



Gramene: It's Not Just For Grasses Anymore

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Integrating functional, genetic & comparative information for discovery and hypothesis based research



Home

GRAMENE Home
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News
• Gramene at grape conference
Gramene is sending a member to the International Grape Genome Program's (IGGP) 3rd Annual Grape Conference in March. Marcela Monaco, who works on Gramene's pathogen team, will be presenting a poster on Gramene release 33 out.
The Gramene team is happy to announce the 3rd annual Gramene release, available at www.gramene.org. This build...
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Presentation materials
Gramene is a curated, open-source, data resource for comparative plant genomics of the grasses. Our goal is to facilitate the study of comparative plant genomics by providing information derived from public projects involving grasses. We provide genomic, protein structure and function analysis, gene expression, and other data types.

Arabidopsis Entry Page

GRAMENE Home
Arabidopsis thaliana (TAIR10)

Description
About Arabidopsis thaliana
Arabidopsis thaliana is a small flowering plant that is widely used as a model organism in plant biology. Arabidopsis is a member of the mustard (Brassicaceae) family, which includes cultivated species such as cabbage and radish. Arabidopsis is not major crop, but it has been extensively studied due to its small size, short life cycle, and ease of genetic manipulation. Arabidopsis thaliana has a genome size of approx. 135 Mbase, and a haploid chromosome number of 5. (From TAIR)

Genome Sequencing and Gene Prediction (Release TAIR10)
The complete genome sequence of Arabidopsis thaliana was first published by the Arabidopsis Genome Initiative in 2000 [1] and was determined by a BAC-by-BAC sequencing strategy anchored to chromosomes using a variety of genetic and physical maps. Gene annotations use cDNA and EST data as well as manual updates informed by cross-species alignments, peptides and community input regarding missing and incorrectly annotated genes. The genome contains approximately 25,000 genes and 100,000 transcripts (AT3G25240.1). Variation (ENSVATH055)

Additional annotations generated by the Gramene/Ensembl Genomes projects include:
• The standard set of Gramene/Ensembl detailed here.
• Phylogenetic tree and whole-genome alignments with several plant and metazoan species, using Ensembl's Compara pipeline.
• The Arabidopsis variation database contains data from the screening of 1179 strains using the Affymetrix 250K Arabidopsis SNP chip, and an open access tool for probe-level analysis is available at the Wellcome Trust Centre for Human Genetics in Oxford. Paula Kornet at the University of Michigan, and funded by the BBSRC, which involved screening of 185 accessions and 185 recombinant inbred strains from the 1001 Genomes Project. Phenotype data has also been added from a GWAS study of 107 phenotypes in 95 inbred lines performed by the Atwell et al. study [2].
• Mappings for probes from the following arrays were also added to the functional genomics schema:
• Arabidopsis ATH1 Genome Array
• Agilent G2510F-0211B
• Agilent G2510F-0150B
• CATTMA

Links
• The Arabidopsis Information Resource
References
1. Arabidopsis Genome Initiative. Analysis of the genome sequence of the flowering plant Arabidopsis thaliana. *Nature*.

Complete Genomes: Arabidopsis thaliana, Arabidopsis lyrata, grapevine, poplar, rice (3), Brachypodium, sorghum, & maize

Produced in collaboration w/[EnsemblPlants](#)

Custom queries and downloads



Export to Excel or text

Orthologs in lyra, grape, poplar, rice, Brachypodium, sorghum maize, & moss									
Ensembl Gene ID	Arabidopsis thaliana genes (TAIR10)	Vitis vinifera	Oryza sativa	Sorghum bicolor	Brachypodium distachyon	Populus tremuloides	Arabidopsis lyrata	Ensembl Gene ID	Physcomitrella patens
AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680
AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680	AT1G08680

All transmembrane-targeted genes, showing InterPro domains, GO terms, and AFFY id's

Ensembl Gene ID	Transmembrane	Signal peptide	Interpro	Interpro Short Description	GO Term Name	GO Term Definition (bp)	GO domain	AFFY domain
AT1G08680	Tmm	Sign	IP500116	Cyto-calnexin	cyto-calnexin	The chemical reactions and pathways involving the transport of one-carbon units across membranes, including the transport of glucose, galactose, and glucose-6-phosphate.	Biological process	AT1G12101
AT1G08680	Tmm	Sign	IP500116	Cyto-calnexin, class_cat	endomembrane system	A complex of membrane proteins that regulates endoplasmic reticulum, Golgi bodies, vesicles, and the plasma membrane envelope. Members of the endomembrane system are involved in the transport of molecules across membranes, through the use of vesicles (Golgi).	Biological process	AT1G12101
AT1G08680	Tmm	Sign	IP500116	Cyto-calnexin, class_cat	metal ion binding	GO0004872	molecular_junction	AT1G12101

All Myb-domain genes with "STOP_GAINED" SNP allele in germplasm

Ensembl Gene ID	Variation ID	Allele	Description	Variation start (bp)	Variation end (bp)	Translation (aa)	Interpro	Description
AT1G05450	ENSVATH055	AT1G05450	STOP_GAINED	62	62	PTSD	IP500454	Myb-like DNA-binding domain
AT1G05450	ENSVATH055	AT1G05450	STOP_GAINED	92	92	PTSD	IP500454	Myb-like DNA-binding domain
AT1G05450	ENSVATH055	AT1G05450	STOP_GAINED	133	133	PTSD	IP500454	Myb-like DNA-binding domain
AT1G05450	ENSVATH055	AT1G05450	STOP_GAINED	212	212	PTSD	IP500454	Myb-like DNA-binding domain
AT1G05450	ENSVATH055	AT1G05450	STOP_GAINED	212	212	PTSD	IP500454	Myb-like DNA-binding domain

Taxon of origin for paralog pairs of cyclin-domain genes that have an ortholog in Physcomitrella

Ensembl Gene ID	Arabidopsis thaliana Ensembl Gene	% Identity	Arabidopsis Identifier	% Identity
AT1G04100	AT1G04100	60	78	Arabidopsis
AT1G04100	AT1G04100	58	78	Arabidopsis
AT1G04100	AT1G04100	55	78	Arabidopsis
AT1G04100	AT1G04100	53	78	Arabidopsis
AT1G04100	AT1G04100	52	78	Arabidopsis
AT1G04100	AT1G04100	41	78	Magnaporthe
AT1G04100	AT1G04100	22	78	Arabidopsis
AT1G04100	AT1G04100	22	78	Arabidopsis
AT1G04100	AT1G04100	22	78	Arabidopsis
AT1G04100	AT1G04100	48	78	Arabidopsis
AT1G04100	AT1G04100	28	80	Arabidopsis
AT1G04100	AT1G04100	44	80	Erythrina

The Browser: Focus on Diversity

8 plant EPO
CATMA-CATMA
AGILENT G2510F-02
AGILENT G2510F-01
AFFY ATH1-121501
EST Cluster (Arabid...
Gene (TAIR)
Config (TAIR)
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