



Gramene Search

search.gramene.org

data.gramene.org

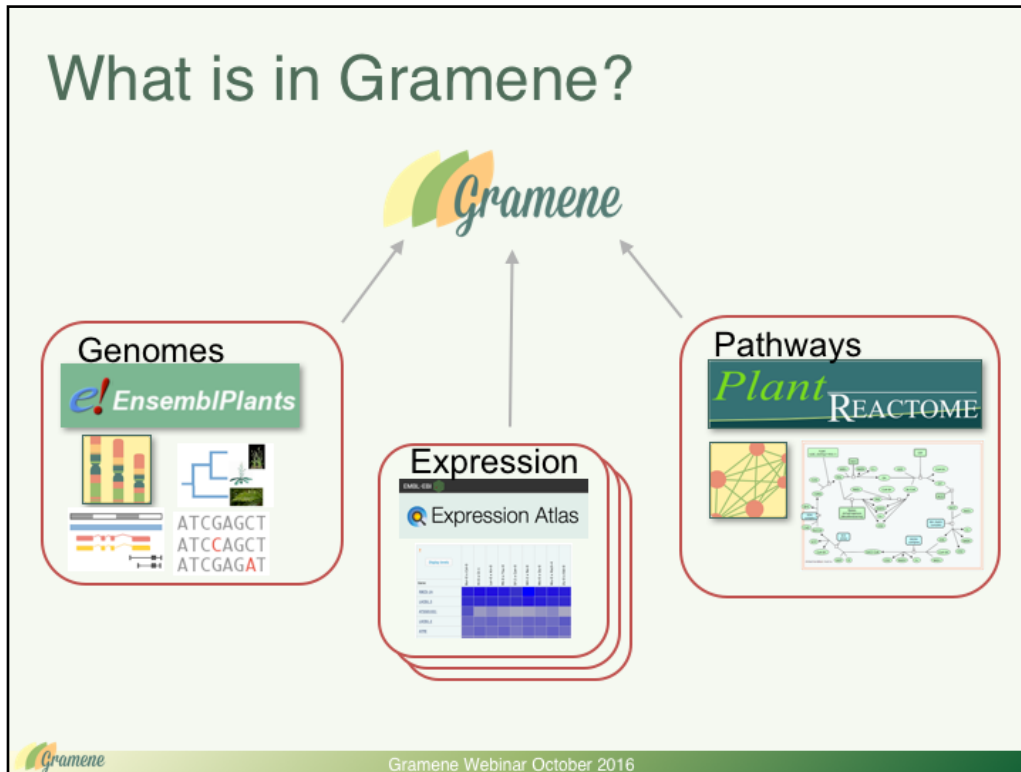
Andrew Olson
Cold Spring Harbor Laboratory
October 4, 2016



Gramene Webinar October 2016

Overview

- The role of search in Gramene
- Demo
- Features in development



<Define Gramene>

The Gramene project encompasses a set of best-in-class software tools that specialize in subsets of functionality.

