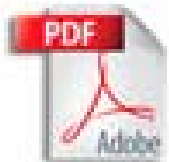


Welcome to the GrameneMart Tutorial

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 "bookmarks" on the left hand side of the Reader for easier navigation.

Action Options are noted in this font.

Notes or comments use this style font.

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

Gramene Home Page

GRAMENE

A Resource for Comparative Grass Genomics

v23 (November 2006)

[Search](#) | [Genomes](#) | [Species](#) | [Download](#) | [Resources](#) | [About](#) | [Help](#) | [Feedback](#)

Quick Search

All Available

Search a single module or all available modules plus online documentation.

Diversity, Pathways, BLAST and Mart not available in this search.

Have Questions...?

- Gramene now has **tutorials** for every module, also recommended for experienced users.
- Ask questions through **Feedback** or **Email**.
- See **FAQ** for questions and answers.

Gramene Tip:

The AGI Maize FPC maps cannot be viewed directly, because they are not reference maps. If you are looking for them, start with a maize genetic map or the rice sequence map, then add the **maize FPC maps** as comparative maps.

- [Browse All Tips](#)

Quick Start

Sequenced genomes for [Rice](#), [Maize](#) & [Arabidopsis](#); Look for [rice/maize synteny](#); Narrow search for sequence alignment with [BLAST](#); search by [Gene Ontology](#).

Search for [Fam](#) or [ProSite](#) or Browse by Gene Ontology using [GO Slim](#).

Search for physical maps for [Rice](#), [Maize](#), [Wheat](#), [Barley](#), [Oats](#), [Sorghum](#), and other grasses, or [Map Viewer \(CMap\)](#) to compare maps of different types and species.

Search for genetic markers (RFLPs, SSRs, etc.), DNA Probes (Primers, Overgos, etc.), Genomic contigs, etc.), and Sequences (GSSs, ESTs, etc.); Use the Simple Sequence Repeat (SSR) [Tool](#); or search by species, including [Rice \(Oryza sativa\)](#), [Maize](#), [Sorghum](#) and [Others](#).

Genomes-Ensembl

Maps-CMap

Markers

QTL

Diversity

Genes

Proteins

Pathways

Ontologies

Literature

Sequences-BLAST

All-GrameneMart

TRAITS: Search the [Genes](#) or [QTL](#) database for important phenotype-related loci such as [Rice Genes](#), [Rice QTL](#), [Maize QTL](#). Don't forget to [search for traits in Ontologies](#).

GENETIC DIVERSITY **NEW**: Search for SNP and SSR markers in [rice](#) and [maize](#) germplasms.

BIOCHEMICAL PATHWAYS **NEW**: Search for [genes](#) of the [metabolic network](#). Compare [rice](#) and [maize](#) pathways.

LITERATURE: Search the literature for your [interests](#).

SUBMISSION: Submit a [Rice Gene](#) or [Ontology Term](#) to Gramene.

Featured News

- NEW**: Gramene Release 23 [release notes](#).
- NEW**: [MaizeSequence.org](#) now available!
- NEW**: [Gramene November Newsletter](#)
- [Rice News Worldwide](#) from IRRI

Visit with us at

- [Data Warehouse Technologies in Bioinformatics](#), December 4-6, 2006.
- [Plant and Animal Genome XV Conference](#), January 13-17, 2007. ([Gramene Workshop](#))

[View Previous Gramene Presentations](#)

[Calendar](#)

Gramene is a curated, open-source, web-accessible data resource for comparative genome analysis in the grasses. Our goal is to facilitate the study of cross-species homology relationships using information derived from public projects involved in genomic and EST sequencing, protein structure and function analysis, genetic and physical mapping, interpretation of biochemical pathways, gene and QTL localization and descriptions of phenotypic characters and mutations.

Note! Although we continually work to make Gramene compatible with all browsers, if you're having difficulty viewing Gramene, try using a different browser. Please report any problems with browsers through [Gramene Feedback](#).

