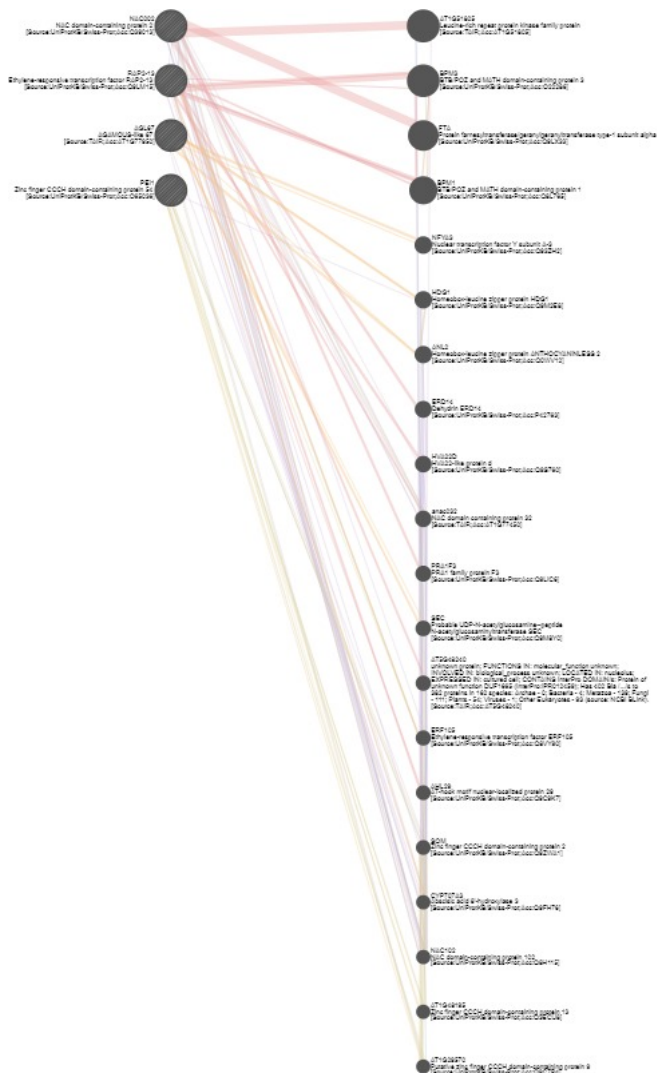


# GeneMANIA report

Created on : 21 June 2020 00:18:46

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Application version : 3.6.0



## Networks

- Physical Interactions
- Predicted
- Co-expression
- Shared protein domains
- Genetic Interactions
- Co-localization

## Functions

N/A

# Search parameters

**Organism** Arabidopsis thaliana (arabidopsis)

**Genes** RAP2-13 , AGL67 , PEI1 , ATAF1

**Network weighting** Automatically selected weighting method

**Networks** **2**

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2011

## **B**

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Bassel-Cutler-2008-Dormant Seed Expression , Bassel-Cutler-2008-Germinating Seed Expression , BIOGRID-SMALL-SCALE-STUDIES , BIOGRID-SMALL-SCALE-STUDIES , Boruc-Russinova-2010 A , Boruc-Russinova-2010 B , Brady-Benfey-2007

## **C**

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Causier-Davies-2012 , Ceserani-Nelson-2009 , Chen-Rhee-2012 , Cutcliffe-Rashotte-2011

## **D**

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Danisman-Immink-2013 , de Folter-Angenent-2005 , Dean Rider-Ogas-2003 , Deeken-Hedrich-2006 A , Dinneny-Benfey-2008 D , Dortay-Heyl-2008 , Dreze-Vidal-2011-combined , Dreze-Vidal-2011-main , Dreze-Vidal-2011-repeat

## **E**

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Efroni-Wagner-2013 , Elrouby-Coupland-2010

## **F**

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Fujiwara-Fukao-2014

## **G**

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Gifford-Birnbaum-2008 , Goda-Shimada-2008 A , Goda-Shimada-2008 B

## **H**

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Hackbusch-Uhrig-2005 , Hackenberg-Grimm-2012

## **I**

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Igawa-Yanagawa-2009 , INTERPRO , IREF-BIND , IREF-BIOGRID , IREF-DIP , IREF-INTACT , IREF-SMALL-SCALE-STUDIES

