

A Comparative Mapping Resource



A Comparative Genomics Resource for Grains



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.

Gramene is a curated, open-source, Web-accessible data resource for comparative genome analysis in the grasses.

As an information resource, Gramene's purpose is to provide added value to data sets available within the public sector to facilitate researchers' ability to leverage the rice genomic sequence to identify and understand corresponding genes, pathways and phenotypes in the crop grasses. This is achieved by building automated and curated relationships between rice and other cereals for both sequence and biology.

Extensive work over the past two decades has shown remarkably consistent conservation of gene order within large segments of linkage groups in rice, maize, sorghum, barley, wheat, rye, sugarcane and other agriculturally important grasses. A substantial body of data supports the notion that the rice genome is significantly colinear at both large and short scales with other crop grasses, opening the possibility of using rice synteny relationships to rapidly isolate and characterize homologues in maize, wheat, barley and sorghum.

Gramene Modules

The best place to begin a search at Gramene is often in the module of what you want. If you want information on a marker, look in the markers module, if you want to learn about a protein, go to the proteins module.

Another good place to start is with the Quick Search on the home page, also found at the top right of all other pages, or in the literature database.

Eventually, you will find that most of the modules are interconnected, and you may move between modules as your search progresses.

www.gramene.org

GRAMENE

A Resource for Comparative Grass Genomics

v22 (August 2006)

[Search](#)
[Genomes](#)
[Species](#)
[Download](#)
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Quick Search

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

[Diversity](#), [Pathways](#), [BLAST](#) and [Mart](#) not available in this search.

Quick Start

sequenced genomes for [Rice](#), [Maize](#) & [Arabidopsis](#); Look for [rice/maize](#) search with [GrameneMart](#); Search for sequence alignment with [BLAST](#); [Protein](#) or [ProSite](#) or Browse by Gene Ontology using [GO Slim](#).

or physical maps for [Rice](#), [Maize](#), [Wheat](#), [Barley](#), [Oats](#), [Sorghum](#), and other comparative Map Viewer ([Map](#)) to compare maps of different types and

Featured News

- NEW: [Gramene November Newsletter](#)
- Gramene Release 22 [release notes](#). Release 23 coming soon!
- [Rice News Worldwide](#) from IRRI

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.

Navigation Bar

- [Genomes-Ensembl](#)
- [Maps-CMap](#)
- [Markers](#)
- [QTL](#)
- [Diversity](#)
- [Genes](#)
- [Proteins](#)
- [Pathways](#)
- [Ontologies](#)
- [Literature](#)
- [Sequences-BLAST](#)
- [All-GrameneMart](#)

Access Gramene modules through the Navigation bar.

This is the list of current modules available. You may also enter through "Quick Start."

Gramene Tip:

In addition to Trait, Plant and Gene Ontology, Gramene has [Environment Ontology](#) and [Gramene Taxonomy Ontology](#).

- [Browse All Tips](#)

TRAITS:

Search the Gramene database for important phenotype-related loci such as [Rice Genes](#), [Rice QTL](#), [Maize](#) or [Arabidopsis](#) to explore traits in [Ontologies](#).

GENETIC DIVERSITY:

Search for genetic variation on loci of [rice](#), [maize](#), and [wheat](#) genotypes.

BIOCHEMICAL PATHWAYS:

Search for an overview of the [metabolic pathways](#) in [Gramene](#).

LITERATURE:

Search for [literature](#) related to [Gramene](#).

SUBMISSION:

Submit [new data](#) to [Gramene](#).

Gramene is a curated, open access resource.

Our goal is to facilitate the projects involved in genome mapping, interpretation of characters and mutations.

Previous Gramene presentations

[Previous Gramene presentations](#)

[USDA](#)
[DAS](#)
[GRAMENE](#)
[RICE](#)
[MAIZE](#)
[WHEAT](#)
[BARLEY](#)
[OATS](#)
[SORGHUM](#)

[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](#).

Note – The presentation of the modules is organized according to their location on the navigation bar. This does not indicate that you should begin with the first module presented, nor end with the last one. Together the modules complement each other by forming the Gramene Database.

Genomes and Gramene Genome Browser

Genome browser is a dynamic graphical display used to browse genomes. Use it to:

- *Search for genes and other features identified from the Rice-Japonica, Maize and Arabidopsis genomes, as well as features from maize, sorghum, barley and wheat that were mapped on the rice genome.*
- *View the location of a particular feature on the rice genome*
- *Examine neighboring genes and markers.*
- *View the gene model of a candidate gene of interest in order to design primers.*
- *Identify the genomic sequence to which a particular gene is mapped.*
- *Look for synteny. Compare the position of features from other species with the location of genes in the rice genome, such as sequenced genetic markers, ESTs, cDNAs, CDSs, genes, insertion and repeat elements.*

Browse a Chromosome or View a Rice-Maize Synteny Map

Find in Genomes

Browser Links

[Genomes Home](#)
[Genomes Help](#)
[Switch Species](#)

browse a genome

Oryzae

Other Poaceae

Other

About Gramene-Ensembl

The Gramene Genome Browser displays genomic data for a wide range of species, including several major cereal genomes and physical maps. The Browser is built on the Ensembl genome browser software system which produces and maintains genome maps for a wide range of species, including several major cereal genomes and physical maps. The Browser is built on the Ensembl genome browser software system which produces and maintains genome maps for a wide range of species, including several major cereal genomes and physical maps.

Browse by Chromosome

1

2

3

4

5

6

7

8

Lookup a Chromosome Location

Chr:

1

 from

1

 -

Rice Synteny Vs Maize FPC Map

Chr 1 vs. Maize

Go

Oryza sativa chromosome 1

50M

100M

150M

200M

250M

300M

350M

400M

450M

500M

Chr 3

Chr 6

Chr 7

Chr 8

Chr 9

Chr 10

Chr 11

Chr 12

Chr 13

Chr 14

Chr 15

Chr 16

Chr 17

Chr 18

Chr 19

Chr 20

Chr 21

Chr 22

Chr 23

Chr 24

Chr 25

Chr 26

Chr 27

Chr 28

Chr 29

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Chr 81

Chr 82

Chr 83

Chr 84

Chr 85

Chr 86

Chr 87

Chr 88

Chr 89

Chr 90

Chr 91

Chr 92

Chr 93

Chr 94

Chr 95

Chr 96

Chr 97

Chr 98

Chr 99

Chr 100

Chromosome 11

50M

100M

150M

200M

250M

300M

350M

400M

450M

500M

Chr 11

TIGR pseudomolecule assembly, release 4, of IRGSP final

This database does not include the portions of clones not used in the assembly which were not used in the assembly have been mapped. Other clones are listed [here](#).

