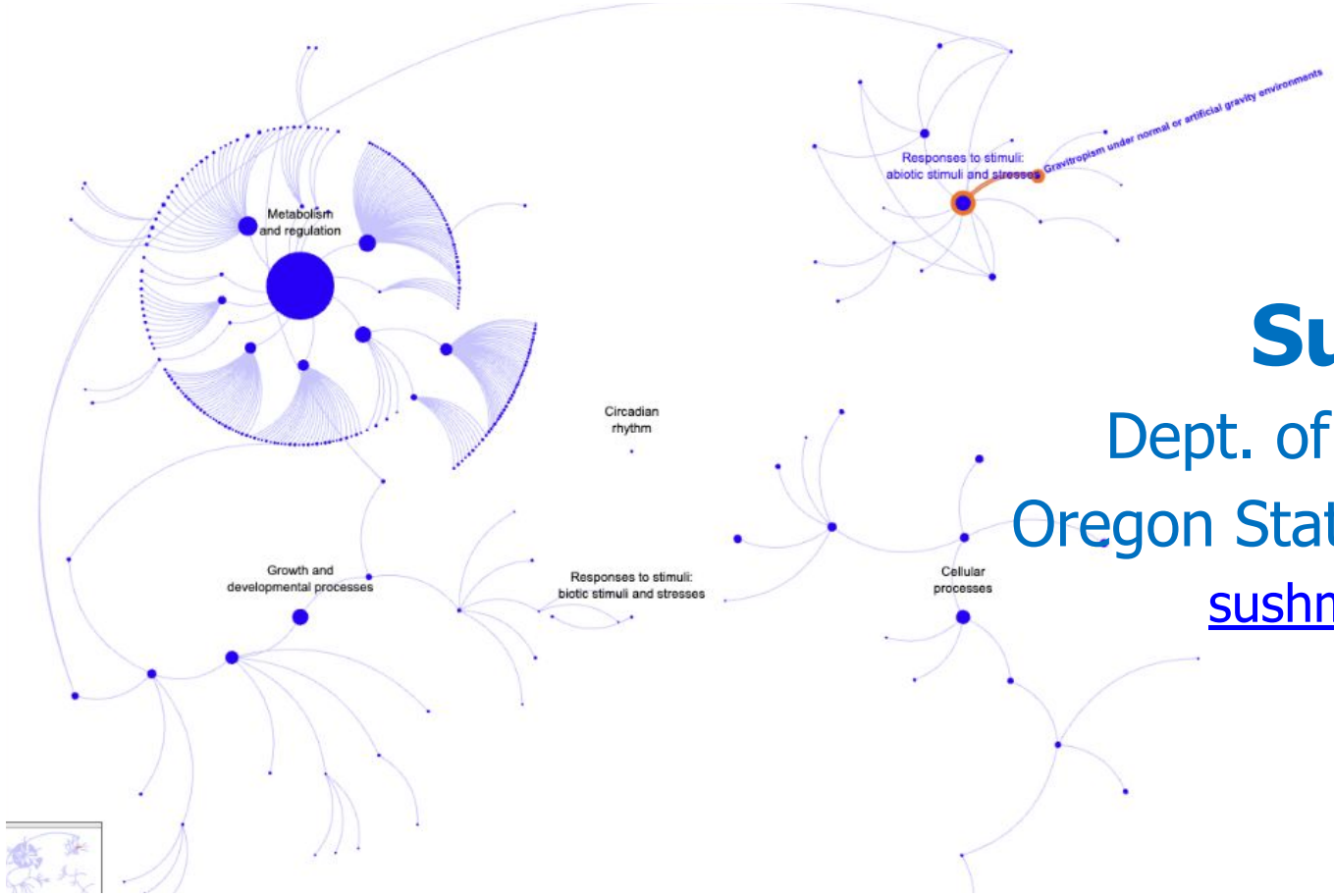
Plant Reactome: Leveraging Neo4j Knowledge Graphs for Pathway Integration, Visualization, Analysis, and Discovery

https://plantreactome.gramene.org



Sushma Naithani

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Oregon State University, Corvallis, OR, USA

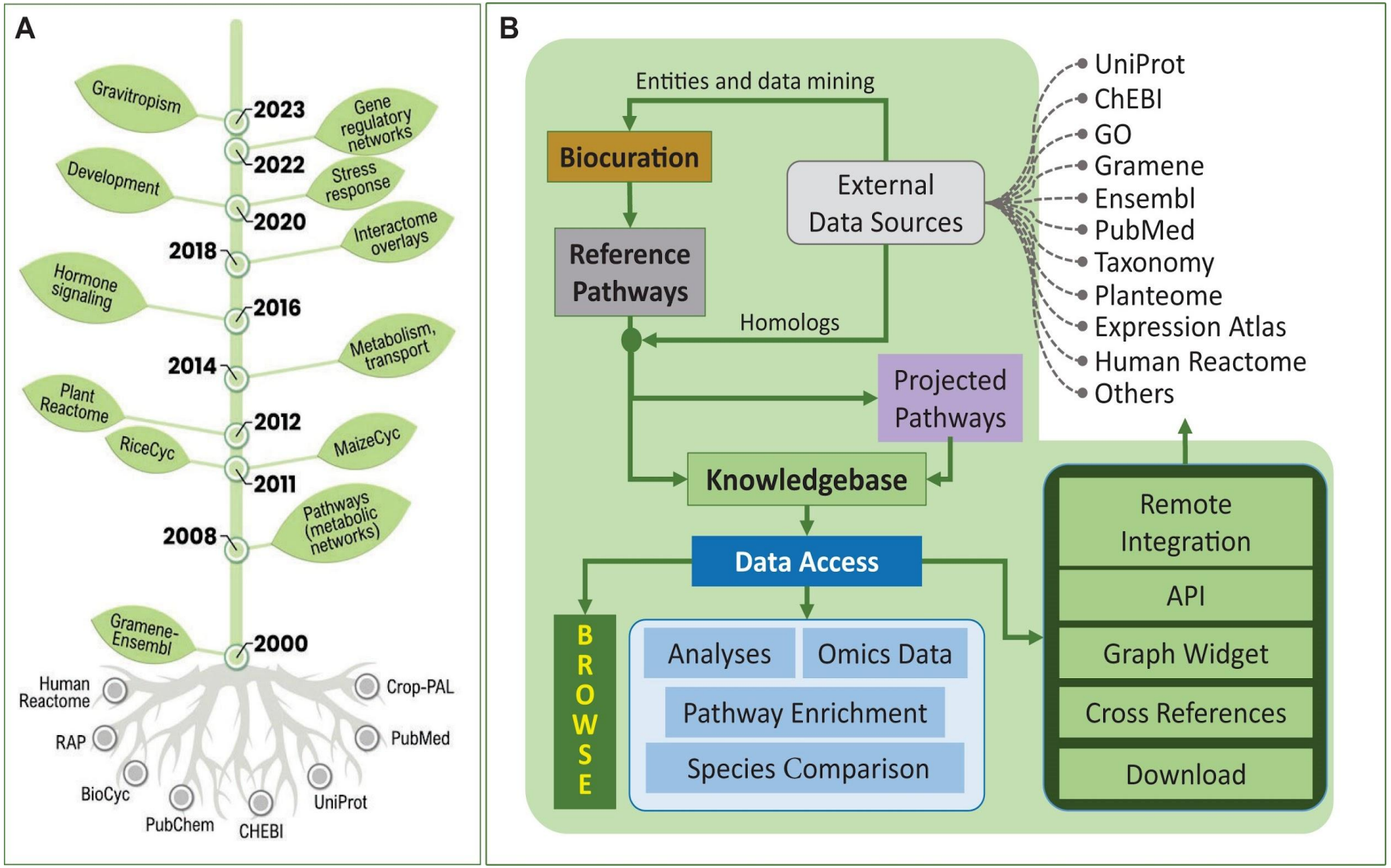
sushma.naithani@oregonstate.edu

Oregon State University

Plant Reactome Gramene Pathways

An overview of the Plant Reactome knowledgebase

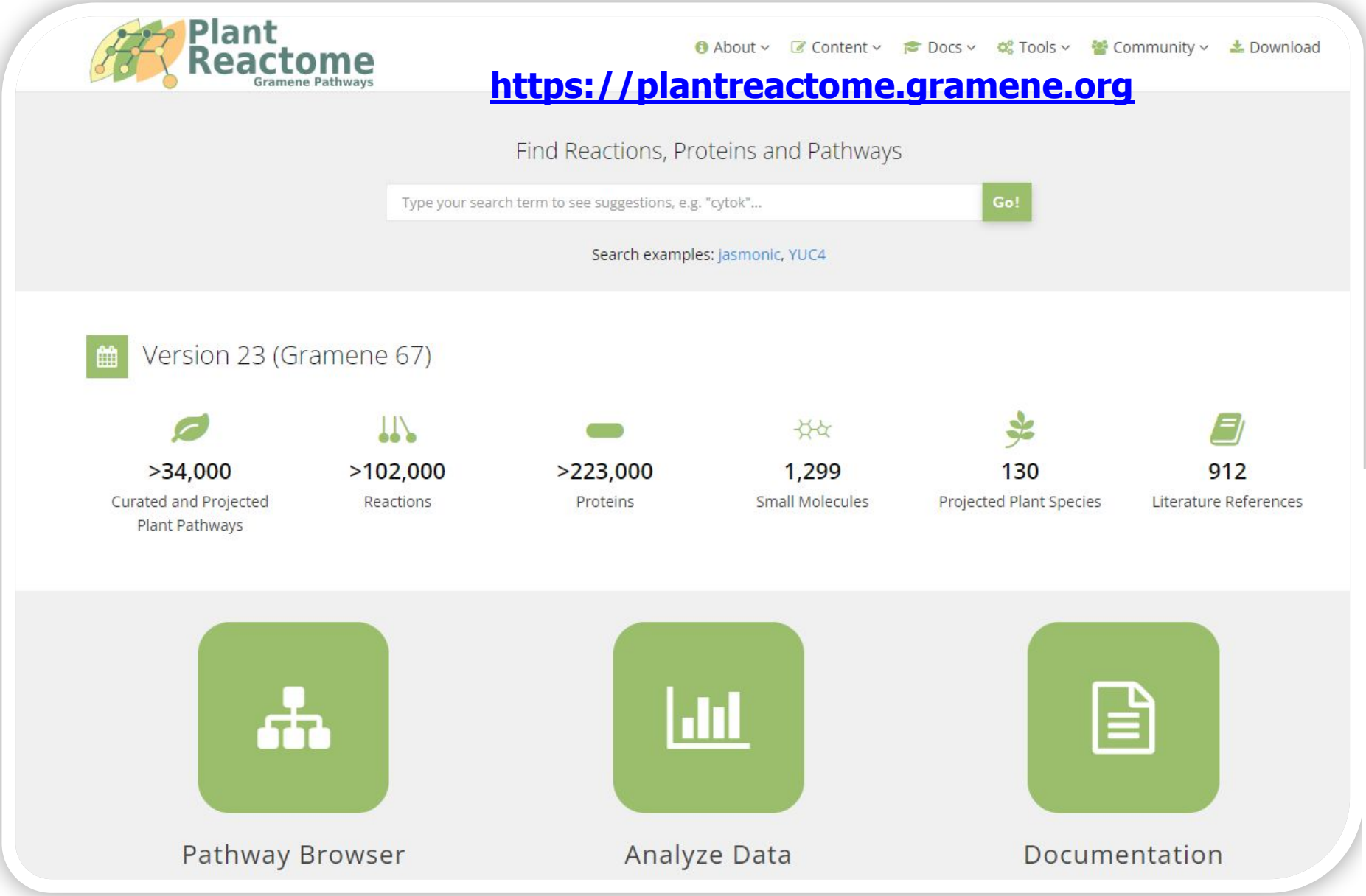
https://plantreactome.gramene.org



- Open access and free-of-cost, FAIR data

Nucleic Acids Res, Volume 52, Issue D1, 5 January 2024, Pages D1538–D1547, https://doi.org/10.1093/nar/gkad1052

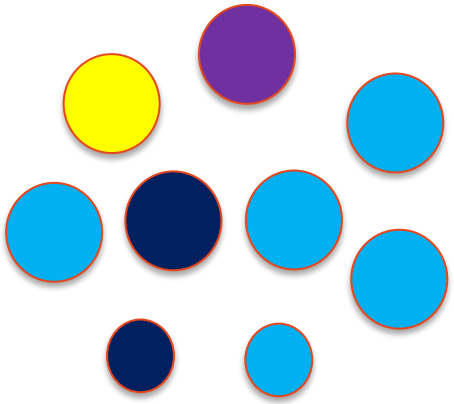
Plant Reactome
Gramene Pathways



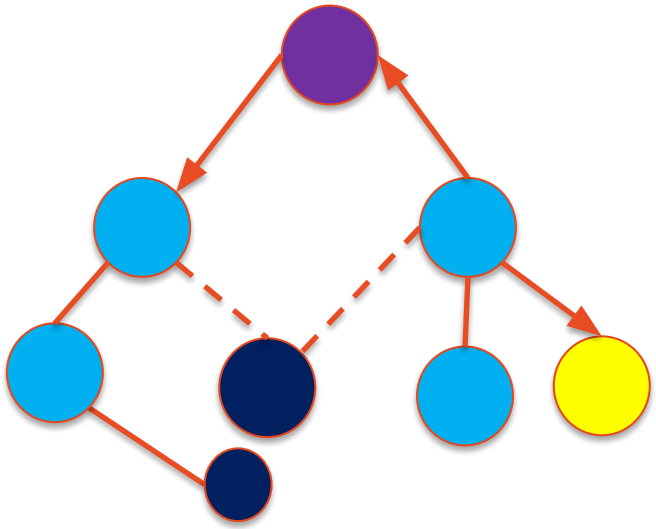
We manually curate reference pathways in rice

- Gene-orthology-based pathway projections for 129 species
- Open access, free-of-cost, FAIR data
- Videos Tutorials, and Training material