SPECIES

Last modified: Wed Nov 8 13:09:58 2006

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11/9/2006

Mart tools are structured as a series of pages to be filled in successively. The steps are outlined at as headers at the top of MartView

Select a Dataset

*Press **Next**. This will move you to the next step, and highlight the headers one by one.*

new START FILTER OUTPUT export

new next

Select the **dataset** for this query

Rice Gene Models (TIGRv4)

Arabidopsis Gene Models (TAIR6)

Maize Gene Models (Gramene FGENESH)

Rice Gene Models (TIGRv4)

Rice Polymorphisms (SNPs)

bio::mart

refresh Help Desk

Summary

▶ start
Not yet initialised

▶ filter
Not yet initialised

▶ output
Not yet initialised

For a bookmarkable version of this page, click [\[here\]](#)

*Select a **dataset** for this query.*

The Summary section at the right hand side is updated accordingly. It is always possible to go back to a previous step and amend the options. Clicking on 'refresh' will update the summary.

Apply a filter to narrow your search

Formulate the Filters: Filter by Region

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

The screenshot shows the bioMart interface with the 'FILTER' tab selected. Under 'DATASET 1', the 'REGION' section has 'Chromosome' checked. A dropdown menu for 'Chromosome' is open, displaying a list of chromosomes (1-9) and gene models (AC025783 to AC078829). The 'Summary' panel on the right shows 'start' and 'Dataset: Rice' with '57752 Entries Total'.

1. If you wish to filter by chromosome or base pair, **select the box** and **enter specific data**

This is the current state of your query, showing the current number of records matching your query and filters. Continue to add filters until the number becomes a manageable size.

Filter by Gene

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

GENE:

<input type="checkbox"/>	with Gramene Curated Gene ID(s)	<input checked="" type="radio"/> Only <input type="radio"/> Excluded
<input type="checkbox"/>	with TIGR Locus ID(s)	
<input type="checkbox"/>	with TIGR FN ID(s)	
<input type="checkbox"/>	with EntrezGene ID(s)	
<input type="checkbox"/>	with TIGR GeneIndex ID(s)	
<input type="checkbox"/>	with Gramene Pathway ID(s)	
<input type="checkbox"/>	with GO ID(s)	
<input type="checkbox"/>	with Refseq DNA ID(s)	
<input type="checkbox"/>	with Refseq DNA Predicted ID(s)	
<input type="checkbox"/>	with Refseq Peptide ID(s)	
<input type="checkbox"/>	with Refseq Peptide Predicted ID(s)	
<input type="checkbox"/>	With SPTreMBL ID(s)	<input checked="" type="radio"/> Only <input type="radio"/> Excluded
<input type="checkbox"/>	Entries with a 3' UTR	<input checked="" type="radio"/> Only <input type="radio"/> Excluded
<input type="checkbox"/>	Gene type	protein_coding
<input type="checkbox"/>	Source	genbank
<input type="checkbox"/>	Status	KNOWN

Browse...

Chromosome name: 12

4143 Entries pass Filters

output

Not yet initialised

Import values from a file

Filter by Gene Ontology

GENE ONTOLOGY:

☒ Molecular function
Evidence code IEA ▼
Molecular function GO:0030234
<browse>

☐ Biological process
Evidence code IEA ▼
Biological process
<browse>

☐ Cellular component
Evidence code IEA ▼
Cellular component
<browse>

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

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

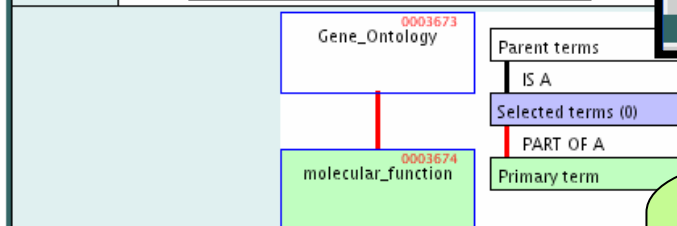
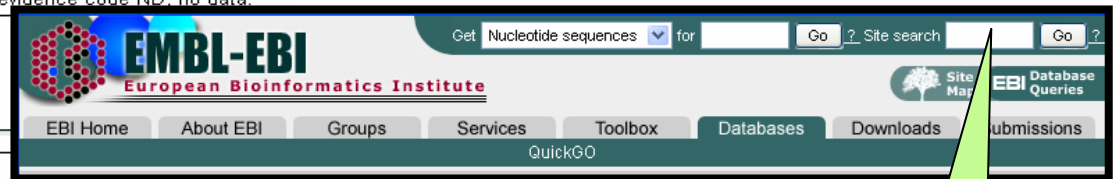
QuickGO