Chromosome 11

Barley_ArrayExemplar_Affy22K Count

1,940

Barley_EST Count

39,462

Barley_ESTcluster_PlantGDB Count

6,397

Barley_ESTcluster_TIGR Count

4,734

Chromosome length

28,462,105

FGENESH Count

4,253

GeneModel Submission Count

1,830

GeneModel TIGR Count

4,297

Maize_Cornchip0_ArrayConsensus_Affy8K Count

256

Maize_ArrayConsensus_Affy18K Count

1,768

Maize_ArrayGene_NSF58K Count

4,591

Maize_BACend Count

2,158

Maize_EST Count

52,888

Maize_ESTcluster_PlantGDB Count

6,862

Maize_ESTcluster_MMPconsensus Count

1,245

Maize_ESTcluster_TIGR Count

2,881

Customize your detailed view display by selecting and deselecting options. Selections will be saved for future visits.

Customize options for Contig View

The screenshot shows the 'Contig View' interface with several customization menus open. At the top, there are tabs for 'Features', 'ESTs', 'GSSs', 'FSTs', 'Arrays', 'Markers', 'DAS Sources', 'Decorations', 'Image size', and 'Help'. Below these, a 'Jump to region' section contains input fields for '10', '1243467', and '1343468', along with a 'Refresh' button. A 'Band' section has an empty input field and another 'Refresh' button. A 'Zoom' section features a slider and buttons for '<1MB', '<200k', '<Window', 'Window>', '200k>', and '1MB>'. Four main customization menus are open: 'Features' (listing items like SNPs, GeneModel TIGR, genbank_tma, etc.), 'ESTs' (listing items like Rice_EST, Rice_ESTcluster_Plan, etc.), 'GSSs' (listing items like Rice_GSS, Rice_GSScluster_Plan, etc.), and 'Markers' (listing items like Rice_MarkerRFLP, Rice_MarkerSSR, etc.). A 'Decorations' menu is also partially visible, listing items like Sequence, Codons, Start/Stop codons, etc. A 'Help' menu is at the bottom right, listing items like Configuring, DAS sources, General, Helpdesk, etc. A blue plus sign is visible in the center of the interface.

Features ▾ ESTs ▾ GSSs ▾ FSTs ▾ Arrays ▾ Markers ▾ DAS Sources ▾ Decorations ▾ Image size ▾ Help ▾

Jump to region 10 : 1243467 - 1343468 Refresh Band: Refresh

<1MB <200k <Window Zoom Window> 200k> 1MB>

Features

- ☐ SNPs
- ☐ SNPs (OMAP)
- ☐ SNPs (dbSNP)
- ☒ Markers
- ☒ GeneModel TIGR
- ☒ genbank_tma
- ☒ genbank_rrna
- ☐ GeneModel Gramene
- ☒ miRNA_genes
- ☐ FGENESH
- ☒ Rice_BAC
- ☐ Rice_QTL
- ☐ Maize_SatMaizea
- ☒ SNPs (dbSNP)
- ☒ SNPs (OMAP:o_satv)
- ☒ SNPs (OMAP:o_satv)
- ☒ SNPs (OMAP:o_satv)

ESTs

- ☐ Rice_EST
- ☐ Rice_ESTcluster_Plan
- ☐ Rice_ESTcluster_TIGR
- ☐ Rice_cDNA_KOME
- ☒ Rice_mRNA
- ☐ RiceIndica_EST_BGI
- ☐ RiceIndica_ESTcluster
- ☒ Barley_EST
- ☐ Barley_ESTcluster_Plan
- ☐ Barley_ESTcluster_TIGR
- ☐ Maize_EST
- ☐ Maize_ESTcluster_MM
- ☐ Maize_ESTcluster_Plan
- ☐ Maize_ESTcluster_TIGR
- ☐ Maize_MAGI_ISU
- ☐ Maize_WGS_JGI
- ☒ Maize_mRNA
- ☐ Maize_EST
- ☐ Other-poaceae_est
- ☐ Other-poaceae_est
- ☒ Sorghum_EST
- ☐ Sorghum_ESTcluster
- ☐ Sorghum_ESTcluster3
- ☐ Sorghum_cDNA
- ☒ Sugarcane_EST
- ☐ Wheat_EST

GSSs

- ☐ RiceAita_BACend
- ☐ RiceAustraliensis
- ☐ RiceBrachyantha
- ☐ RiceCoarctata_BAC
- ☐ RiceGlaberrima_BAC
- ☐ RiceIndica_BAC
- ☒ RiceMinuta_BAC
- ☐ RiceNivara_BAC
- ☐ RiceOfficialis_BACend_OMAP
- ☐ RicePunctata_BACend_OMAP
- ☐ RiceRidley_BACend_OMAP
- ☒ RiceRufipogon_BACend_OMAP
- ☐ Maize_BACend
- ☐ Maize_HiCot_Benneizen
- ☐ Maize_HiCotCluster_TIGR
- ☒ Maize_HiCotMethylFilterCluster
- ☐ Maize_MethylFilter_CSHL
- ☐ Maize_MethylFilter_Orion
- ☐ Ryegrass_MethylFilter_Orion
- ☐ Ryegrass_MethylFilterCluster_Orion
- ☐ Sorghum_GSS_Klein
- ☐ Sorghum_MethylFilter_Orion
- ☐ Sorghum_V

Arrays

- ☐ Rice_ArrayConsensus_Affy57K
- ☐ Rice_ArrayOligo_NSF20K
- ☐ Rice_ArrayOligo_Yale58K
- ☐ Rice_MpssTag
- ☐ Barley_ArrayExample_Affy22K
- ☐ Maize_ArrayConsensus_Affy18K
- ☐ Maize_ArrayOligo_NSF58K
- ☐ MaizeCorro0_ArrayConsensus_Affy8K
- ☐ Sugarcane_ArrayConsensus_Affy8K
- ☐ Wheat_ArrayConsensus_Affy51K

Markers

- ☒ Rice_MarkerRFLP
- ☒ Rice_MarkerSSR
- ☒ Maize_Marker
- ☒ Sorghum_Marker
- ☒ Wheat_Marker
- ☐ nonRice_MarkerRFLP

Decorations

- ☐ Sequence
- ☐ Codons
- ☐ Start/Stop codons
- ☒ Contigs
- ☒ Ruler
- ☒ Scale
- ☐ %GC
- ☒ Show
- ☒ Show
- ☒ Show
- ☐ Show # bumps/glyphs
- ☐ Half-height glyphs
- ☐ Concise labels

Help

- Configuring
- DAS sources
- General
- Helpdesk

Width 600px
* Width 700px
Width 800px

Width 1400px
Width 1500px
Width 1600px

Be patient when making changes,, it may take a few minutes to retrieve all data.