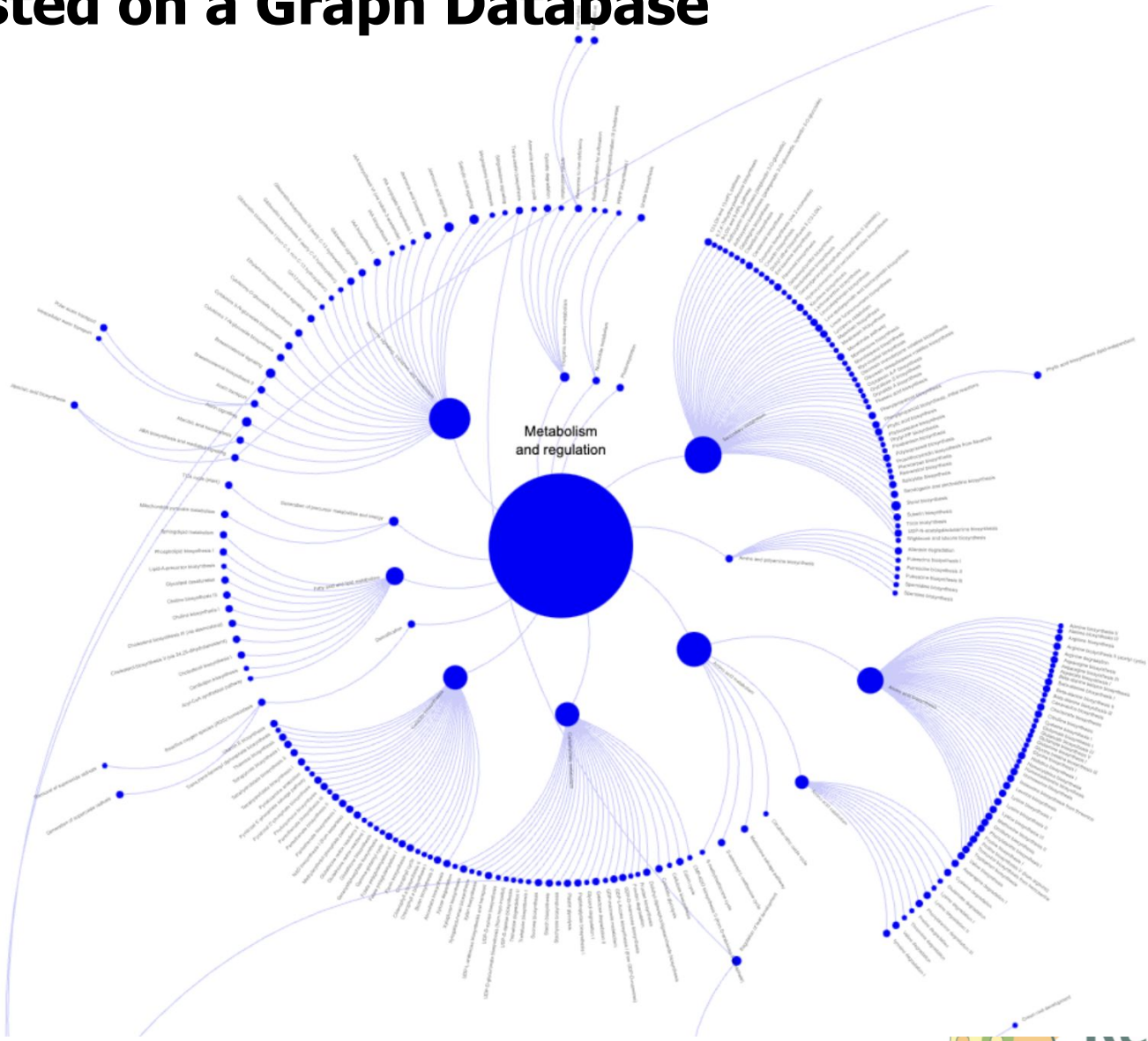
Plant Reactome is a Reaction Network hosted on a Graph Database



Entities



Relationships

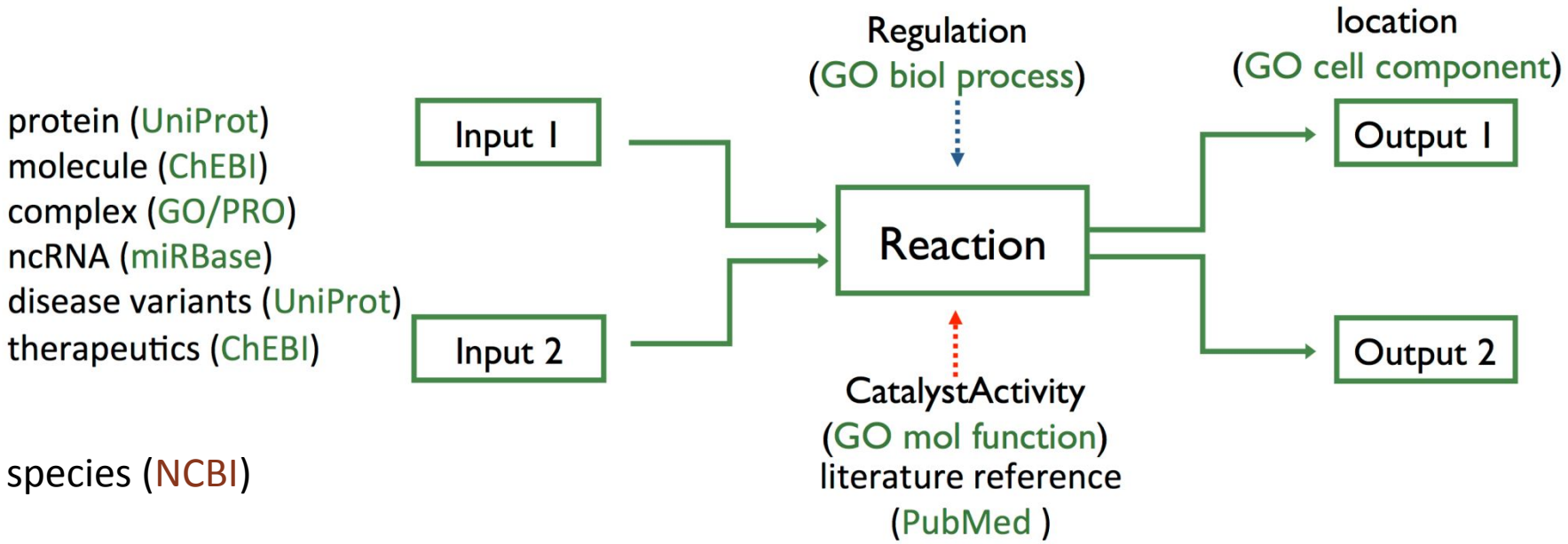


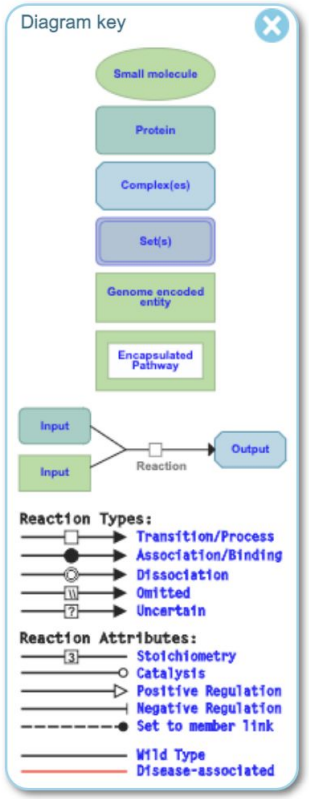
Plant Reactome is a Reaction Network Database

- Explicitly describes biological processes as reactions that transport, transform, and reorganize physical entities.

- Thus, provides molecular representations of many biological events;

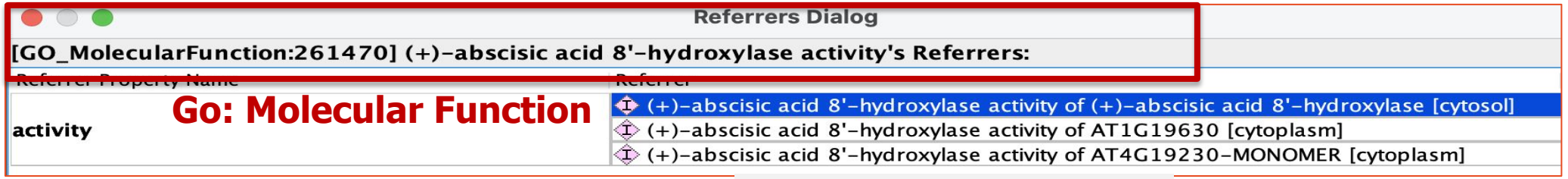
The Reaction:





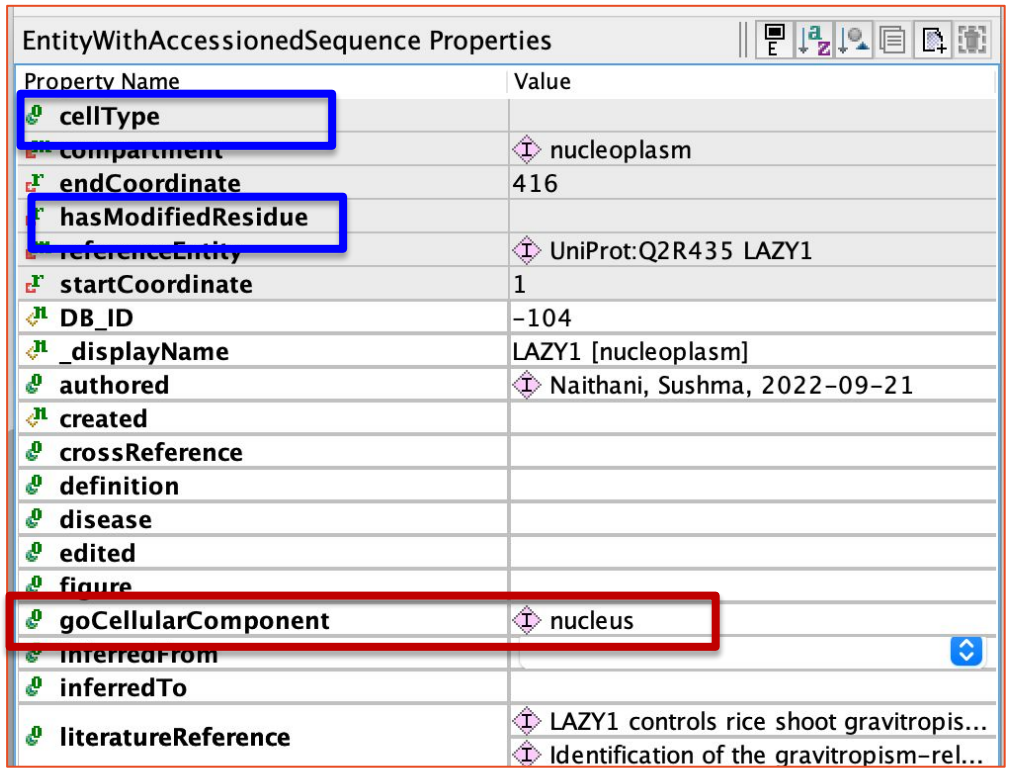
Interoperability at the level of data annotation

