. It contains a 'REGION:' section with a checked 'Chromosome' filter and unchecked 'Base pair' and 'Genomic features' filters. A dropdown menu is open over the 'Chromosome' filter, showing a list of chromosomes from 1 to 22, with '12' selected. Below the 'REGION:' section is a 'GENE:' section. At the bottom right, there are logos for 'das', 'USDA', and 'ORNL'.

1 - For example - select the region of your choice

2 - Then click on "count" to update your summary. There are 4198 genes on chromosome 12 of the *Oryza sativa japonica* genome.

Formulate the Filters: Optionally Filter by Region

The screenshot shows a web interface for filtering a dataset of 4198 genes out of a total of 58406. The interface is divided into a left sidebar and a main query area.

Left Sidebar:

- Dataset:** 4198 / 58406 Genes
- Filters:** Chromosome: 12
- Attributes:** [None selected]
- Dataset:** [None Selected]

Main Query Area:

Please restrict your query using criteria below

REGION:

- Chromosome:** 12
- Base pair:**
 - Gene Start (bp): 1
 - Gene End (bp): 10000000
- Genomic features:**
 - Type of feature: FPContig name
 - ID(s): [Empty text box]
 - Choose File: no file selected

Callouts:

- A callout pointing to the 'Attributes' section states: "You can search for all genes between two individual BasePairs".
- A callout pointing to the 'Genomic features' section states: "You can search for all genes on one or more FPContigs".

Formulate the Filters: Optionally Filter by Gene

If you wish to filter by these criteria, **select the box** and **enter specific data**

GENE:

ID LIST FILTERS: with EntrezGene ID(s) Only Excluded

ID list limit: Ensembl Gene ID(s) no file selected

Transcript count >=

Gene type: miRNA, protein_coding, pseudogene, siRNA, transposon_pseudogene

Import values from a file

Formulate the Filters: Optionally Filter by Gene Ontology

If you wish to filter by gene ontology, **select the box** and **enter specific data**

The screenshot shows a web interface with a top navigation bar containing 'New', 'Count', 'Results', 'XML', 'Perl', and 'Help'. On the left, a sidebar displays 'Dataset 23 / 58406 Genes' and a 'Filters' section with 'Chromosome: 12', 'Evidence code (Molecular function) : IEA', and 'Molecular function : GO:0030234'. The main content area is titled 'GENE ONTOLOGY:' and contains several rows of filter options:

- Evidence code (Molecular function) [IEA]
- Molecular function [GO:0030234] [browse]
- Evidence code (Biological process) [IEA]
- Biological process [] [browse]
- Evidence code (Cellular component) [IEA]
- Cellular component [] []

Then click on "count" to update your summary. There are 23 genes on chromosome 12 of with our selected ontology.

Use the "browse" button to go to EBI's **QuickGO** to find your GO term (*see next slide*).

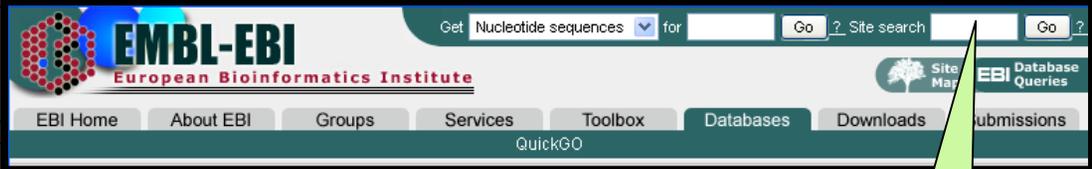
QuickGO

QuickGO **GO Term GO:0003674**

[?](#) = h

Term ID ?	GO:0003674
Name ?	molecular_function
Last updated ?	2001-03-30 04:29:44.0
Definition ?	Elemental activities, such as catalysis or binding, describing the actions of a gene product at the molecular level. A given gene product may exhibit one or more molecular functions
Synonyms ?	molecular function unknown
Comment ?	Note that this term should be used for the annotation of gene products whose molecular function is unknown by annotating to this node with the evidence code ND, no data.
Hierarchy ?	<ul style="list-style-type: none"> View this term's parents in a denormalised tree. View with neither graph nor tree. Hide all selected terms except the primary one Add more terms to the selection with a search
Child terms ?	<ul style="list-style-type: none"> GO:0016209: antioxidant activity GO:0005488: binding GO:0003824: catalytic activity GO:0030188: chaperone regulator activity GO:0042056: chemoattractant activity GO:0045499: chemorepellant activity GO:0031992: energy transducer activity GO:0030234: enzyme regulator activity GO:0003774: motor activity GO:0045735: nutrient reservoir activity GO:0008369: obsolete molecular function GO:0031386: protein tag GO:0004871: signal transducer activity GO:0005198: structural molecule activity

You should be on the ontology you entered from



Browse to find most appropriate term. (Click a term to see it's child terms) Note the term ID of choice (copy) and return to filter page (paste).