Select options to customize the view. Closing menus will refresh your map

Maps and CMap

Identify the location of a particular gene, trait, QTL or marker - and the grass species they have been mapped to - on genetic, QTL, physical, sequence, and deletion maps .

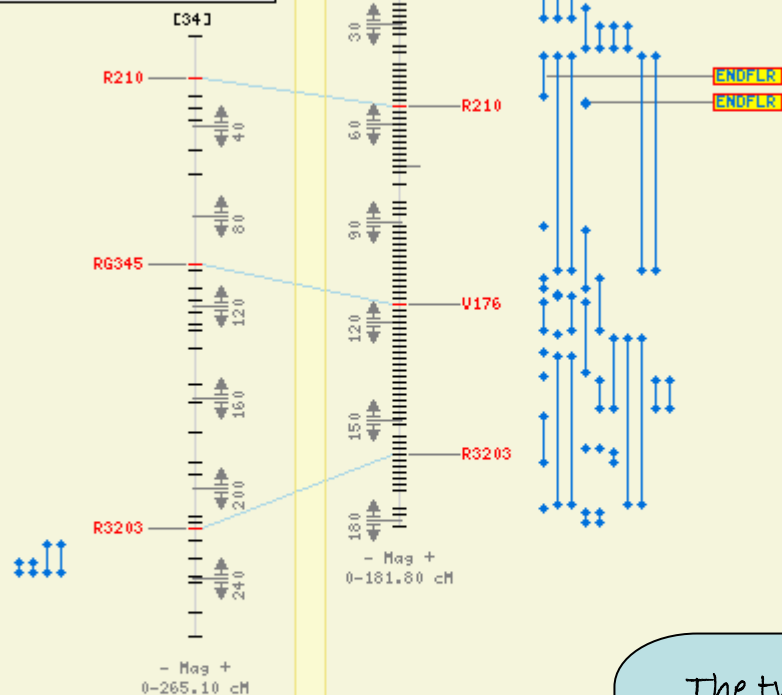
Use the CMap viewer to examine the co-linearity of a particular region in one chromosome or species to another; or infer which linkage group in one species is most conserved with a linkage group in another species. .

Determine which maps are the best for making comparisons.

Compare Maps and Customize Options

Rice
CNZU Azu/IR1552 RI QTL 2004
1
[i ? M F N]

Rice
JRGP Nip/Kas F2 QTL 2000
1
[i ? M F N]



Feature Types:

- ☐ Centromere
- ☐ Marker
- ☒ QTL

Features in red have correspondences

Evidence Types:

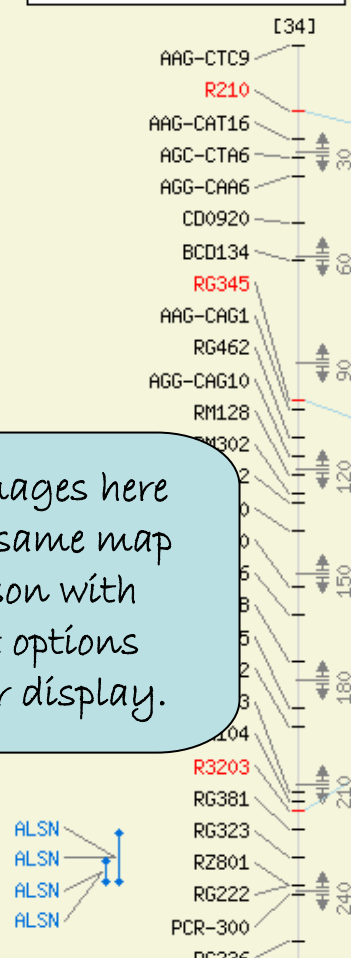
Lightblue line denotes Automated name-based

Menu Symbols:

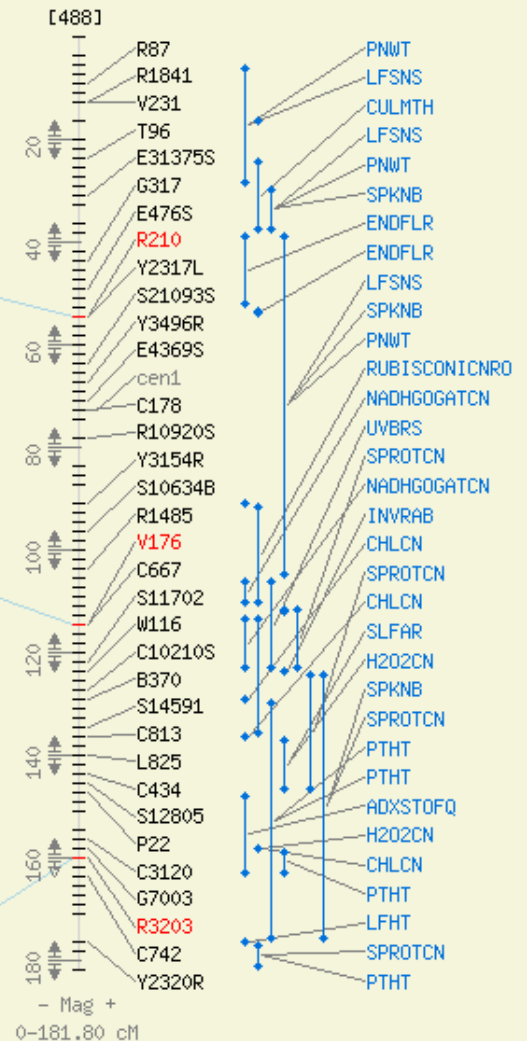
- ☒ Map Set Info
- ☒ Map Details
- ☐ Map History

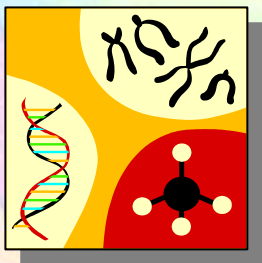
The two images here reflect the same map comparison with different options selected for display.

Rice
CNZU Azu/IR1552 RI QTL 2004
1
[i ? M F N]



Rice
JRGP Nip/Kas F2 QTL 2000
1
[i ? M F N]





Markers Database

Locate a specific marker based upon name, type or species.

View marker information, including ID, germplasm and genome positioning.

Get marker-type specific information.

Link to the Maps, Literature and Ontologies Databases.