Controlled vocabularies for entities and events

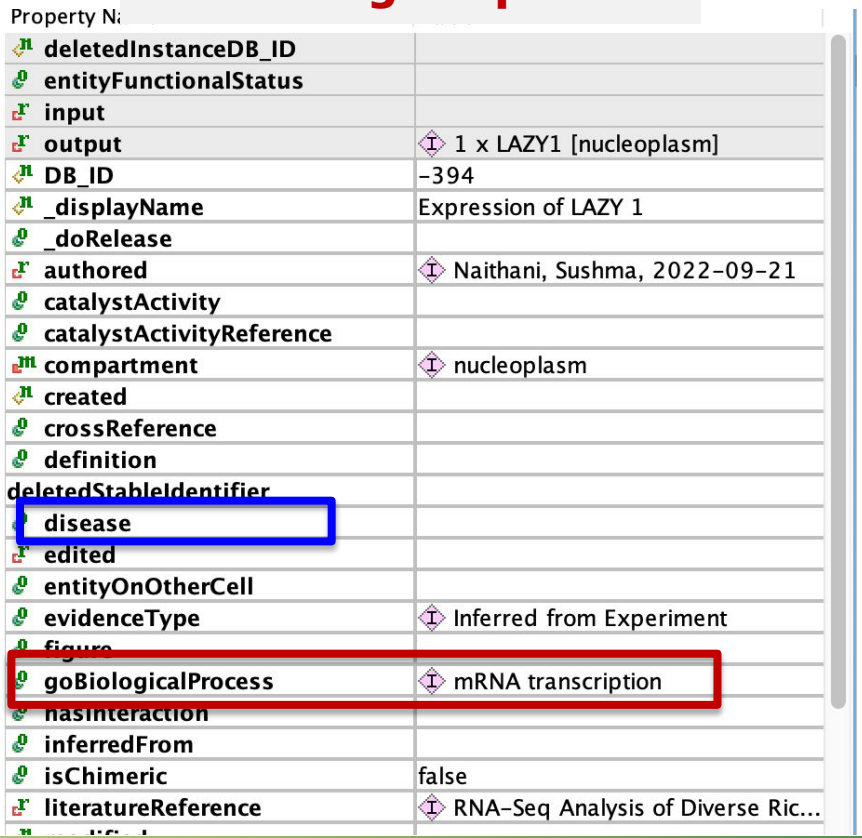


Go: Molecular Function

Entities: proteins, Gene, transcripts
GO: Cellular Component



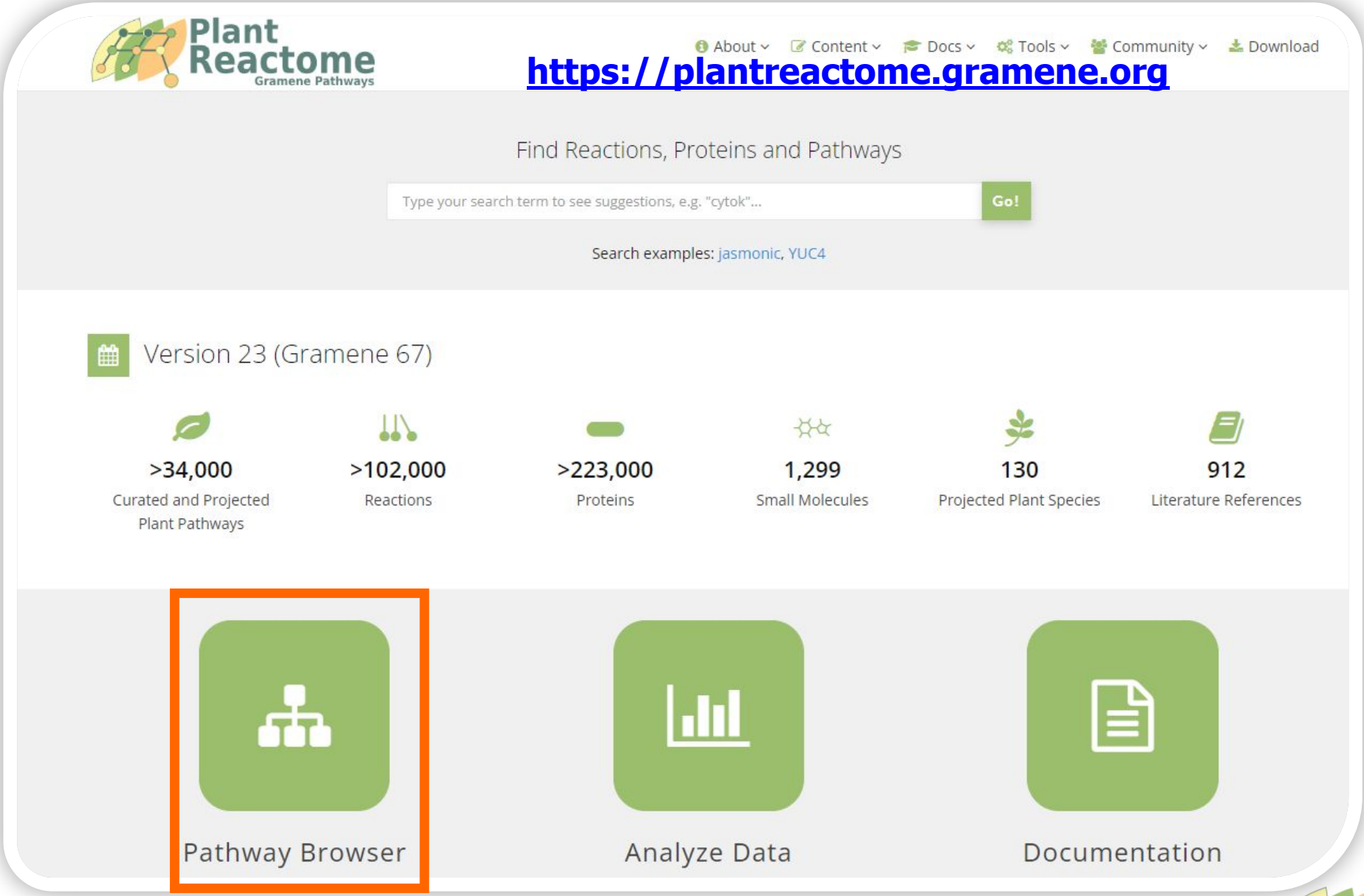
Reactions:
GO: Biological process

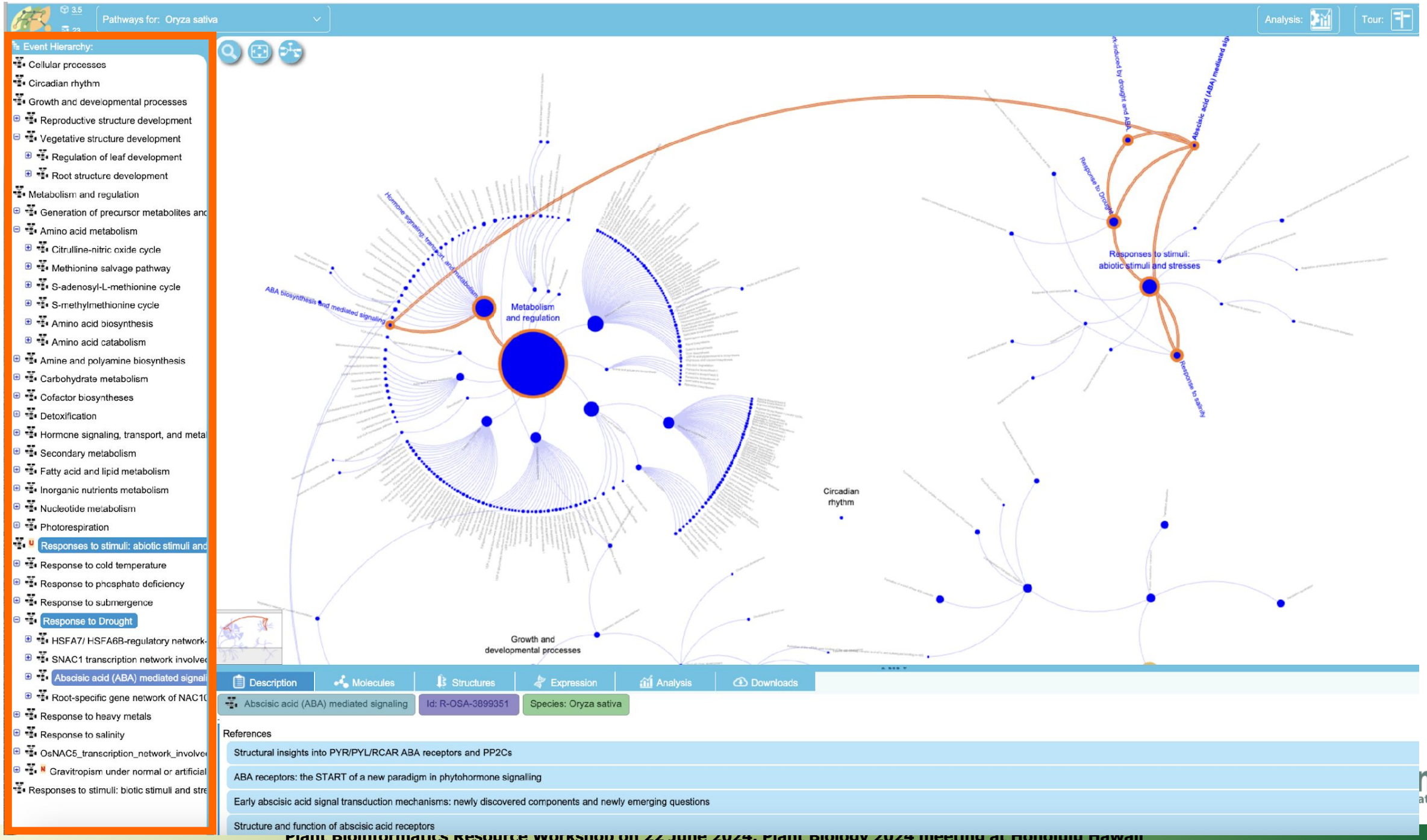


We have provision in our data schema to accommodate Details

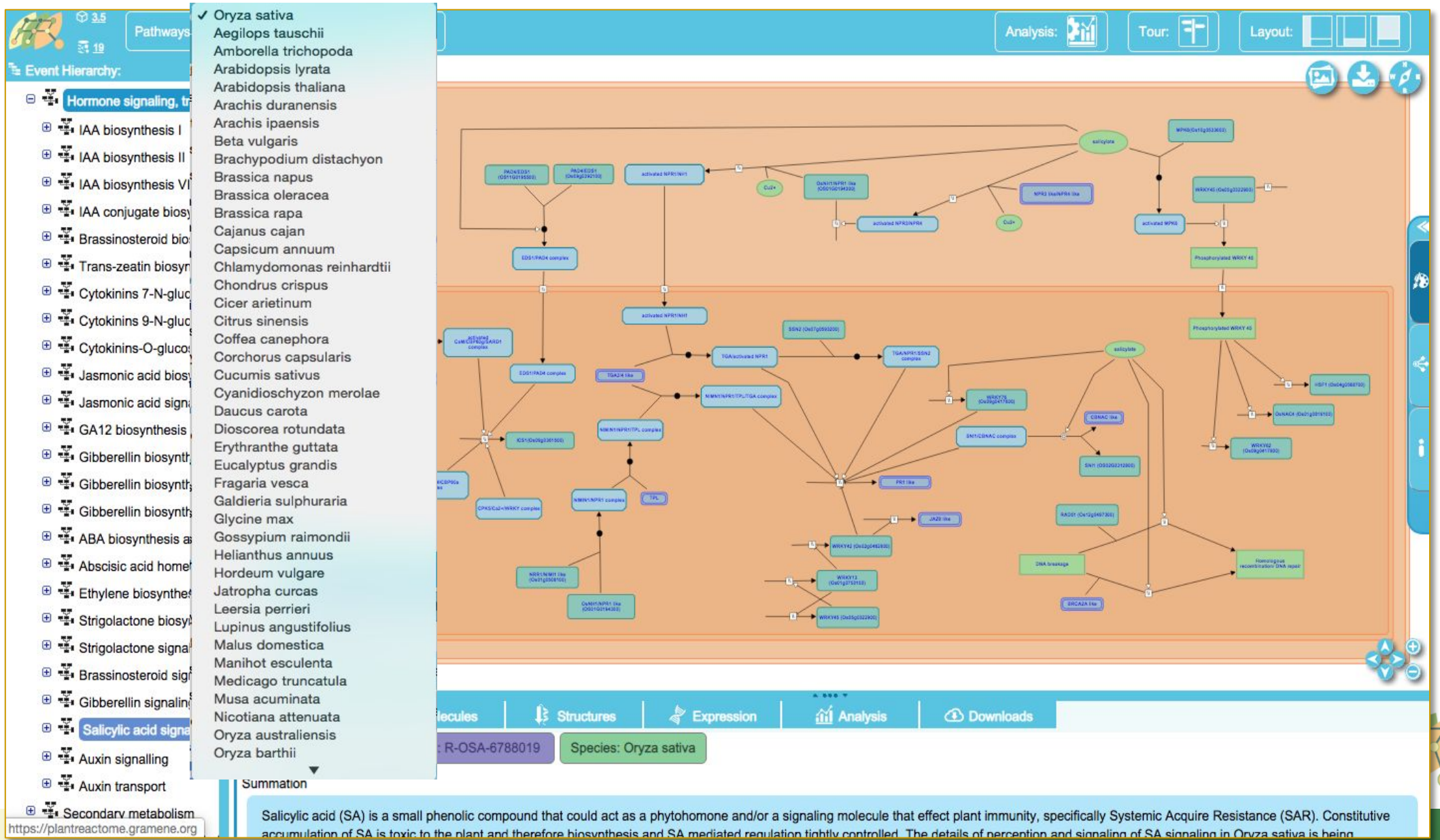
- Cell type
- Protein modifications
- Disease models and pathogens

Plant Reactome
Gramene Pathways


Plant Reactome
Gramene Pathways
About
Content
Docs
Tools
Community
Download
https://plantreactome.gramene.org
Find Reactions, Proteins and Pathways
Type your search term to see suggestions, e.g. "cytok"...
Go!
Search examples: jasmonic, YUC4
Version 23 (Gramene 67)
>34,000
Curated and Projected Plant Pathways
>102,000
Reactions
>223,000
Proteins
1,299
Small Molecules
130
Projected Plant Species
912
Literature References
Pathway Browser
Analyze Data
Documentation


Pathways for: Oryza sativa
Analysis:
Tour:
Event Hierarchy:
Cellular processes
Circadian rhythm
Growth and developmental processes
Reproductive structure development
Vegetative structure development
Regulation of leaf development
Root structure development
Metabolism and regulation
Generation of precursor metabolites and
Amino acid metabolism
Citrulline-nitric oxide cycle
Methionine salvage pathway
S-adenosyl-L-methionine cycle
S-methylmethionine cycle
Amino acid biosynthesis
Amino acid catabolism
Amine and polyamine biosynthesis
Carbohydrate metabolism
Cofactor biosyntheses
Detoxification
Hormone signaling, transport, and meta
Secondary metabolism
Fatty acid and lipid metabolism
Inorganic nutrients metabolism
Nucleotide metabolism
Photorespiration
Responses to stimuli: abiotic stimuli and
Response to cold temperature
Response to phosphate deficiency
Response to submergence
Response to Drought
HSFA7/ HSFA6B-regulatory network-
SNAC1 transcription network involve
Abscisic acid (ABA) mediated signali
Root-specific gene network of NAC1
Response to heavy metals
Response to salinity
OsNAC5_transcription_network_involve
Gravitropism under normal or artificial
Responses to stimuli: biotic stimuli and stre
Metabolism and regulation
Hormone signaling, transport, and metabolism
ABA biosynthesis and mediated signaling
Responses to stimuli: abiotic stimuli and stresses
Response to Drought
Abscisic acid (ABA) mediated signaling
Responses to salinity
Circadian rhythm
Growth and developmental processes
Description
Molecules
Structures
Expression
Analysis
Downloads
Abscisic acid (ABA) mediated signaling
Id: R-OSA-3899351
Species: Oryza sativa
References
Structural insights into PYR/PYL/RCAR ABA receptors and PP2Cs
ABA receptors: the START of a new paradigm in phytohormone signalling
Early abscisic acid signal transduction mechanisms: newly discovered components and newly emerging questions
Structure and function of abscisic acid receptors

