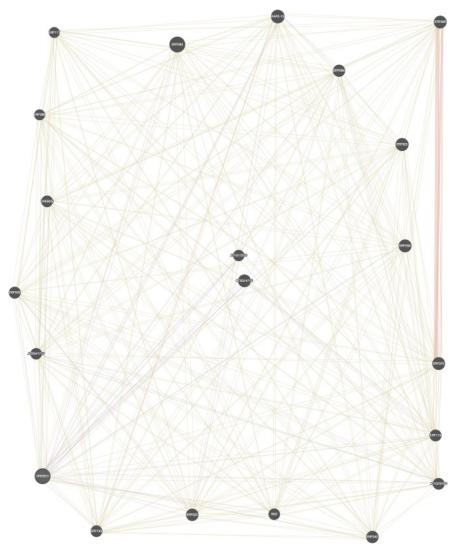
# GeneMANIA report

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#### Networks

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

#### **Functions**

N/A

### Search parameters

Organism Arabidopsis thaliana (arabidopsis)

Genes DREB2D

Network Automatically selected weighting method

weighting

Networks 2

2011

 $\mathbf{B}$ 

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

 $\mathbf{C}$ 

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

 $\mathbf{D}$ 

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

 $\mathbf{E}$ 

Efroni-Wagner-2013, Elrouby-Coupland-2010

F

Fujiwara-Fukao-2014

 $\mathbf{G}$ 

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

 $\mathbf{H}$ 

Hackbusch-Uhrig-2005, Hackenberg-Grimm-2012

T

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

.]

Jones-Frommer-2014

 $\mathbf{K}$ 

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

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

#### $\mathbf{M}$

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

#### N

Nozue-Maloof-2011

#### P

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

#### ${f Q}$

Queval-Noctor-2012

#### $\mathbf{R}$

Risseeuw-Crosby-2003, Ronemus-Martienssen-2006

#### $\mathbf{S}$

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

#### $\mathbf{T}$

Tamura-Hara-Nishimura-2010

#### V

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

#### $\mathbf{W}$

Waidmann-Jonak-2014

₹	

Yamaoka-Hara-Nishimura-2013

### ${f Z}$

Zuber-Gallardo-2010 A

## Genes

Gene	Description	Rank
DREB2D	Dehydration-responsive element-binding protein 2D [Source:UniProtKB/Swiss-Prot;Acc:Q9LQZ2]	N/A
ERF096	Ethylene-responsive transcription factor ERF096 [Source:UniProtKB/Swiss-Prot;Acc:Q9LSX0]	1
RAP2-13	Ethylene-responsive transcription factor RAP2-13 [Source:UniProtKB/Swiss-Prot;Acc:Q9LM15]	2
ERF025	Ethylene-responsive transcription factor ERF025 [Source:UniProtKB/Swiss-Prot;Acc:Q9FJ90]	3
ERF056	Ethylene-responsive transcription factor ERF056 [Source:UniProtKB/Swiss-Prot;Acc:Q9SIE4]	4
ERF070	Ethylene-responsive transcription factor ERF070 [Source:UniProtKB/Swiss-Prot;Acc:Q9C995]	5
ERF069	Ethylene-responsive transcription factor ERF069 [Source:UniProtKB/Swiss-Prot;Acc:Q8W4I5]	6
AT3G14710	F-box/FBD/LRR-repeat protein At3g14710 [Source:UniProtKB/Swiss-Prot;Acc:Q9LUC4]	7
ERF022	Ethylene-responsive transcription factor ERF022 [Source:UniProtKB/Swiss-Prot;Acc:Q9LQ28]	8
ERF042	Ethylene-responsive transcription factor ERF042 [Source:UniProtKB/Swiss-Prot;Acc:Q52QU1]	9
ERF086	Ethylene-responsive transcription factor ERF086 [Source:UniProtKB/Swiss-Prot;Acc:Q6J9Q2]	10
ERF003	Ethylene-responsive transcription factor ERF003 [Source:UniProtKB/Swiss-Prot;Acc:Q94AW5]	11
ERF114	Ethylene-responsive transcription factor ERF114 [Source:UniProtKB/Swiss-Prot;Acc:Q9FH54]	12
AT1G79700	AP2-like ethylene-responsive transcription factor At1g79700 [Source: UniProtKB/Swiss-Prot;Acc:A0JPZ8]	13
ERF105	Ethylene-responsive transcription factor ERF105 [Source:UniProtKB/Swiss-Prot;Acc:Q8VY90]	14
DREB2G	Dehydration-responsive element-binding protein 2G [Source:UniProtKB/Swiss-Prot;Acc:P61827]	15
AT2G41710	AP2-like ethylene-responsive transcription factor At2g41710 [Source: UniProtKB/Swiss-Prot;Acc:Q8GWK2]	16
SNZ	AP2-like ethylene-responsive transcription factor SNZ [Source:	17