Tab through Marker Data

Tab Through Marker Data

View Rice SSR "RM1"

Details Source/Library Map Positions (21) Associations (1) Images (0)

ID	16402333
Name	RM1
Synonyms (2)	RM001 RM1 (K)
Type	SSR
Species	Oryza sativa (Rice)
Germplasm	
Description	
Repeat Motif	
Remarks	

Details Source/Library **Map Positions (21)** Associations (1) Images (0)

Species	Map Type	Map Set	Name	Map	Start	Stop	Map Links	Comments
Oryza sativa (Rice)	Sequence	Gramene Annotated Nipponbare Sequence 2006	RM1	Chr. 1	4,633,595 bp	4,633,672 bp	View in Genome Browser View Comparative Map	
	Genetic	Cornell SSR 2001	RM1	1	29.7 cM	29.7 cM	View Comparative Map	
		KRGRP 1998	RM1	1	12.9 cM		View Comparative Map	
	QTL	AGEBC KDM105/CT999 RI QTL 2000	RM1 (K)	1c	79.4 cM		View Comparative Map	
		Brazil BG90-2/RS16 QTL 2002	RM1	1	5.5 cM		View Comparative Map	
							View Comparative Map	

Details Source/Library Map Positions (21) **Associations (1)** Images (0)

Direction	Name	Type	Species	Analysis	Assoc. Type
From	RM1	SSR Primer Pair	Oryza sativa	primer_pair	primer_pair

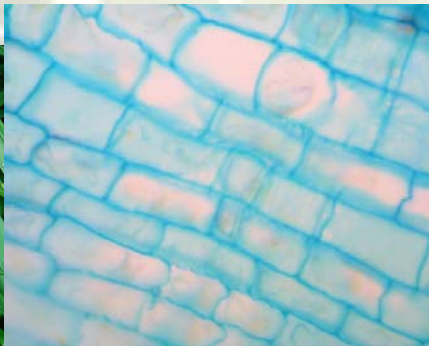
QTL Database

QTL (Quantitative Trait Loci) are a statistical creation that identifies a particular region of the genome as containing a gene (or genes) that is associated with the trait being assayed or measured.

Learn which trait is associated with a QTL, find where it is located on a map, and construct comparisons with other maps.

Determine which markers delimit a QTL

Determine what genes are located in the same region as other genes



Trait Categories

Traits at Gramene are categorized according to:

Abiotic stress: Traits related to stresses from abiotic environment, e.g., water, light, temperature, or chemical.

Anatomy: Traits directly measuring plant parts such as root, stem or leaf.

Biochemical: Biochemical and physiological traits, e.g., enzyme activity.

Biotic stress: Traits related to stresses from pests and pathogens.

Development: Traits related to plant and plant part development. Also includes maturity related traits.

Quality: Traits of economic importance that may affect product quality.

Sterility or fertility: Traits related to male and female flower sterility or fertility, including incompatibility.

Vigor: Traits related to growth and dormancy.

Yield: Traits contributing directly to yield based on economic value.

QTL Data

Details for QTL "CQA2" (vegetative growth time)

QTL Accession ID	CQA2									
Species	Oryza sativa (Rice)									
Trait Symbol	VGTM									
Trait Name	vegetative growth time									
Species Ontology	GR_tax:013681									
Trait Ontology	TO:0000369									
Published Symbol	QTL2b									
Trait Synonym(s)										
Trait Category	Development									
Chromosome	2									
Mappings	Species	Map Type	Map Set	Name	Map	Start	Stop	Map Links	Method	
	Oryza sativa (Rice)	QTL	FAUF Gui630/Twj DH QTL 2001	VGTM	2	69	69	View in Mappings DB View Comparative Map	Experimental	
Comments	The trait VGTM, is defined as the number of days spent in the vegetative growth stage by the plant. This growth phase also contributes to the total number of days to heading. The QTL was detected by Multiple-trait Composite Interval Mapping (MCIM).									
DBXRefs	Gramene Literature	Zhou-Y Li-W Wu-W Chen-Q Mao-D Worland-A-J, Genetic dissection of heading time and its components in rice., Theoretical and applied genetics, 102(8), 2001, pp. 1236-1242								

Gramene Diversity

Gramene Genetic Diversity database contains SSR and SNP allelic data and passport descriptions for rice, maize and wheat germplasms. It also holds phenotypic data for maize.

The ultimate goal is to make this database a source of rice, maize, and wheat bio-information from/for evolutionary, domestication, association, and genetic diversity studies. It also could potentially be useful for applications such as germplasm management, marker assisted selection and DNA-based variety identification.



Diversity Data

[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

View Germplasm "IR36"

[Search Again](#)

Accession name	IR36	Collector	
Institute(s) holding accession	IRGC/IRRI	Collection number	
Accession number	RA5352	Collection source	
Synonym(s)	IRGC 30416 (Search at IRIS/IRRI)	Collection code	
Stock source	McCouch	Collection/release date	
Stock number	RA5352	Locality	San Ildefonso, Bulacan
Germplasm type	N/A	City	
Genus	Oryza	Elevation	15
Species	sativa	Latitude	15° 4' N
Subspecies	indica	Longitude	120° 55' E
Subtaxa	indica	State/province	Luzon
Taxonomy xref	GR_tax:013682	Country	Phillipines

Experiments

There is allele data for germplasm "RA5352" from 1 experiment.

Title	Design	Polymorphism Type	Allele Scoring Protocol	Producer	Originator	Comments	
Genetic structure and diversity in Oryza sativa L.	234 rice accessions from wide geographical regions of the world	SSR	PCR products were size separated by capillary electrophoresis using ABI 3700 DNA analyzer; SSRs were analysed with GenScan 3.1.2 software and scored with Genotyper 2.5 software.		McCouch/Tai	Prediction of population structure was model-based (STRUCTURE) and based on data from 169 genomic SSRs. For more information, see the paper by Garris et al., 2005 .	Show Allele Data

[Phenotype Search](#) | [GDPC Browser](#) | [Help](#) | [Tutorial](#) | [FAQ](#)
Genetic structure and diversity in Oryza sativa L."

1 of 7 | Next

Number	Locus name	Genotype	View All Genotypes on Marker
IR36	RM1	86, 108	All Genotypes On "RM1"
IR36	RM2	167	All Genotypes On "RM2"
IR36	RM5	112	All Genotypes On "RM5"
IR36	RM7	181	All Genotypes On "RM7"
IR36	RM11	139	All Genotypes On "RM11"
IR36	OSR13	94	All Genotypes On "OSR13"
IR36	RM13	139	All Genotypes On "RM13"
IR36	RM16	181	All Genotypes On "RM16"
IR36	RM17	157, 183	All Genotypes On "RM17"
IR36	RM19	225	All Genotypes On "RM19"
IR36	RM21	159	All Genotypes On "RM21"
IR36	RM22	195	All Genotypes On "RM22"
IR36	RM25	145	All Genotypes On "RM25"
IR36	RM31	138	All Genotypes On "RM31"
IR36	RM44	103, 111	All Genotypes On "RM44"
IR36	RM55	227	All Genotypes On "RM55"
IR36	RM72	159	All Genotypes On "RM72"
IR36	RM85	104	All Genotypes On "RM85"
IR36	RM87	151	All Genotypes On "RM87"
IR36	RM104	238	All Genotypes On "RM104"
IR36	RM105	126	All Genotypes On "RM105"
IR36	RM106	293	All Genotypes On "RM106"
IR36	RM108	74	All Genotypes On "RM108"
IR36	RM109	87	All Genotypes On "RM109"
IR36	RM112	422	All Genotypes On "RM112"