Exploring Pathways in Pathway Browser



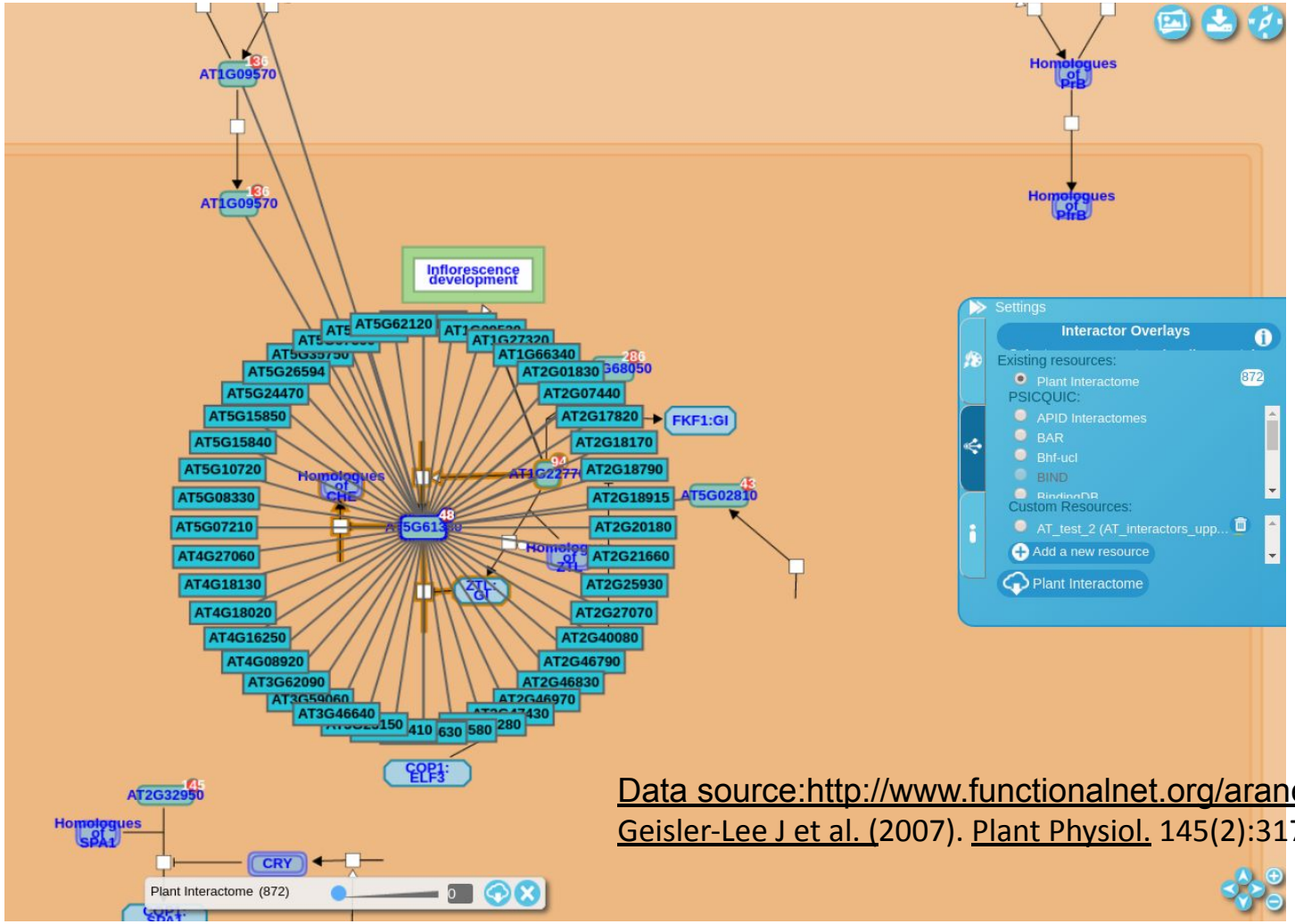
Plant Reactome
Gramene Pathways

Pathway Projections in Arabidopsis

Plant Reactome
Gramene Pathways

Displaying Gene Interaction Data on Plant Reactome Pathways

Synthesizing gene-gene interactions information



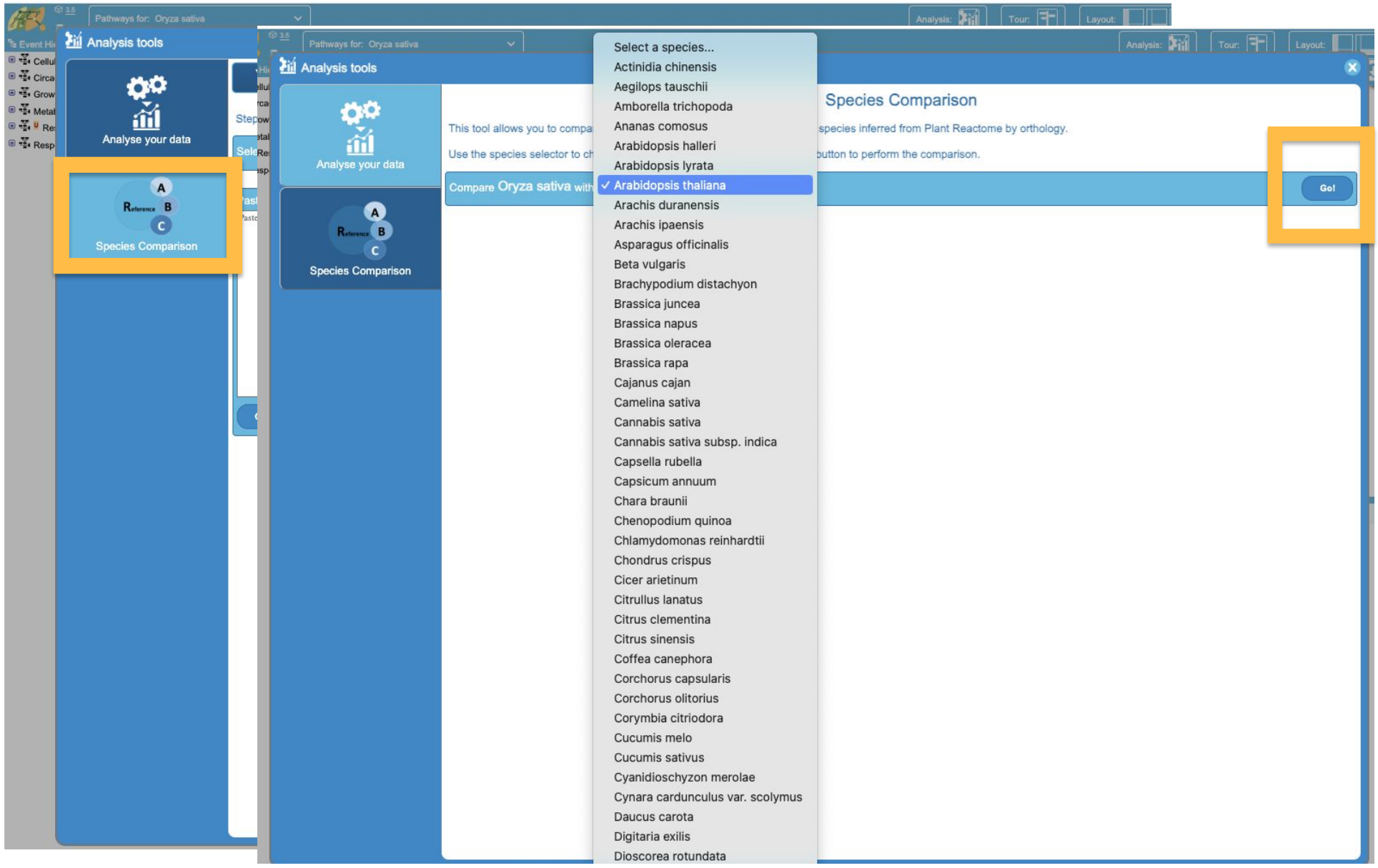
Users can also upload their own data

Users can send us the data from their favorite species

Data source:http://www.functionalnet.org/aranet/

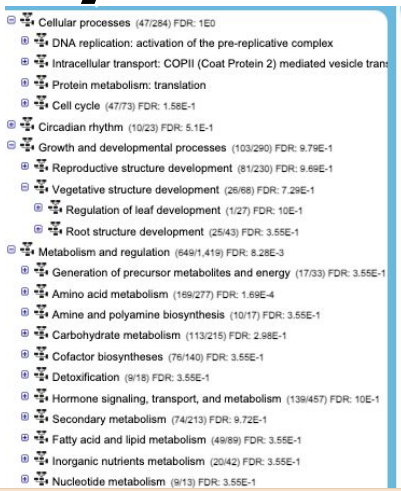
Geisler-Lee J et al. (2007). Plant Physiol. 145(2):317-29

