A Comparative Genomic Mapping Resource for Grains

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 substantially 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.

The technological core of Gramene is the Oracle database management system, a commercial relational database system that is stable and well supported.

Bioinformatics is…

- Computer or information science combined with biology:
  - nucleotide and protein sequences
  - taxonomy info
  - genomic info – model organisms
  - maps

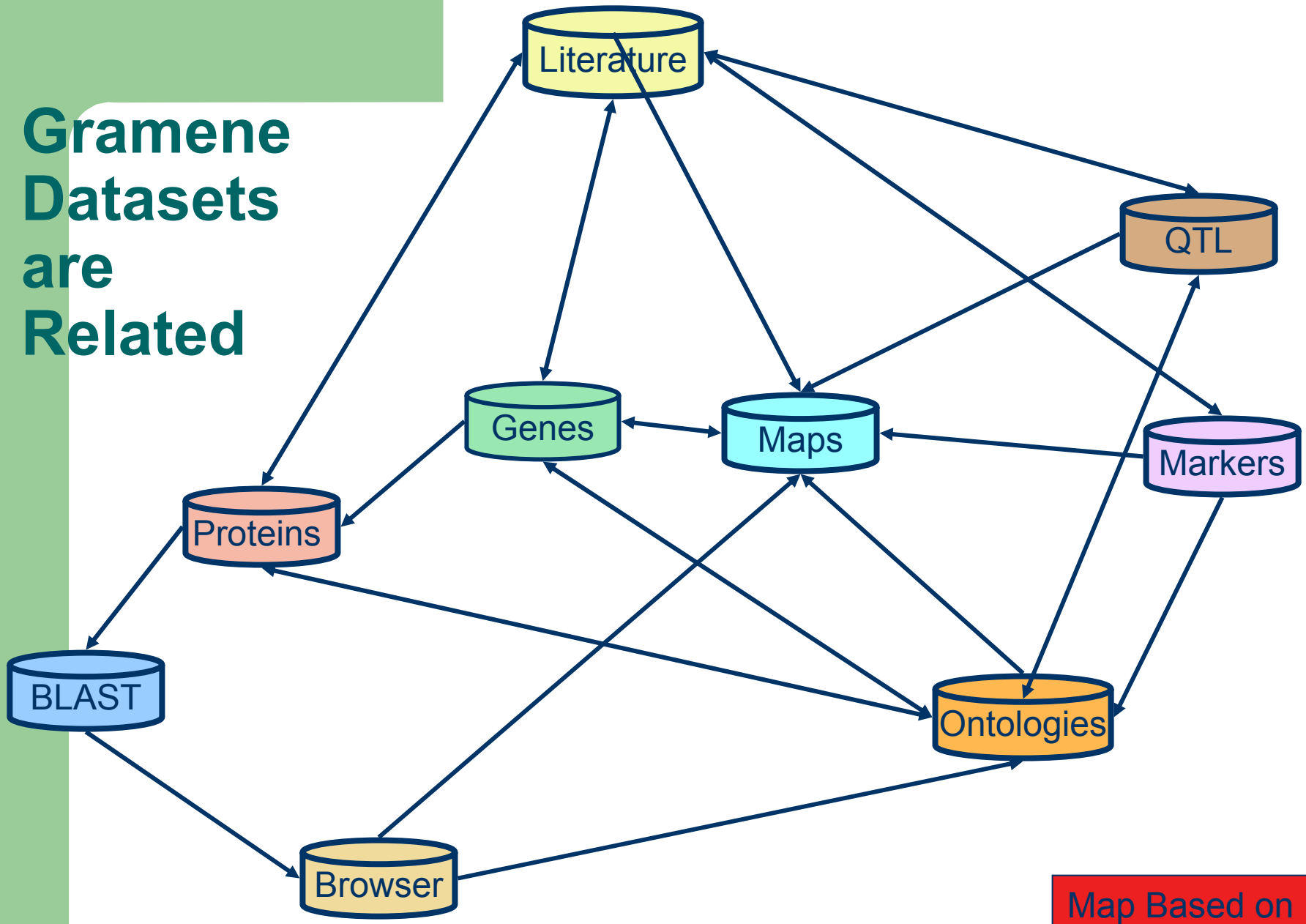
Uses of bioinformatics…

- Disease research
- Disease prevention
- Studying the origin of life and evolution
- Feeding the world: Bioengineered food, faster and better plant breeding
- Forensics
- Preserving biodiversity
- Industry

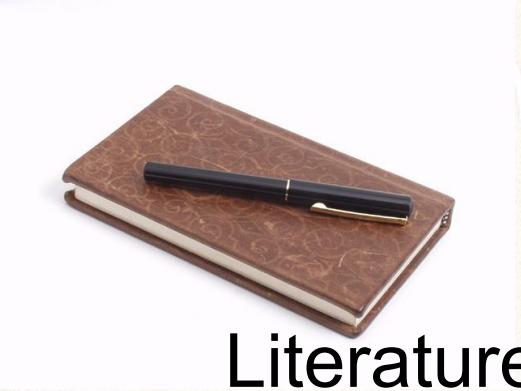
Major Databases

- Human Genome
- Rat Genome
- Mouse Genome
- Yeast
- Fruitfly
- Worm Base
- Gramene
- GrainGenes
- Maize GDB
- NCBI/GenBank
- Arabidopsis (TAIR)