## **J**

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Jones-Frommer-2014

## **K**

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Kim-Vierstra-2013 , Klopffleisch-Jones-2011 , Kram-Carter-2009 , Kuroda-Matsui-2012

## **L**

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Lalonde-Frommer-2010 , Lee-Rhee-2010 AraNet , Lee-Rhee-2010 Co-citation worm2arabidopsis , Lee-Rhee-2010 Co-citation yeast2arabidopsis , Lee-Rhee-2010 co-expression human2arabidopsis , Lee-Rhee-2010 Co-expression worm2arabidopsis , Lee-Rhee-2010 Co-expression yeast2arabidopsis , Lee-Rhee-2010 Co-inheritance , Lee-Rhee-2010 Gene neighbourhoods , Lee-Rhee-2010 Genetic interactions worm2arabidopsis , Lee-Rhee-2010 Genetic interactions yeast2arabidopsis , Lee-Rhee-2010 Protein complexes human2arabidopsis , Lee-Rhee-2010 Protein complexes yeast2arabidopsis , Lee-Rhee-2010 Protein interactions , Lee-Rhee-2010 Protein interactions fly2arabidopsis , Lee-Rhee-2010 protein interactions from complexes yeast2arabidopsis , Lee-Rhee-2010 Protein interactions human2arabidopsis , Lee-Rhee-2010 Protein interactions worm2arabidopsis , Lee-Rhee-2010 protein interactions yeast2arabidopsis , Lee-Rhee-2010 Shared protein domains , Lee-Rhee-2010 shared protein domains human2arabidopsis , Lee-Rhee-2010 shared protein domains yeast2arabidopsis , Lee-Rhee-2010 Y2H human2arabidopsis , Lee-Rhee-2010 Y2H worm2arabidopsis , Lee-Rhee-2010 Y2H yeast2arabidopsis , Lumba-McCourt-2014

## **M**

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Malitsky-Aharoni-2008 , Manzano-Del Pozo-2008 , Mirabella-Schuurink-2015 , Moreno-Risueno-Benfey-2015

## **N**

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Nozue-Maloof-2011

## **P**

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Pandey-Albert-2010 , PFAM , Piya-Hewezi-2014 , Popescu-Dinesh-Kumar-2007 , PPI-Predicted (Interologs)

## **Q**

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Queval-Noctor-2012

## **R**

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Risseuw-Crosby-2003 , Ronemus-Martienssen-2006

## **S**

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Sako-Yamaguchi-2014 , Schmid-Lohmann-2003 A , Schmid-Lohmann-2003 B , Sozzani-Benfey-2010 , Swatek-Thelen-2011

## **T**

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Tamura-Hara-Nishimura-2010

## **V**

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Van Leene-De Jaeger-2010 , Vernoux-Traas-2011

## **W**

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Waidmann-Jonak-2014

## Y

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Yamaoka-Hara-Nishimura-2013

## Z

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Zuber-Gallardo-2010 A

# Genes

Gene	Description	Rank
PEI1	Zinc finger CCCH domain-containing protein 54 [Source:UniProtKB/Swiss-Prot;Acc:O65036]	N/A
AGL67	AGAMOUS-like 67 [Source:TAIR;Acc:AT1G77950]	N/A
RAP2-13	Ethylene-responsive transcription factor RAP2-13 [Source:UniProtKB/Swiss-Prot;Acc:Q9LM15]	N/A
NAC002	NAC domain-containing protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q39013]	N/A
AT1G51805	Leucine-rich repeat protein kinase family protein [Source:TAIR;Acc:AT1G51805]	1
BPM3	BTB/POZ and MATH domain-containing protein 3 [Source:UniProtKB/Swiss-Prot;Acc:O22286]	2
FTA	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [Source:UniProtKB/Swiss-Prot;Acc:Q9LX33]	3
BPM1	BTB/POZ and MATH domain-containing protein 1 [Source:UniProtKB/Swiss-Prot;Acc:Q8L765]	4
NFYA3	Nuclear transcription factor Y subunit A-3 [Source:UniProtKB/Swiss-Prot;Acc:Q93ZH2]	5
HDG1	Homeobox-leucine zipper protein HDG1 [Source:UniProtKB/Swiss-Prot;Acc:Q9M2E8]	6
ANL2	Homeobox-leucine zipper protein ANTHOCYANINLESS 2 [Source:UniProtKB/Swiss-Prot;Acc:Q0WV12]	7
ERD14	Dehydrin ERD14 [Source:UniProtKB/Swiss-Prot;Acc:P42763]	8
HVA22D	HVA22-like protein d [Source:UniProtKB/Swiss-Prot;Acc:Q9S760]	9
anac032	NAC domain containing protein 32 [Source:TAIR;Acc:AT1G77450]	10
PRA1F3	PRA1 family protein F3 [Source:UniProtKB/Swiss-Prot;Acc:Q9LIC6]	11
SEC	Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC [Source:UniProtKB/Swiss-Prot;Acc:Q9M8Y0]	12
AT5G48240	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1665 (InterPro:IPR012459); Has 402 Bla /.../s to 382 proteins in 162 species: Archae - 0; Bacteria - 4; Metazoa - 139; Fungi - 111; Plants - 54; Viruses - 1; Other Eukaryotes - 93 (source: NCBI BLink). [Source:TAIR;Acc:AT5G48240]	13