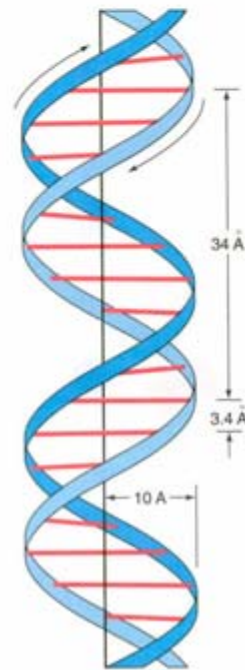
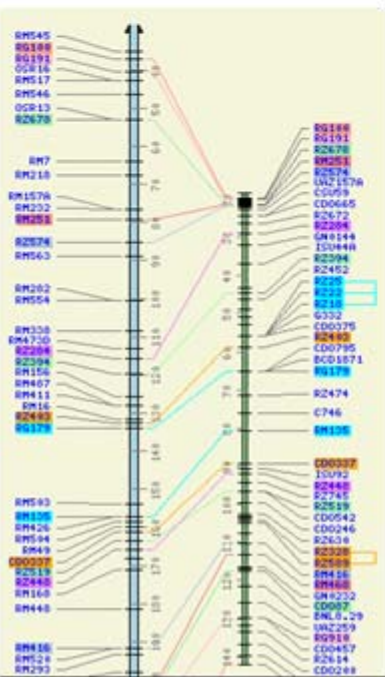
Gene & Allele Database

Retrieve descriptions of alleles associated with morphological, developmental, and agronomically important phenotypes and variants of physiological characters, biochemical functions and isozymes.

Get a gene's information, including information on name of the gene, gene symbol, related phenotypes (traits), images, allele and germplasm.

Link to Literature and Ontology databases.

View associated maps and sequencing data.




Summary for Gene: *d1* (GR:0060184)

General Info | Allele and Germplasm | Sequence Association | Map Position | Ontology Association | References


General Information	
Accession	GR:0060184
Gene Symbol	<i>d1</i>
Gene Name	<i>dwarf-1</i>
Gene Synonym(s)	<i>dwf1</i> , daikoku dwarf, G-protein alpha subunit, GA1, GP-alpha-1, Guanine nucleotide-binding protein alpha-1 subunit, RGA1
Species	<i>Rice</i>
Chromosome No.	5
Gene Type	CDS (Protein coding)
Has Phenotype	yes
Description	A typical small grain dwarf type with short and stout stems, short, sinuate but broad leaves with dark green color, erect and compact panicles and small, round floral glumes. Internodes are thick and sometimes the second internode does not elongate.

1.




1. Dwarf type of an isogenic line (*d1*) in the 'Shiokari' background.

2.



2. Dwarf plant with dark green leaves and small grains (on right).

3.



3. Dwarf plant with dark green leaves and small grains (on right).

The protein is encoded by a single copy gene in rice. It is the alpha subunit of the heterotrimeric G-protein complex. Immunoblot analysis using anti-RGA1 revealed that the RGA1 protein is most abundant in mature roots. It exists at particularly high levels in the immature embryo after pellicle highly reduced hypersensitive response to infection by an avirulent race of rice blast. A leaves of the mutants infected with rice blast was delayed for 24 h relative to the wild type. Expression induced by sphingolipid elicitors (SE) were strongly suppressed in *d1* cell. Active OsRac1, a small GTPase Rac of rice, in *d1* mutants restored SE-dependent defense. The gene expression was induced by an avirulent race of rice blast and SE applied.

Allele
d1.wt1, *d1.1*, *d1.2*, *d1.3*, *d1.4*, *d1.5*, *d1.6*, *d1.7*, *d1.8*, *A59*, *C19*, *Nipponbare*, *D25*, *E017*, *Akage-1*, *CM392*, *Kin*, *CM1361-1*, *DK22*, *ID-1*, *DKT-1*, *DKT-2*, *Daikoku*, *HO532*, *HO541*, *HO552*, *CM382*, *CM1792*, *T65d1* (Taichung 65-Daikoku dwarf)

Germplasm

Sequence Association	
Protein	Gramene Protein: P49083 , Q43604
Nucleotide (DNA)	GenBank Nucleotide: AB026176 , AB026177 , AB026178 , AB026179 , AB026180 , AB026181 , AB026182 , AB026183 , AB026184 , AB026185 , AB026186 , AB026187 , AB026188 , AB026189 , AB026190 , AB026191 , AB026192 , AB026193 , AB026194 , AB026195 , AB026196 , AB026197 , AB026198 , AB026199 , AB026200 , AB026201 , AB026202 , AB026203 , AB026204 , AB026205 , AB026206 , AB026207 , AB026208 , AB026209 , AB026210 , AB026211 , AB026212 , AB026213 , AB026214 , AB026215 , AB026216 , AB026217 , AB026218 , AB026219 , AB026220 , AB026221 , AB026222 , AB026223 , AB026224 , AB026225 , AB026226 , AB026227 , AB026228 , AB026229 , AB026230 , AB026231 , AB026232 , AB026233 , AB026234 , AB026235 , AB026236 , AB026237 , AB026238 , AB026239 , AB026240 , AB026241 , AB026242 , AB026243 , AB026244 , AB026245 , AB026246 , AB026247 , AB026248 , AB026249 , AB026250 , AB026251 , AB026252 , AB026253 , AB026254 , AB026255 , AB026256 , AB026257 , AB026258 , AB026259 , AB026260 , AB026261 , AB026262 , 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Proteins Database

Provides collective information on proteins from grasses (family *Poaceae/Gramineae*), and are annotated according to Gene Ontology and Plant Ontology.

- Gene Ontology (GO)
 - Molecular function of the gene product.
 - Biological process in which the gene product is involved.
 - Cellular component where the gene product is localized.
- Plant Ontology
 - Plant structure where the gene is expressed (PO)
 - Plant growth stage at which the gene is expressed (GRO)

*** Only rice (*Oryza*) protein entries are manually curated.**

Proteins



Find a protein and conduct a BLAST query on it.

Determine the molecular function, biological process or cellular location of a particular rice protein.

Find protein sequence information and orthologs from other species.

Find which proteins are members of a protein family (Pfam & PROSITE).

Link to ontology and literature databases.