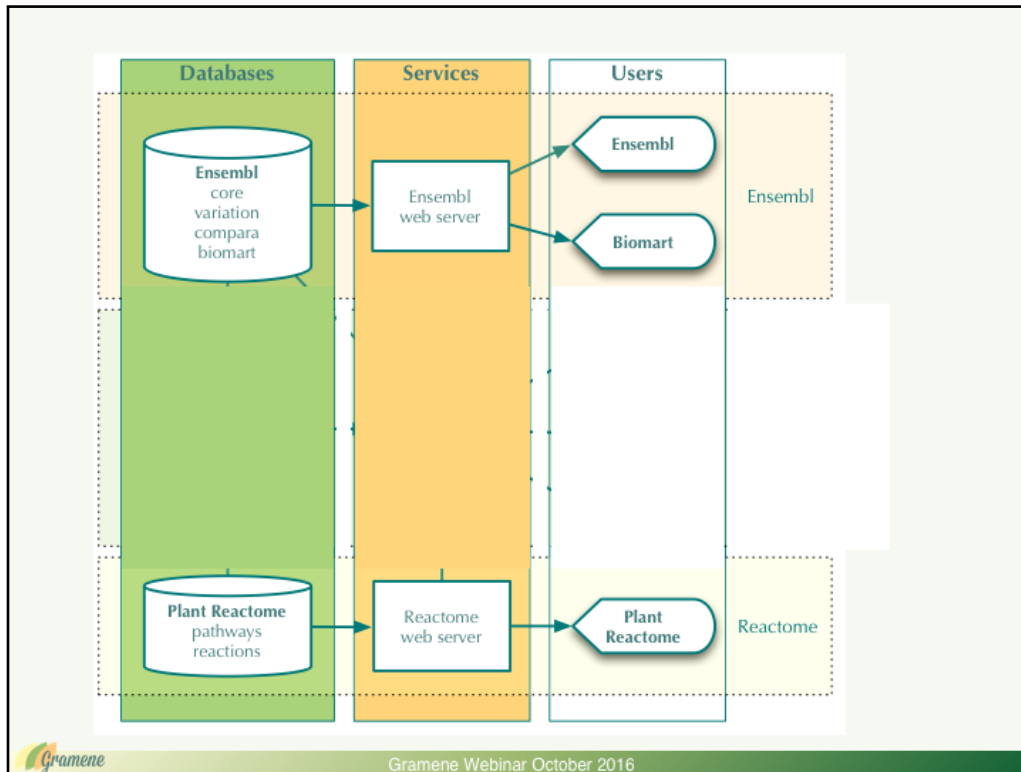
Most significantly:-

- Ensembl for Genomes and Comparative Genomics
- Plant Reactome for pathways and metabolic networks

And also:-

- ATLAS for expression

We also are working with databases like EVA – variation archive – to simplify integration of variation data.



When you think about the architecture of these tools, you see siloes databases, services and user interfaces.

We have been working to build a data warehouse that combines these data and makes them searchable together.

Goals of Search Interface

- Search all Gramene data
- Enable powerful, expressive searches
- Provide:-
 - useful summaries and visualizations
 - links to specialized tools
- REALLY FAST
- [demo](#)

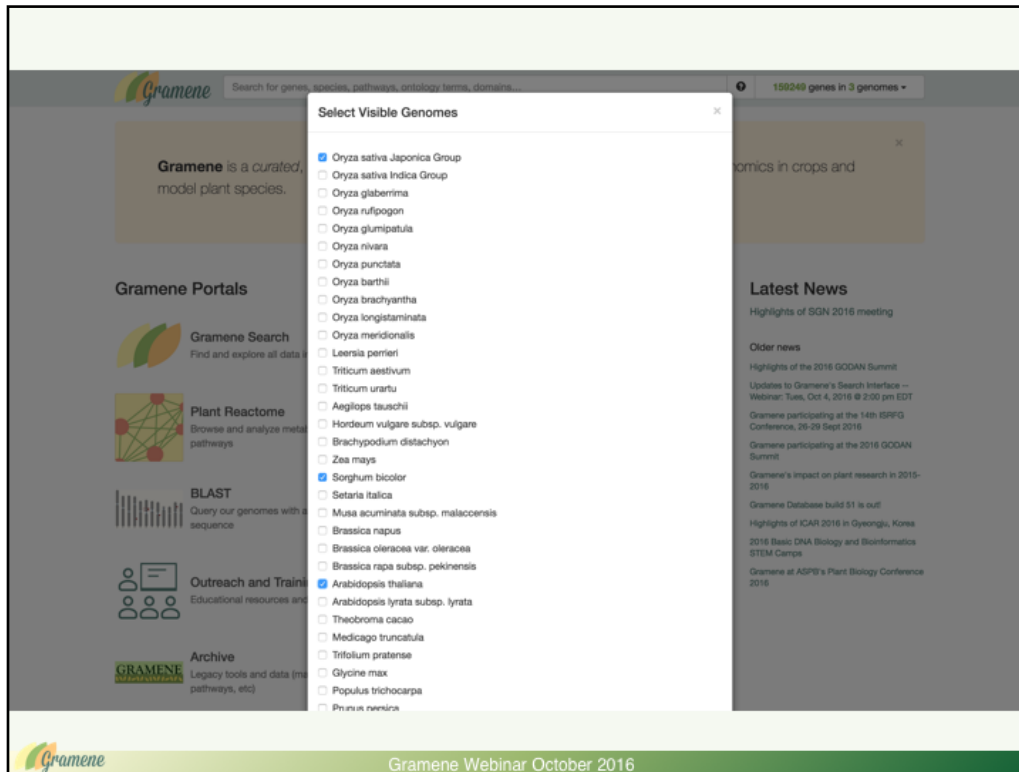
The screenshot displays the Gramene website's main interface. At the top, there is a search bar with the text "Search for genes, species, pathways, ontology terms, domains..." and a status indicator on the right that reads "1761223 genes in 44 genomes". Below the search bar is a light orange banner with the text: "Gramene is a curated, open-source, integrated data resource for comparative functional genomics in crops and model plant species." The main content area is divided into two columns. The left column, titled "Gramene Portals", lists several services: "Gramene Search" (Find and explore all data in Gramene database), "Plant Reactome" (Browse and analyze metabolic and regulatory pathways), "BLAST" (Query our genomes with a DNA or protein sequence), "Outreach and Training" (Educational resources and webinars), and "Archive" (Legacy tools and data (markers, Cysc pathways, etc)). The right column, titled "Latest News", lists recent updates: "Highlights of SGN 2016 meeting", "Older news", "Highlights of the 2016 GODAN Summit", "Updates to Gramene's Search Interface -- Webinar: Tues, Oct 4, 2016 @ 2:30 pm EDT", "Gramene participating at the 14th ISFPG Conference, 26-29 Sept 2016", "Gramene participating at the 2016 GODAN Summit", "Gramene's impact on plant research in 2015-2016", "Gramene Database build 51 is out!", "Highlights of ICAR 2016 in Gyeongju, Korea", "2016 Basic DNA Biology and Bioinformatics STEM Camps", and "Gramene at ASPB's Plant Biology Conference 2016". The footer of the page includes the Gramene logo and the text "Gramene Webinar October 2016".