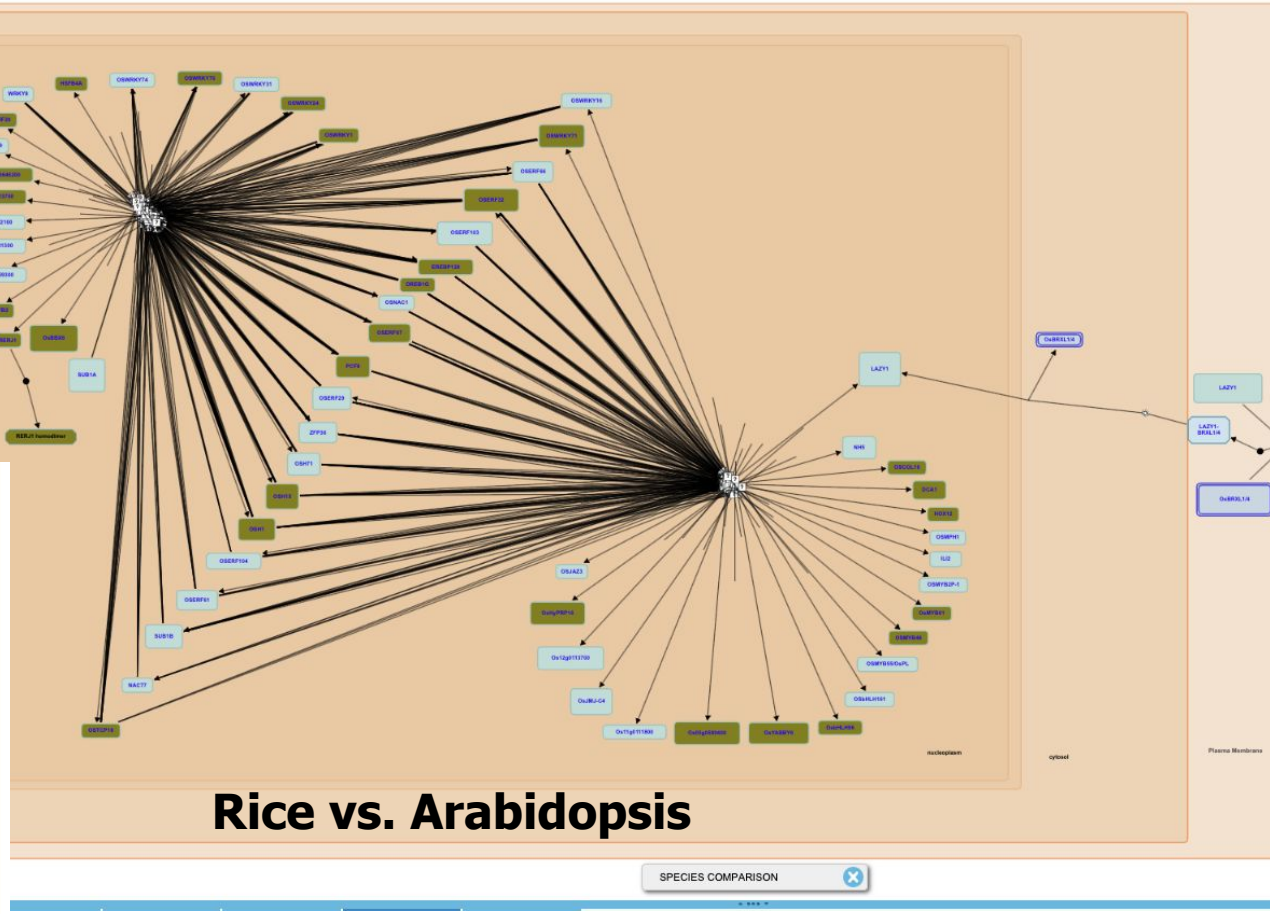
Plant Reactome Gramene Pathways

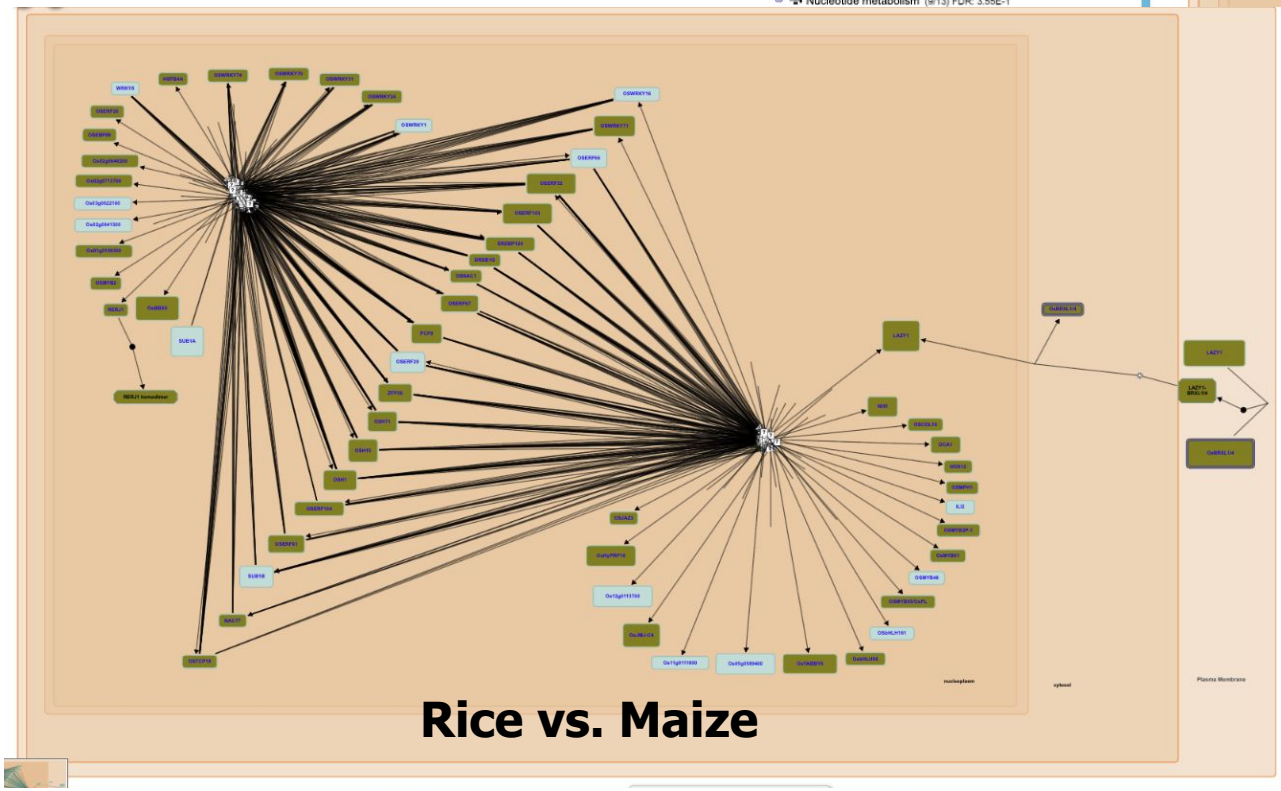


Plant Reactome
Gramene Pathways

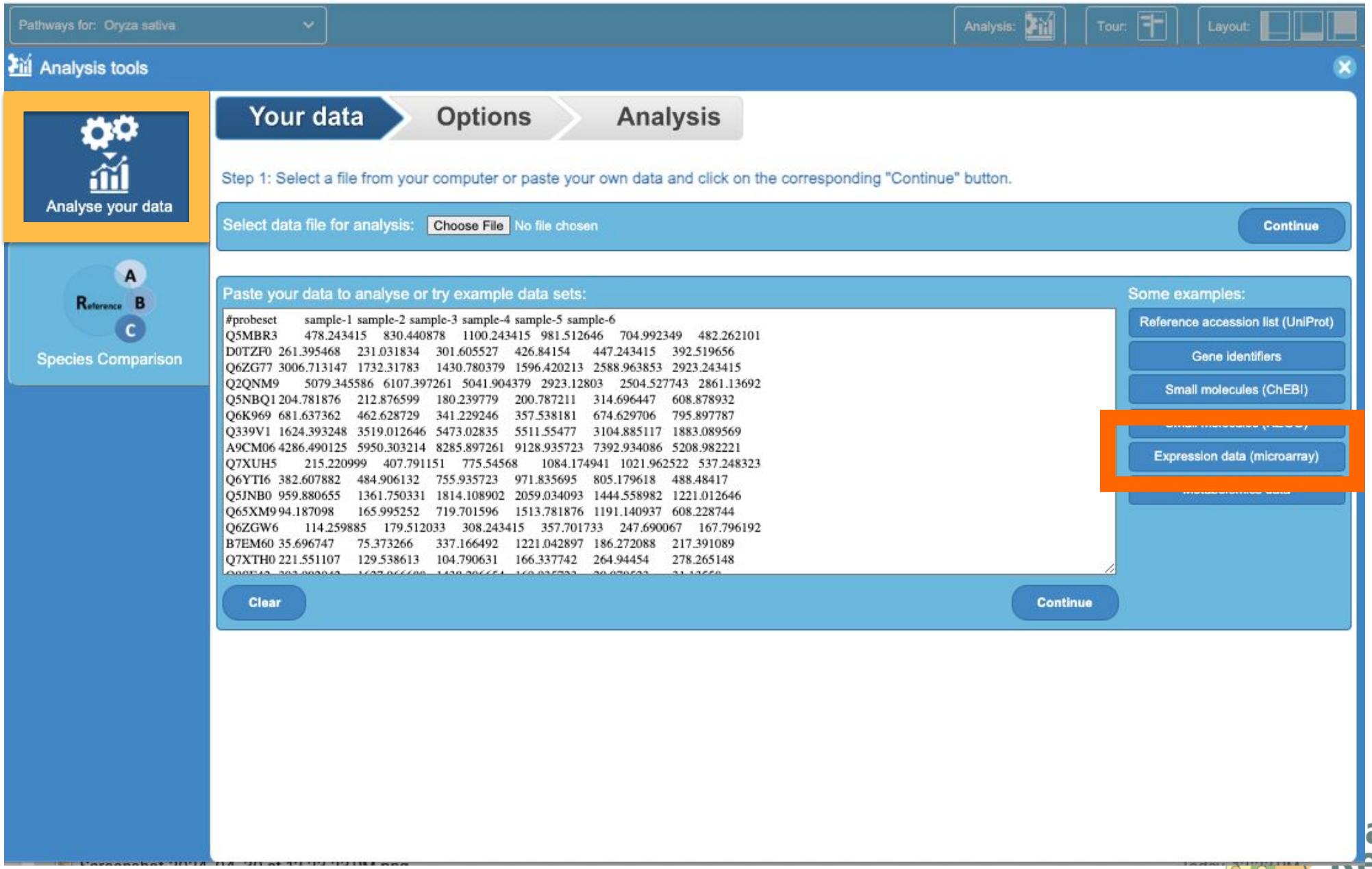
Analysis Tools: Species Comparisons





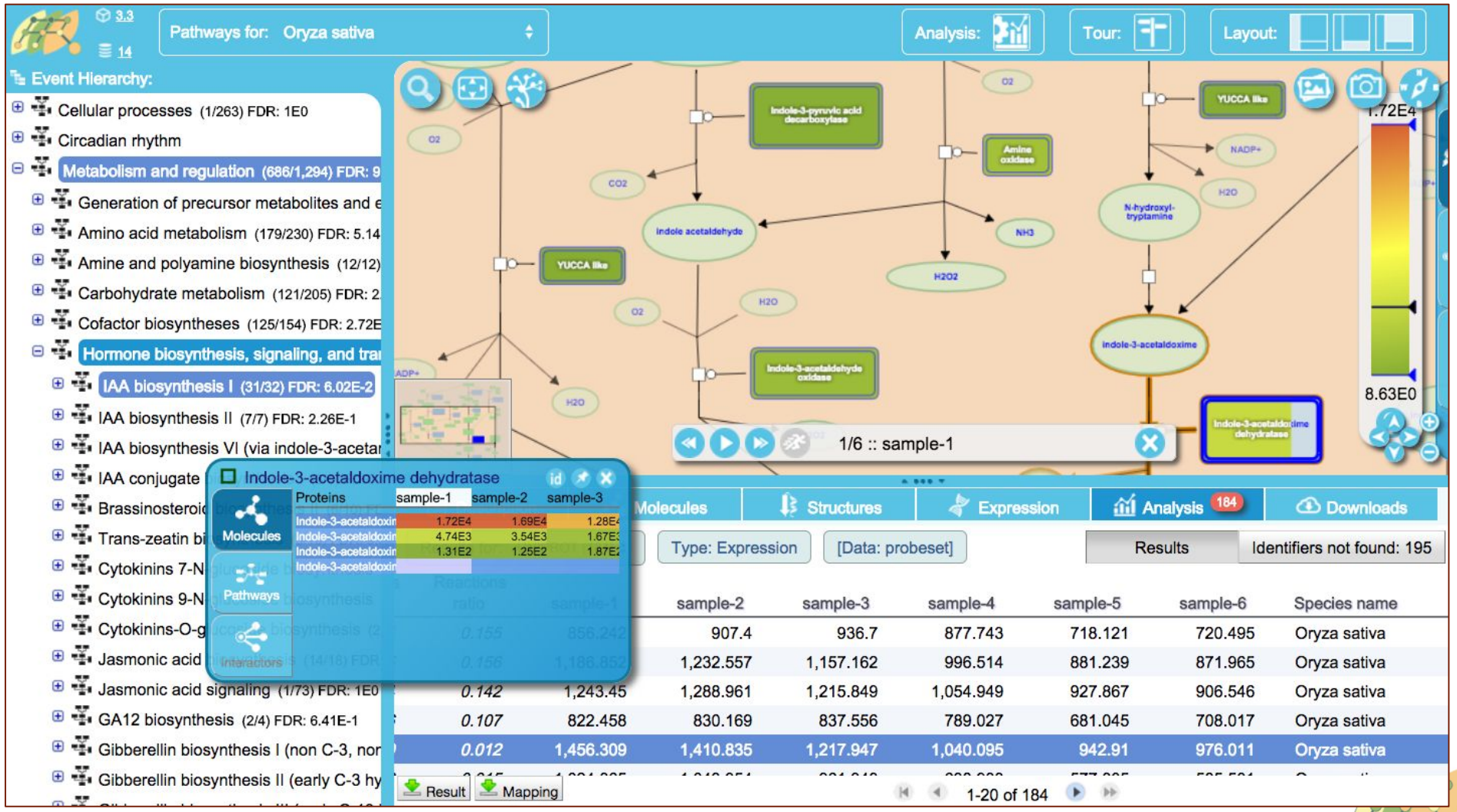


Plant Reactome
Gramene Pathways


Pathways for: Oryza sativa
Analysis:
Tour:
Layout:
Analysis tools
Analyse your data
Species Comparison
Your data
Options
Analysis
Step 1: Select a file from your computer or paste your own data and click on the corresponding "Continue" button.
Select data file for analysis:
Choose File
No file chosen
Continue
Paste your data to analyse or try example data sets:
#probeset sample-1 sample-2 sample-3 sample-4 sample-5 sample-6
Q5MBR3 478.243415 830.440878 1100.243415 981.512646 704.992349 482.262101
D0TZF0 261.395468 231.031834 301.605527 426.84154 447.243415 392.519656
Q6ZG77 3006.713147 1732.31783 1430.780379 1596.420213 2588.963853 2923.243415
Q2QNM9 5079.345586 6107.397261 5041.904379 2923.12803 2504.527743 2861.13692
Q5NBQ1 204.781876 212.876599 180.239779 200.787211 314.696447 608.878932
Q6K969 681.637362 462.628729 341.229246 357.538181 674.629706 795.897787
Q339V1 1624.393248 3519.012646 5473.02835 5511.55477 3104.885117 1883.089569
A9CM06 4286.490125 5950.303214 8285.897261 9128.935723 7392.934086 5208.982221
Q7XUH5 215.220999 407.791151 775.54568 1084.174941 1021.962522 537.248323
Q6YTI6 382.607882 484.906132 755.935723 971.835695 805.179618 488.48417
Q5JNB0 959.880655 1361.750331 1814.108902 2059.034093 1444.558982 1221.012646
Q65XM9 94.187098 165.995252 719.701596 1513.781876 1191.140937 608.228744
Q6ZGW6 114.259885 179.512033 308.243415 357.701733 247.690067 167.796192
B7EM60 35.696747 75.373266 337.166492 1221.042897 186.272088 217.391089
Q7XTH0 221.551107 129.538613 104.790631 166.337742 264.94454 278.265148
Clear
Continue
Some examples:
Reference accession list (UniProt)
Gene identifiers
Small molecules (ChEBI)
Expression data (microarray)

Analysis Tools

Users can upload their own omics data and download analysis results



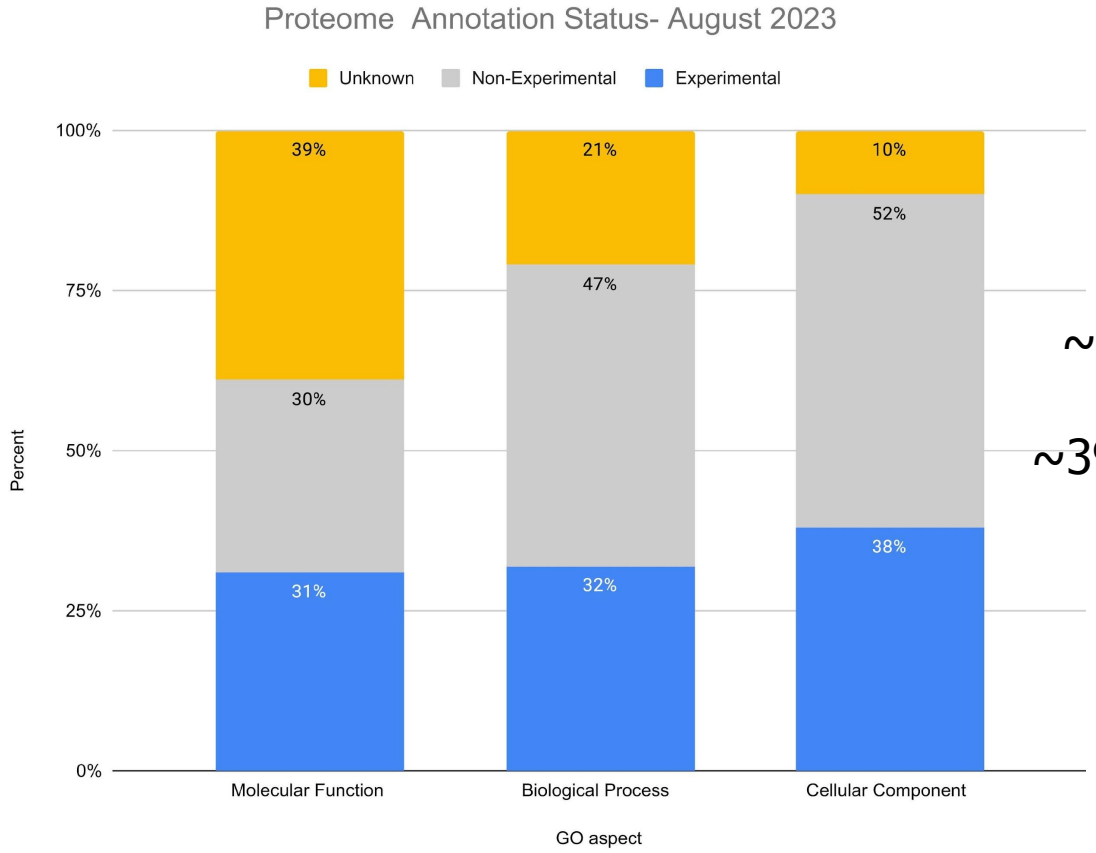
Plant Reactome
Gramene Pathways

LIMITATIONS
for
Pathway Biocuration

The annotation status of the Arabidopsis proteome as of 2024

Arabidopsis thaliana genome was published in 2000

~27,000 genes



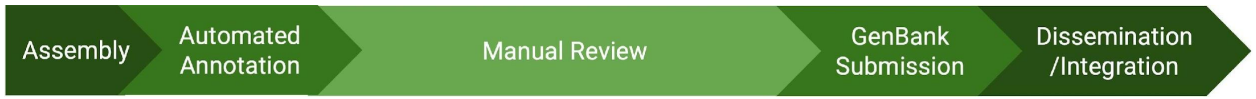
tair

Molecular Function

~30% experimental evidence

~39% genes: unknown function

~30% have only GO



2000 ☐---------- Phases of genome reannotation--------- ☐2024

Genetics, Volume 227, Issue 1, May 2024, iyae027, https://doi.org/10.1093/genetics/iyae027

Plant Reactome Gramene Pathways

The annotation status of the Rice proteome as of 2021

Rice genome
Draft genome in 2002
and high-quality 2005

~ 39,045 protein-coding genes

Research | Open access | Published: 19 April 2022

New Data and New Features of the FunRiceGenes (Functionally Characterized Rice Genes) Database: 2021 Update

Fangfang Huang, Yingru Jiang, Tiantian Chen, Haoran Li, Mengjia Fu, Yazhou Wang, Yufang Xu, Yang Li, Zhengfu Zhou, Lihua Jia, Yidan Ouyang & Wen Yao

Rice **15**, Article number: 23 (2022) | Cite this article

4125 Accesses | **12** Citations | **2** Altmetric | Metrics

Up to Nov 2021

- ~ 4100 functionally characterized rice genes
- ~ 6000 members of different gene families
- 22.3% of the 39,045 annotated protein-coding genes in the rice genome.

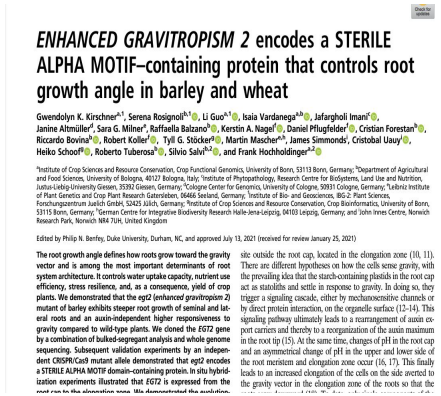
Plant Reactome
Gramene Pathways

Can we use existing knowledge from other species to curate pathways in the Plant Reactome?

Plant Reactome
Gramene Pathways

Use of gene-orthology relationships to improve functional annotation of a rice gene

Barley EGT2 is a Transcriptional regulator of root growth angle



ENHANCED GRAVITROPISM 2 encodes a STERILE ALPHA MOTIF–containing protein that controls root growth angle in barley and wheat

Gwendolyn K. Kirschner[a,1], Serena Rosignoli[b,1], Li Guo[a,1], Isaia Vardanega[a,b], Jafargholi Imani[c], Janine Altmüller[d], Sara G. Milner[e], Raffaella Balzano[b], Kerstin A. Nagel[f], Daniel Pflugfelder[f], Cristian Forestan[b], Riccardo Bovina[b], Robert Koller[b], Tyll G. Stöcker[a,b], Martin Mascher[e,h], James Simmonds[i], Cristobal Uauy[i], Heiko Schoof[g], Roberto Tuberosa[b], Silvio Salvi[b,2], and Frank Hochholdinger[a,2]

[a]Institute of Crop Sciences and Resource Conservation, Crop Functional Genomics, University of Bonn, 53113 Bonn, Germany; [b]Department of Agricultural and Food Sciences, University of Bologna, 40127 Bologna, Italy; [c]Institute of Phytopathology, Research Centre for BioSystems, Land Use and Nutrition, Justus-Liebig-University Giessen, 35392 Giessen, Germany; [d]Cologne Center for Genomics, University of Cologne, 50931 Cologne, Germany; [e]Leibniz Institute of Plant Genetics and Crop Plant Research Gatersleben, 06466 Seeland, Germany; [f]Institute of Bio- and Geosciences, IBG-2: Plant Sciences, Forschungszentrum Juelich GmbH, 52425 Jülich, Germany; [g]Institute of Crop Sciences and Resource Conservation, Crop Bioinformatics, University of Bonn, 53115 Bonn, Germany; [h]German Centre for Integrative Biodiversity Research Halle-Jena-Leipzig, 04103 Leipzig, Germany; and [i]John Innes Centre, Norwich Research Park, Norwich NR4 7UH, United Kingdom

Edited by Philip N. Benfey, Duke University, Durham, NC, and approved July 13, 2021 (received for review January 25, 2021)

The root growth angle defines how roots grow toward the gravity vector and is among the most important determinants of root system architecture. It controls water uptake capacity, nutrient use efficiency, stress resilience, and, as a consequence, yield of crop plants. We demonstrated that the *egt2* (*enhanced gravitropism 2*) mutant of barley exhibits steeper root growth of seminal and lateral roots and an auxin-independent higher responsiveness to gravity compared to wild-type plants. We cloned the *EGT2* gene by a combination of bulked-segregant analysis and whole genome sequencing. Subsequent validation experiments by an independent CRISPR/Cas9 mutant allele demonstrated that *egt2* encodes a STERILE ALPHA MOTIF domain–containing protein. In situ hybridization experiments illustrated that *EGT2* is expressed from the

site outside the root cap, located in the elongation zone (10, 11). There are different hypotheses on how the cells sense gravity, with the prevailing idea that the starch-containing plastids in the root cap act as statoliths and settle in response to gravity. In doing so, they trigger a signaling cascade, either by mechanosensitive channels or by direct protein interaction, on the organelle surface (12–14). This signaling pathway ultimately leads to a rearrangement of auxin export carriers and thereby to a reorganization of the auxin maximum in the root tip (15). At the same time, changes of pH in the root cap and an asymmetrical change of pH in the upper and lower side of the root meristem and elongation zone occur (16, 17). This finally leads to an increased elongation of the cells on the side averted to the gravity vector in the elongation zone of the roots so that the

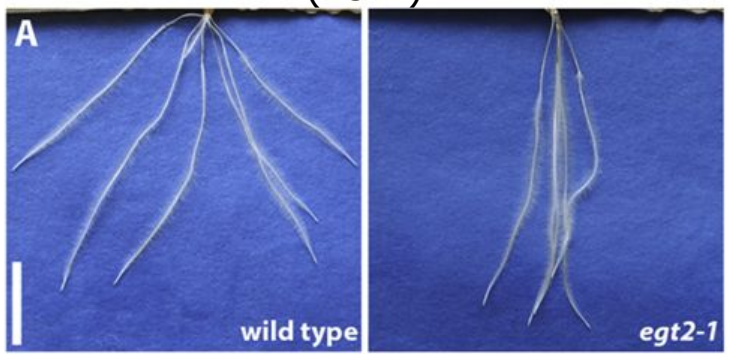
Barley

Arabidopsis

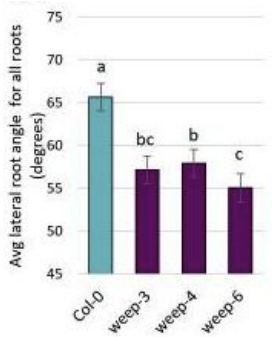
Rice

HORVU.MOREX.r3.5HG0447830 (EGT2) — AT3G07760 (AtSAM5) — **Os12g0514600**

Unknown Function



(Kirschner et al., 2021; PMID: 34446550)



