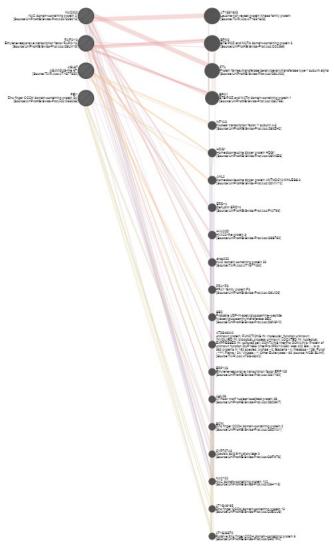
GeneMANIA report

Created on: 21 June 2020 00:18:46

Last database update : 13 March 2017 $00{:}00{:}00$

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 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

 ${\it Igawa-Yanagawa-2009}~,~ {\it INTERPRO}~,~ {\it IREF-BIND}~,~ {\it IREF-BIOGRID}~,~ {\it IREF-INTACT}~,~ {\it IREF-SMALL-SCALE-STUDIES}~$

J

Jones-Frommer-2014

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
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-acetylglucosaminepeptide 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

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 Solvention of forml induction pathways using global expression analysis. Schmid et al (2003). Development To-expression with 625,625 interactions from GEO Schmid-Lohmann-2003 A O.539 Solvention of forml induction pathways using global expression analysis. Schmid et al (2003). Development To-expression with 604,695 interactions from GEO Solvention of forml induction pathways using global expression analysis. Schmid et al (2008). Proc	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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1 700	Shared protein domains	3.00%
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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%
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