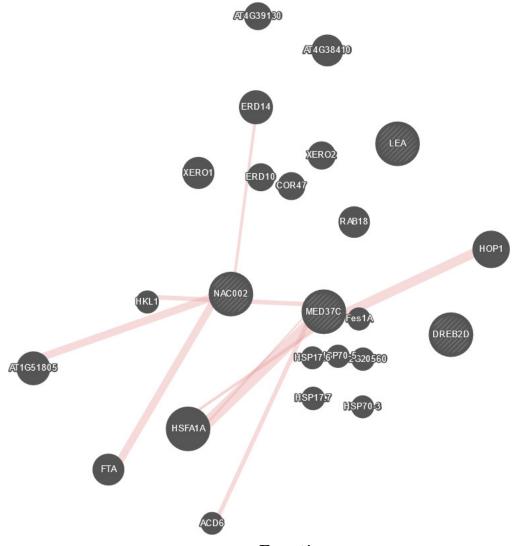
GeneMANIA report

Created on : 24 June 2020 21:00:51

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, LEA, ATAF1, HSP70

Network Automatically selected weighting method

weighting

Networks

2011

 \mathbf{B}

 $\mathbf{2}$

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

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

.]

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)

\mathbf{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 |
| LEA | Probable dehydrin LEA [Source:UniProtKB/Swiss-Prot;Acc:Q96261] | N/A |
| NAC002 | NAC domain-containing protein 2 [Source:UniProtKB/Swiss-Prot;Acc: Q39013] | N/A |
| MED37C | Probable mediator of RNA polymerase II transcription subunit 37c [Source:UniProtKB/Swiss-Prot;Acc:Q9LHA8] | N/A |
| HSFA1A | Heat stress transcription factor A-1a [Source:UniProtKB/Swiss-Prot;Acc: P41151] | 1 |
| НОР1 | Hsp70-Hsp90 organizing protein 1 [Source:UniProtKB/Swiss-Prot;Acc: Q9LNB6] | 2 |
| ERD14 | Dehydrin ERD14 [Source:UniProtKB/Swiss-Prot;Acc:P42763] | 3 |
| AT1G51805 | Leucine-rich repeat protein kinase family protein [Source:TAIR;Acc: AT1G51805] | 4 |
| XERO1 | Dehydrin Xero 1 [Source:UniProtKB/Swiss-Prot;Acc:P25863] | 5 |
| FTA | Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [Source:UniProtKB/Swiss-Prot;Acc:Q9LX33] | 6 |
| AT4G38410 | Dehydrin family protein [Source:TAIR;Acc:AT4G38410] | 7 |
| RAB18 | Dehydrin Rab18 [Source:UniProtKB/Swiss-Prot;Acc:P30185] | 8 |
| XERO2 | Dehydrin Xero 2 [Source:UniProtKB/Swiss-Prot;Acc:P42758] | 9 |
| ERD10 | Dehydrin ERD10 [Source:UniProtKB/Swiss-Prot;Acc:P42759] | 10 |
| COR47 | Dehydrin COR47 [Source:UniProtKB/Swiss-Prot;Acc:P31168] | 11 |
| AT4G39130 | Dehydrin family protein [Source:TAIR;Acc:AT4G39130] | 12 |
| HSP17.7 | 17.7 kDa class II heat shock protein [Source:UniProtKB/Swiss-Prot;Acc: O81822] | 13 |
| AT2G20560 | DNAJ heat shock family protein [Source:TAIR;Acc:AT2G20560] | 14 |
| HSP70-5 | Heat shock 70 kDa protein 5 [Source:UniProtKB/Swiss-Prot;Acc: Q9S9N1] | 15 |
| Fes1A | Fes1A [Source:TAIR;Acc:AT3G09350] | 16 |
| HSP17.6 | 17.6 kDa class II heat shock protein [Source:UniProtKB/Swiss-Prot;Acc: P29830] | 17 |
| HKL1 | Hexokinase-3 [Source:UniProtKB/Swiss-Prot;Acc:Q9LPS1] | 18 |
| HSP70-3 | Heat shock 70 kDa protein 3 [Source:UniProtKB/Swiss-Prot;Acc:O65719] | 19 |

| Gene | Description | Rank |
|------|---|------|
| ACD6 | ankyrin repeat family protein [Source:TAIR;Acc:AT4G14400] | 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 Schmid-Lohmann-2003 A O.539 Schmid-Lohmann-2005 A O.549 Schmid-Lohmann-2005 A O.559 Schmid-Lohmann-2005 A | 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 | |
| boolean modeling of transcriptome data reveals novel modes of heterotrimeric G-protein action. Pasidey et al (2010). Mol Syst Not Coccupression with 686.557 interactions from GEO Goda-Shimada-2008 A The At-GenEygress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Goda et al (2008). Pasit J Coccupression with 679.444 interactions from GEO Wirabella-Schuurink-2015 Wirabella-Schuurink-2015 Wirabella-Schuurink-2015 Wirabella-Schuurink-2016 Wirabella-Schuurink-2018 O.579 Wirabella-Schuurink-2008 O.579 Coccupression with 698.788 interactions from GEO Cocken-Hodrich-2006 A Interaction from GEO Cocken-Hodrich-2006 A The integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Decken et al (2008). Pasit Cell Cocken-Hodrich-2006 A The integrated view of gene expression from GEO Cocken-Hodrich-2006 Cocken-Hodrich-2008 Cocken-Hodrich-2008 Cocken-Hodrich-2008 Cocken-Hodrich-2008 Cocken-Hodrich-2008 Cocken-Hodrich-2008 Cocken-Hodrich-2008 Cocken-Hodrich-2008 Cocken-Hodrich-2008 Cocken-Polyson with 694,896 interactions from GEO Malitsky-Aharoni-2008 Moreno-Risueno-Benfey-2015 Transcriptonal control of sisse formation throughout root development. Moreno-Risueno et al (2015). Science Cockepression with 648,813 interactions from GEO Moreno-Risueno-Benfey-2015 Transcriptonal control of sisse formation throughout root development. Moreno-Risueno et al (2015). Science Cockepression with 625,625 interactions from GEO Sozzani-Benfey-2010 Spatiotemporal regulation of cell-cycle genes by SiORTROOT links potterning and growth. Sozzani et al (2010). Nature Cockepression with 604,619 interactions fro | Co-expression with 693,336 interactions from GEO | |
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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) . Nat $Biotechnol$ | |
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| 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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