The highlighted region on the top right is the search status (currently all gene in all genomes)

Click on it to select genomes of interest

The screenshot displays the Gramene website interface. At the top, there is a search bar with the text "Search for genes, species, pathways, ontology terms, domains..." and a dropdown menu showing "1761223 genes in 44 genomes". Below the search bar, a message states: "Gramene is a curated, open-source, integrated data resource for comparative functional genomics in crops and model plant species." The main content area is divided into two columns. The left column, titled "Gramene Portals", includes links to "Gramene Search", "Plant Reactome", "BLAST", "Outreach and Training", and "Archive". The right column, titled "Latest News", lists recent events such as "Highlights of SGN 2016 meeting" and "Updates to Gramene's Search Interface". The footer of the page contains the Gramene logo and the text "Gramene Webinar October 2016".

By default you search across all species
 Or you can select a subset from a list



The list of species (in the same order as in the species tree)

Future plans include making this list easier to navigate by laying it out on the species tree, color coding clades such as monocots and dicots, and highlighting model organisms and crop species.

The screenshot shows the Gramene website interface. At the top, there is a search bar with the text "Search for genes, species, pathways, ontology terms, domains...". To the right of the search bar, it displays "1761223 genes in 44 genomes" and a dropdown menu with options "Show All Species" and "Pick Species from List". Below the search bar, a message states: "Gramene is a curated, open-source, integrated data resource for comparative functional genomics in crops and model plant species."

The main content area is divided into two columns. The left column is titled "Gramene Portals" and includes the following items:

- Gramene Search**: Find and explore all data in Gramene database
- Plant Reactome**: Browse and analyze metabolic and regulatory pathways
- BLAST**: Query our genomes with a DNA or protein sequence
- Outreach and Training**: Educational resources and webinars
- Archive**: Legacy tools and data (markers, Cysc pathways, etc)

The right column includes:

- Genome Browser**: Browse genomes with annotations, variation and comparative tools
- Plant Expression ATLAS**: Browse plant expression results at EBI ATLAS
- Gramene Mart**: An advanced query interface powered by BioMart
- Bulk Downloads**: FTP download of our data

On the far right, there is a "Latest News" section with the following content:

- Highlights of SGN 2016 meeting
- Older news
- Highlights of the 2016 GGDAN Summit
- Updates to Gramene's Search Interface -- Webinar: Tues, Oct 4, 2016 @ 2:30 pm EDT
- Gramene participating at the 14th ISFGF Conference, 28-29 Sept 2016
- Gramene participating at the 2016 GGDAN Summit
- Gramene's impact on plant research in 2015-2016
- Gramene Database build 51 is out!
- Highlights of ICAR 2016 in Gyeongju, Korea
- 2016 Basic DNA Biology and Bioinformatics STEM Camps
- Gramene at ASPB's Plant Biology Conference 2016

At the bottom of the page, the Gramene logo is on the left, and the text "Gramene Webinar October 2016" is centered.