Gene	Description	Rank
ERF105	Ethylene-responsive transcription factor ERF105 [Source:UniProtKB/Swiss-Prot;Acc:Q8VY90]	14
AHL29	AT-hook motif nuclear-localized protein 29 [Source:UniProtKB/Swiss-Prot;Acc:Q9C9K7]	15
SOM	Zinc finger CCCH domain-containing protein 2 [Source:UniProtKB/Swiss-Prot;Acc:Q9ZWA1]	16
CYP707A3	Abscisic acid 8'-hydroxylase 3 [Source:UniProtKB/Swiss-Prot;Acc:Q9FH76]	17
NAC102	NAC domain-containing protein 102 [Source:UniProtKB/Swiss-Prot;Acc:Q8H115]	18
AT1G48195	Zinc finger CCCH domain-containing protein 13 [Source:UniProtKB/Swiss-Prot;Acc:Q3ECU8]	19
AT1G29570	Putative zinc finger CCCH domain-containing protein 9 [Source:UniProtKB/Swiss-Prot;Acc:Q9C7P4]	20

# Networks

<b>Physical Interactions</b>	66.87%
Cutcliffe-Rashotte-2011	12.88%
CRFs form protein-protein interactions with each other and with members of the cytokinin signalling pathway in Arabidopsis via the CRF domain. Cutcliffe et al (2011). <i>J Exp Bot</i>	
Physical Interactions with 68 interactions from BioGRID	
Sako-Yamaguchi-2014	12.06%
Proteomic analysis of the 26S proteasome reveals its direct interaction with transit peptides of plastid protein precursors for their degradation. Sako et al (2014). <i>J Proteome Res</i>	
Physical Interactions with 187 interactions from BioGRID	
Danisman-Immink-2013	8.79%
Analysis of functional redundancies within the Arabidopsis TCP transcription factor family. Danisman et al (2013). <i>J Exp Bot</i>	
Physical Interactions with 119 interactions from iRefIndex	
Causier-Davies-2012	4.47%
The TOPLESS interactome: a framework for gene repression in Arabidopsis. Causier et al (2012). <i>Plant Physiol</i>	
Physical Interactions with 110 interactions from BioGRID	
Kim-Vierstra-2013	4.09%
Advanced proteomic analyses yield a deep catalog of ubiquitylation targets in Arabidopsis. Kim et al (2013). <i>Plant Cell</i>	
Physical Interactions with 891 interactions from iRefIndex	
Vernoux-Traas-2011	2.92%
The auxin signalling network translates dynamic input into robust patterning at the shoot apex. Vernoux et al (2011). <i>Mol Syst Biol</i>	
Physical Interactions with 404 interactions from iRefIndex	
IREF-DIP	2.28%
Physical Interactions with 339 interactions from iRefIndex	
Igawa-Yanagawa-2009	2.24%
Isolation and identification of ubiquitin-related proteins from Arabidopsis seedlings. Igawa et al (2009). <i>J Exp Bot</i>	
Physical Interactions with 159 interactions from iRefIndex	
Boruc-Russinova-2010 B	2.05%
Functional modules in the Arabidopsis core cell cycle binary protein-protein interaction network. Boruc et al (2010). <i>Plant Cell</i>	
Physical Interactions with 27 interactions from BioGRID	
BIOGRID-SMALL-SCALE-STUDIES	1.77%
Physical Interactions with 5,720 interactions from BioGRID	
Fujiwara-Fukao-2014	1.73%
Interactomics of Qa-SNARE in Arabidopsis thaliana. Fujiwara et al (2014). <i>Plant Cell Physiol</i>	
Physical Interactions with 464 interactions from BioGRID	
Boruc-Russinova-2010 A	1.69%
Functional modules in the Arabidopsis core cell cycle binary protein-protein interaction network. Boruc et al (2010). <i>Plant Cell</i>	
Physical Interactions with 40 interactions from BioGRID	

