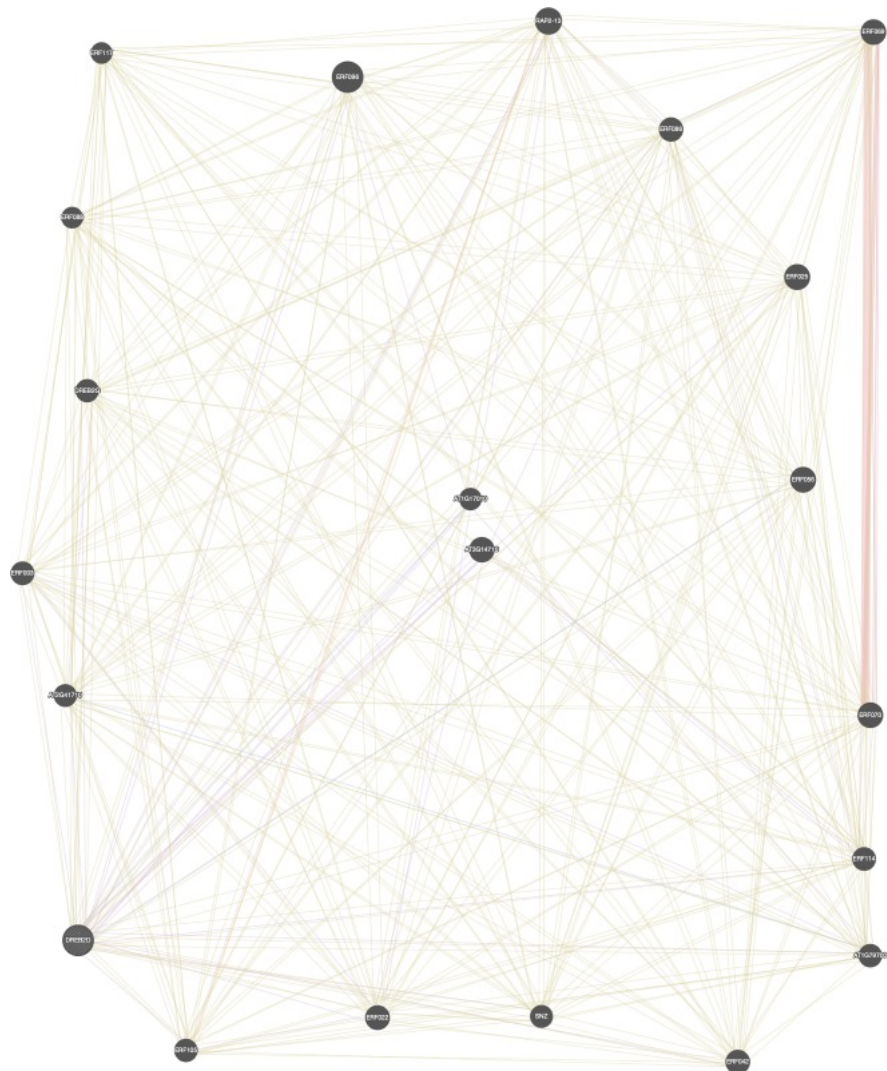


GeneMANIA report

Created on : 24 June 2020 22:13:08
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 DREB2D

Network weighting Automatically selected weighting method

Networks 2

2011

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

C

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

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

E

Efroni-Wagner-2013 , Elrouby-Coupland-2010

F

Fujiwara-Fukao-2014

G

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

H

Hackbusch-Uhrig-2005 , Hackenberg-Grimm-2012

I

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

J

Jones-Frommer-2014

K

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

L

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

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)

Q

Queval-Noctor-2012

R

Risseuw-Crosby-2003 , Ronemus-Martienssen-2006

S

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

T

Tamura-Hara-Nishimura-2010

V

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

W

Waidmann-Jonak-2014

Y

Yamaoka-Hara-Nishimura-2013

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). <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 | |

| | |
|--|---------------|
| 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). <i>Front Plant Sci</i> | |
| 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). <i>Nat Biotechnol</i> | |
| 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). <i>Dev Cell</i> | |
| Physical Interactions with 456 interactions from iRefIndex | |
| Manzano-Del Pozo-2008 | 0.85% |
| Identification of ubiquitinated proteins in Arabidopsis. Manzano et al (2008). <i>Plant Mol Biol</i> | |
| 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 | |
| Lalonde-Frommer-2010 | 0.48% |
| 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 | |
| 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). <i>PLoS One</i> | |
| 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). <i>Mol Syst Biol</i> | |
| 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% |

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

| | |
|---|---------------|
| 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). <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 | |

| | |
|--|--------|
| 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). <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 | |
| 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). <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 | |

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|--|---------------|
| Co-expression | 12.73% |
| 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 | |
| Shared protein domains | 3.00% |
| PFAM | 1.76% |

| | |
|---|-------|
| Shared protein domains | 3.00% |
| <hr/> | |
| PFAM | |
| Shared protein domains with 680,094 interactions from Pfam | |
| <hr/> | |
| INTERPRO | 1.23% |
| Shared protein domains with 743,516 interactions from InterPro | |
| <hr/> | |
| 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 | |
| Genetic Interactions | 2.87% |
| <hr/> | |
| BIOGRID-SMALL-SCALE-STUDIES | 2.87% |
| Genetic Interactions with 219 interactions from BioGRID | |
| Co-localization | 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 | |