GeneMANIA report

Created on : 1 July 2021 22:01:17
Last database update : 13 April 2021 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	FUS3
Network weighting	Automatically selected weighting method
Networks	**2**

2011

A

Altmann-Falter-Braun-2020 , Arae-Chiba-2017

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 , Bustos-Paz-Ares-2010

C

Carianopol-Gazzarrini-2020 , Causier-Davies-2012 , Ceserani-Nelson-2009 , Chang-Bailey-Serres-2012 , Chen-Rhee-2012 , Cutcliffe-Rashotte-2011

D

Danisman-Immink-2013 , de Folter-Angenent-2005 , Deeken-Hedrich-2006 A , Dinneny-Benfey-2008 D , Dinneny-Benfey-2008 F , 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

H

Hackbusch-Uhrig-2005 , Hackenberg-Grimm-2012

I

Igawa-Yanagawa-2009 , INTERPRO , IREF-bar , IREF-bind , IREF-bind-translation , IREF-biogrid , IREF-dip , IREF-intact , IREF-intcomplex , IREF-mint , IREF-quickgo , IREF-SMALL-SCALE-STUDIES , IREF-uniprotpp

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

Manzano-Del Pozo-2008 , Mott-Belkhadir-2019 , Mukhtar-Dangl-2011 , Mustroph-Bailey-Serres-2009 B , Mustroph-Bailey-Serres-2009 C

P

Pandey-Albert-2010 , PFAM , Piya-Hewezi-2014 , Popescu-Dinesh-Kumar-2007 , Popescu-Dinesh-Kumar-2009 , PPI-Predicted (Interologs)

Q

Queval-Noctor-2012

R

Risseeuw-Crosby-2003 , Ronemus-Martienssen-2006

S

Sako-Yamaguchi-2014 , Schmid-Lohmann-2003 B , Schuler-Bauer-2011 , Smakowska-Luzan-Belkhadir-2018 , Swatek-Thelen-2011

T

Tamura-Hara-Nishimura-2010 , Tintor-Saijo-2013 , Trigg-Ecker-2017

V

Van Leene-De Jaeger-2010 , Van Leene-De Jaeger-2019 , Vernoux-Traas-2011

W

W

Waidmann-Jonak-2014

Y

Yamaoka-Hara-Nishimura-2013

Z

Zhang-Fernie-2018 , Zuber-Gallardo-2010 A

Genes

Gene	Description	Rank
FUS3	B3 domain-containing transcription factor FUS3 [Source:UniProtKB/ Swiss-Prot;Acc:Q9LW31]	N/A
ET2	ET2 [Source:UniProtKB/TrEMBL;Acc:A0A178URY3]	1
AT3G25730	AP2/ERF and B3 domain-containing transcription factor ARF14 [Source:UniProtKB/Swiss-Prot;Acc:Q9LS06]	2
TEM1	AP2/ERF and B3 domain-containing transcription repressor TEM1 [Source:UniProtKB/Swiss-Prot;Acc:Q9C6M5]	3
RAV1	AP2/ERF and B3 domain-containing transcription factor RAV1 [Source: UniProtKB/Swiss-Prot;Acc:Q9ZWM9]	4
VAL2	B3 domain-containing transcription repressor VAL2 [Source:UniProtKB/ Swiss-Prot;Acc:Q5CCK4]	5
VAL1	B3 domain-containing transcription repressor VAL1 [Source:UniProtKB/ Swiss-Prot;Acc:Q8W4L5]	6
AT4G33280	AP2/B3-like transcriptional factor family protein [Source:TAIR;Acc: AT4G33280]	7
ARF17	auxin response factor 17 [Source:TAIR;Acc:AT1G77850]	8
AT2G33860	Auxin response factor 3 [Source:UniProtKB/Swiss-Prot;Acc:O23661]	9
AT1G50680	AP2/ERF and B3 domain-containing transcription factor At1g50680 [Source:UniProtKB/Swiss-Prot;Acc:Q9C6P5]	10
AT5G60130	B3 domain-containing protein At5g60130 [Source:UniProtKB/Swiss-Prot; Acc:Q9LVG1]	11
AT1G51120	AP2/ERF and B3 domain-containing transcription factor At1g51120 [Source:UniProtKB/Swiss-Prot;Acc:Q9C688]	12
REM4	Putative B3 domain-containing protein REM4 [Source:UniProtKB/ Swiss-Prot;Acc:Q9SB79]	13
ARF10	Auxin response factor (Fragment) [Source:UniProtKB/TrEMBL;Acc: C0SV66]	14
AT3G06160	AP2/B3-like transcriptional factor family protein [Source:UniProtKB/ TrEMBL;Acc:F4J9Q0]	15
AT5G57720	B3 domain-containing protein At5g57720 [Source:UniProtKB/Swiss-Prot; Acc:Q9FHH1]	16
AT5G25470	B3 domain-containing protein At5g25470 [Source:UniProtKB/Swiss-Prot; Acc:Q1PDT6]	17
AT3G28853	Putative B3 domain-containing protein At3g28853 [Source:UniProtKB/	18