Gramene Datasets are Related



Map Based on Module Data

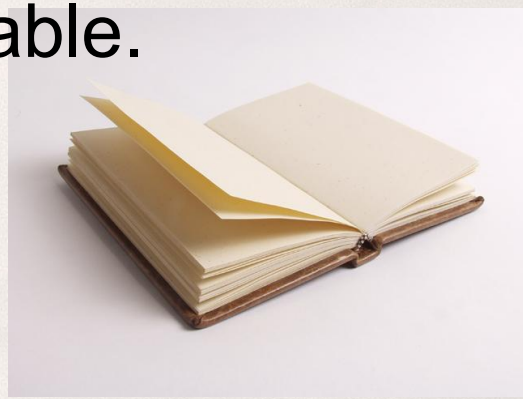


Literature

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

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

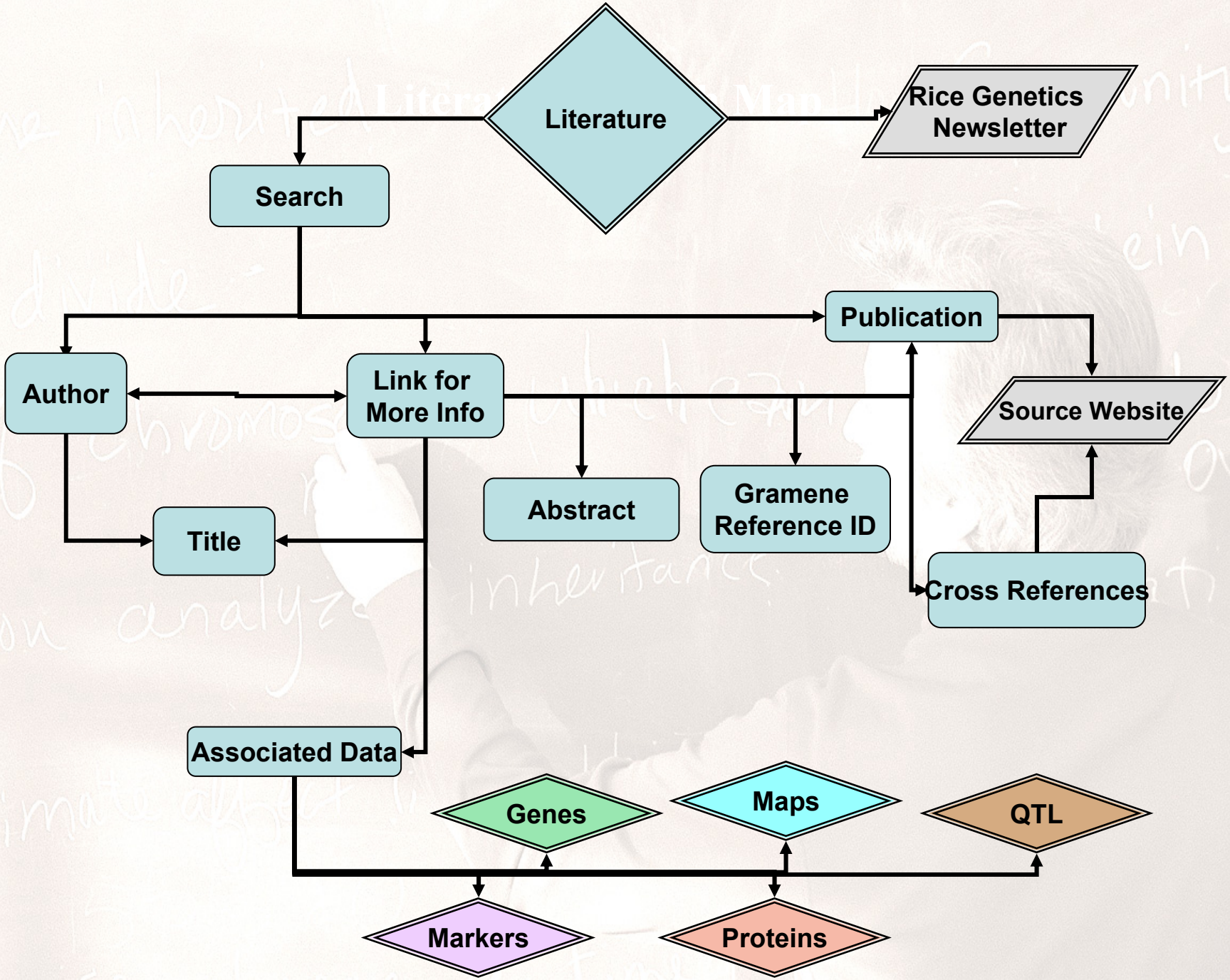
Literature search results provide links to publication sources and other Gramene databases where available.