Revert back to all species

The screenshot shows the Gramene website interface. At the top, there is a search bar with the text "Search for genes, species, pathways, ontology terms, domains..." and a notification "1761223 genes in 44 genomes". Below the search bar is a dropdown menu titled "Features" which is currently open. The dropdown menu contains several sections:

- Suggestions:** "Suggested terms are provided as you type:" followed by a search input field and a list of suggestions: "Arabidopsis (meta)", "Arabidopsis (meta subsp. meta)", "Lysine (Lys) motif containing protein 2", and "TEXT SEARCH" with filters for "Exactly 'y'", "Starts with 'y'", "y*o*", and "y*o*".
- Visualization:** "See the distribution of results across all genomes:" with a small visualization chart.
- Gene view:** "Concise view of available information about a gene:" with a small gene view interface showing "PAD4 Arabidopsis thaliana" and tabs for "Gene Structure", "Homology", "Domains", and "Cross-reference".
- For Example:** "You can use to ask sophisticated questions about the genes across all of our databases concerning crop and model plant genomes:" followed by two bullet points:
 - What are the homologs of Arabidopsis thaliana's PAD4 gene in the Cryzeae?
 - What cytosolic genes in A. thaliana and Z. mays are in the pyruvate metabolism pathway and bind either NAD or NADP?
- BLAST:** "Query our genomes with a DNA or protein sequence" with a "bioMart" logo.
- bioMart:** "An advanced query interface powered by BioMart".
- Outreach and Training:** "Educational resources and webinars" with an icon of three people.
- Bulk Downloads:** "FTP download of our data" with a download icon.
- Archive:** "Legacy tools and data (markers, Cyc pathways, etc)" with a "GRAMENE" logo.

At the bottom of the page, there is a footer with the Gramene logo and the text "Gramene Webinar October 2016".

The little help icon loads a small guide

Gramene
1761223 genes in 44 genomes

TOP
jasmonic acid biosynthesis 276 | Jasmonic acid signaling 81 | Wound-induced_Wun1 139 | Prosystemin/Systemin 2 | JAR1 74

PLANT REACTOME
jasmonic acid biosynthesis 276 | Jasmonic acid signaling 81 | Jasmonate conjugation 81

INTERPRO
MeTrfase_7 1022 | Allene_ox_cyc 81 | Wound-induced_Wun1 139 | Prosystemin/Systemin 2 | JAR1 74 | Ninja_fam 261 | Jas 500

GENE
jasmonate-zim-domain protein 5 1 | jasmonate-zim-domain protein 1 1 | jasmonic acid carboxyl methyltransferase 1 | jasmonate-zim-domain protein 8 1 | JASMONIC ACID RESPONSIVE 3 1 | JASMONATE-ZIM-DOMAIN PROTEIN 9 1 | jasmonate-zim-domain protein 6 1 | JASMONATE-ZIM-DOMAIN PROTEIN 2 1 | jasmonate-zim-domain protein 7 1 | JASMONATE RESISTANT 1 1 | All genes that contain the word "jasmi" | All genes that contain a word that starts with "jasmi"

GO PROCESS
response to jasmonic acid 2593 | jasmonic acid and ethylene-dependent systemic resistance 106 | cellular response to jasmonic acid stimulus 1717 | jasmonic acid mediated signaling pathway 1710 | response to jasmonic acid stimulus involved in jasmonic acid and ethylene-dependent systemic resistance 13 | regulation of jasmonic acid metabolic process 65 | response to cyclopentenone 263 | jasmonic acid biosynthetic process 905 | jasmonic acid and ethylene-dependent systemic resistance, ethylene mediated signaling pathway 23 | regulation of jasmonic acid mediated signaling pathway 136

GO FUNCTION
jasmonyl-ile conjugate hydrolase activity 1 | jasmonate O-methyltransferase activity 25 | jasmonate-amino synthetase activity 23 | jasmonyl-isoleucine-12-hydroxylase activity 1 | methyl jasmonate esterase activity 17

Gramene Webinars
Plant
BLAS
Outre
Archiv

GRAMENE
Legacy tools and data (markers, Cyt pathways, etc)

Gramene Webinars October 2016

Start typing jasmonic acid signaling

Suggested filters appear grouped by category, with top scoring matches displayed first

The screenshot shows the Gramene website interface. At the top, there is a search bar with the text "Search for genes, species, pathways, ontology terms, domains..." and a status indicator "81 genes in 33 genomes". Below the search bar, the selected query is "Plant Reactome | Jasmonic acid signaling".

