



# Metabolic and Regulatory Networks for Cereals

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## Introduction

Gramene is an open-source, curated comparative plant genomics database ([www.gramene.org](http://www.gramene.org)). In order to represent the metabolomes of cereal crops and thereby support their analysis and comparison, we develop and curate pathway databases for cereal species. The Gramene portal includes pathways for rice (RiceCyc), sorghum (SorghumCyc), maize (MaizeCyc, developed in collaboration with MaizeGDB; [maizecyc.maizegdb.org](http://maizecyc.maizegdb.org)) and *Brachypodium* (BrachyCyc). The portal also mirrors other crop and model species-specific pathway databases and reference pathway databases MetaCyc and PlantCyc. Having all the individual pathway databases at one site facilitates inter- and intra-specific comparisons between pathways and associated genes, and searches for patterns of coexpression. The integrated Omics Viewer tool allows users to overlay and visualize transcriptomic, proteomic, and metabolomic datasets with expressed values on pathway maps in a cellular overview in real time. Moving beyond the MetaCyc based pathway databases, Gramene in collaboration with the Reactome project ([www.reactome.org](http://www.reactome.org)) is in the process of developing metabolic and regulatory networks for rice and Arabidopsis on the Reactome platform, which would integrate plant-specific regulatory, signaling and metabolic pathways from multiple sources. Funded by USDA ARS 1907-21000-030, 3625-21000-051 and NSF IOS-0703908

## Gramene Home Page

## Pathways Home Page Navigation

## Comparative Analysis

## Pathway Information

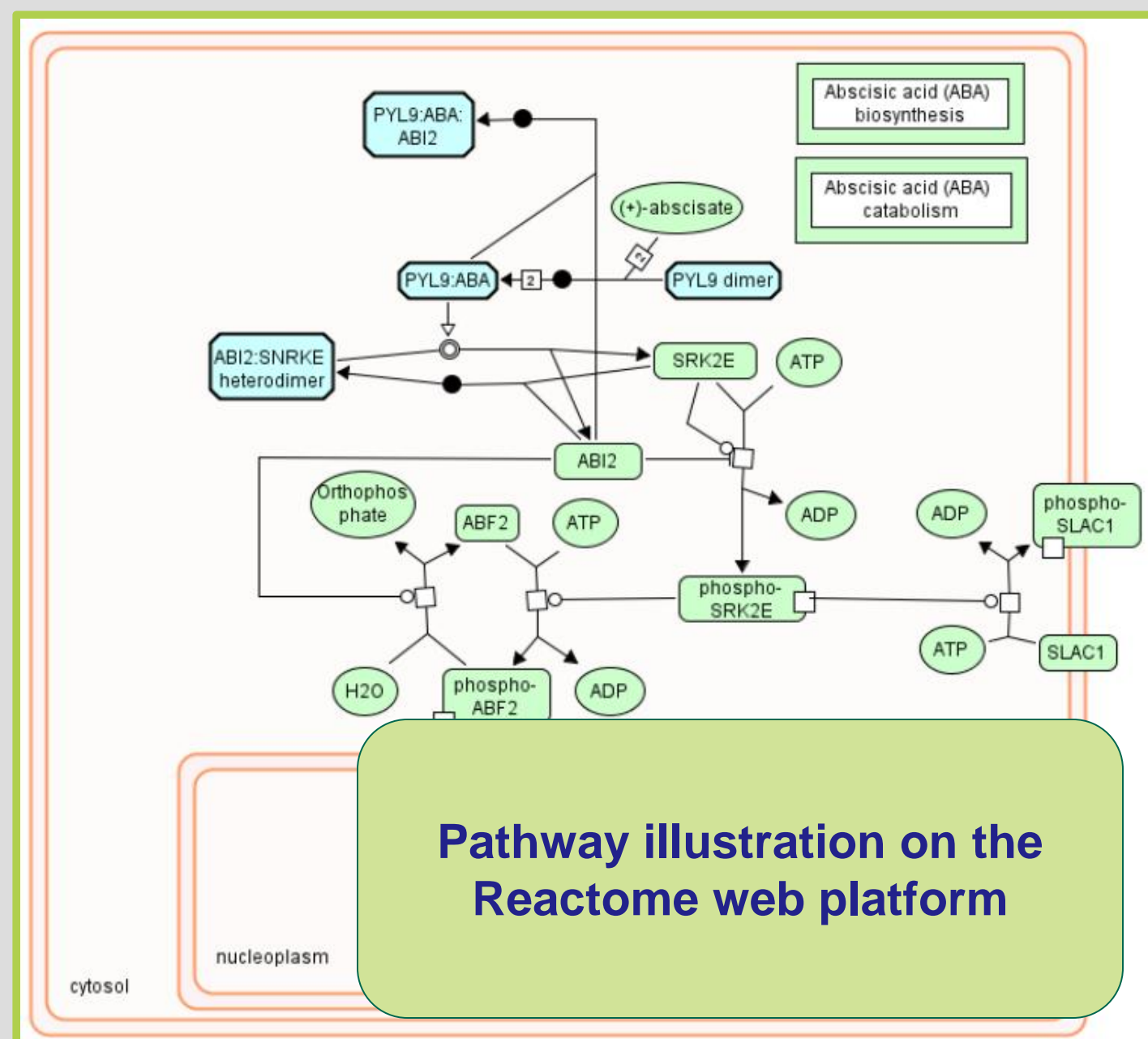
- Gramene is a collaboration between CSHL, Cornell University and Oregon State University supported by National Science Foundation (Grant No. 0703908)
- The data content and web interface of the database is updated semi-annually.
- For up-to-date information, please visit Gramene website ([www.gramene.org](http://www.gramene.org)) or send feedback to [gramene@gramene.org](mailto:gramene@gramene.org)
- Your contribution to pathway curation is welcome

## Conversion of rice and Arabidopsis pathways to the Reactome platform

### Pathway Data Sources

- RiceCyc v3.2 (hosted by the Gramene project) <http://pathway.gramene.org/gramene/riccyc.shtm>
- AraCyc v8.0 (provided by TAIR) <http://www.arabidopsis.org/biocyc/>
- <http://www.ArabidopsisReactome.org/>
- Human pathway projections from <http://www.reactome.org/> for both *O. sativa* and *A. thaliana*

Over 500 curated and projected pathways for each species



In support of the Gramene project's efforts to integrate and expand plant-specific regulatory, signaling, and metabolic pathways, we have converted rice and Arabidopsis pathway data drawn from the curated RiceCyc and AraCyc databases, originally developed by Gramene and the Plant Metabolic Network, respectively, in the BioCyc format.

Data was exported in the BioPAX Level 2 format and then imported into the Reactome database schema using a modified version of the Reactome BioPAX importer. The converted pathways were then merged into the Reactome central database for curatorial activities. Based on gene orthology predictions generated by Ensembl's Compara pipeline, we imported additional pathways -- such as cell cycle and DNA repair -- projected from sequence similarity to curated human pathways. A small set of manually-curated pathways have also been imported from the prior version of Arabidopsis Reactome (<http://www.arabidopsisreactome.org>).

We are currently populating manually-curated gene networks for other well-known plant pathways, and future plans include additional pathway references for maize. We expect this plant-specific instance of Reactome to become a central hub for pathway curation and enrichment in the plant community.