Literature

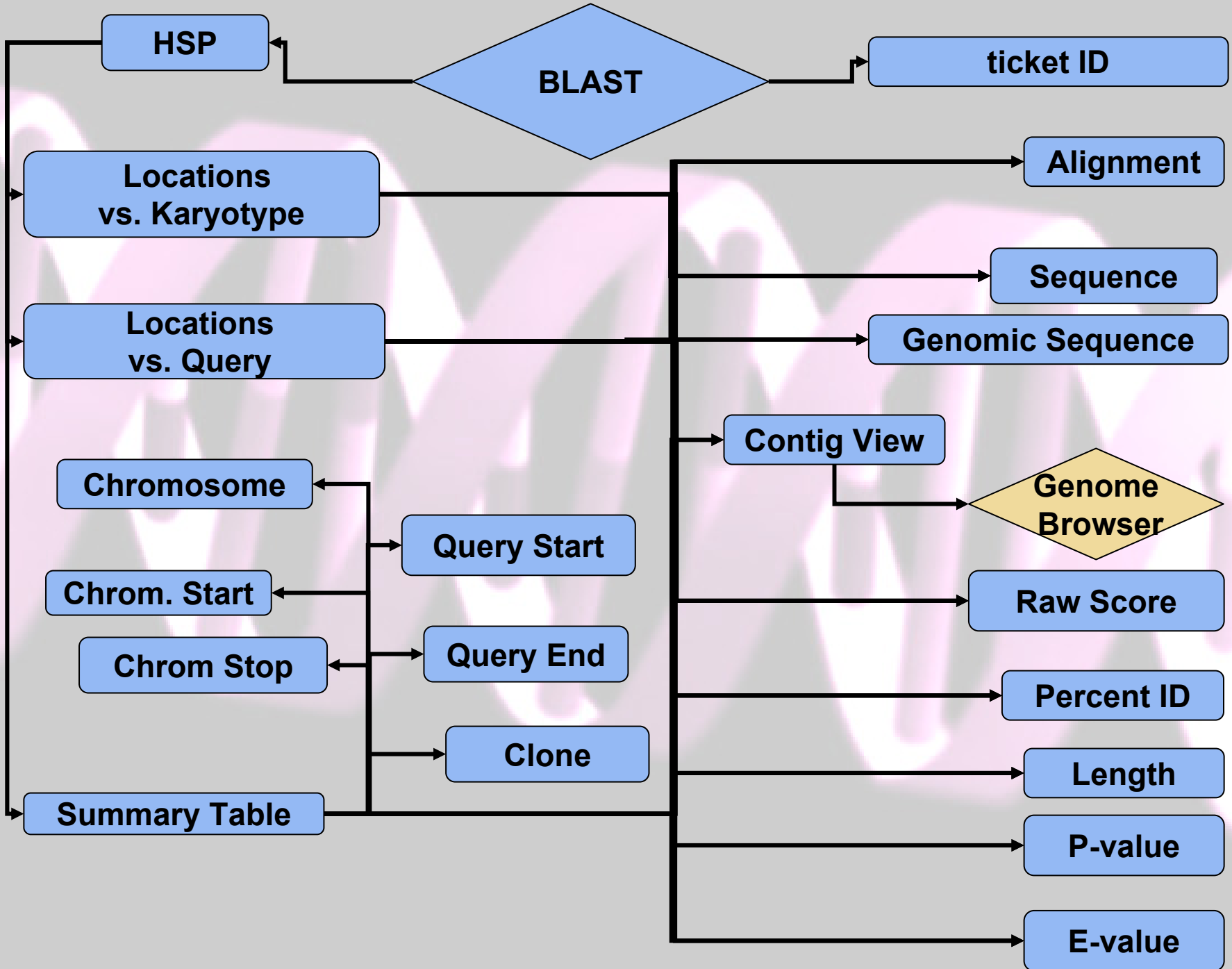
Find articles about genes, proteins, QTL, markers, or ontology.

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


Literature
Rice Genetics Newsletter
Search
Publication
Author
Link for More Info
Source Website
Abstract
Gramene Reference ID
Title
Cross References
Associated Data
Genes
Maps
QTL
Markers
Proteins

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.


HSP
BLAST
ticket ID
Locations vs. Karyotype
Locations vs. Query
Alignment
Sequence
Genomic Sequence
Contig View
Genome Browser
Chromosome
Chrom. Start
Chrom Stop
Query Start
Query End
Clone
Raw Score
Percent ID
Length
P-value
E-value
Summary Table

Gramene Genome Browser

- ***Genome browser is a dynamic graphical display used to browse genomes.***
- ***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.***

Genome Browser

Link to maps and ontologies from the genome browser.

View synteny between rice and maize

Upload your data to view in a karyotype ideogram.

Download genetic information

Customize your results specifically for the information you need.

Browse a Chromosome or View a Synteny Map

Oryza sativa (japonica) Genome Browser v18

Current Release TIGR v3

- TIGR pseudomolecule assembly release 3 of IRGSP finished sequence.
- Clones which were not used in the assembly have been mapped as features, and are listed here
- Feature data sets mapped to the genome can be viewed in summary and detailed form.
- Putative orthologs between rice, *Arabidopsis* and maize gene models were generated using Ensembl's compara pipeline.
- Syntenic regions between the maize FPC map and the rice genome assembly were estimated, and loaded into Ensembl.

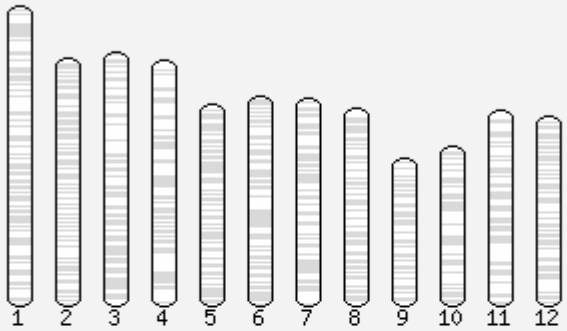
Example entry points

- Gene: LOC_Os01g14200
- Transcript: LOC_Os08g23430.1
- Chromosome: 12
- Contig: AP003727