Gene	Description	Rank
	UniProtKB/Swiss-Prot;Acc:Q6PV67]	
AT1G17010	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein [Source:TAIR;Acc:AT1G17010]	18
ERF117	Ethylene-responsive transcription factor ERF117 [Source:UniProtKB/Swiss-Prot;Acc:Q9M9B2]	19
ERF088	Ethylene-responsive transcription factor ERF088 [Source:UniProtKB/Swiss-Prot;Acc:Q3E703]	20

# Networks

Physical Interactions	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). $J Exp Bot$	
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 $(2014)$ . $J$ Proteome $Res$	
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). $J \ Exp \ Bot$ 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 ubiquity lation targets in Arabidopsis. Kim et al (2013). Plant Cell Physical Interactions with 891 interactions from iRef Index	
Vernoux-Traas-2011	2.92%
The auxin signalling network translates dynamic input into robust patterning at the shoot apex. Vernoux et al $(2011)$ . $Mol Syst$ $Biol$	
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). $J Exp Bot$ 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). Plant Cell Physiol 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). Plant Cell Physical Interactions with 40 interactions from BioGRID	

Physical Interactions	66.87%
Piya-Hewezi-2014	1.63%
Protein-protein interaction and gene co-expression maps of ARFs and Aux/IAAs in Arabidopsis. Piya et al (2014). Front Plant $Sci$	
Physical Interactions with 142 interactions from BioGRID	
IREF-BIND	1.62%
Physical Interactions with 794 interactions from iRefIndex	
Lee-Rhee-2010 Protein interactions	1.59%
Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). $Nat\ Biotechnol$	
Physical Interactions with 751 interactions from supplementary material	
Lumba-McCourt-2014	1.01%
A mesoscale abscisic acid hormone interactome reveals a dynamic signaling landscape in Arabidopsis. Lumba et al (2014). $Dev$ $Cell$	
Physical Interactions with 456 interactions from iRefIndex	
Manzano-Del Pozo-2008	0.85%
Identification of ubiquitinated proteins in Arabidopsis. Manzano et al (2008). Plant Mol Biol	
Physical Interactions with 170 interactions from iRefIndex	
Hackbusch-Uhrig-2005	0.66%
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	0.4007
Lalonde-Frommer-2010	0.48%
A membrane protein/signaling protein interaction network for Arabidopsis version AMPv2. Lalonde et al (2010). Front Physiol Physical Interactions with 282 interactions from BioGRID	
Yamaoka-Hara-Nishimura-2013	0.44%
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	
Kuroda-Matsui-2012	0.35%
A comprehensive analysis of interaction and localization of Arabidopsis SKP1-like (ASK) and F-box (FBX) proteins. Kuroda et al $(2012)$ . $PLoS\ One$	
Physical Interactions with 657 interactions from iRefIndex	
Van Leene-De Jaeger-2010	0.33%
Targeted interactomics reveals a complex core cell cycle machinery in Arabidopsis thaliana. Van Leene et al (2010). Mol Syst Biol	
Physical Interactions with 447 interactions from BioGRID	
IREF-INTACT	0.33%
Physical Interactions with 9,433 interactions from iRefIndex	
IREF-SMALL-SCALE-STUDIES	0.23%
Physical Interactions with 6,133 interactions from iRefIndex	
Chen-Rhee-2012	0.16%

Physical Interactions	66.87%
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 controla 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	

Predicted	14.02%
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 $(2010)$ . $Nat$ $Biotechnol$	
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 $(2010)$ . $Nat$ $Biotechnol$	
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). $Nat\ Biotechnol$	
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). $Nat\ Biotechnol$	
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 $(2010)$ . $Nat$ $Biotechnol$	
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 $(2010)$ . $Nat$ $Biotechnol$	
Predicted with 1,905 interactions from supplementary material	
PPI-Predicted (Interologs)	0.34%
A predicted interactome for Arabidopsis. Geisler-Lee et al (2007). Plant Physiol	
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). $Nat\ Biotechnol$	
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 $(2010)$ . $Nat$ $Biotechnol$	
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). $Nat$ $Biotechnol$	
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 $(2010)$ . $Nat$ $Biotechnol$	
Predicted with 735,927 interactions from supplementary material	

