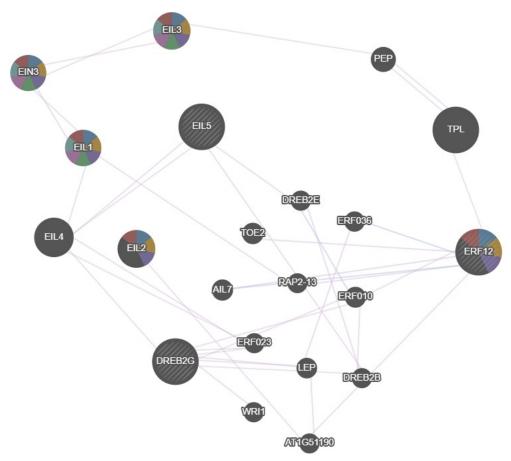
# GeneMANIA report

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#### Networks

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

#### **Functions**

- phosphorelay signal transduction system
- cellular response to ethylene stimulus
- response to ethylene
- cellular response to iron ion
- cellular response to metal ion
- cellular response to inorganic substance
- ethylene-activated signaling pathway

### Search parameters

Organism Arabidopsis thaliana (arabidopsis)

Genes ERF12, DREB2G, EIL5

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

 $\mathbf{K}$ 

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 |
|--------|--|------|
| EIL5   | ETHYLENE INSENSITIVE 3-like 5 protein [Source:UniProtKB/Swiss-Prot;Acc:Q9FJQ5]                   | N/A  |
| DREB2G | Dehydration-responsive element-binding protein 2G [Source:UniProtKB/Swiss-Prot;Acc:P61827]       | N/A  |
| ERF12  | Ethylene-responsive transcription factor 12 [Source:UniProtKB/Swiss-Prot;Acc:Q94ID6]             | N/A  |
| TPL    | Protein TOPLESS [Source:UniProtKB/Swiss-Prot;Acc:Q94AI7]   | 1    |
| HY5    | Transcription factor HY5 [Source:UniProtKB/Swiss-Prot;Acc:O24646]                                | 2    |
| EIL4   | Putative ETHYLENE INSENSITIVE 3-like 4 protein [Source: UniProtKB/Swiss-Prot;Acc:Q9LX16]         | 3    |
| EIL2   | ETHYLENE INSENSITIVE 3-like 2 protein [Source:UniProtKB/Swiss-Prot;Acc:O23115]                   | 4    |
| EIL3   | ETHYLENE INSENSITIVE 3-like 3 protein [Source:UniProtKB/Swiss-Prot;Acc:O23116]                   | 5    |
| EIL1   | ETHYLENE INSENSITIVE 3-like 1 protein [Source:UniProtKB/Swiss-Prot;Acc:Q9SLH0]                   | 6    |
| EIN3   | Protein ETHYLENE INSENSITIVE 3 [Source:UniProtKB/Swiss-Prot; Acc:O24606]                         | 7    |
| LOL1   | Protein LOL1 [Source:UniProtKB/Swiss-Prot;Acc:Q93ZB1]  | 8    |
| PEP    | RNA-binding KH domain-containing protein PEPPER [Source: UniProtKB/Swiss-Prot;Acc:Q9SZH4]        | 9    |
| TOE2   | AP2-like ethylene-responsive transcription factor TOE2 [Source: UniProtKB/Swiss-Prot;Acc:Q9LVG2] | 10   |
| AIL7   | AP2-like ethylene-responsive transcription factor AIL7 [Source: UniProtKB/Swiss-Prot;Acc:Q6J9N8] | 11   |
| ERF010 | Ethylene-responsive transcription factor ERF010 [Source:UniProtKB/Swiss-Prot;Acc:Q9FH94]         | 12   |
| LEP    | Ethylene-responsive transcription factor LEP [Source:UniProtKB/Swiss-Prot;Acc:Q9M644]            | 13   |
| ERF036 | Ethylene-responsive transcription factor ERF036 [Source:UniProtKB/Swiss-Prot;Acc:Q9LU18]         | 14   |
| WRI1   | Ethylene-responsive transcription factor WRI1 [Source:UniProtKB/Swiss-Prot;Acc:Q6X5Y6]           | 15   |
| DREB2E | Dehydration-responsive element-binding protein 2E [Source:UniProtKB/                             | 16   |

| Gene      | Description  | Rank |
|-----------|--|------|
|           | Swiss-Prot;Acc:O80917]   |      |
| DREB2B    | Dehydration-responsive element-binding protein 2B [Source:UniProtKB/Swiss-Prot;Acc:O82133]       | 17   |
| ERF023    | Ethylene-responsive transcription factor ERF023 [Source:UniProtKB/Swiss-Prot;Acc:Q1ECI2]         | 18   |
| AT1G51190 | AP2-like ethylene-responsive transcription factor PLT2 [Source: UniProtKB/Swiss-Prot;Acc:Q5YGP7] | 19   |
| RAP2-13   | Ethylene-responsive transcription factor RAP2-13 [Source:UniProtKB/Swiss-Prot;Acc:Q9LM15]        | 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<br>lation targets in Arabidopsis. Kim et al (2013). Plant Cell Physical Interactions with 891 interactions from iRef<br>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 |        |
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| Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO  Shared protein domains  3.00%   | Co-expression with 625,625 interactions from GEO   |        |
| Co-expression with 604,619 interactions from GEO  Shared protein domains  3.00%  | Sozzani-Benfey-2010  | 0.51%  |
| •  | Spatiotemporal regulation of cell-cycle genes by SHORTROOT links patterning and growth. Sozzani et al (2010). Nature Co-expression with 604,619 interactions from GEO                    |        |
| 1 700  | Shared protein domains   | 3.00%  |
| $2\mathrm{FAM}$  | PFAM   | 1.76%  |

| Shared protein domains  | 3.00% |
|---|-------|
| PFAM  |       |
| Shared protein domains with 680,094 interactions from Pfam  |       |
| 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                                   |       |
| Co-localization with 831,109 interactions from GEO  |       |