Lookup

Chr: 1 from 1 - 100000 Go

Browse a Chromosome



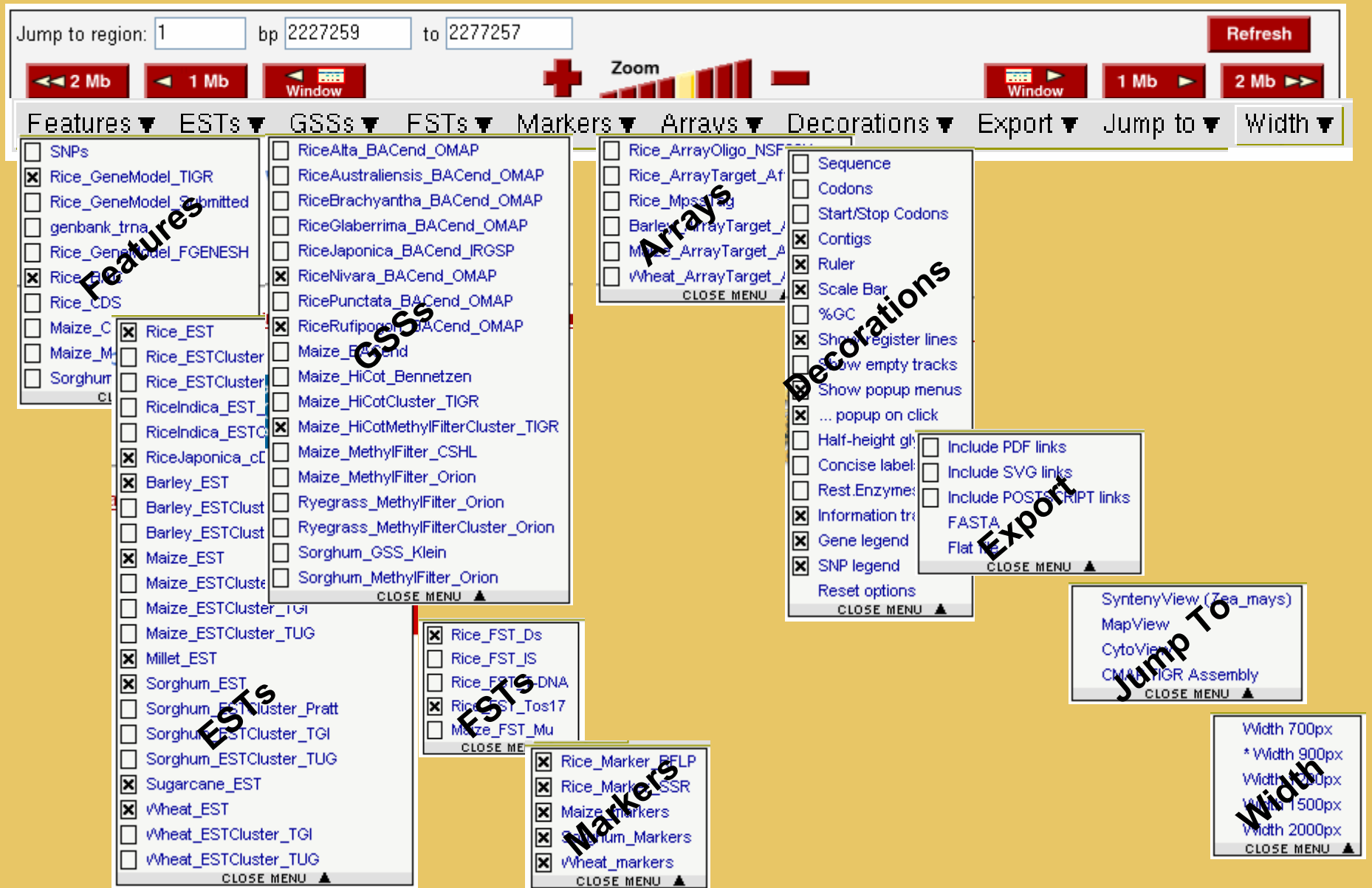
Rice Synteny Vs Maize FPC Map

Rice Chr 1 vs. Maize Go

- Rice Chr 1 vs. Maize
- Rice Chr 2 vs. Maize
- Rice Chr 3 vs. Maize
- Rice Chr 4 vs. Maize
- Rice Chr 5 vs. Maize
- Rice Chr 6 vs. Maize
- Rice Chr 7 vs. Maize
- Rice Chr 8 vs. Maize
- Rice Chr 9 vs. Maize
- Rice Chr 10 vs. Maize
- Rice Chr 11 vs. Maize
- Rice Chr 12 vs. Maize

Rice-japo ... rabidopsis

Customize options for Contig View



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:

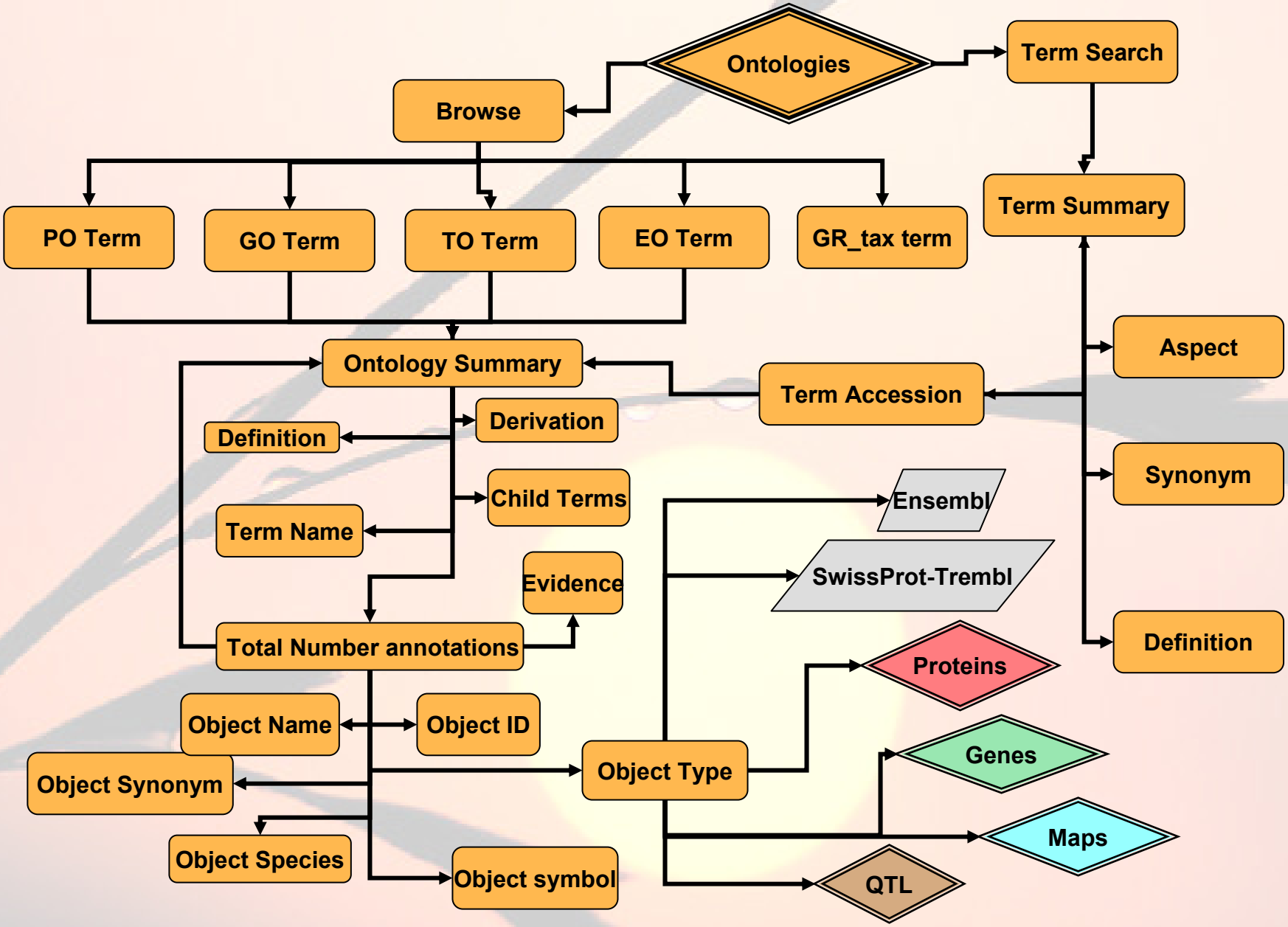
- Find Ensembl rice genes (from TIGR's rice genome assembly), proteins from SWISSPROT-TrEMBL representing Poaceae (grass) family, rice genes, QTL and map sets.