Protein Detail Page: General Information

[General Information](#) | [Associations](#) | [Similarity to Other Proteins](#) | [Features](#) | [References Used for Curation](#) | [FASTA Sequence](#)

General Information about P93436

Accession	P93436
Name	Alcohol dehydrogenase class 3
Symbol	ADHIII
Synonym(s)	FALDH, FDH, GSH-FDH, Glutathione-dependent formaldehyde dehydrogenase
E.C. Number(s)	1.1.1.1, 1.2.1.1
Gene Name(s)	<i>AdhIII</i>
Organelle	Not available
Best hits to TIGR rice gene models	LOC_Os02g57040 Click here to generate a BLASTP query

Accession Numbers	GenBank	SWISSPROT
	P93436	P93436
Organism(s)	Species	Cultivar
	Oryza sativa (indica cultivar-group)	Not available

Associations

Term Type	Term	Reference	Evidence
Molecular Function	zinc ion binding		
	formaldehyde dehydrogenase activity (GO:0004472)	Viridiplantae Green plants -Embryophytes (plants) -Magnoliophytes (flowering plants) -Monocots Grasses Rice Maize Sorghum Wheat Barley Rye Oat Sugarcane -Dicots Brassicaceae Arabidopsis Fabaceae (Legumes) Solanaceae Cucurbitaceae	
	alcohol dehydrogenase	Others : Fungi Metazoa	
	alcohol dehydrogenase, zinc-dependent	3D protein structures : BLink from NCBI Sequence Annotated by Structure (SAS)	
Biological Process	regulation of carbohydrate metabolism		
Cellular Component	cytoplasm (GO:0005832)		
Keywords	NAD , Oxidoreductase		

Similarity to Other Proteins

Protein Features

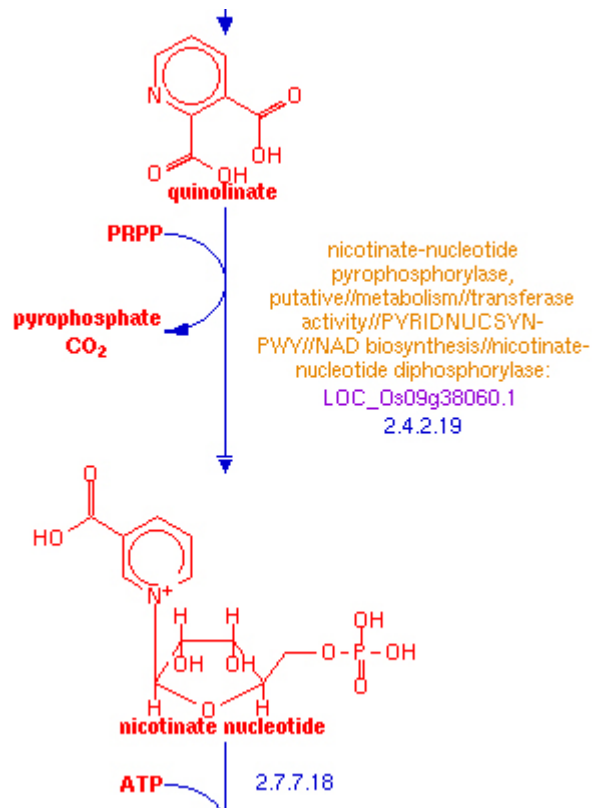
Pfam (Infor)	PF00107 ; adh_zinc	All Members of this Family
	PF08240 ; ADH_N	All Members of this Family
Prosite (Infor)	PS00059 ; ADH_ZINC	Residues from 70 : GHEAAGIVESVGEGV All Members of this Family
Physio-chemical features	P93436	
ProtoMap (Info)	ADHX_ORYSA	

References Used for Curation

- [Dolferus-R Osterman-J-C Peacock-W-J Dennis-E-S](#)
Cloning of the Arabidopsis and rice formaldehyde dehydrogenase genes: implications for the origin of plant ADH enzymes
Genetics, 1997, vol.146, pp.1131-1141
- [Jaiswal-P Ren-L Zhao-W Schmidt-S-C Ratnapu-K-K Lincoln-S McCouch-S](#)
Gene Ontology Annotation By The Gramene Database
Gramene database, 2003, vol.1, pp.1-1

[Search the Literature Database for Additional References](#)

Pathways (RiceCyc)



RiceCyc allows biochemical pathways to be analyzed and visualized.

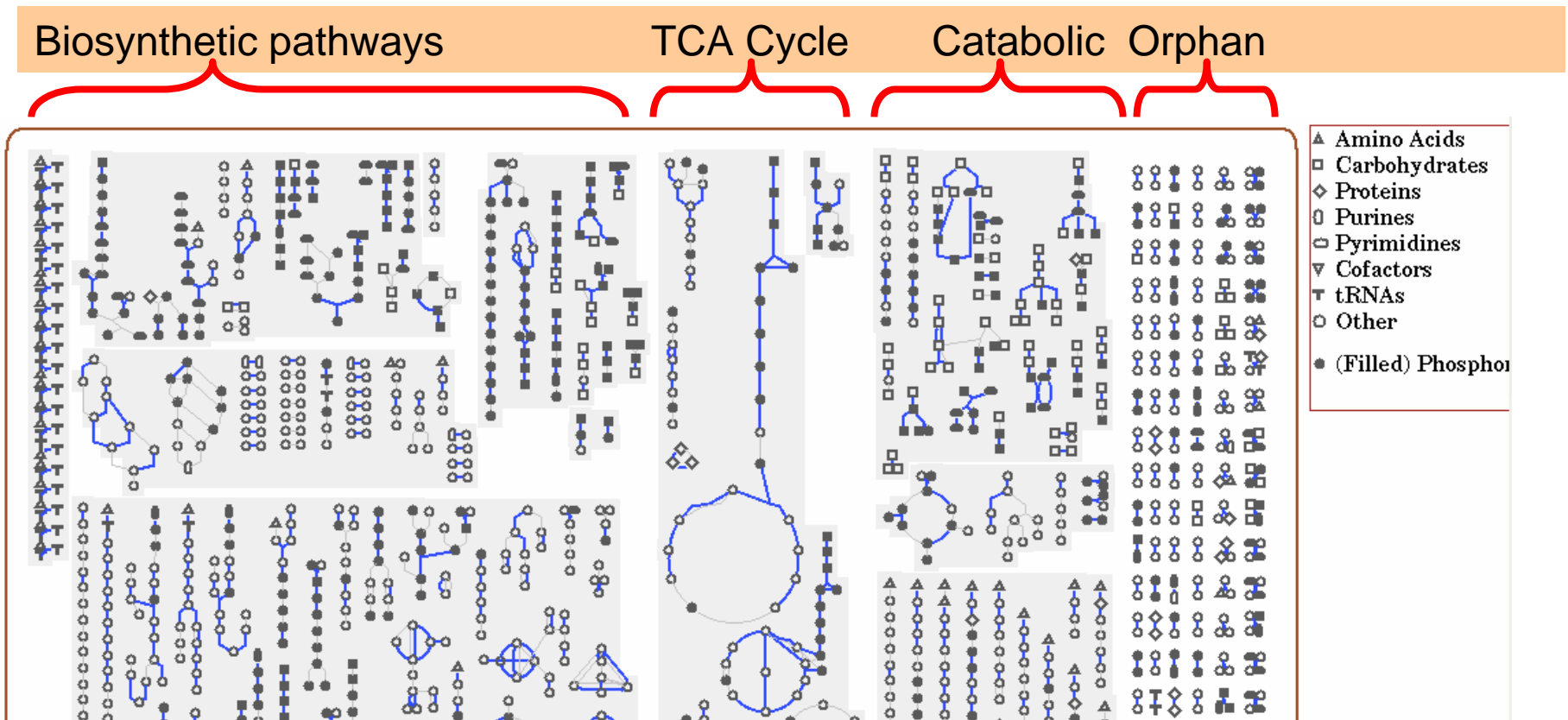
To access a more detailed overview of the program's features and the data contained within please refer to the Pathways links available from the Pathways home page.