Or use the search function

Formulate the Filters: Optionally Filter by Species Homologs

The screenshot shows a web interface for filtering genes. The sidebar on the left displays 'Dataset 23 / 58406 Genes' and 'Filters' (Chromosome: 12, Evidence code (Molecular function) : IEA, Molecular function : GO:0030234). The main area has sections for 'GENE ONTOLOGY' and 'MULTI SPECIES COMPARISONS'. The 'MULTI SPECIES COMPARISONS' section is circled, and a dropdown menu is open showing species options like 'Orthologous Maize Genes' which is selected. Radio buttons for 'Only' and 'Excluded' are also visible.

If you wish to compare with other available species, **select the box** and indicate whether to **compare only** or **exclude** that species.

Formulate the Filters: Optionally Filter by Protein Information

Dataset 23 / 58406 Genes

Filters

Chromosome: 12
Evidence code (Molecular function) : IEA
Molecular function : GO:0030234

Attributes

Ensembl Gene ID
Ensembl Transcript ID

Dataset

[None Selected]

MULTI SPECIES COMPARISONS:

Homolog filters

PROTEIN:

Limit to genes with these family or domain IDs:

Limit to genes with these family or domain IDs:

PFAM ID(s)

Choose File no file selected

with PROFILE ID(s)
with PFAM ID(s)
with coil(s)
with low complexity region(s)
with PRINTS ID(s)
with PROSITE ID(s)
with InterPro ID(s)

PFAM ID(s)
PRINTS ID(s)
PROFILE ID(s)
PROSITE ID(s)
Ensembl Family ID(s)
Interpro ID(s)

If you wish to filter by protein, **select the box**, make a selection from the **drop down menu** and **enter specific data**

Use the **Choose File** button to import values from a file

Formulate the Filters: Optionally Filter by SNP information

New **Count** **Results** **XML** **Perl** **Help**

Dataset 23 / 58406 Genes

Filters

Chromosome: 12
Evidence code (Molecular function) : IEA
Molecular function : GO:0030234

Attributes

Ensembl Gene ID
Ensembl Transcript ID

Dataset
[None Selected]

MULTI SPECIES COMPARISONS:

Homolog filters Paralogous Rice (Japonica) Genes Only Excluded

PROTEIN:

Limit to genes with these family or domain IDs: with PROFILE ID(s)

Limit to genes with these family or domain IDs: PFAM ID(s)

SNP:

Snp type Coding Only Excluded

Synonymous status Frameshifting SNPs Only Excluded

Associated with validated SNPs Only Excluded

Dropdown 1 (Snp type):
Coding
Intronic
5utr
5upstream
3utr
3downstream

Dropdown 2 (Synonymous status):
✓ Frameshifting SNPs
Synonymous SNPs
Non-synonymous SNPs
Stop gained SNPs
Stop lost SNPs
Splice site SNPs
Essential splice site SNPs

After Filtering, go to Attributes

The screenshot shows a web interface with a dark green header containing buttons for 'New', 'Count', 'Results', 'XML', 'Perl', and 'Help'. Below the header, the left sidebar displays 'Dataset 23 / 58406 Genes' with 'Filters' (Chromosome: 12, Evidence code: IEA, Molecular function: GO:0030234) and 'Attributes' (Ensembl Gene, Ensembl Transcription). The main content area has a title 'Please select columns to be included in the output and hit 'Results' when ready' and radio buttons for 'Features' (selected), 'Homologs', 'Structures', 'Sequences', and 'SNPs'. Below these are expandable sections for 'GENE:', 'EXTERNAL:', 'PROTEIN:', and 'GENOMIC REGION:'.

Output fields can be selected from Features, Structures, SNPs, Homologs or Sequences. Select to navigate between them. Each type must be run individually.