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

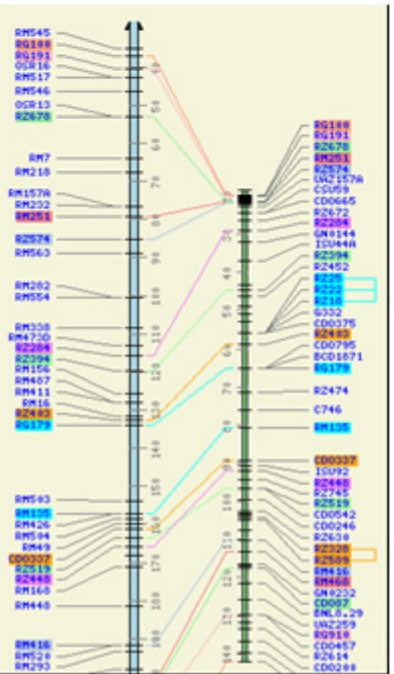
- Using ontologies will assist users in their searches.
- An Ontology is a glossary of keywords arranged in a structured order/network based on the biological concept that describes the keyword's relationship in an ontology tree.
- Researchers are working towards a standardized ontology, thus facilitating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


Ontologies
Term Search
Browse
Term Summary
PO Term
GO Term
TO Term
EO Term
GR_tax term
Aspect
Ontology Summary
Term Accession
Derivation
Definition
Synonym
Child Terms
Ensembl
Term Name
SwissProt-Trembl
Evidence
Definition
Total Number annotations
Proteins
Object Name
Object ID
Genes
Object Type
Object Synonym
Maps
Object Species
Object symbol
QTL