The main content area features a phylogenetic tree on the left, a heatmap in the center, and a list of species on the right. The heatmap uses different colors to represent chromosomes across various species. Below the heatmap, the top result is expanded to show details for **JAR1** (AT2G46370) in *Arabidopsis thaliana*, described as an "Auxin-responsive GH3 family protein". It also shows a "Model Species Homolog" for **JAR1** in *Arabidopsis thaliana*, described as "Jasmonic acid-amido synthetase JAR1".

At the bottom of the page, the Gramene logo and the text "Gramene Webinar October 2016" are visible.

Note the selected suggestion becomes displayed below the search box, numbers in the search status area are updated

Taxagenomic distribution shows species tree (based on ncbi taxonomy)

Count of genes in each species

Linear view of each genome – color by chromosome. Unanchored portions of a genome are gray and don't show the position of search results

Below is a list view – arabidopsis results appear first because they tend to be best annotated

Non-arabidopsis genes have a model species homolog to provide some hints of annotation to a gene

Gramene Search for genes, species, pathways, ontology terms, domains... 81 genes in 33 genomes -

Plant Reactome | Jasmonic acid signaling X

Phylogenetic tree and species list:

- Brassica napus 0
- B. oleracea oleracea 3
- B. napo polinensis 3
- Arabidopsis thaliana 1
- A. lyrata lyrata 1
- Theobroma cacao 2
- Medicago truncatula 1
- Trifolium pratense 0
- Glycine max 1
- Populus trichocarpa 1
- Prunus persica 2
- Vitis vinifera 2
- Solanum tuberosum 2
- Solanum lycopersicum 3
- B. vulgaris vulgaris 0
- Antirrhinum majus 1
- S. moellendorffii 0
- P. sativum 1
- C. reinhardtii 0
- O. lucimarinus CCE9901 0
- G. sulphuraria 0
- C. merriamii 102 0
- Chondrus crispus 0

JAR1 AT2G46370 Arabidopsis thaliana
Auxin-responsive GHD family protein

TAIR Curated Description: Encodes a jasmonate-amido synthetase that is a member of the GHD family of proteins. JAR1 catalyzes the formation of a biologically active jasmonyl-...

Location Homology X-refs

Genome location: Chromosome 2:19033741-19036659
Currently viewing: 2:19033450-19036950

Search Gramene: All on Chromosome 2, All within 2:19033450-19036950

Links to other resources: Gramene Ensembl, PhytoMine, Araport

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The location view shows a lightweight genome browser that lets you see the annotated gene structure. You can scroll and zoom in/out

Gramene Search for genes, species, pathways, ontology terms, domains... 81 genes in 33 genomes -

Plant Reactome | Jasmonic acid signaling

JAR1 AT2G46370 Arabidopsis thaliana
Auxin-responsive G13 family protein

TAIR Curated Description
Encodes a jasmonate-amido synthetase that is a member of the G13 family of proteins. JAR1 catalyzes the formation of a biologically active jasmonyl-...

Location Homology X-refs

Genome location: Chromosome 2:19033741-19036659
Currently viewing: 2:19032592-19036094

Search Gramene
All on Chromosome 2
All within 2:19032592-19036094

Links to other resources
Gramene Ensembl
PhytoMine
Araport

Gramene Webinar October 2016

Scroll to exon junction

Gramene Search for genes, species, pathways, ontology terms, domains... 81 genes in 33 genomes -

Plant Reactome | Jasmonic acid signaling X

Phylogenetic tree and heatmap showing gene presence across 33 species:

- Brassica napus 0
- B. oleracea oleracea 3
- B. napo polinensis 3
- Arabidopsis thaliana 1
- A. lyrata lyrata 1
- Theobroma cacao 2
- Medicago truncatula 1
- Trifolium pratense 0
- Glycine max 1
- Populus trichocarpa 1
- Prunus persica 2
- Vitis vinifera 2
- Solanum tuberosum 2
- Solanum lycopersicum 9
- B. vulgaris vulgaris 0
- Antirrhinum majus 1
- S. moellendorffii 0
- P. sativum 1
- C. reinhardtii 0
- O. laccinermis CCE9901 0
- G. sulphuraria 0
- C. merriamii 102
- Chondrus crispus 0

JAR1 AT2G46370 Arabidopsis thaliana
Auxin-responsive G43 family protein

TAIR Curated Description
Encodes a jasmonate-amido synthetase that is a member of the G43 family of proteins. JAR1 catalyzes the formation of a biologically active jasmonyl-...