After your output is a manageable size, click on “Attributes” to select your output options

By default this shows the first 10 results in hyper-linked HTML format but the number and format can be altered using the drop downs above this preview.

Results -Features

Export all results: TSV Unique results only

Email notification:

View: 10 20 50 100 150 200 All HTML CSV TSV ADF Unique results only

Ensembl Gene ID	Ensembl Transcript ID	Gene Start (bp)	Description
LOC_Os12g36210	LOC_Os12g36210.1	22159864	subtilisin putative, expressed
LOC_Os12g12010	LOC_Os12g12010.1	6582236	verticillium precursor, expressed
LOC_Os12g16890	LOC_Os12g16890.1	9686394	prolamin expressed
LOC_Os12g37480	LOC_Os12g37480.1	22966329	18 enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor, putative, expressed
LOC_Os12g10930	LOC_Os12g10930.1		NLOE, putative
LOC_Os12g05900	LOC_Os12g05900.1		ac GTPase activating protein 1, putative, expressed
LOC_Os12g05900	LOC_Os12g05900.1		ac GTPase activating protein 1, putative, expressed
LOC_Os12g39210	LOC_Os12g39210.1		yclin-A2, putative, expressed
LOC_Os12g30020	LOC_Os12g30020.1		yclin-T1, putative, expressed
LOC_Os12g30020	LOC_Os12g30020.1		yclin-T1, putative, expressed

If you want to save your results, options in the top section of the page allow you to select an export format.

In addition you can choose to show unique results in cases where there is redundancy due to the data model but note this can affect how long it takes to retrieve your results.

Hyperlinks to Genome data

Export Results

Note for particularly intensive queries server time-outs can be a problem, in which case use one of the Web file options.

The screenshot shows a web interface with a dark green header bar containing buttons for 'New', 'Count', 'Results', 'XML', 'Perl', and 'Help'. Below the header, there is a section for 'Dataset 23 / 58406 Genes' with a 'Filters' section showing 'Chromosome: 12'. To the right, there is an 'Export all results to' section with a 'File' input field, a dropdown menu, and a 'Unique results only' checkbox. The dropdown menu is open, showing options: HTML, CSV, TSV, XLS (selected), and ADF. A 'Go' button is located to the right of the 'Unique results only' checkbox.

HTML is web-page format, with active links to Genomes data
CSV - comma separated values
TSV - Tab separated values
XLS - excel file
ADF -

Query Script

The screenshot shows the BioMart interface with a toolbar at the top containing buttons for 'New', 'Count', 'Results', 'XML', 'Perl', and 'Help'. The main content area is divided into a left sidebar and a main panel. The sidebar shows 'Dataset 23 / 58406 Genes' with filters for 'Chromosome: 12', 'Evidence code (Molecular function): IEA', and 'Molecular function: GO:00302'. Below the filters are 'Attributes' including 'Ensembl Gene ID', 'Ensembl Transcript ID', 'Gene Start (bp)', 'Gene End (bp)', 'Prosite ID', and 'PFAM ID'. The main panel has radio buttons for 'Features', 'Homologs', 'Structures', and 'Sequences'. A large text box displays a Perl script for the BioMart API, with red arrows pointing from the 'XML' and 'Perl' buttons to it. The script includes comments and code for setting a registry file and running a query. Below the script, two boxes show the XML output: one for the query parameters and another for the dataset details. A green callout box contains text explaining that the XML format is generated by clicking the 'XML' button and the Perl script is generated by clicking the 'Perl' button. The date '10/18/07' is visible in the bottom left corner.

```
# An example script demonstrating the use of BioMart API.
# This perl API representation is only available for configuration versions >= 0.5
use strict;
use BioMart::Initializer;
use BioMart::Query;
use BioMart::QueryRunner;

my $confFile = "PATH TO YOUR REGISTRY FILE UNDER biomart-perl/conf/. For Biomart Central Registry navigate to
               http://www.biomart.org/biomart/martservice?type=registry";

#
# NB: change action to 'clean' if you wish to start a fresh configuration
# and to 'cached' if you want to skip configuration step on subsequent runs from the same registry
#

my $registryFile = "PATH TO YOUR REGISTRY FILE UNDER biomart-perl/conf/. For Biomart Central Registry navigate to
                  http://www.biomart.org/biomart/martservice?type=registry";

my $action = "cached";

my $queryRunner = BioMart::QueryRunner->new(
    registryFile => $confFile, 'action' => $action);

my $query = BioMart::Query->new(
    registry => $registryFile, 'virtualSchemaName' => 'default');

my $count = $queryRunner->count($query);

print "Count: " . $count . "\n";
```