A Comparative Mapping Resource

GRAMENE

Gene & Allele Database

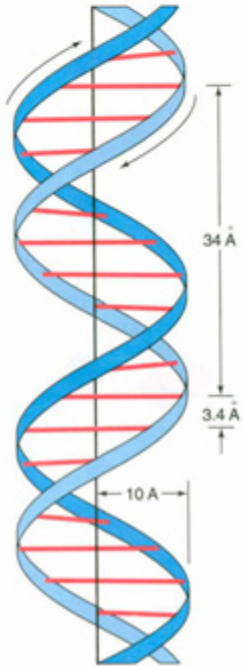


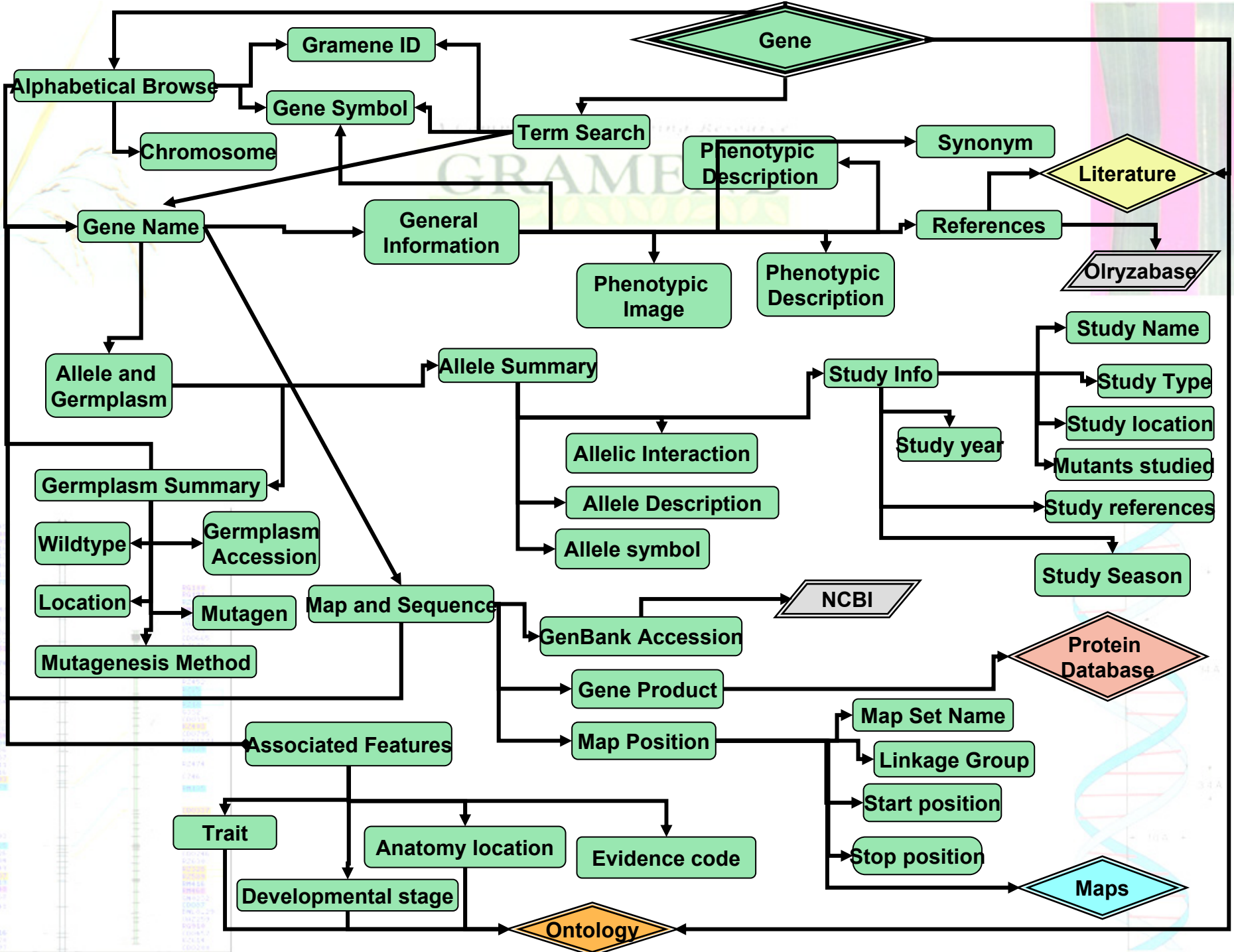
Retrieve descriptions of alleles associated with morphological, developmental, and agronomically important phenotypes and variants of physiological characters, biochemical functions and isozymes.

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.




Gene
Gramene ID
Alphabetical Browse
Gene Symbol
Term Search
Chromosome
Synonym
Phenotypic Description
Literature
Gene Name
General Information
References
Phenotypic Image
Phenotypic Description
Oryzabase
Study Name
Allele and Germplasm
Allele Summary
Study Info
Study Type
Study year
Study location
Allelic Interaction
Mutants studied
Germplasm Summary
Allele Description
Study references
Wildtype
Germplasm Accession
Allele symbol
Study Season
Location
Mutagen
Map and Sequence
NCBI
GenBank Accession
Protein Database
Mutagenesis Method
Gene Product
Map Set Name
Map Position
Associated Features
Linkage Group
Start position
Trait
Anatomy location
Evidence code
Stop position
Maps
Developmental stage
Ontology