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

You should be on the ontology you selected



Child terms [?]	<p>GO:0016209: antioxidant activity</p> <p>GO:0005488: binding</p> <p>GO:0003824: catalytic activity</p> <p>GO:0030188: chaperone regulator activity</p> <p>GO:0042056: chemoattractant activity</p> <p>GO:0045499: chemorepellant activity</p> <p>GO:0031992: energy transducer activity</p> <p>GO:0030234: enzyme regulator activity</p> <p>GO:0003774: motor activity</p> <p>GO:0045735: nutrient reservoir activity</p> <p>GO:0008369: obsolete molecular function</p> <p>GO:0031386: protein tag</p> <p>GO:0004871: signal transducer activity</p> <p>GO:0005198: structural molecule activity</p>
------------------------	---

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

Compare Species

MULTI SPECIES COMPARISONS:

<input type="checkbox"/>	Osativa paralog	<input checked="" type="radio"/> Only
	Osativa paralog	<input type="radio"/> Excluded
	Athaliana homolog	
	Zmays homolog	

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

Filter by Protein

PROTEIN

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

☐ with InterPro ID(s) ☒ Only ☐ Excluded

☐ Limit to genes with these domain ID(s)

Interpro ID(s)
Interpro ID(s)
PFAM ID(s)
PRINTS ID(s)
PROFILE ID(s)

Browse...

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

Use the 'Browse' button to import values from a file

Filter by SNP

SNP:

☐ Coding ☒ Only ☐ Excluded

☐ Intronic

☐ 5utr

☐ 5upstream

☐ 3utr

☐ 3downstream

☐ Synonymous SNPs ☒ Only ☐ Excluded

☐ Associated with validated SNPs ☒ Only ☐ Excluded

Apply the filter

After selecting a filter click on “refresh”

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

Summaries from three progressive filters (different example)

bio::mart

[refresh](#) [Help Desk](#)

Summary

► **start**

- Dataset: Rice
- Gene Models (TIGRv4)

① 57752 Entries Total

► **filter**

- Chromosome name: 12
- Evidence code: IEA
- Molecular function: GO:0030234

① 8 Entries pass Filters

► **output**

① Not yet initialised

bio::mart

[refresh](#) [Help Desk](#) [Tutorial](#)

Summary

► **start**

- Dataset: Oryza sativa genes

① 58752 Entries Total

► **filter**

① Not yet initialised

► **output**

① Not yet initialised

bio::mart

[refresh](#) [Help Desk](#) [Tutorial](#)

Summary

► **start**

- Dataset: Oryza sativa genes

① 58752 Entries Total

► **filter**

- Chromosome name: 9

① 3465 Entries pass Filters

► **output**

① Not yet initialised

bio::mart

[refresh](#) [Help Desk](#) [Tutorial](#)

Summary

► **start**

- Dataset: Oryza sativa genes

① 58752 Entries Total

► **filter**

- Chromosome name: 9
- Homologous Maize genes: Only

① 70 Entries pass Filters

► **output**

① Not yet initialised

After Filtering, go to Output



After your output is a manageable size, click on “**next**” to go to the output page.

Output - Features

Select the Attribute Page

Features

Features

Structures

SNPs

Homologs

Sequences

Name

Start Position (bp)

End Position (bp)

Strand

GENE:

Ensembl Attributes

☒ Ensembl Gene ID

☐ Ensembl Peptide ID

☐ External Gene DB

☐ Ensembl cDNA length

☐ Transcript count

☐ Description

☐ Source

☒ Ensembl Transcript ID

☐ External Gene ID

☐ Ensembl CDS length

☐ Ensembl Peptide length

☐ % GC content

☐ Biotype

☐ Status

GO Attributes

☐ GO description

☐ GO description

External References (max 3)

☐ TIGR GeneIndex ID

☐ UniProt/SPTreMBL ID

☐ Gramene Curated Gene

☐ RefSeq DNA ID

☐ RefSeq Peptide ID

☐ TIGR GeneIndex ID

☐ UniProt/SPTreMBL ID

☐ Gramene Curated Gene

☐ RefSeq DNA ID

☐ RefSeq Peptide ID

Select the output format:

☒ HTML

☐ Text, comma separated

☐ MS Excel

☐ Text, pipe separated

☐ Text, tab separated

☐ Predefined ADF attributes

File compression:

☒ None

☐ gzip (.gz)

Enter a name for this result set:

Name:

Enter a value to open results in new window (REQUIRES POP-UP UNBLOCKING), or to provide a name for file download.