Johnson et al., 2022 (PMID: 35685275)

Gene Name for Os12g0514600 ☐ OsEGT2

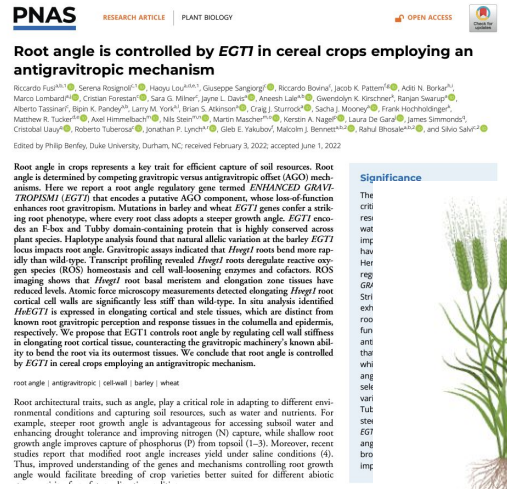
Functional Annotation ☐ transcriptional Fact

Pathway ☐ root growth angle formation

Response to Gravitropism ☐ anti-gravitropic offset, negative gravitropic response

Reactome Gramene Pathways

Gene-orthology relationships to predict potential functions of a rice gene


PNAS RESEARCH ARTICLE | PLANT BIOLOGY OPEN ACCESS

Root angle is controlled by *EGT1* in cereal crops employing an antigravitropic mechanism

Riccardo Fusi[a,b,1], Serena Rosignoli[a,1], Haoyu Lou[a,b,c,1], Giuseppe Sangiorgi[d], Riccardo Bovina[a], Jacob K. Pattern[e,2], Aditi N. Borkar[a,b], Marco Lombardi[a,b], Cristian Forestan[a], Sara G. Milner[a], Jayne L. Davet[a], Aneesh Lale[a,b], Gwendolyn K. Kirschner[a], Ranjan Swarup[a], Alberto Tassinari[a], Bipin K. Pandey[a,b], Larry M. York[a,f], Brian S. Atkinson[a], Craig J. Sturrock[a], Sacha J. Mooney[a], Frank Hochholdinger[g], Matthew R. Tucker[a,f], Axel Himmelbach[h], Nils Stein[h,i], Martin Mascher[h,i], Kerstin A. Nagel[j], Laura De Gara[k], James Simmonds[l], Cristobal Uauy[l], Roberto Tuberosa[a], Jonathan P. Lynch[a,f], Gleb E. Yakubov[f], Malcolm J. Bennett[a,b,2], Rahul Bhosale[a,b,2], and Silvio Salvi[a,2]

Edited by Philip Benfey, Duke University, Durham, NC; received February 3, 2022; accepted June 1, 2022

Root angle in crops represents a key trait for efficient capture of soil resources. Root angle is determined by competing gravitropic versus antigravitropic offset (AGO) mechanisms. Here we report a root angle regulatory gene termed *ENHANCED GRAVITROPISM1* (*EGT1*) that encodes a putative AGO component, whose loss-of-function enhances root gravitropism. Mutations in barley and wheat *EGT1* genes confer a striking root phenotype, where every root class adopts a steeper growth angle. *EGT1* encodes an F-box and Tubby domain-containing protein that is highly conserved across plant species. Haplotype analysis found that natural allelic variation at the barley *EGT1* locus impacts root angle. Gravitropic assays indicated that *Hvegt1* roots bend more rapidly than wild-type. Transcript profiling revealed *Hvegt1* roots deregulate reactive oxygen species (ROS) homeostasis and cell wall-loosening enzymes and cofactors. ROS imaging shows that *Hvegt1* root basal meristem and elongation zone tissues have reduced levels. Atomic force microscopy measurements detected elongating *Hvegt1* root cortical cell walls are significantly less stiff than wild-type. In situ analysis identified *HvEGT1* is expressed in elongating cortical and stele tissues, which are distinct from known root gravitropic perception and response tissues in the columella and epidermis, respectively. We propose that EGT1 controls root angle by regulating cell wall stiffness in elongating root cortical tissue, counteracting the gravitropic machinery's known ability to bend the root via its outermost tissues. We conclude that root angle is controlled by *EGT1* in cereal crops employing an antigravitropic mechanism.

root angle | antigravitropic | cell-wall | barley | wheat

Significance

Root architectural traits, such as angle, play a critical role in adapting to different environmental conditions and capturing soil resources, such as water and nutrients. For example, steeper root growth angle is advantageous for accessing subsoil water and enhancing drought tolerance and improving nitrogen (N) capture, while shallower root growth angle improves capture of phosphorus (P) from topsoil (1–3). Moreover, recent studies report that modified root angle increases yield under saline conditions (4). Thus, improved understanding of the genes and mechanisms controlling root growth angle would facilitate breeding of crop varieties better suited for different abiotic

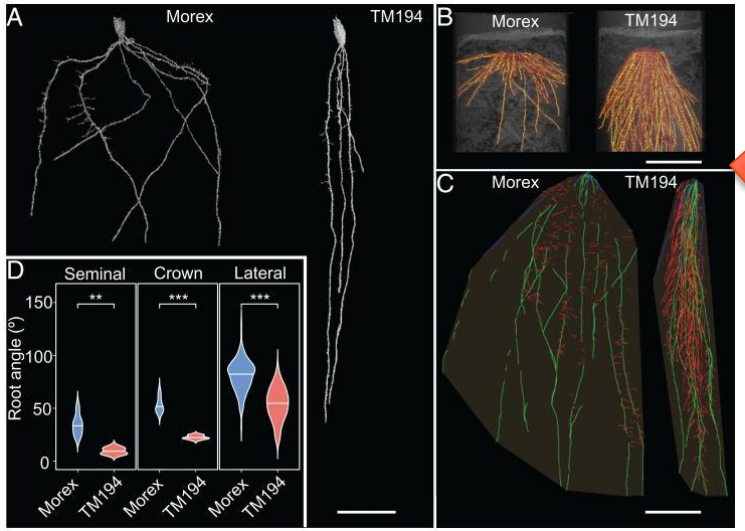
egt1 mutant has a steep root growth angle phenotype

hypergravitropic root phenotype

EGT1 appears to function as a component of an antigravitropic offset mechanism that regulates tissue stiffness, which impacts final root growth angle.

Barley

Wild type egt1 TILLING mutant TM194



Functional Annotation ☐ **transcriptional Factor**

Pathway ☐ **root growth angle formation**

Response to Gravitropism ☐ anti-gravitropic offset, negative gravitropic response

Arabidopsis thaliana (AT2G18280) TLP6, TULP2 (a TF)

gene-orthology projection

Manual Curation

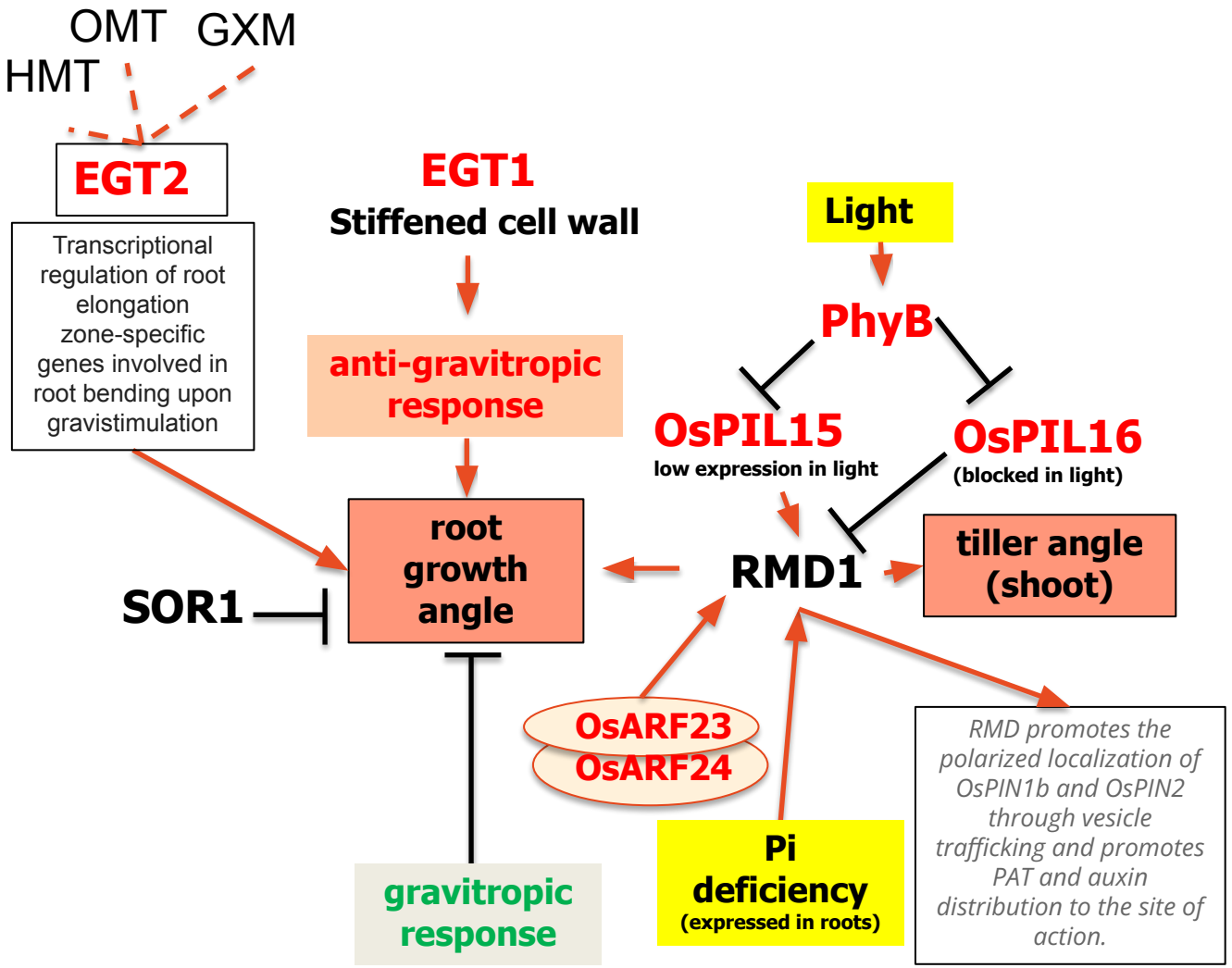
Oryza sativa Os02g0705300 OsTLP8 (TF)

HORVU6Hr1G068970 (EGT1) (Fusi et al., 2022; PMID: 35881796)

HORVU.MOREX.r3.6HG0607550

Plant Reactome Gramene Pathways

Gene-gene interaction network based on evidence from rice and other species



> Proc Natl Acad Sci U S A. 2014 Jul 15;111(28):10377-82. doi: 10.1073/pnas.1401680111. Epub 2014 Jun 30.

Rice actin-binding protein RMD is a key link in the auxin–actin regulatory loop that controls cell growth

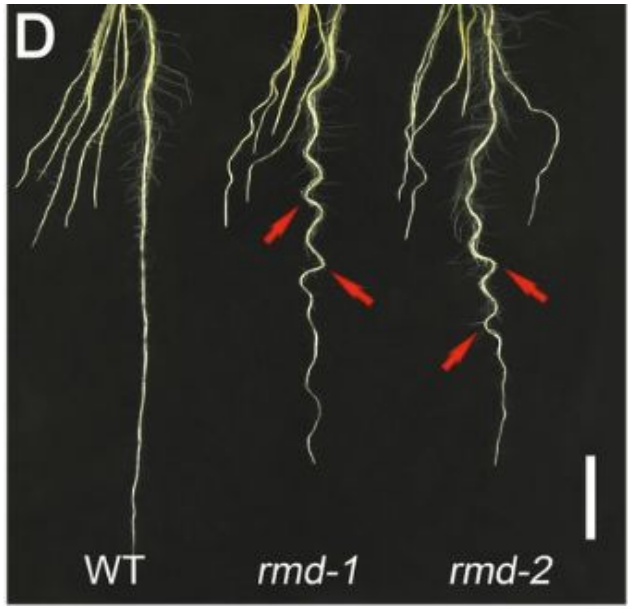
Gang Li [1], Wanqi Liang [1], Xiaoqing Zhang [1], Haiyun Ren [2], Jianping Hu [3], Malcolm J Bennett [4], Dabing Zhang [5]

Affiliations + expand

PMID: 24982173 PMCID: PMC4104909 DOI: 10.1073/pnas.1401680111

Abstract

The plant hormone auxin plays a central role in plant growth and development. Auxin transport and signaling depend on actin organization. Despite its functional importance, the mechanistic link between actin filaments (F-actin) and auxin intracellular signaling remains unclear. Here, we report that the actin-organizing protein Rice Morphology Determinant (RMD), a type II formin from rice (Oryza sativa), provides a key link. Mutants lacking RMD display abnormal cell growth and altered configuration of F-actin array direction. The rmd mutants also exhibit an inhibition of auxin-mediated cell elongation, decreased polar auxin transport, altered auxin distribution gradients in root tips, and suppression of plasma membrane localization of auxin transporters O. sativa PIN-FORMED 1b (OsPIN1b) and OsPIN2 in root cells. We demonstrate that RMD is required for endocytosis, exocytosis, and auxin-mediated OsPIN2 recycling to the plasma membrane. Moreover, RMD expression is directly regulated by heterodimerized O. sativa auxin response factor 23 (OsARF23) and OsARF24, providing evidence that auxin modulates the orientation of F-actin arrays through RMD. In support of this regulatory loop, osarf23 and lines with reduced expression



(Li et al., 2014; PMID: 24982173)

Plant Reactome
Gramene Pathways

Re-use and Re-analysis of Transcriptome Data

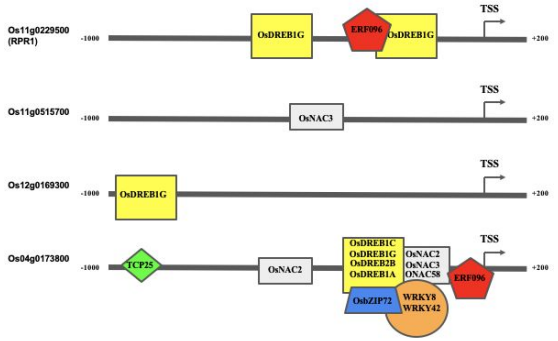
Biocuration of rice transcription factor network involved in stress response