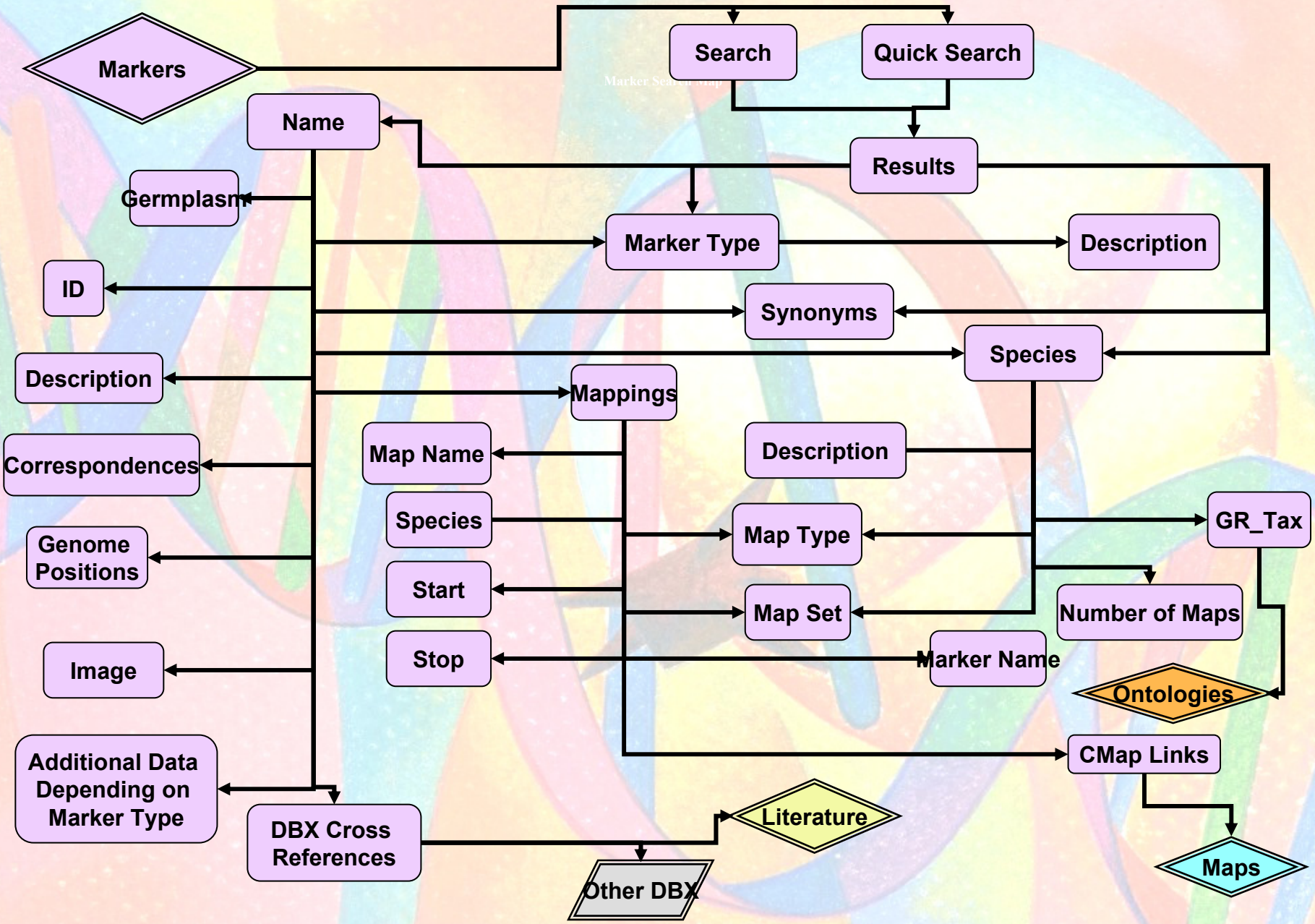
Markers Database

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.


Markers
Search
Quick Search
Name
Results
Germplasm
Marker Type
Description
ID
Synonyms
Species
Description
Mappings
Correspondences
Map Name
Description
Species
Map Type
GR_Tax
Genome Positions
Start
Map Set
Number of Maps
Stop
Marker Name
Image
Ontologies
Additional Data Depending on Marker Type
CMap Links
DBX Cross References
Literature
Other DBX
Maps

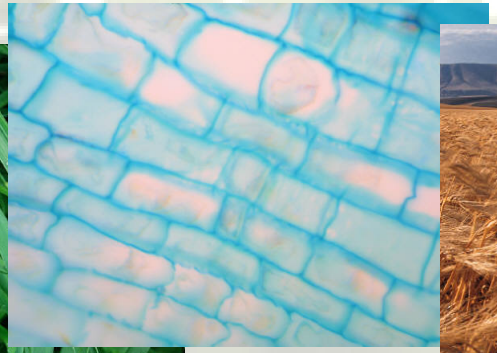
QTL Database

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.

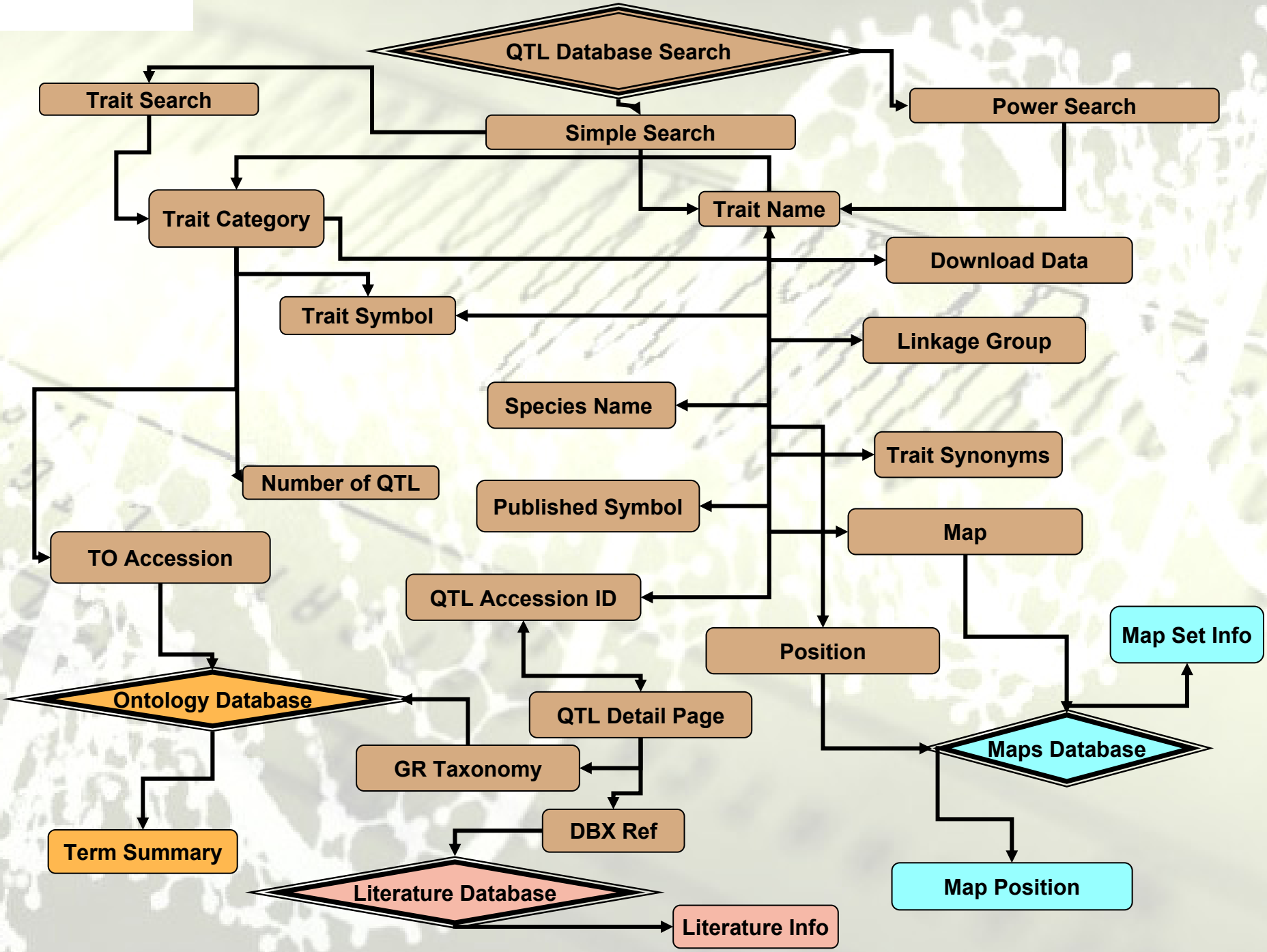
Development: Traits related to plant and plant part development. Also includes maturity related traits.