[back](#) [export](#)

For more information of this page, click [here](#)

Select output options you want by clicking on the box to the left of an option to check it.

Output fields can be selected from Features, Structures, SNPs, Homologs and Sequences. Select to navigate between them.

Options at the bottom of the Export page allow you to select HTML, text or Excel formats, and may vary depending on output field selected.

Click Export (see next slide)

Output - Structure and SNPs

The image displays two screenshots of a web application interface for selecting attributes. A green arrow points from the 'Structures' dropdown in the left screenshot to the 'SNPs' dropdown in the right screenshot, indicating that the available options vary based on the selected output type.

Left Screenshot (Structures selected):

- Select the Attribute Page:** Structures
- REGION:**
 - Chromosome Attributes:**
 - ☐ Chromosome
 - ☐ End Position (bp)
 - ☐ Start Position (bp)
 - ☐ Strand
- GENE:**
 - Ensembl Attributes:**
 - ☒ Ensembl Gene ID
 - ☐ Ensembl Peptide ID
 - ☐ External Gene DB
 - ☐ Ensembl Peptide length
 - ☐ Transcript Count
 - ☒ Biotype
 - ☐ Ensembl Transcript ID
 - ☐ External Gene ID
 - ☐ Ensembl CDS length
 - ☐ Ensembl Peptide Length
 - ☐ Description
- EXON:**
 - Exon Attributes:**
 - ☐ Exon Start (Chr bp)
 - ☐ Coding Start (Chr bp)
 - ☐ Ensembl CDS Start (Chr bp)
 - ☐ Constitutive Exon
 - ☐ Exon End (Chr bp)
 - ☐ Coding End (Chr bp)
 - ☐ Ensembl CDS End (Chr bp)

Right Screenshot (SNPs selected):

- Select the Attribute Page:** SNPs
- REGION:**
 - Chromosome Attributes:**
 - ☐ Chromosome Name
 - ☐ End Position (bp)
 - ☐ Start Position (bp)
 - ☐ Strand
- GENE:**
 - Ensembl Attributes:**
 - ☒ Ensembl Gene ID
 - ☐ Ensembl Peptide ID
 - ☐ External Gene DB
 - ☐ Ensembl cDNA length
 - ☐ Transcript count
 - ☐ Description
 - ☒ Ensembl Transcript ID
 - ☐ External Gene ID
 - ☐ Ensembl CDS length
 - ☐ Ensembl Peptide length
 - ☐ % GC content
 - Gene SN Attributes:**
 - ☐ Synonymous SNP count
 - ☐ Non-synonymous SNP count
- GENE ASSOCIATED SNPS:**
 - SNP Attributes:**
 - ☐ RefGene ID
 - ☐ Variation status
 - ☐ Allele
 - ☐ Mapweight
 - ☐ SNP Chromosome Strand
 - ☐ Chromosome Location (bp)
- Gene Location and Effect:**
 - ☐ Location in Gene (coding etc)
 - ☐ Synonymous Status
 - ☐ Peptide Shift

Output - Homologs and Sequences

Homologs ▼

REGION:

Chromosome Attributes

☐ Chromosome Name ☐ Start Position (bp)

☐ End Position (bp) ☐ Strand

GENE:

Ensembl Attributes

☒ Ensembl Gene ID ☒ Ensembl Transcript ID

☐ Ensembl Peptide ID ☐ External Gene ID

☐ External Gene DB ☐ Ensembl CDS length

☐ Ensembl cDNA length ☐ Ensembl Peptide length

☐ Transcript count ☐ GC content

☐ Description

PARALOGS

Rice Paralog Attributes

☐ Paralog Ensembl Gene ID ☐ Paralog Ensembl Peptide ID

☐ Paralog External ID ☐ Paralog External DB

☐ Paralog Chromosome ☐ Paralog Chr Start (bp)