<b>Physical Interactions</b>	<b>66.87%</b>
<b>Piya-Hewezi-2014</b>	<b>1.63%</b>
Protein-protein interaction and gene co-expression maps of ARFs and Aux/IAAs in Arabidopsis. Piya et al (2014). <i>Front Plant Sci</i>	
Physical Interactions with 142 interactions from BioGRID	
<b>IREF-BIND</b>	<b>1.62%</b>
Physical Interactions with 794 interactions from iRefIndex	
<b>Lee-Rhee-2010 Protein interactions</b>	<b>1.59%</b>
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Physical Interactions with 751 interactions from supplementary material	
<b>Lumba-McCourt-2014</b>	<b>1.01%</b>
A mesoscale abscisic acid hormone interactome reveals a dynamic signaling landscape in Arabidopsis. Lumba et al (2014). <i>Dev Cell</i>	
Physical Interactions with 456 interactions from iRefIndex	
<b>Manzano-Del Pozo-2008</b>	<b>0.85%</b>
Identification of ubiquitinated proteins in Arabidopsis. Manzano et al (2008). <i>Plant Mol Biol</i>	
Physical Interactions with 170 interactions from iRefIndex	
<b>Hackbusch-Uhrig-2005</b>	<b>0.66%</b>
A central role of Arabidopsis thaliana ovate family proteins in networking and subcellular localization of 3-aa loop extension homeodomain proteins. Hackbusch et al (2005). <i>Proc Natl Acad Sci U S A</i>	
Physical Interactions with 169 interactions from iRefIndex	
<b>Lalonde-Frommer-2010</b>	<b>0.48%</b>
A membrane protein/signaling protein interaction network for Arabidopsis version AMPv2. Lalonde et al (2010). <i>Front Physiol</i>	
Physical Interactions with 282 interactions from BioGRID	
<b>Yamaoka-Hara-Nishimura-2013</b>	<b>0.44%</b>
Identification and dynamics of Arabidopsis adaptor protein-2 complex and its involvement in floral organ development. Yamaoka et al (2013). <i>Plant Cell</i>	
Physical Interactions with 150 interactions from iRefIndex	
<b>Kuroda-Matsui-2012</b>	<b>0.35%</b>
A comprehensive analysis of interaction and localization of Arabidopsis SKP1-like (ASK) and F-box (FBX) proteins. Kuroda et al (2012). <i>PLoS One</i>	
Physical Interactions with 657 interactions from iRefIndex	
<b>Van Leene-De Jaeger-2010</b>	<b>0.33%</b>
Targeted interactomics reveals a complex core cell cycle machinery in Arabidopsis thaliana. Van Leene et al (2010). <i>Mol Syst Biol</i>	
Physical Interactions with 447 interactions from BioGRID	
<b>IREF-INTACT</b>	<b>0.33%</b>
Physical Interactions with 9,433 interactions from iRefIndex	
<b>IREF-SMALL-SCALE-STUDIES</b>	<b>0.23%</b>
Physical Interactions with 6,133 interactions from iRefIndex	
<b>Chen-Rhee-2012</b>	<b>0.16%</b>



## Chen-Rhee-2012

Uncovering Arabidopsis membrane protein interactome enriched in transporters using mating-based split ubiquitin assays and classification models. Chen et al (2012). *Front Plant Sci*

Physical Interactions with 486 interactions from iRefIndex

## Efroni-Wagner-2013

0.14%

Regulation of leaf maturation by chromatin-mediated modulation of cytokinin responses. Efroni et al (2013). *Dev Cell*