- **Re-use/re-analysis of Omics data**
- **Review of published papers**

Literature and transcriptome data review

Compilation of gene list

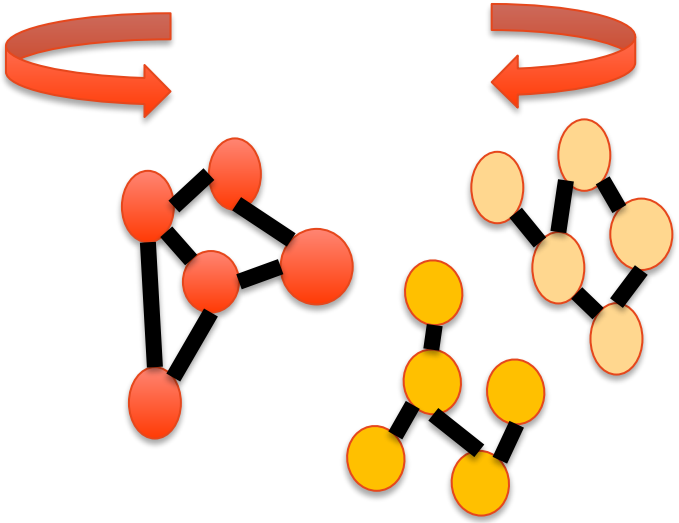
Manual biocuration of genes: improved functional annotation with linked evidence



- **Sequence Data**
- **ChIP-qPCR**
- **ChIP-Seq**
- **TSS-mapping**

Transcriptome Data
Co-expression analysis

Identification of the genes belonging to same network

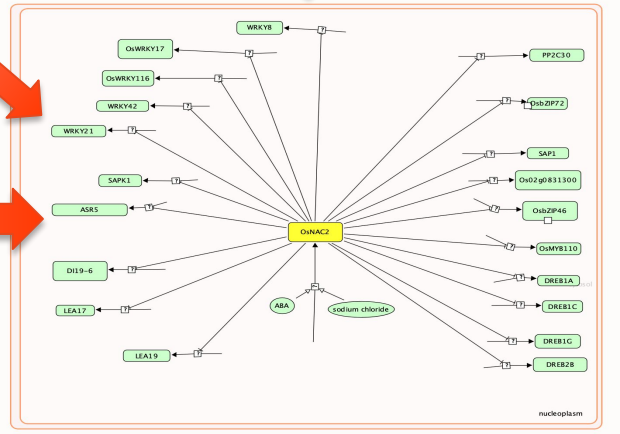


Promoter analysis of the genes

Score TF-Target relationship

Biocuration in Reactome Curator Tool

Integration into the Plant Reactome & Orthology projections



Reactome
Gramene Pathways

Open Access Article

Biocuration of a Transcription Factors Network Involved in Submergence Tolerance during Seed Germination and Coleoptile Elongation in Rice (*Oryza sativa*)

by Sushma Naithani [1,*], Bijayalaxmi Mohanty [2], Justin Elser [1], Peter D'Eustachio [3] and Pankaj Jaiswal [1]

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[2] NUS Environmental Research Institute, National University of Singapore, Singapore 117411, Singapore

[3] Department of Biochemistry and Molecular Pharmacology, NYU Grossman School of Medicine, New York, NY 10016, USA

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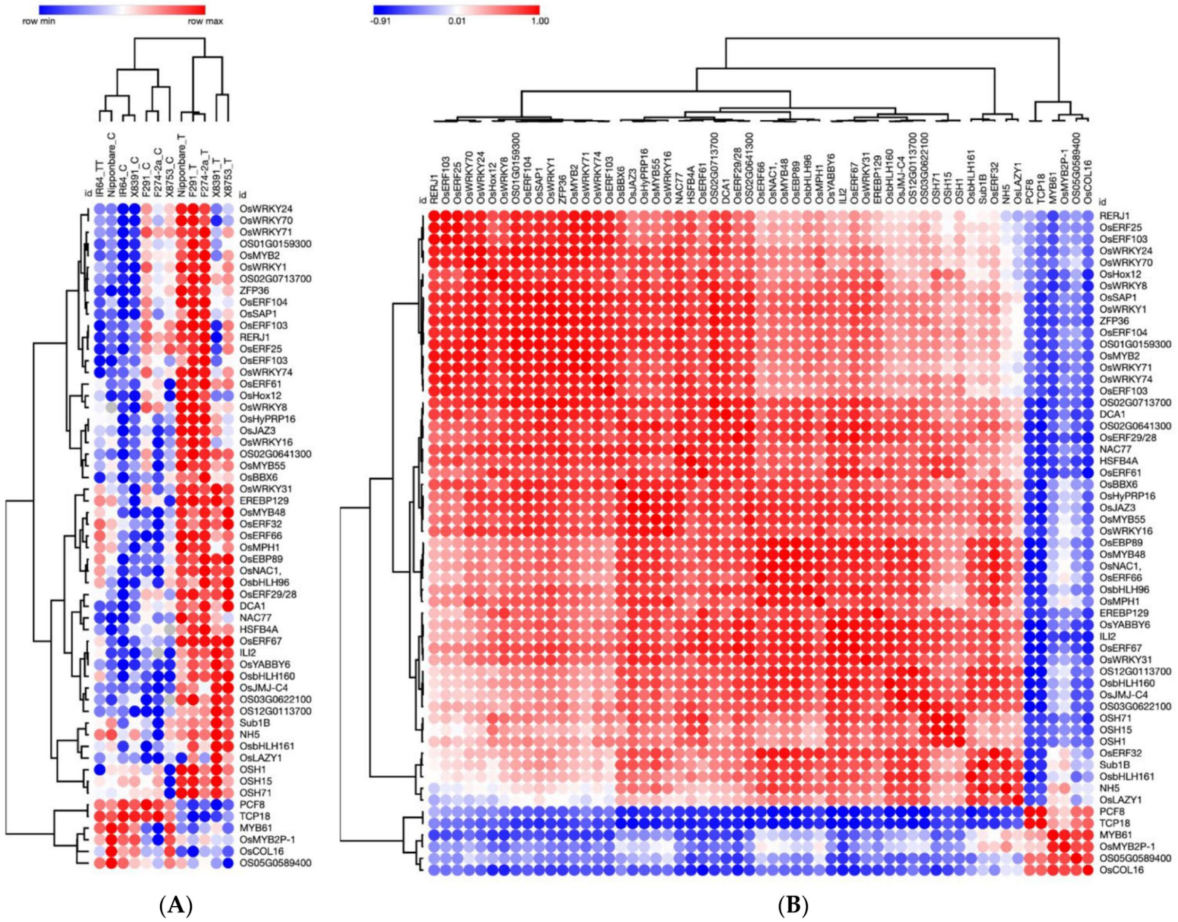
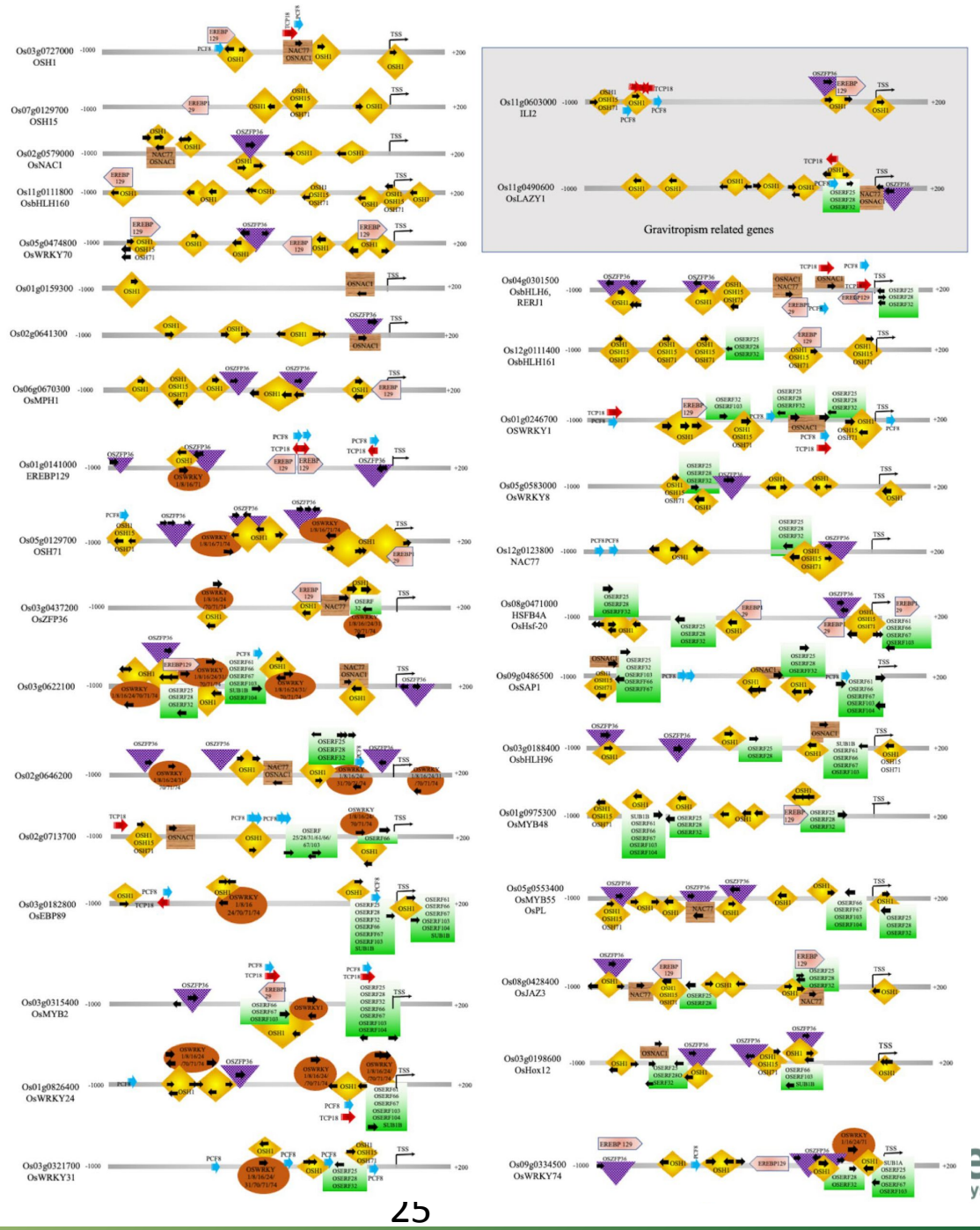
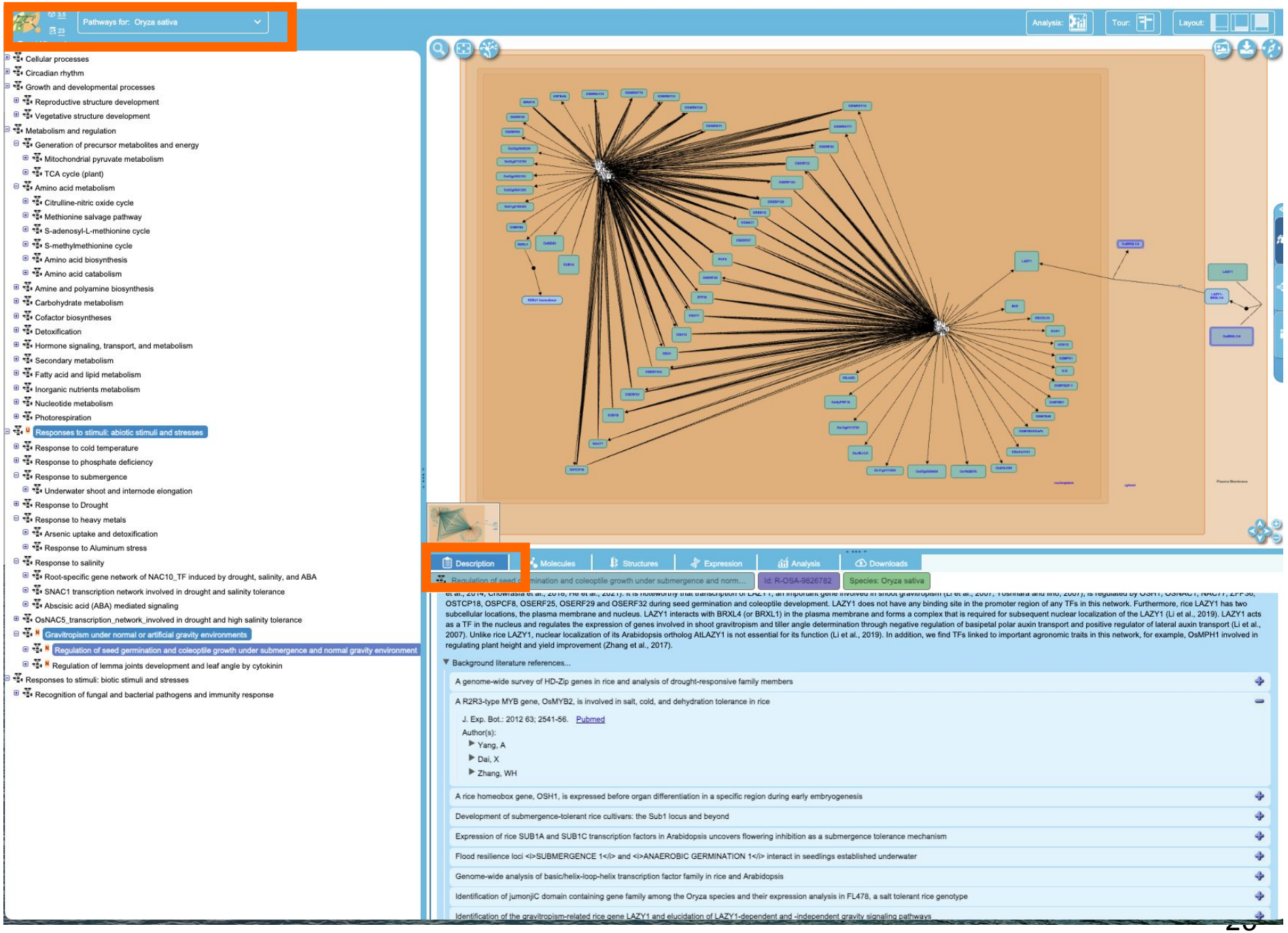
Plants **2023**, *12*(11), 2146; https://doi.org/10.3390/plants12112146