Location Homology X-refs

Genome location: Chromosome 2:19033741-19036659
Currently viewing: 2:19034302-19034383

1,300 19,034,300 19,034,340 19,034,380 19,034

T C G A A A T C T G A T G C A C T T T T T C T T T T A T C T A C T T C A G G A A T T T G G A A A G G T T G A A A C T T T T G A C A T G A A C A G A G T C A T

Search Gramene
All on Chromosome 2
All within 2:19034302-19034383

Links to other resources
Gramene Ensembl
PhytoMine
Araport

Gramene Webinar October 2016

Zoom to 100bp zoom level to see splice acceptor sequence and start codon

Gramene Search for genes, species, pathways, ontology terms, domains... 81 genes in 33 genomes -

Plant Reactome | Jasmonic acid signaling

OS05G0143800 *Oryza sativa* Japonica Group
unknown
Location Homology X-refs

GH3.5 OS05G0586200 *Oryza sativa* Japonica Group
Jasmonic acid-amido synthetase JAR1
Location Homology X-refs

Genome location: **Chromosome 5:29200200-29205715**
Currently viewing: 5:29199649-29206266

Search Gramene

All on Chromosome 5
All within 5:29199649-29206266

Links to other resources

Gramene Ensembl
PhytoMine
Arasport

DFL2 *Arabidopsis thaliana*
Auxin-responsive GH3 family protein
Model Species Homolog

JAR1 *Arabidopsis thaliana*
Jasmonic acid-amido synthetase JAR1
Model Species Homolog

GH3.12 OS11G0186500 *Oryza sativa* Japonica Group
Probable indole-3-acetic acid-amido synthetase GH3.12
Location Homology X-refs

Zm00001d009714 *Zea mays*
ensembl.gramene.org/oryza_sativa/Gene/Summary?g=OS05G0586200

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Expanded location tab on rice gene GH3.5

Click Gramene Ensembl link to go the gene page

Gramene BLAST BioMart Tools Downloads Help Feedback UploadData Login/Register

Search Oryza sativa Japonica...

Oryza sativa Japonica (IROSP-1.0) Location: 5:29,200,200-29,205,715 Gene: GH3.5 Transcript: GH3.5

Gene-based displays

- Summary
 - Splice variants
 - Transcript comparison
 - Gene alleles
- Sequence
 - Secondary Structure
 - Gene families
 - Literature
- Plant Compara
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
 - Pan-taxonomic Compara
 - Gene Tree
 - Orthologues
- Ontologies
 - GO: Biological process
 - GO: Cellular component
 - GO: Molecular function
 - Phenotypes
- Genetic Variation
 - Variant table
 - Structural variants
 - Variant image
- Gene expression
- Regulation
- External references
- Supporting evidence
- ID History

Gene: GH3.5 OS05G0588200

Description Jasmonic acid-amido synthetase JAR1 [Source:UniProt/SWISSPROT;Acc:Q6581]

Location Chromosome 5: 29,200,200-29,205,715 forward strand.

About this gene This gene has 1 transcript (splice variant), 84 orthologues and 12 paralogues.

Transcripts [Hide transcript table](#)

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
GH3.5	OS05G0588200-01	2407	881aa	Protein coding	Q6581	NM_001062925 NP_001056460	

Summary

Name GH3.5 (UniProtKB Gene Name)

UniProtKB This gene has proteins that correspond to the following UniProtKB identifiers: [Q6581](#)

Gene type Protein coding

Annotation method Gene annotation by [International Rice Genome Sequencing Project \(IRGSP\)](#) dated 2013-04-24. [Read more...](#)

[Go to Region In Detail for more tracks and navigation options \(e.g. zooming\)](#)

Gene Legend: Protein Coding (red), IRGSP (red), Non-Protein Coding (blue), RNA gene (purple)

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The ensembl gene page

Gene: GH3.5 OS05G0588200

Description: Jasmonic acid-amido synthetase JAR1 [Source:UniProt/SWISSPROT;Acc:Q6I581]

Location: Chromosome 5: 29,200,200-29,205,715 forward strand.