Predicted	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 $(2010)$ . $Nat$ $Biotechnol$	
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 $(2010)$ . $Nat$ $Biotechnol$	
Predicted with 39,767 interactions from supplementary material	
Co-expression Co-expression	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 $(2009)$ . $BMC\ Plant\ Biol$	
Co-expression with 672,038 interactions from GEO	
Ronemus-Martienssen-2006	0.94%
$\label{eq:microRNA-targeted} MicroRNA-targeted and small interfering RNA-mediated mRNA degradation is regulated by argonaute, dicer, and RNA-dependent RNA polymerase in Arabidopsis. Ronemus et al (2006). Plant Cell$	
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). Development	
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 $(2008)$ . Plant Physiol	
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). Plant Physiol	0.0070
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). Science	
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). $Plant\ J$	
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). Plant Cell Environ	
Co-expression with 655,914 interactions from GEO	

The seed composition of Arabidopsis mutants for the group 3 sulface transporters indicates a role in sulfate translocation within reveloping seeds. Zuber et al (2010). Plant Physiol 10-respectation with 693,536 interactions from GEO  Pandey-Albert-2010  Boolean modeling of transcripture data reveals navel modes of beterotrineric G-protein action. Pandey et al (2010). Mol Syst 56d  Coopersonion with 693,557 interactions from GEO  Goda-Shimada-2008 A  10.599  Goda-Shimada-2008 A  10.579  Goda-Shimada-2015  WikiYol and WikiYo act downstream of the green leaf volatile E-2-becenal in Arabidopsis. Mirabella et al (2015). Plant J  10. respection with 698,546 interactions from GEO  Gifford-Bimbaum-2008  10.579  Goda-Ghimada-2008 A  10.579	Co-expression	12.73%
Comparison with 683,356 interactions from GEO	Zuber-Gallardo-2010 A	0.61%
Pandey-Albert-2010  Sonders modeling of transcriptome data reveals movel modes of heterotrimeric G protein action. Pandey et al (2010). Mol Syst Not Co-expression with 688-587 interactions from GEO  Godds-Shiimada-2008 A  The AtGenExpression with 688-587 interactions from GEO  Godds-Shiimada-2008 A  The AtGenExpression with 679-444 interactions from GEO  Mirabella-Schuurink-2015  WRKY0 and WRKY6 act downstream of the green leaf volatile E-3-beavenal in Arabidopsis. Mirabella et al (2015). Plant J  To expression with 595-546 interactions from GEO  Gifford-Birnbaum-2008  Colleged responses meditate developmental plasticity. Gifford et al (2008). Proc Natl Acad Sci U S A  Decken-Hedrich-2006 A  In integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2006). Plant CM  That CM  To expression with 604.786 interactions from GEO  Dean Rider-Ogas-2003  Conditator repression of regulators of embryonic identity by PICKLE during germination in Arabidopsis. Dean Rider et al (2003). Proc Natl Acad Sci U S A  To expression with 116,036 interactions from GEO  Malitsky-Aharoni-2008  The transcript and metabolite networks affected by the two clades of Arabidopsis glurosinolate biosynthesis regulators. Malitsky al (2008). Proc Natl Acad Sci U S A  To expression with 155,045 interactions from GEO  Moreno-Risueno-Benfey-2015  Transcriptional court of citiens form GEO  Moreno-Risueno-Benfey-2015  Transcriptional court of citiens form GEO  Moreno-Risueno-Benfey-2015  Transcriptional court of citiens form GEO  Schmid-Lohmann-2003 A  O.539  Solvetion of foral induction pathways using global expression analysis. Schmid et al (2003). Development  To-expression with 625,625 interactions from GEO  Solvetion of foral induction pathways using global expression analysis. Schmid et al (2003). Development  To-expression with 69,645 interactions from GEO  Solvetion of foral induction pathways using global expression analysis. Schmid et al (2008). Proc Natl Acad Sci U S A  O.539  Solve	The seed composition of Arabidopsis mutants for the group 3 sulfate transporters indicates a role in sulfate translocation within developing seeds. Zuber et al $(2010)$ . Plant Physiol	
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Shared protein domains	3.00%
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INTERPRO	1.23%
Shared protein domains with 743,516 interactions from InterPro	
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 $(2010)$ . $Nat$ $Biotechnol$	
Shared protein domains with $50,665$ interactions from supplementary material	
Genetic Interactions	2.87%
BIOGRID-SMALL-SCALE-STUDIES	2.87%
Genetic Interactions with 219 interactions from BioGRID	
Co-localization	0.52%
Brady-Benfey-2007	0.52%
A high-resolution root spatiotemporal map reveals dominant expression patterns. Brady et al (2007). Science	
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