Physical Interactions with 354 interactions from BioGRID

## Jones-Frommer-2014

0.05%

Border control--a membrane-linked interactome of Arabidopsis. Jones et al (2014). *Science*

Physical Interactions with 10,436 interactions from BioGRID

## Dreze-Vidal-2011-repeat

0.04%

Evidence for network evolution in an Arabidopsis interactome map. (2011). *Science*

Physical Interactions with 1,015 interactions from supplementary material

**Predicted**

14.02%

## Lee-Rhee-2010 Co-citation worm2arabidopsis

1.70%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 5,553 interactions from supplementary material

## Lee-Rhee-2010 Protein interactions human2arabidopsis

1.66%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 102,798 interactions from supplementary material

## Lee-Rhee-2010 Co-citation yeast2arabidopsis

1.62%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 52,241 interactions from supplementary material

## Lee-Rhee-2010 protein interactions from complexes yeast2arabidopsis

1.45%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 10,826 interactions from supplementary material

## Lee-Rhee-2010 Gene neighbourhoods

1.32%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 94,649 interactions from supplementary material

## Lee-Rhee-2010 Genetic interactions yeast2arabidopsis

0.78%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 30,482 interactions from supplementary material

## Lee-Rhee-2010 Protein complexes human2arabidopsis

0.69%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 2,153 interactions from supplementary material

<b>Predicted</b>	<b>14.02%</b>
Lee-Rhee-2010 protein interactions yeast2arabidopsis	0.60%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 25,127 interactions from supplementary material	
Lee-Rhee-2010 Protein complexes yeast2arabidopsis	0.59%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 128,410 interactions from supplementary material	
Lee-Rhee-2010 Co-expression worm2arabidopsis	0.54%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 92,935 interactions from supplementary material	
Lee-Rhee-2010 shared protein domains yeast2arabidopsis	0.52%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 24,095 interactions from supplementary material	
Lee-Rhee-2010 Co-expression yeast2arabidopsis	0.45%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 102,740 interactions from supplementary material	
Lee-Rhee-2010 Y2H worm2arabidopsis	0.35%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 1,905 interactions from supplementary material	
PPI-Predicted (Interologs)	0.34%
A predicted interactome for Arabidopsis. Geisler-Lee et al (2007). <i>Plant Physiol</i>	
Predicted with 18,204 interactions from collaborator	
Lee-Rhee-2010 Protein interactions worm2arabidopsis	0.32%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 1,806 interactions from supplementary material	
Lee-Rhee-2010 shared protein domains human2arabidopsis	0.29%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 21,634 interactions from supplementary material	
Lee-Rhee-2010 Co-inheritance	0.28%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 82,768 interactions from supplementary material	
Lee-Rhee-2010 AraNet	0.24%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 735,927 interactions from supplementary material	

<b>Predicted</b>	14.02%
Lee-Rhee-2010 Protein interactions fly2arabidopsis	0.16%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 7,978 interactions from supplementary material	
Lee-Rhee-2010 co-expression human2arabidopsis	0.11%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Predicted with 39,767 interactions from supplementary material	
<b>Co-expression</b>	12.73%
Kram-Carter-2009	0.95%
Uncovering the Arabidopsis thaliana nectary transcriptome: investigation of differential gene expression in floral nectariferous tissues. Kram et al (2009). <i>BMC Plant Biol</i>	
Co-expression with 672,038 interactions from GEO	
Ronemus-Martienssen-2006	0.94%
MicroRNA-targeted and small interfering RNA-mediated mRNA degradation is regulated by argonaute, dicer, and RNA-dependent RNA polymerase in Arabidopsis. Ronemus et al (2006). <i>Plant Cell</i>	
Co-expression with 176,825 interactions from GEO	
Schmid-Lohmann-2003 B	0.86%
Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). <i>Development</i>	
Co-expression with 134,679 interactions from GEO	
Bassel-Cutler-2008-Dormant Seed Expression	0.69%
Elucidating the germination transcriptional program using small molecules. Bassel et al (2008). <i>Plant Physiol</i>	
Co-expression with 424,666 interactions from collaborator	
Nozue-Maloof-2011	0.66%
Genomic analysis of circadian clock-, light-, and growth-correlated genes reveals PHYTOCHROME-INTERACTING FACTOR5 as a modulator of auxin signaling in Arabidopsis. Nozue et al (2011). <i>Plant Physiol</i>	
Co-expression with 686,407 interactions from GEO	
Bassel-Cutler-2008-Germinating Seed Expression	0.66%
Elucidating the germination transcriptional program using small molecules. Bassel et al (2008). <i>Plant Physiol</i>	
Co-expression with 418,628 interactions from collaborator	
Dinneny-Benfey-2008 D	0.63%
Cell identity mediates the response of Arabidopsis roots to abiotic stress. Dinneny et al (2008). <i>Science</i>	
Co-expression with 709,273 interactions from GEO	
Goda-Shimada-2008 B	0.62%
The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Goda et al (2008). <i>Plant J</i>	
Co-expression with 677,499 interactions from GEO	
Queval-Noctor-2012	0.62%
Day length is a key regulator of transcriptomic responses to both CO(2) and H(2)O(2) in Arabidopsis. Queval et al (2012). <i>Plant Cell Environ</i>	
Co-expression with 655,914 interactions from GEO	