Gramene has incorporated the latest TIGR 4 genome into this release to create an *Oryza sativa* specific pathway dataset.

Data is under development and subject to change. If you do see any errors in the dataset please feel free to contact us through the feedback provided at the top of Gramene webpages.



Metabolic Map Overview



The flow of the pathway is from the top of the page to the bottom

Ontologies

This database is a collective resource of structured controlled vocabularies (Ontologies) for knowledge domains and their associations.

Plant Ontology ([PO](#))

Plant Structure (morphology, organs, tissue and cell types)*

Growth stages (plant growth and developmental stages) ([GRO](#))

Trait Ontology ([TO](#))

Plant traits and phenotypes

Gene Ontology ([GO](#))

Molecular function

Biological process

Cellular component

Environment Ontology ([EO](#))

Gramene's taxonomy ontology ([GR_tax](#))

Associations:

Find Ensembl rice genes (from TIGR's rice genome assembly), proteins from SWISSPROT-TrEMBL representing Poaceae (grass) family, rice genes, QTL and map sets.

Note: Remember that different ontologies are for different purposes and do not overlap with each other.

For more information on each ontology type please visit the current ontologies section at Gramene

Ontologies

- Using ontologies will assist users in their searches.
- An Ontology is a glossary of keywords arranged in a structured order/network based on the biological concept that describes the keyword's relationship in an ontology tree.
- Researchers are working towards a standardized ontology, thus facilitating searching in different databases.






Ontology Relationships and Associations

 [Term](#) | [Annotations](#)

Summary for TO Term: *cold tolerance* (TO:0000303)

Term Name	cold tolerance
Synonym	COLDTL, CTol.
Aspect	Trait
Definition	Tolerance to cold temperatures if plant is exposed to below permissive temperature limits. Observe differences in vigor along with subtle changes in leaf color. The optimum time to make observations would be the seedling, tillering (sensu Poaceae), flowering and mature stages.
External References	GR:pj IRRI:SES

Derivation

- [all \(all\)](#) #391761 
 - [i] [trait ontology \(TO:0000387\)](#) #12358 
 - [i] [stress trait \(TO:0000164\)](#) #1995 
 - [i] [abiotic stress trait \(TO:0000168\)](#) #1343 
 - [i] [temperature response trait \(TO:0000432\)](#) #74 
 - [i] **cold tolerance** (TO:0000303) #49

Parent Term (1)

- [i] [temperature response trait \(TO:0000432\)](#)

Total Number of Annotations:	49 objects, 49 associations gene (18) QTL (31)
gene:	Oryza sativa (18)
QTL:	Oryza sativa (31)

Literature



Literature searches are a good option for beginning your Gramene search.

Search for citations on rice, as well as other species.

Literature search results provide links to publication sources and other Gramene databases where available.




Literature

Find articles about genes, proteins, QTL, markers, or ontology.

Link to maps described in the given citations, as well as the gene, QTL, protein and marker databases.

Literature detail

Gramene's ID for that reference

Search result	
Reference ID	11062
Title	The Oryza bacterial artificial chromosome library resource: Construction and analysis of 12 deep-coverage large-insert BAC libraries that represent the 10 genome types of the genus Oryza
Source	Genome research , 2006, 16, pp.140-147
Authors	Ammiraju-J-S , Luo-M , Goicoechea-J-L , Wang-W , Kudrna-D , Mueller-C , Talag-J , Kim-H , Sisneros-N-B , Blackmon-B , Fang-E , Tomkins-J-B , Brar-D , Mackill-D , McCouch-S , Kurata-N , Lambert-G , Galbraith-D-W , Arumuganathan-K , Rao-K , Walling-J-G , Gill-N , Yu-Y , SanMiguel-P , Soderlund-C , Jackson-S , Wing-R-A
Abstract	<p>Rice (<i>Oryza sativa</i> L.) is the most important food crop in the world and a model system for plant biology. With the completion of a finished genome sequence we must now functionally characterize the rice genome by a variety of methods, including comparative genomic analysis between cereal species and within the genus <i>Oryza</i>. <i>Oryza</i> contains two cultivated and 22 wild species that represent 10 distinct genome types. The wild species contain an essentially untapped reservoir of agriculturally important genes that must be harnessed if we are to maintain a safe and secure food supply for the 21st century. As a first step to functionally characterize the rice genome from a comparative standpoint, we report the construction and analysis of a comprehensive set of 12 BAC libraries that represent the 10 genome types of <i>Oryza</i>. To estimate the number of clones required to generate 10 genome equivalent BAC libraries we determined the genome sizes of nine of the 12 species using flow cytometry. Each library represents a minimum of 10 genome equivalents, has an average insert size range between 123 and 161 kb, an average organellar content of 0.4%-4.1% and nonrecombinant content between 0% and 5%. Genome coverage was estimated mathematically and empirically by hybridization and extensive contig and BAC end sequence analysis. A preliminary analysis of BAC end sequences of clones from these libraries indicated that LTR retrotransposons are the predominant class of repeat elements in <i>Oryza</i> and a roughly linear relationship of these</p>
Cross-reference	

Click here to link to cross-referenced resources.

Please note:

To request reprints, please contact the authors or the source/journal website. Due to copyright issues Gramene does not distribute reprints.

BLAST

- BLAST is a tool.
- Search for sequence similarity matches in the Gramene database.
- Select the best target database for your search.
- Choose the best algorithm for your search.
- Fine-tune search parameters.
- Display match results.