☐ Paralog Chr End (bp) ☐ % Coverage

☐ Paralog % Coverage ☐ Paralog % Identity

ORTHOLOGS (Max 3 Species):

Maize Ortholog Attributes

☐ Maize Gene ID ☐ Maize Clone

☐ Maize Clone Start (bp) ☐ Maize Clone End (bp)

☐ Orthology Type ☐ Peptide ID

☐ % Coverage ☐ % Identity

☐ Maize Peptide ID ☐ Maize % Coverage

☐ Maize % Identity

Arabidopsis Ortholog Attributes

☐ Arabidopsis Gene ID ☐ Arabidopsis External ID

☐ Arabidopsis External DB ☐ Arabidopsis Chromosome

☐ Arabidopsis Chr Start (bp) ☐ Arabidopsis Chr End (bp)

☐ Orthology Type ☐ Peptide ID

☐ % Coverage ☐ % Identity

☐ Arabidopsis Peptide ID ☐ Arabidopsis % Coverage

☐ Arabidopsis % Identity

Select the **Attribute Page**

Sequences ▼

SEQUENCES:

Type of Sequence to Export (all in 5'-3' direction):

☐ Unsplied (Gene) ☐ Flank (Transcript)

☐ Flank (Gene) ☐ Flank-coding region (Transcript)

☐ Flank-coding region (Gene) ☐ Exon sequences (Transcript)

☐ Exon sequences (Gene) ☐ cDNA sequences

☐ 5' UTR ☐ 3' UTR

☐ Coding sequence ☐ Peptide

☐ Upstream flank

☐ Downstream flank

Header Information

Gene Attributes

☒ Chromosome ☒ Ensembl Gene ID

☐ External Gene ID ☐ External Gene DB

☐ Description

Transcript Attributes

☐ Ensembl Transcript ID ☐ Ensembl Peptide ID

☐ Transcript Type ☐ Strand

☐ End Position (bp) ☐ Ensembl CDS length

☐ 5 UTR End (Chr bp) ☐ 3 UTR End (Chr bp)

Exon Attributes

☐ Ensembl Exon ID ☐ Exon Start (Chr bp)

☐ Exon End (Chr bp) ☐ Coding Start (Chr bp)

☐ Coding End (Chr bp) ☐ Exon Rank in Transcript

Options vary with Output type

Results

Each selected output field will depend upon your filters, output type, and output options.

>LOC_Os12g18560|invertase inhibitor domain inhibitor homolog, putative[1]11686.e00708[1]10731000|10731144|1|
 AAGAAGCAATTAACCAAGCACTAGCTATTCTAGCTTAGCCTCGCTAAACCAACCAACATCGTAAAAATCTCTTTGATAG
 TGGACATCGGAGGCACTGATTAATTAAGTAGCTAGCTAGTTACAGGCCCAAGGAGAGAAACACCAATGGGCATCAATGGCG
 CATCGGCAATGGTGCTCATCTGCTCTCTGCTGCTGGTCTCTCGCTCGAGCACTCTGTCTGCTACGGGGCGGGGCTCTT
 TCCAAAGCAGGGCATGGCGGCTGGCCAGCCCAAGCGGCTGGCCGCCAGCGGCTCGGTACGGCGCGCGCGCGCGCCAGC
 AGCGCGCGCGGCTGGTGCTGCTGCACTGCAACTCCACCTCTACTACGACCTCTGGCTGGCGAGCTCTCGCGGACAC
 GCGCCAGCGCGGACCTGCTGCGGGAATGCTGCTCATCTGCGGCTCTCGCGCGCGCGCGCCCAAGCATCGCGGCGGGG
 GCTCTGGCGCTGGCGAAGCGACCGGACGCGGGGACGACGGCGGGCTCGCGCGGCGCGCGCGCGCGCGGCGCTGTG
 GCTGCTGCCCACTGCGCGGCGCAAGTACGGCGACGCGCGCGGAGCGGCTCGCGCGCGCGCAAGGGCTCATCGCGCG
 CATACGACATGGGCTCGTGTCACGTACAGCGCGCGCGGAGATCCCGGAGTGTGAGGACAGCTGTTCGCGGCGG
 CGCGGAGACATCCCGCGGAGCTCGCGCGACAGAGGTGGCGCTCAGGACGCTTGTCTGCTGCGGCTGTGACAT
 CTCTCTACGCTCATCCAGCAACTAGCAGCTCTGCTTGTACGAGCTCAAGTTTACCCCAACCAAGCTTAAGTACT
 CGTATAGGTACAAATGGTGCAATATATAGTACTGTATAATACTACTGATCAAGATACATATAGTGTATATAGTAC
 TATTTTATCTTTTTTTTGGCAAGGGCGCATATCAATTAATTTGTGTGTGCCCAATTAATAGAGTGAATCCATGCA
 TATGTCTTTTGTGTAATTGTATTATCATCCATAGAGGAGTGTCTGTAGTAGTGCAAAAGGTACATCGGCGCGCGGCA
 GTATGATGATTCTCA