<b>Co-expression</b>	<b>12.73%</b>
Zuber-Gallardo-2010 A	0.61%
The seed composition of Arabidopsis mutants for the group 3 sulfate transporters indicates a role in sulfate translocation within developing seeds. Zuber et al (2010). <i>Plant Physiol</i>	
Co-expression with 693,336 interactions from GEO	
Pandey-Albert-2010	0.60%
Boolean modeling of transcriptome data reveals novel modes of heterotrimeric G-protein action. Pandey et al (2010). <i>Mol Syst Biol</i>	
Co-expression with 686,557 interactions from GEO	
Goda-Shimada-2008 A	0.59%
The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Goda et al (2008). <i>Plant J</i>	
Co-expression with 679,444 interactions from GEO	
Mirabella-Schuurink-2015	0.57%
WRKY40 and WRKY6 act downstream of the green leaf volatile E-2-hexenal in Arabidopsis. Mirabella et al (2015). <i>Plant J</i>	
Co-expression with 598,546 interactions from GEO	
Gifford-Birnbaum-2008	0.57%
Cell-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). <i>Proc Natl Acad Sci U S A</i>	
Co-expression with 669,788 interactions from GEO	
Deeken-Hedrich-2006 A	0.54%
An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Deeken et al (2006). <i>Plant Cell</i>	
Co-expression with 604,796 interactions from GEO	
Dean Rider-Ogas-2003	0.54%
Coordinate repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). <i>Plant J</i>	
Co-expression with 116,036 interactions from GEO	
Malitsky-Aharoni-2008	0.53%
The transcript and metabolite networks affected by the two clades of Arabidopsis glucosinolate biosynthesis regulators. Malitsky et al (2008). <i>Plant Physiol</i>	
Co-expression with 559,163 interactions from GEO	
Moreno-Risueno-Benfey-2015	0.53%
Transcriptional control of tissue formation throughout root development. Moreno-Risueno et al (2015). <i>Science</i>	
Co-expression with 648,813 interactions from GEO	
Schmid-Lohmann-2003 A	0.53%
Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). <i>Development</i>	
Co-expression with 625,625 interactions from GEO	
Sozzani-Benfey-2010	0.51%
Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). <i>Nature</i>	
Co-expression with 604,619 interactions from GEO	
<b>Shared protein domains</b>	<b>3.00%</b>
PFAM	1.76%

<b>Shared protein domains</b>	3.00%
<hr/>	
PFAM	
Shared protein domains with 680,094 interactions from Pfam	
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INTERPRO	1.23%
Shared protein domains with 743,516 interactions from InterPro	
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Lee-Rhee-2010 Shared protein domains	0.01%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). <i>Nat Biotechnol</i>	
Shared protein domains with 50,665 interactions from supplementary material	
<b>Genetic Interactions</b>	2.87%
<hr/>	
BIOGRID-SMALL-SCALE-STUDIES	2.87%
Genetic Interactions with 219 interactions from BioGRID	
<b>Co-localization</b>	0.52%
<hr/>	
Brady-Benfey-2007	0.52%
A high-resolution root spatiotemporal map reveals dominant expression patterns. Brady et al (2007). <i>Science</i>	
Co-localization with 831,109 interactions from GEO	