Gene	Description	Rank
	Swiss-Prot;Acc:Q9LH88]	
AT4G01580	B3 domain-containing protein At4g01580 [Source:UniProtKB/Swiss-Prot; Acc:Q9ZSH7]	19
VDD	B3 domain-containing protein At5g18000 [Source:UniProtKB/Swiss-Prot; Acc:Q9FJG2]	20

Swiss-Prot;Acc:Q9LH88]

AT4G01580   B3 domain-containing protein At4g01580 [Source:UniProtKB/Swiss-Prot; Acc:Q9ZSH7]

Networks

Physical Interactions   52.06%

Danisman-Immink-2013   9.90%

Analysis of functional redundancies within the Arabidopsis TCP transcription factor family. Danisman et al (2013). *J Exp Bot*

Physical Interactions with 94 interactions from iRefIndex

IREF-intcomplex   6.27%

Physical Interactions with 6 interactions from iRefIndex

Boruc-Russinova-2010 A   6.16%

Functional modules in the Arabidopsis core cell cycle binary protein-protein interaction network. Boruc et al (2010). *Plant Cell*

Physical Interactions with 69 interactions from BioGRID

Causier-Davies-2012   3.88%

The TOPLESS interactome: a framework for gene repression in Arabidopsis. Causier et al (2012). *Plant Physiol*

Physical Interactions with 110 interactions from BioGRID

Sako-Yamaguchi-2014   2.59%

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 189 interactions from BioGRID

IREF-dip   2.15%

Physical Interactions with 357 interactions from iRefIndex

Popescu-Dinesh-Kumar-2009   1.78%

MAPK target networks in Arabidopsis thaliana revealed using functional protein microarrays. Popescu et al (2009). *Genes Dev*

Physical Interactions with 1,111 interactions from BioGRID

IREF-bind-translation   1.65%

Physical Interactions with 678 interactions from iRefIndex

IREF-quickgo   1.63%

Physical Interactions with 1,510 interactions from iRefIndex

Boruc-Russinova-2010 B   1.53%

Functional modules in the Arabidopsis core cell cycle binary protein-protein interaction network. Boruc et al (2010). *Plant Cell*

Physical Interactions with 29 interactions from BioGRID

Fujiwara-Fukao-2014   1.38%

Interactomics of Qa-SNARE in Arabidopsis thaliana. Fujiwara et al (2014). *Plant Cell Physiol*

Physical Interactions with 456 interactions from iRefIndex

Van Leene-De Jaeger-2010   1.29%

Targeted interactomics reveals a complex core cell cycle machinery in Arabidopsis thaliana. Van Leene et al (2010). *Mol Syst Biol*

Physical Interactions with 507 interactions from BioGRID

Lumba-McCourt-2014   1.21%

A mesoscale abscisic acid hormone interactome reveals a dynamic signaling landscape in Arabidopsis. Lumba et al (2014). *Dev Cell*

Physical Interactions 52.06%

Lumba-McCourt-2014

Physical Interactions with 379 interactions from BioGRID

IREF-SMALL-SCALE-STUDIES 1.10%

Physical Interactions with 7,477 interactions from iRefIndex

IREF-uniprotpp 1.04%

Physical Interactions with 106 interactions from iRefIndex

Kuroda-Matsui-2012 1.03%

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 130 interactions from BioGRID

IREF-mint 1.01%

Physical Interactions with 135 interactions from iRefIndex

BIOGRID-SMALL-SCALE-STUDIES 1.01%

Physical Interactions with 5,948 interactions from BioGRID

Lee-Rhee-2010 Protein interactions 0.97%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Physical Interactions with 746 interactions from supplementary material

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Van Leene-De Jaeger-2019 0.90%

Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. Van Leene et al (2019). *Nat Plants*

Physical Interactions with 181 interactions from BioGRID

IREF-bind 0.74%

Physical Interactions with 670 interactions from iRefIndex

Altmann-Falter-Braun-2020 0.54%

Extensive signal integration by the phytohormone protein network. Altmann et al (2020). *Nature*