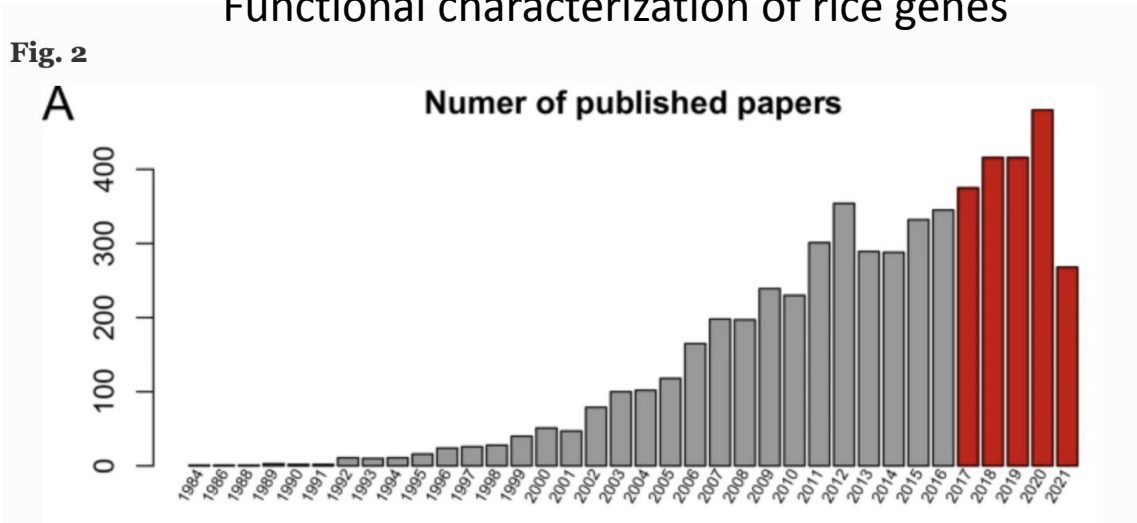


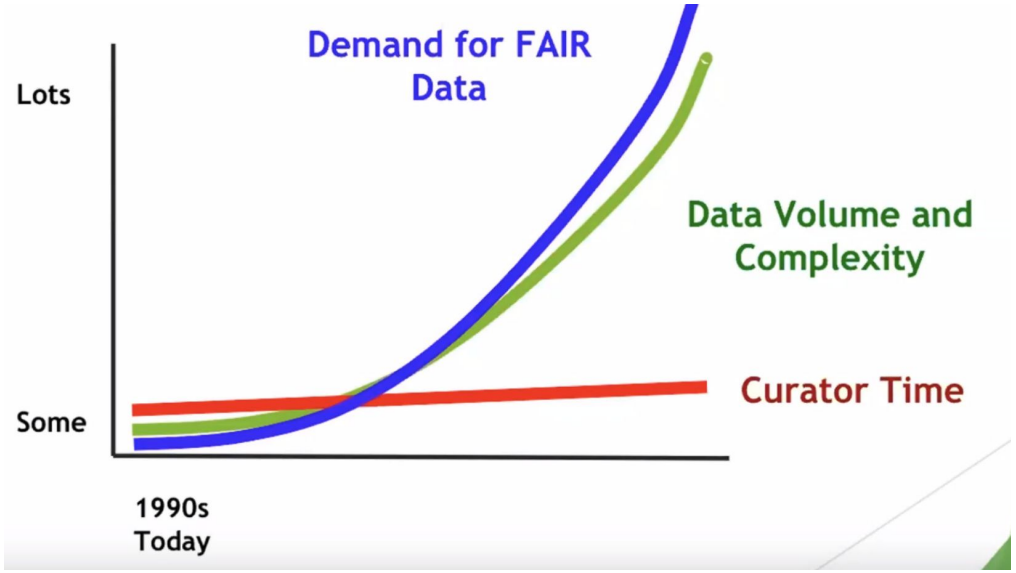



Pathways for: Oryza sativa
Analysis:
Tour:
Layout:
Cellular processes
Circadian rhythm
Growth and developmental processes
Reproductive structure development
Vegetative structure development
Metabolism and regulation
Generation of precursor metabolites and energy
Mitochondrial pyruvate metabolism
TCA cycle (plant)
Amino acid metabolism
Citrulline-nitric oxide cycle
Methionine salvage pathway
S-adenosyl-L-methionine cycle
S-methylmethionine cycle
Amino acid biosynthesis
Amino acid catabolism
Amine and polyamine biosynthesis
Carbohydrate metabolism
Cofactor biosyntheses
Detoxification
Hormone signaling, transport, and metabolism
Secondary metabolism
Fatty acid and lipid metabolism
Inorganic nutrients metabolism
Nucleotide metabolism
Photorespiration
Responses to stimuli: abiotic stimuli and stresses
Response to cold temperature
Response to phosphate deficiency
Response to submergence
Underwater shoot and internode elongation
Response to Drought
Response to heavy metals
Arsenic uptake and detoxification
Response to Aluminum stress
Response to salinity
Root-specific gene network of NAC10_TF induced by drought, salinity, and ABA
SNAC1 transcription network involved in drought and salinity tolerance
Abscisic acid (ABA) mediated signaling
OsNAC5_transcription_network_involved in drought and high salinity tolerance
Gravitropism under normal or artificial gravity environments
Regulation of seed germination and coleoptile growth under submergence and normal gravity environment
Regulation of lemma joints development and leaf angle by cytokinin
Responses to stimuli: biotic stimuli and stresses
Recognition of fungal and bacterial pathogens and immunity response
Description
Molecules
Structures
Expression
Analysis
Downloads
Species: Oryza sativa
OSTCP18, OSPCF8, OSERF25, OSERF29 and OSERF32 during seed germination and coleoptile development. LAZY1 does not have any binding site in the promoter region of any TFs in this network. Furthermore, rice LAZY1 has two subcellular locations, the plasma membrane and nucleus. LAZY1 interacts with BRXL4 (or BRXL1) in the plasma membrane and forms a complex that is required for subsequent nuclear localization of the LAZY1 (Li et al., 2019). LAZY1 acts as a TF in the nucleus and regulates the expression of genes involved in shoot gravitropism and tiller angle determination through negative regulation of basipetal polar auxin transport and positive regulator of lateral auxin transport (Li et al., 2007). Unlike rice LAZY1, nuclear localization of its Arabidopsis ortholog AtLAZY1 is not essential for its function (Li et al., 2019). In addition, we find TFs linked to important agronomic traits in this network, for example, OsMPH1 involved in regulating plant height and yield improvement (Zhang et al., 2017).
Background literature references...
A genome-wide survey of HD-Zip genes in rice and analysis of drought-responsive family members
A R2R3-type MYB gene, OsMYB2, is involved in salt, cold, and dehydration tolerance in rice
J. Exp. Bot.: 2012 63; 2541-56. Pubmed
Author(s):
Yang, A
Dai, X
Zhang, WH
A rice homeobox gene, OSH1, is expressed before organ differentiation in a specific region during early embryogenesis
Development of submergence-tolerant rice cultivars: the Sub1 locus and beyond
Expression of rice SUB1A and SUB1C transcription factors in Arabidopsis uncovers flowering inhibition as a submergence tolerance mechanism
Flood resilience loci SUBMERGENCE 1 and ANAEROBIC GERMINATION 1 interact in seedlings established underwater
Genome-wide analysis of basic/helix-loop-helix transcription factor family in rice and Arabidopsis
Identification of jumonjiC domain containing gene family among the Oryza species and their expression analysis in FL478, a salt tolerant rice genotype
Identification of the gravitropism-related rice gene LAZY1 and elucidation of LAZY1-dependent and -independent gravity signaling pathways

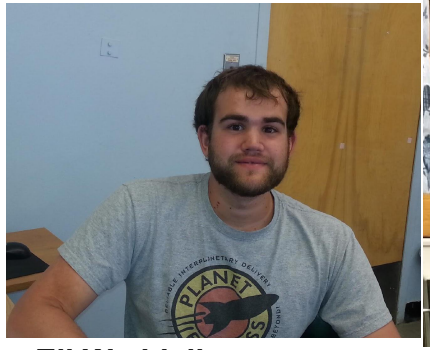
Needed: Increased Support for Biocuration

Functional characterization of rice genes





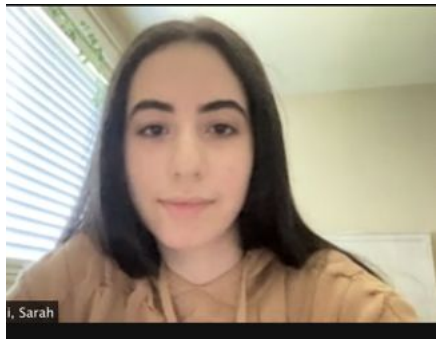
Our Undergraduate Biocurators : Plant Gene and Pathway Curation



Eli Waddell 2013-2014

Christina Partipilo
2014-2016

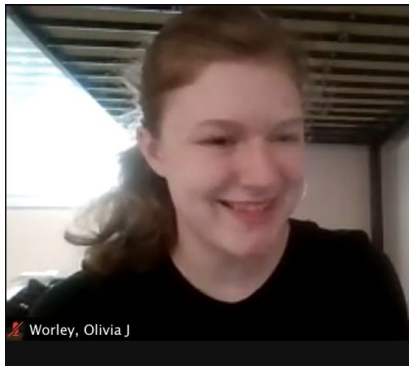
Ami (Amitavo) Ganguli
URSA-Fellow, 2021 winter-spring



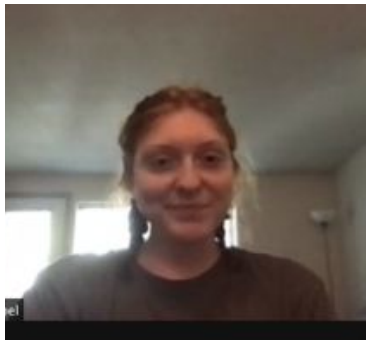
Sarah El-Husseini
URSA-Fellow, 2021 winter-spring
Honors Thesis (2021-2022)

Shayla Rao (spring 2020)

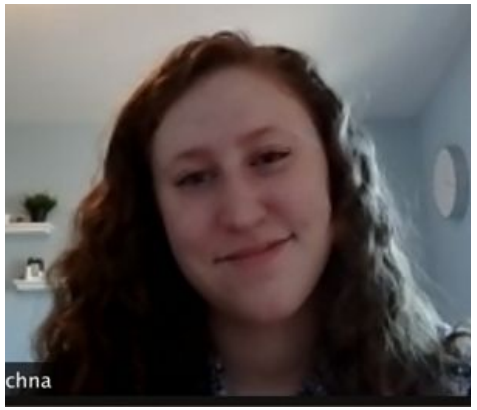
Callan Stowell
(winter-spring 2020)
URSA-fellow



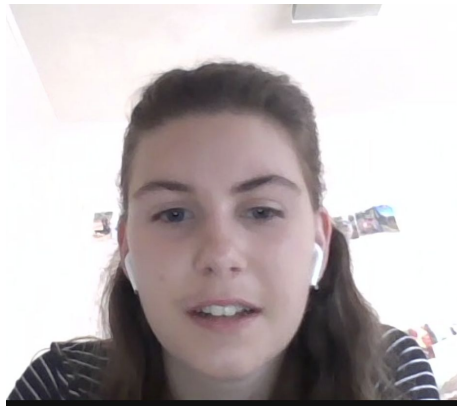
Olivia Worley
URSA-Fellow, 2021 winter-spring



Maddie Goebel
URSA-Fellow, 2021 winter-spring



Gwendolyn Michna
URSA-Fellow, 2021 winter-spring



Kennedy Sparks
URSA-Fellow, 2022 winter-spring

Quentin Beers
URSA-Fellow, 2021 winter-spring

Elizabeth Hooks
URSA-Fellow, winter-spring 2022, continued until Fall 2023

Tutorials and Videos on Gramene YouTube Channel

tinyurl.com/grchannel

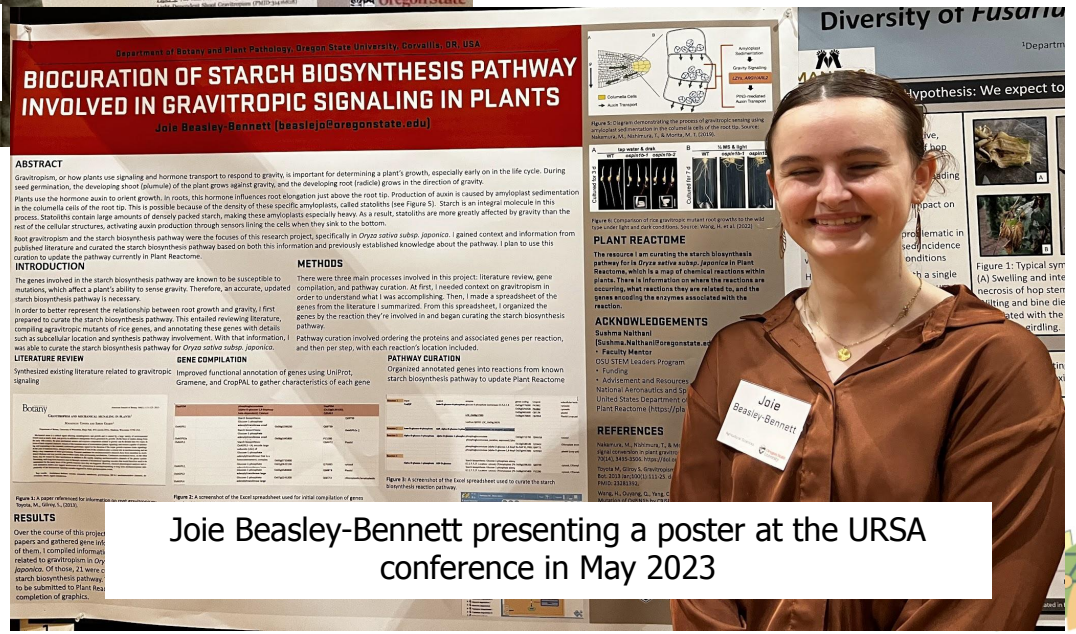
Plant Reactome
Gramene Pathways

We train undergraduate students in critical review of scientific literature and gene biocuration

Riley Callahan and Jenna Rosenau presenting their work at the URSA conference in May 2023

Madeleine Zeller
(Fall 2023)

Tongsak, Annette
URSA-Fellow, 2023 winter-spring



Joie Beasley-Bennett presenting a poster at the URSA conference in May 2023

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URSA undergraduate Research Fellows of 2024 working on Biocuration of genes and pathways

Siena Buchanan
second-year biology major

Isabella Ramirez
second-year microbiology major

Carolyn Crofford
Bioresource Research and Sustainability major

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Biocuration of a gene family using transcriptome data to infer tissue specific expression and association with stress response

Daemon A. Dikeman (2019-2020)
(Honors Thesis, undergraduate)
Joined Ph.D. at Univ. of Maine

> PeerJ. 2021 Mar 15;9:e11052. doi: 10.7717/peerj.11052. eCollection 2021.

Beyond gene ontology (GO): using biocuration approach to improve the gene nomenclature and functional annotation of rice S-domain kinase subfamily

Sushma Naithani [1], Daemon Dikeman [1], Priyanka Garg [1], Noor Al-Bader [1], Pankaj Jaiswal [1]

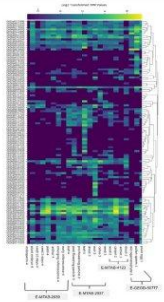
Affiliations + expand

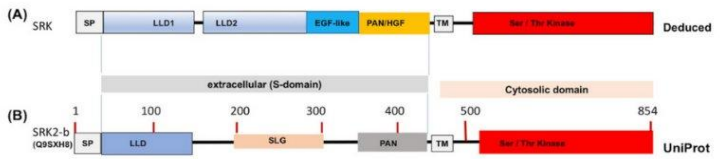
PMID: 33777532 PMCID: PMC7971086 DOI: 10.7717/peerj.11052

Free PMC article

Abstract

The S-domain subfamily of receptor-like kinases (SDRLKs) in plants is poorly characterized. Most members of this subfamily are currently assigned gene function based on the *S*-locus Receptor Kinase from Brassica that acts as the female determinant of self-incompatibility (SI). However, Brassica like SI mechanisms does not exist in most plants. Thus, automated Gene Ontology (GO) pipelines are not sufficient for functional annotation of SDRLK subfamily members and lead to erroneous association with the GO biological process of SI. Here, we show that manual bio-curation can help to correct and improve the gene annotations and association with relevant biological processes. Using publicly available genomic and transcriptome datasets, we conducted a detailed





PeerJ Life & Environment
Views: 736
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Sushma Naithani group, OSU
Undergraduate Biocurators

Bijayalaxmi Mohanty
Community Biocurator

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- Justin Elser (Software Dev)
- Parul Gupta (biocuration)

NYU Langone Medical Center
- Peter D'Eustachio (Biocuration)

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- Guanming Wu

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- IntAct

Cold Spring Harbor Laboratory
- Doreen Ware (PI)
- Andrew Olson

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Thanks

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