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE Query>
<Query virtualSchemaName = "default" formatter = "TSV" header = "0"
uniqueRows = "0" count = "" datasetConfigVersion = "1.6" >

  <Dataset name = "ojaponica_gene_ensembl" interface = "default" >
    <Filter name = "evidence_code" value = "IEA" />
    <Filter name = "mol_function" value = "GO:00302" />
    <Filter name = "chromosome_name" value = "12" />
    <Attribute name = "ensembl_gene_id" />
    <Attribute name = "ensembl_transcript_id" />
    <Attribute name = "start_position" />
    <Attribute name = "end_position" />
    <Attribute name = "prosite" />
    <Attribute name = "pfam" />
    <Attribute name = "description" />
  </Dataset>
</Query>
```

```
my $query_runner = BioMart::QueryRunner->new(
    registryFile => $confFile, 'action' => $action);

my $query = BioMart::Query->new(
    registry => $registryFile, 'virtualSchemaName' => 'default');

my $count = $query_runner->count($query);

print "Count: " . $count . "\n";
```

A summary of your current query in BioMart Query XML format can be achieved by clicking the XML button on the toolbar. This is useful for people accessing BioMart via the martservice webservice interface. Similarly a BioMart perl API script to run the same query can be generated by clicking the Perl button. For more detailed help please see the documentation at www.biomart.org.

10/18/07

Attributes - Structures

The screenshot displays a web application interface for data management. At the top, there are navigation tabs: "New", "Count", "Results", "XML", "Perl", and "Help".

On the left side, there is a sidebar with the following sections:

- Dataset 23 / 58406 Genes**
- Filters**: Chromosome: 12, Evidence code (Molecular function) : IEA, Molecular function : GO:0030234
- Attributes**: Ensembl Gene ID, Chromosome, Biotype, Gene Start (bp), Gene End (bp), Ensembl Exon ID
- Dataset**: [None Selected]

The main content area is divided into two sections:

- GENE:** Under "Ensembl Attributes", several options are checked: Ensembl Gene ID, Chromosome, Gene Start (bp), Gene End (bp), Transcript Start (bp), Transcript End (bp), and Strand. Other options like Ensembl Transcript ID, Ensembl Peptide ID, Ensembl CDS length, Ensembl CDNA length, Ensembl Peptide Length, Transcript Count, Description, and Biotype are unchecked.
- EXON:** Under "Exon Attributes", "Ensembl Exon ID" is checked, while "Exon Rank", "Exon Start (bp)", "Exon End (bp)", and "Coding Start" are unchecked.

At the top of the main content area, there are radio buttons for "Features", "Structures", "SNPs", "Homologs", and "Sequences". The "Structures" option is selected and circled in red.

A green callout box with a black border contains the text: "In addition to Features, there are other output options."

Below the main content area, there is an "Export" section with the following options:

- Export all results to: File (dropdown), TSV (dropdown), Unique results only (checkbox), Go (button)
- Email notification to: (text input)
- View: 20 (dropdown), rows as CSV (dropdown), Unique results only (checkbox)

The "rows as CSV" option is circled in red.

Below the export options, there is a table of results. The table has the following columns: Ensembl Gene ID, Chromosome, Biotype, Gene Start (bp), Gene End (bp), Ensembl Exon ID. The table contains several rows of data, including:

Ensembl Gene ID	Chromosome	Biotype	Gene Start (bp)	Gene End (bp)	Ensembl Exon ID
LOC_Os12g36210	12	protein_coding	22159864	22160429	LOC_Os12g36210.1.exon1
LOC_Os12g12010	12	protein_coding	6582236	6585235	LOC_Os12g12010.1.exon1
LOC_Os12g16890	12	protein_coding	9686394	9687123	LOC_Os12g16890.1.exon1
LOC_Os12g37480	12	protein_coding	22966329	22967418	LOC_Os12g37480.1.exon1