About this gene: This gene has 1 transcript (splice variant), 84 orthologues and 12 paralogues.

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
GH3.5	OS05G0588200-01	2407	881aa	Protein coding	Q6I581	NM_001062995 NP_001056460	

Gene expression

Showing 4 experiments: 9 Davidson, 7 Sakai, 4 Zhang et al., Anderson et al.

Sort by: Default | Download all results

Legend: Below cutoff, Low, Medium, High, No data available

Click Gene expression in the sidebar

This expression atlas view widget is something we'd like to incorporate into the gramene search results

Gramene Search for genes, species, pathways, ontology terms, domains... 1761223 genes in 44 genomes -

Gramene is a curated, open-source, integrated data resource for comparative functional genomics in crops and model plant species.

Gramene Portals

- Gramene Search**
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Browse genomes with annotations, variation and comparative tools
- Plant Reactome**
Browse and analyze metabolic and regulatory pathways
- Plant Expression ATLAS**
Browse plant expression results at EBI ATLAS
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FTP download of our data
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Legacy tools and data (markers, Cys pathways, etc)

Latest News

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Back to the search homepage to do a new search for RFL1

Gramene Search for genes, species, pathways, ontology terms, domains... 9 genes in 2 genomes

Gene | RFL1 X

RFL1 AT1G12210 Arabidopsis thaliana
RPS5-like 1
Location Homology X-refs

Bra019755 Brassica rapa subsp. pekinensis
AT1G12210 (E=2e-222) RFL1 | RFL1 (RPS5-like 1); ATP binding / protein binding
Location Homology X-refs

RFL1 Arabidopsis thaliana
Disease resistance protein RFL1

TAIR Curated Description
RFL1 has high sequence similarity to the adjacent disease resistance (R) gene RPS5.

Model Species Homology
RFL1 Arabidopsis thaliana
Disease resistance protein RFL1

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Note only a few genes are annotated with this term (9 genes in 2 genomes)

Gramene Search for genes, species, pathways, ontology terms, domains... 9 genes in 2 genomes -

Gene | RFL1 X

RFL1 AT1G12210 Arabidopsis thaliana
RPS5-like 1

Location Homology X-refs

TAIR Curated Description
RFL1 has high sequence similarity to the adjacent disease resistance (R) gene RPS5.

Compara Gene Tree
This phylogram shows the relationships between this genes and others similar to it, as determined by Ensembl Compara.

Gene Tree

Search Gramene

Show All Homologs 1114

Show Orthologs 13

Show Paralogs 25

Links to other resources
Ensembl Gene Tree view

Gramene Webinar October 2016

Click the homolog tab to see the gene tree (1114 genes!)

The tree branches are opened up to show the current gene of interest (RFL1)

The right hand side of the display is a view of the multiple species alignment. Colors correspond to interpro domains.

Gramene Search for genes, species, pathways, ontology terms, domains... 9 genes in 2 genomes

Gene | RFL1 X

RFL1 AT1G12210 Arabidopsis thaliana
RPS5-like 1

Location Homology X-refs

TAIR Curated Description
RFL1 has high sequence similarity to the adjacent disease resistance (R) gene RPS5.

Compara Gene Tree
This phylogram shows the relationships between this genes and others similar to it, as determined by Ensembl Compara.

Gene Tree

Gene Tree

- Magnoliophyta: 44 genes, 1 paralog
- rosids: 45 genes, 2 paralogs
 - Brassicaceae: 20 genes, 1 paralog
 - Brassicaceae: 14 genes, 4 paralogs
 - Brassicaceae: 28 genes, 2 paralogs
 - Brassicaceae: 13 genes, 2 paralogs
 - Brassicaceae: 13 genes
 - Arabidopsis lyrata subsp. lyrata: 2 par
 - AT1G12210
 - Brassicaceae: 21 genes, 3 paralogs
 - AT5G03020
 - Brassicaceae: 5 genes
 - Brassicaceae: 7 genes
 - Brassicaceae: 31 genes, 4 paralogs
 - Brassicaceae: 5 genes, 2 paralogs
 - Tp57577_TGAC_v2_gene4011
- rosids: 42 genes
- Magnoliophyta: 162 genes
- commelinids: 34 genes
- AMTR1_000062p00089640
- Magnoliophyta: 624 genes, 2 paralogs

Search Gramene

Show All Homologs 1114

Show Orthologs 13

Show Paralogs 25

Links to other resources
Ensembl Gene Tree view

IPR032675 - L_dom-like
Leucine-rich repeat domain, L domain-like
Shared by 963 of 1114 (86.4%) genes in this gene tree.
Shared by all 7 genes in this clade.