Physical Interactions with 1,741 interactions from BioGRID

Tamura-Hara-Nishimura-2010 0.53%

Identification and characterization of nuclear pore complex components in Arabidopsis thaliana. Tamura et al (2010). *Plant Cell*

Physical Interactions with 474 interactions from BioGRID

Carianopol-Gazzarrini-2020 0.49%

An abscisic acid-responsive protein interaction network for sucrose non-fermenting related kinase1 in abiotic stress response. Carianopol et al (2020). *Commun Biol*

Physical Interactions with 164 interactions from BioGRID

IREF-intact 0.42%

Physical Interactions with 26,649 interactions from iRefIndex

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Klopffleisch-Jones-2011 0.24%

Arabidopsis G-protein interactome reveals connections to cell wall carbohydrates and morphogenesis. Klopffleisch et al (2011). *Mol Syst Biol*

Physical Interactions with 307 interactions from BioGRID

Physical Interactions   52.06%

Dreze-Vidal-2011-repeat   0.23%

Evidence for network evolution in an Arabidopsis interactome map. (2011). *Science*

Physical Interactions with 1,015 interactions from supplementary material

Smakowska-Luzan-Belkhadir-2018   0.22%

An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. Smakowska-Luzan et al (2018). *Nature*

Physical Interactions with 2,514 interactions from iRefIndex

Mukhtar-Dangl-2011   0.11%

Independently evolved virulence effectors converge onto hubs in a plant immune system network. Mukhtar et al (2011). *Science*

Physical Interactions with 748 interactions from iRefIndex

Lalonde-Frommer-2010   0.05%

A membrane protein/signaling protein interaction network for Arabidopsis version AMPv2. Lalonde et al (2010). *Front Physiol*

Physical Interactions with 270 interactions from iRefIndex

Predicted   21.72%

Lee-Rhee-2010 Protein interactions human2arabidopsis   3.58%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 102,757 interactions from supplementary material

Lee-Rhee-2010 Co-citation worm2arabidopsis   2.83%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 5,549 interactions from supplementary material

Lee-Rhee-2010 Co-citation yeast2arabidopsis   2.40%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 52,030 interactions from supplementary material

Lee-Rhee-2010 Gene neighbourhoods   1.95%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 94,430 interactions from supplementary material

Lee-Rhee-2010 protein interactions yeast2arabidopsis   1.64%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 25,047 interactions from supplementary material

Lee-Rhee-2010 protein interactions from complexes yeast2arabidopsis   1.53%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 10,822 interactions from supplementary material

Lee-Rhee-2010 Protein complexes yeast2arabidopsis   1.39%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 128,042 interactions from supplementary material

Predicted   21.72%

Lee-Rhee-2010 Co-expression yeast2arabidopsis   1.08%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 102,549 interactions from supplementary material

Lee-Rhee-2010 Genetic interactions yeast2arabidopsis   1.06%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 30,329 interactions from supplementary material

Lee-Rhee-2010 Protein complexes human2arabidopsis   0.86%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 2,147 interactions from supplementary material

Lee-Rhee-2010 Co-expression worm2arabidopsis   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 92,816 interactions from supplementary material

Lee-Rhee-2010 Co-inheritance   0.64%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 82,730 interactions from supplementary material

PPI-Predicted (Interologs)   0.41%

A predicted interactome for Arabidopsis. Geisler-Lee et al (2007). *Plant Physiol*

Predicted with 18,163 interactions from collaborator

Lee-Rhee-2010 AraNet   0.39%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 734,223 interactions from supplementary material

Lee-Rhee-2010 co-expression human2arabidopsis   0.27%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 39,769 interactions from supplementary material

Lee-Rhee-2010 shared protein domains yeast2arabidopsis   0.26%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 23,986 interactions from supplementary material

Lee-Rhee-2010 Y2H human2arabidopsis   0.18%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 6,664 interactions from supplementary material

Lee-Rhee-2010 Genetic interactions worm2arabidopsis   0.17%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 1,269 interactions from supplementary material

Predicted   21.72%

Lee-Rhee-2010 Protein interactions fly2arabidopsis   0.14%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 7,953 interactions from supplementary material

Lee-Rhee-2010 shared protein domains human2arabidopsis   0.14%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 21,600 interactions from supplementary material

Lee-Rhee-2010 Y2H worm2arabidopsis   0.03%

Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. Lee et al (2010). *Nat Biotechnol*

Predicted with 1,903 interactions from supplementary material

Co-expression   18.12%

Kram-Carter-2009   1.43%

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 672,952 interactions from GEO

Bassel-Cutler-2008-Dormant Seed Expression   1.07%

Elucidating the germination transcriptional program using small molecules. Bassel et al (2008). *Plant Physiol*