BLAST Results

new SETUP CONFIG RESULTS **DISPLAY**

refresh Online Help
FAQ Tutorial

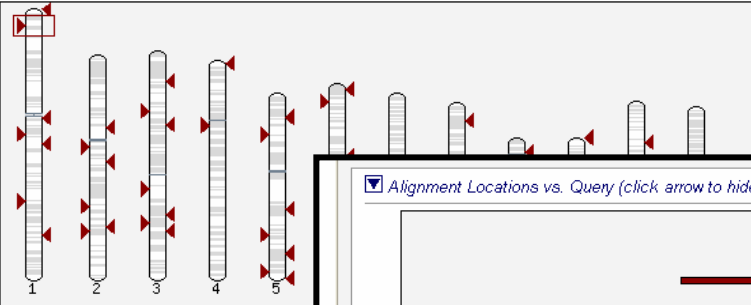
Summary

- setup
 - Rice
 - Genomic sequence
 - BLASTN
 - Low sensitivity
- configure

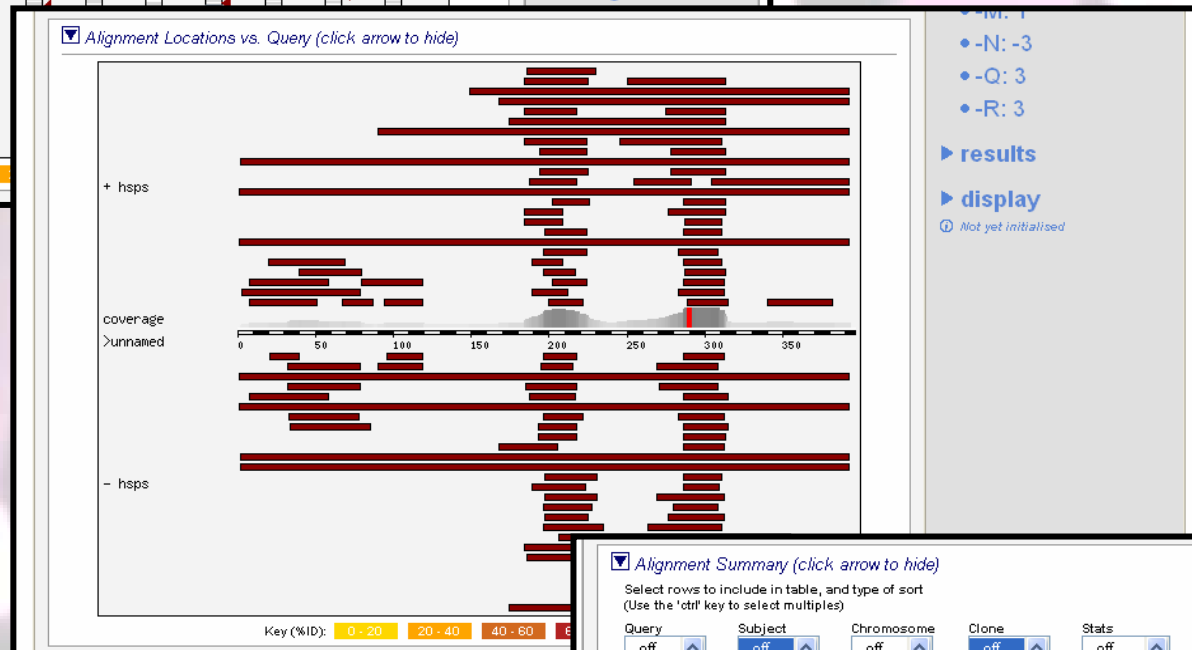
Displaying unnamed sequence alignments vs Rice LATESTGP database

Showing top 100 alignments of 167, sorted by Raw Score

☒ Alignment Locations vs. Karyotype (click arrow to hide)



Key (%ID): 0 - 20



☒ Alignment Summary (click arrow to hide)

Select rows to include in table, and type of sort
(Use the 'ctrl' key to select multiples)

Query	Subject	Chromosome	Clone	Stats	Sort By...
<input type="checkbox"/> _off	<input type="checkbox"/> off	<input type="checkbox"/> off	<input type="checkbox"/> off	<input type="checkbox"/> off	>Clone
<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Score	<Score
<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> E-val	>Score

Links	Query Start	Chromosome Name	Start	Stats Score	E-val
[A] [S] [G] [C]	1	Chr:1	2817113	379	1.1e-217
[A] [S] [G] [C]	1	Chr:1	2834924	343	3.2e-196
[A] [S] [G] [C]	1	Chr:1	2871274	339	4.6e-193
[A] [S] [G] [C]	2	Chr:1	2841537	334	8.9e-190
[A] [S] [G] [C]	2	Chr:1	2854476	334	8.9e-190
[A] [S] [G] [C]	1	Chr:1	2883597	331	6.8e-188
[A] [S] [G] [C]	2	Chr:1	2888984	300	6.8e-169
[A] [S] [G] [C]	90	Chr:5	28350554	216	3.8e-155



GrameneMart

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.

Data mining - apply filters and select output

new

START

FILTER

OUTPUT

export

back

export

FeaturesStructuresSequences

REGION:

Chromosome Attributes

☒ Chromosome Name

☒ Start Position (bp)

☒ End Position (bp)

☒ Strand

GENE:

Gene Attributes

☒ TIGR Gene LOC ID

☐ TIGR Transcript LOC ID

☒ Transcript count

☐ Description

External References

☐ GO ID

☐ GO description

☐ GO evidence code

MULTI SPECIES:

Arabidopsis Homolog Attributes

☐ Arabidopsis TIGR Gene ID

☐ Arabidopsis Chr Name

☐ Arabidopsis Chr Start (bp)

☐ Arabidopsis Chr End (bp)

☐ Arabidopsis Chr Strand

☐ Arabidopsis Homology Description

☐ Arabidopsis DN/DS

☐ Arabidopsis % Pep Covered

☐ Arabidopsis % Pep ID

Maize Homolog Attributes

☐ Maize FGENESH Gene ID

☐ Maize Clone

☐ Maize Clone Start (bp)

☐ Maize Clone End (bp)

☐ Maize Clone Strand

☐ Maize Homology Description

☐ DN/DS

☐ Maize % Pep Covered

☐ Maize % Pep ID

bio::mart

refresh

Help Desk

Tutorial

Summary

start

Dataset: Oryza sativa genes

58752 Entries Total

filter

Chromosome name: 12

Evidence code: IEA

Molecular function

Select the output format:

☒ HTML

☐ Text, fixed width

☐ Text, comma separated

☐ Text, tab separated

☐ MS Excel

☐ 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

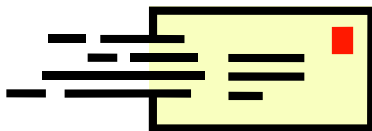
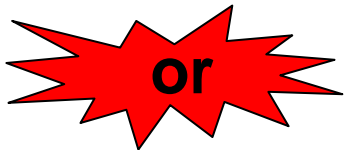
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