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Popover on an interpro domain shows how many genes in the gene tree are annotated with this domain, and for collapsed clades it shows the number of genes in the clade with the domain

Click on Show All Homologs to update the search filter



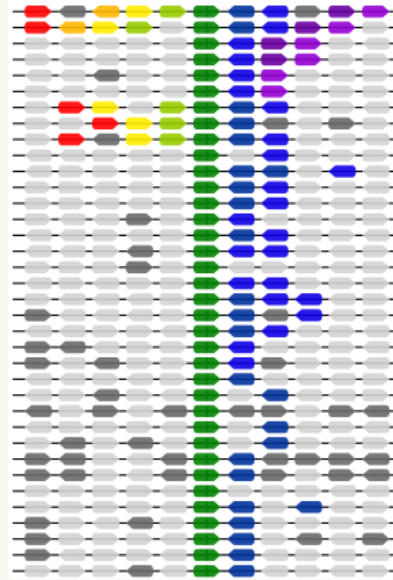
The taxagenomic distribution shows that there was a large expansion in the dicots relative to the monocots

Features in development

- Download search results
- Link from BLAST results to Gramene search
- Improve UI for selecting genomes of interest
- Customize filter logic
- Index Atlas expression data for search
- Atlas and Plant Reactome viewers
- Gene family neighborhood conservation viewer

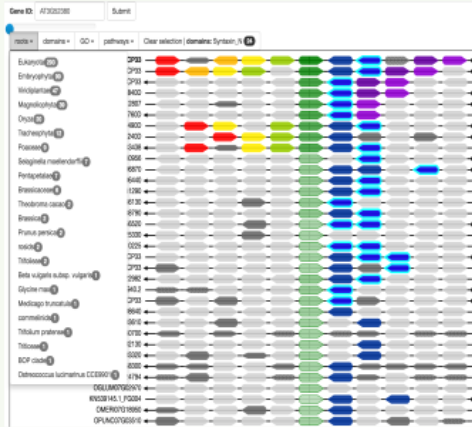
Neighborhood conservation

- Given a query gene and a set of orthologous genes, display the neighboring genes and assign colors based on the gene families of the neighbors of the query gene.
- It can show aspects of gene neighborhoods that are conserved across a gene family



Extend basic functionality

- Use shape to distinguish biotypes
- Use shading in center column to show % identity to query gene
- Add arrows to indicate direction of neighborhood
- Highlight genes by property



[demo](#)

Gramene - Exploring Function through Comparative
Genomics and Network Analysis
NSF IOS 1127112 (2011- 2017)

Doreen Ware, PI (USDA ARS, CSHL)

Michael Campbell, Kapeel Chougule, Yinping Jiao, Sunita Kumari, **Joe Mulvaney**, Andrew Olson, Joshua Stein, Marcela K. Tello-Ruiz, Jim Thomason, Peter van Buren, Bo Wang, Sharon Wei

Pankaj Jaiswal, Co-PI (OSU)

Noor Al-Bader, Justin Elser, Matthew Geniza, Parul Gupta, Justin Preece, Sushma Naithani

Paul Kersey / Robert Petryszuk (EMBL-EBI)

Dan Bolser, Christopher Grabmuller, Chuang Kee Ong, Dan Staines, Brandon Walts / Elisabet Barrera, Maria Keays, Oliver Mannion, Nuno Fonseca, Laura Huerta Martinez

Lincoln Stein (OICR)

Peter D' Eustachio (NYU); Guanming Wu, Robin Haw, Joel Weiser, Sheldon McKay; Antonio Fabregat (EBI)

Crispin Taylor (ASPB)

Patty Lockhart; Weijia Xu (TACC), Amit Gupta(TACC)



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We're hiring!



<https://cshl.peopleadmin.com/postings/10733>



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