>LOC_Os12g07050|expressed protein[1]11686.e16863[1]25195068[25195825]25195262|25195825|25195068|25195261
 ATGGGGCTCTCTCACTTACTACCGGCGACCTGCTCTCTGCTCGCGCGCGCGCTGCTCTCGCATACGGCGCGGCTCTCGCC
 CGCGCGCGGCGGGGTGGACAGCGTGGCGGAGTGTGTCACGCCATCAAGGAGCTTGTGGAGGTGGGCTTCTCGGAGCGCG
 CTTGCGGTGGCTCTGCGCGCGGCTGGCGCGGCGCACGGCGGACGGCCAGGCCACTCTGATCGCGGCGGCGCTGGCGCGCGG
 CGCGGGGACCTGGGCGAGGACGACGCCCTGGCGCGGCGCGCGCGCGCGCGGAGCGGCGGCGGAGAGCGGAGCGGAGTGGT
 GGAGCGGCTGGCGGACTCTGTGACGGGTGCTCGGTGGCGCGGCTGCGGCTGATGCGGGGATCGCGGCGCGCGCGGCGG
 AGCGCGGAGTGCTGCTGTGCTGCGGCGGAGCGCGGATGGGCTGGCGCGGCGCTGACCTGCGCGCGCGCGCGG
 ATGGGACGGGCGCAAGCAGGATTTCAGCGGCTCACACCATGGCCACCGCGCTGCTCAACAGCTGCGCGGCGCACGCGGCT
 TGGGCACTCTTT
 TTAATGTAACT

GR Gene LOC ID Transcript count

LOC_Os12g18560	1	6.e04040 1 4747198 4747452 4747198 4747452 CTCGTGGCGGCA AGGTGGTCCCG TCGCGCAGACT
LOC_Os12g40750	1	44445 1 22155417 22155925 22155834 22155925 22155 ATAGCTCATCAT TCGCGTCTCCG ACCCCAACCATC GTATCATATGCA GTATTTTTTTTC
LOC_Os12g09090	1	
LOC_Os12g36210	1	

Chromosome Name	Start Position (bp)	End Position (bp)	Strand	TIGR Gene LOC ID	Transcript count
12	10731000	10732135	1	LOC_Os12g18560	1
12	25195068	25195825	-1	LOC_Os12g40750	1
12	4747198	4747452	-1	LOC_Os12g09090	1
12	22155417	22155925	-1	LOC_Os12g36210	1
12	22160052	22160556	-1	LOC_Os12g36220	1
12	22164736	22165247	-1	LOC_Os12g36240	1
12	22961703	22962786	-1	LOC_Os12g37480	1
12	1392077	1392652	-1	LOC_Os12g03510	1

Links to Genome Browser

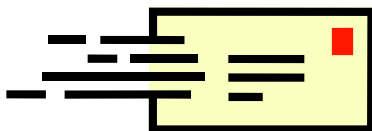
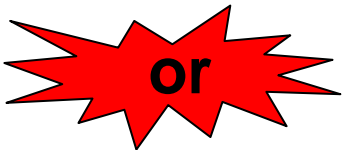
For Further Information

- 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 at gramene@gramene.org