LOC_Os12g10930	12	protein_coding	5903561	5906601	LOC_Os12g10930.1.exon3
LOC_Os12g10930	12	protein_coding	5903561	5906601	LOC_Os12g10930.1.exon2
LOC_Os12g10930	12	protein_coding	5903561	5906601	LOC_Os12g10930.1.exon1
LOC_Os12g05900	12	protein_coding	2707478	2712514	LOC_Os12g05900.1.exon5
LOC_Os12g05900	12	protein_coding	2707478	2712514	LOC_Os12g05900.1.exon4
LOC_Os12g05900	12	protein_coding	2707478	2712514	LOC_Os12g05900.1.exon3
LOC_Os12g05900	12	protein_coding	2707478	2712514	LOC_Os12g05900.1.exon2
LOC_Os12g05900	12	protein_coding	2707478	2712514	LOC_Os12g05900.2.exon4
LOC_Os12g05900	12	protein_coding	2707478	2712514	LOC_Os12g05900.2.exon3
LOC_Os12g05900	12	protein_coding	2707478	2712514	LOC_Os12g05900.2.exon2
LOC_Os12g05900	12	protein_coding	2707478	2712514	LOC_Os12g05900.2.exon1
LOC_Os12g39210	12	protein_coding	24109067	24111320	LOC_Os12g39210.1.exon1
LOC_Os12g39210	12	protein_coding	24109067	24111320	LOC_Os12g39210.1.exon2
LOC_Os12g39210	12	protein_coding	24109067	24111320	LOC_Os12g39210.1.exon3
LOC_Os12g39210	12	protein_coding	24109067	24111320	LOC_Os12g39210.1.exon4

A green callout box with a black border contains the text: "And results can be viewed in different formats and numbers of results."

Attributes - SNPs

New **Count** **Results** **XML** **Perl** **Help**

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

Features Homologs
 Structures Sequences
 SNPs

Gene SNP Attributes

Synonymous SNP count Non-synonymous SNP count

Dataset 23 / 58406 Genes

Filters

Chromosome: 12
 Evidence code (Molecular function) : IEA
 Molecular function : GO:0030234

Attributes

Synonymous SNP count
 Non-synonymous SNP count

Dataset

[None Selected]

New **Count** **Results** **XML** **Perl** **Help**

Export all results to Unique results only

Email notification to

View rows as Unique results only

	1
	2
3	4
5	2
5	2
	4
3	8
15	4
14	5
21	10
11	4
11	12
3	1
1	2
5	3
1	6
1	

An example of options and results for SNPs

Attributes - Homologs

New Count Results XML Perl Help

Dataset 23 / 58406 Genes

Filters

Chromosome: 12
Evidence code (Molecular function) : IEA
Molecular function : GO:0030234

Attributes

Ensembl Gene ID
Ensembl Transcript ID

Dataset

[None Selected]

Features Homologs
 Structures Sequences
 SNPs

GENE:

Ensembl Attributes

<input checked="" type="checkbox"/> Ensembl Gene ID	<input type="checkbox"/> External Gene ID
<input checked="" type="checkbox"/> Ensembl Transcript ID	<input type="checkbox"/> External Gene DB
<input type="checkbox"/> Ensembl Peptide ID	<input type="checkbox"/> Ensembl Peptide length
<input type="checkbox"/> Chromosome Name	<input type="checkbox"/> Transcript count
<input type="checkbox"/> Gene Start (bp)	<input type="checkbox"/> % GC content
<input type="checkbox"/> Gene End (bp)	<input type="checkbox"/> Description
<input type="checkbox"/> Strand	

PARALOGS:

Rice (Japonica) Paralogs Attributes

<input type="checkbox"/> Rice (Japonica) Paralogs Chr Start (bp)	<input type="checkbox"/> % Coverage
<input type="checkbox"/> Rice (Japonica) Paralogs Ensembl Gene ID	<input type="checkbox"/> % Identity
<input type="checkbox"/> Rice (Japonica) Paralogs External ID	<input type="checkbox"/> Rice (Japonica) Paralog Ensembl Peptide ID
<input type="checkbox"/> Rice (Japonica) Paralogs External DB	<input type="checkbox"/> Rice (Japonica) Paralog % Coverage
<input type="checkbox"/> Rice (Japonica) Paralogs Gene Name	<input type="checkbox"/> Rice (Japonica) Paralog % Identity
<input type="checkbox"/> Rice (Japonica) Paralogs Gene Start (bp)	<input type="checkbox"/> Ancestor
<input type="checkbox"/> Ensembl Peptide ID	

ARABIDOPSIS ORTHOLOGS:

RICE (INDICA) ORTHOLOGS:

Maize ORTHOLOGS:

POPLAR ORTHOLOGS:

SORGHUM ORTHOLOGS:

C.ELEGANS ORTHOLOGS:

DROSOPHILA ORTHOLOGS:

HUMAN ORTHOLOGS:

YEAST ORTHOLOGS:

An example of options for homologs

Options vary with attribute type

Help file

The screenshot shows the Ensembl MartView interface. At the top, there is a toolbar with buttons for 'New', 'Count', 'Results', and 'Help'. A green callout box with a white border and a pointer to the 'Help' button contains the text 'Click on "help" for help document'. Below the toolbar, the main content area is titled 'e! HelpView' and 'Ensembl MartView'. The left sidebar contains a 'Dataset' section with '[None Selected]' and a 'Filters' section with 'Chromosome: 12', 'Evidence code (Molecular IEA)', and 'Molecular function : GO:00...'. The main content area has a search bar with 'martview' and a 'Go' button. Below the search bar, there are navigation links: 'HOME · BLAST · SITEMAP' and 'Contact helpdesk'. The main content area is divided into sections: 'Help with help!', 'General', 'Full text search', 'Entry Points', and 'Data Displays'. The 'Entry Points' section includes links for 'Ensembl BLASTView', 'Ensembl ExaSearch', 'Ensembl HelpView', 'Ensembl Homepage', 'Ensembl TextView', 'Ensembl User Accounts', and 'Ensembl User Groups'. The 'Data Displays' section includes links for 'Ensembl AlignSliceView', 'Ensembl AlignView', 'Ensembl ChromoView', 'Ensembl ContigView', 'Ensembl CytoView', 'Ensembl DomainView', 'Ensembl DotterView', 'Ensembl ExonView', 'Ensembl FamilyView', and 'Ensembl FastaView'. The main content area contains text explaining the MartView interface, including instructions on how to navigate, query, and filter results. At the bottom, there is a copyright notice: '© 2007 WTSJ / EBI. Ensembl is available to download for public use - please see the code licence for details.'

FAQ

The screenshot shows the GRAMENE website's navigation menu and a list of frequently asked questions. The menu includes: Search, Genomes, Species, Download, Resources, About, Help, Feedback, Site Map, Help Documents, Release Notes, Tutorials and Exercises, Glossary, FAQs, Gramene Documentation, Workshop Materials, and Mailing Lists. The 'FAQs' link is highlighted with a mouse cursor. A callout bubble points to the 'Feedback' link with the text 'Use Feedback to ask a question'. Another callout bubble points to the 'FAQs' link with the text 'Search FAQ'. A third callout bubble points to the first FAQ question with the text 'FAQs may be able to answer some of your questions.' A fourth callout bubble points to the first FAQ question with the text 'Click on a question or FAQ section to open and close the information.' The first FAQ question is: 'Do you have a list of all rice/arabidopsis orthologs with their respective ids'. The answer text is partially visible: 'We suggest using the GrameneMart searches to generate this list. If you are not familiar with this please follow the tutorials provided at <http://www.gramene.org/multi/martview> to get started. For your specific query select the search filters appropriately. Here is a simplified way using your query. -Go to <http://www.gramene.org/multi/martview> select the rice data set and click the NEXT button on top. By doing this you will be taken to the features section. -Click on the next button. -Click on the TCGR gene. -Click on the type of output you want -Click on EXPORT button. -This should give you a list of orthologs.

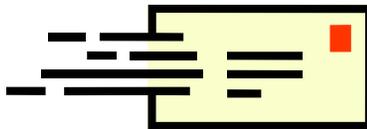
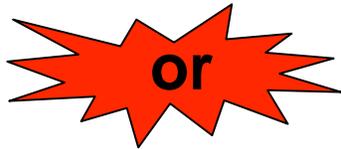
For Further Information

- Data mining using EnSmart (oriented towards human data mining at Ensembl)
 - www.ensembl.org/Homo_sapiens/helpview?se=1;kw=martview
- BioMart documents
 - www.biomart.org/install.html

Contact Gramene



Use the feedback button, located at the top of every page, to provide feedback or to ask questions about Gramene.



Email Gramene users at gramene@gramene.org