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 Database Search
Trait Search
Power Search
Simple Search
Trait Category
Trait Name
Download Data
Trait Symbol
Linkage Group
Species Name
Trait Synonyms
Number of QTL
Published Symbol
Map
TO Accession
QTL Accession ID
Map Set Info
Position
Ontology Database
QTL Detail Page
Maps Database
GR Taxonomy
DBX Ref
Term Summary
Map Position
Literature Database
Literature Info

Proteins Database

Provides collective information on proteins from grasses (family *Poaceae/Gramineae), a*nd 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

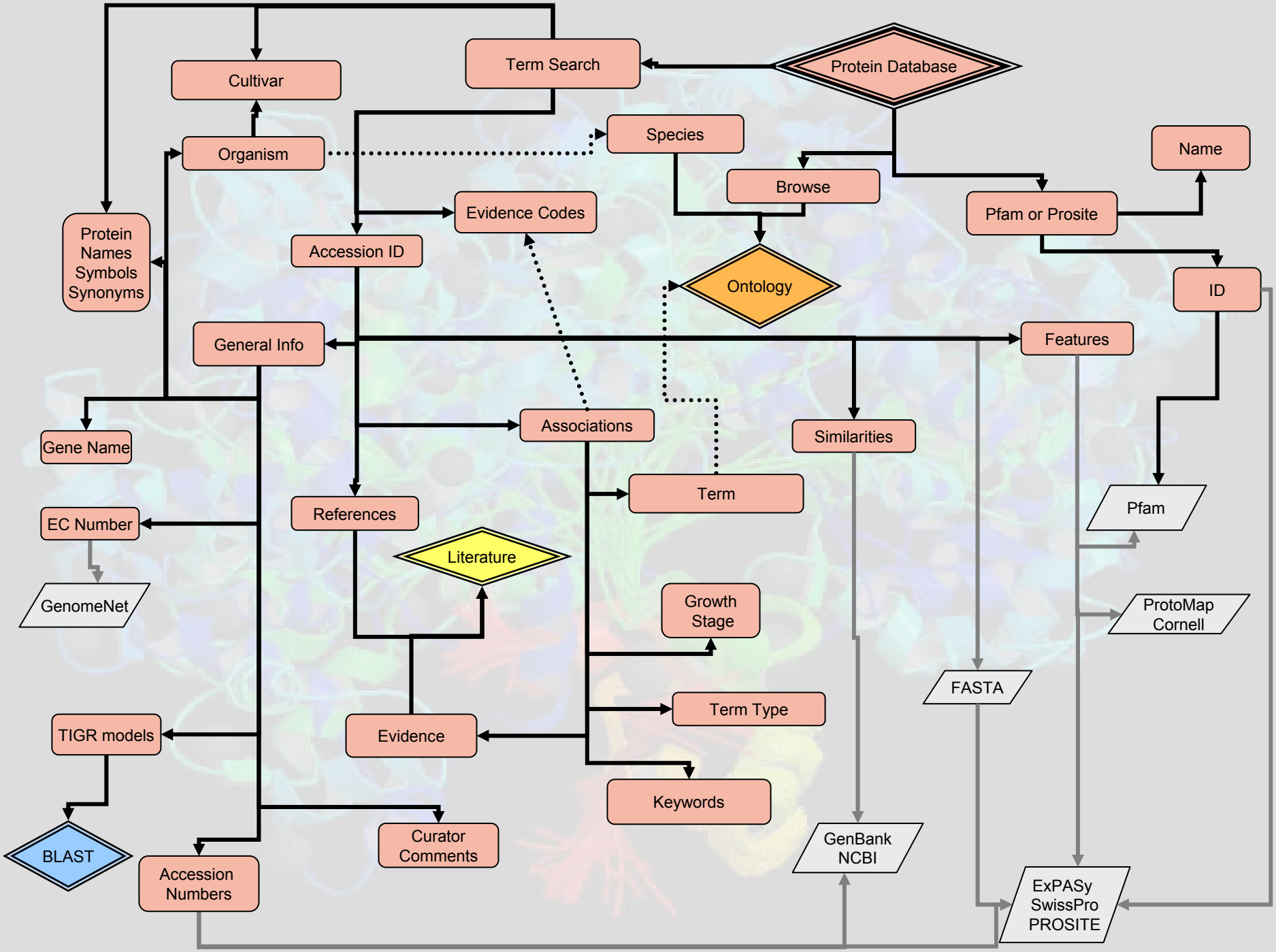
Find a protein and conduct a BLAST query on it.

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 Database
Term Search
Cultivar
Organism
Species
Browse
Name
Pfam or Prosite
Evidence Codes
Accession ID
Protein Names Symbols Synonyms
Ontology
ID
General Info
Features
Gene Name
Associations
Similarities
Term
References
EC Number
Pfam
Literature
GenomeNet
Growth Stage
ProtoMap Cornell
FASTA
Term Type
TIGR models
Evidence
Keywords
BLAST
Curator Comments
GenBank NCBI
Accession Numbers
ExPASy SwissPro PROSITE

Welcome to the Maps and CMap Tutorial

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.

GrameneMart

- Batch Data Sequence Retrieval
- Select a Gramene dataset to search against.
- Add filters to the dataset to increase its specificity.
- Choose the fields to include in the report.
- Generate a batch report in a format that can be imported into local tools, such as Excel.

GrameneMart is based upon Biomart. Mart 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