Co-expression with 426,202 interactions from collaborator

Bassel-Cutler-2008-Germinating Seed Expression   1.00%

Elucidating the germination transcriptional program using small molecules. Bassel et al (2008). *Plant Physiol*

Co-expression with 420,272 interactions from collaborator

Zuber-Gallardo-2010 A   0.99%

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*

Co-expression with 694,429 interactions from GEO

Ronemus-Martienssen-2006   0.98%

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 179,027 interactions from GEO

Tintor-Saijo-2013   0.95%

Layered pattern receptor signaling via ethylene and endogenous elicitor peptides during Arabidopsis immunity to bacterial infection. Tintor et al (2013). *Proc Natl Acad Sci U S A*

Co-expression with 656,153 interactions from GEO

Schuler-Bauer-2011   0.92%

Transcriptome analysis by GeneTrail revealed regulation of functional categories in response to alterations of iron homeostasis in Arabidopsis thaliana. Schuler et al (2011). *BMC Plant Biol*

Co-expression with 654,167 interactions from GEO

Bustos-Paz-Ares-2010   0.92%

A central regulatory system largely controls transcriptional activation and repression responses to phosphate starvation in Arabidopsis. Bustos et al (2010). *PLoS Genet*

Co-expression 18.12%

Bustos-Paz-Ares-2010

Co-expression with 691,702 interactions from GEO

Schmid-Lohmann-2003 B 0.92%

Dissection of floral induction pathways using global expression analysis. Schmid et al (2003). *Development*

Co-expression with 137,061 interactions from GEO

Queval-Noctor-2012 0.91%

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 657,861 interactions from GEO

Gifford-Birnbaum-2008 0.87%

Cell-specific nitrogen responses mediate developmental plasticity. Gifford et al (2008). *Proc Natl Acad Sci U S A*

Co-expression with 674,136 interactions from GEO

Pandey-Albert-2010 0.86%

Boolean modeling of transcriptome data reveals novel modes of heterotrimeric G-protein action. Pandey et al (2010). *Mol Syst Biol*

Co-expression with 689,348 interactions from GEO

Deeken-Hedrich-2006 A 0.83%

An integrated view of gene expression and solute profiles of Arabidopsis tumors: a genome-wide approach. Deeken et al (2006). *Plant Cell*

Co-expression with 609,443 interactions from GEO

Chang-Bailey-Serres-2012 0.82%

Transient MPK6 activation in response to oxygen deprivation and reoxygenation is mediated by mitochondria and aids seedling survival in Arabidopsis. Chang et al (2012). *Plant Mol Biol*

Co-expression with 683,527 interactions from GEO

Dinneny-Benfey-2008 D 0.80%

Cell identity mediates the response of Arabidopsis roots to abiotic stress. Dinneny et al (2008). *Science*

Co-expression with 707,355 interactions from GEO

Mustroph-Bailey-Serres-2009 B 0.80%

Profiling translatomes of discrete cell populations resolves altered cellular priorities during hypoxia in Arabidopsis. Mustroph et al (2009). *Proc Natl Acad Sci U S A*

Co-expression with 790,223 interactions from GEO

Goda-Shimada-2008 A 0.80%

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 684,584 interactions from GEO

Arae-Chiba-2017 0.77%

Co-ordinated Regulations of mRNA Synthesis and Decay during Cold Acclimation in Arabidopsis Cells. Arae et al (2017). *Plant Cell Physiol*

Co-expression with 573,695 interactions from GEO

Dinneny-Benfey-2008 F 0.75%

Cell identity mediates the response of Arabidopsis roots to abiotic stress. Dinneny et al (2008). *Science*

Co-expression 18.12%

Dinneny-Benfey-2008 F

Co-expression with 650,698 interactions from GEO

Mustroph-Bailey-Serres-2009 C 0.75%

Profiling translatomes of discrete cell populations resolves altered cellular priorities during hypoxia in Arabidopsis. Mustroph et al (2009). *Proc Natl Acad Sci U S A*

Co-expression with 803,119 interactions from GEO

Shared protein domains 4.90%

INTERPRO 2.76%

Shared protein domains with 758,071 interactions from InterPro

PFAM 2.14%

Shared protein domains with 677,172 interactions from Pfam

Genetic Interactions 2.44%

BIOGRID-SMALL-SCALE-STUDIES 2.44%

Genetic Interactions with 225 interactions from BioGRID

Co-localization 0.76%

Brady-Benfey-2007 0.76%

A high-resolution root spatiotemporal map reveals dominant expression patterns. Brady et al (2007). *Science*

Co-localization with 819,905 interactions from GEO